Institut für Nutzpflanzenwissenschaften und Ressourcenschutz (INRES)

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Rheinischen Friedrich-Wilhelms-Universität Bonn

Identification and functional characterization of *ENHANCED GRAVITROPISM 2* controlling the root setpoint angle in barley (*Hordeum vulgare* L.)

Supplementary Tables

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Appendix

Supplementary Tables for Chapter 2

Title: *ENHANCED GRAVITROPISM 2* encodes a STERILE ALPHA MOTIF–containing protein that controls root growth angle in barley and wheat

Kirschner GK, Rosignoli S, **Guo L**, Vardanega I, Imani J, Altmüller J, Milner SG, Balzano R, Nagel KA, Pflugfelder D, Forestan C, Bovina R, Koller R, Stöcker TG, Mascher M, Simmonds J, Uauy C, Schoof H, Tuberosa R, Salvi S, Hochholdinger F

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Table S1. Mutated high confidence protein coding genes in the egt2 mapping intervall on chromosome 5H

Gene ID	Start	End	Gene length	Gene function	5´Position of mutation	Type of mutation	ID of mutation
HORVU5Hr1G027890	160633192	160636469	3278	Sterile alpha motif (SAM) domain-containing protein	160635280	G to A	chr5H_part1_160635280_A
HORVU5Hr1G029670	178370028	178374066	4039	F-box family protein	178376238	C to T	chr5H_part1_178376238_T
HORVU5Hr1G029910	182793217	182822426	29210	ATPase-like fidgetin	182789159	C to T	chr5H_part1_182789159_T
HORVU5Hr1G030940	192355205	192356197	993	50S ribosomal protein L14	192351249	C to T	chr5H_part1_192351249_T
HORVU5Hr1G031470	199378390	199523314	144925	Chaperone protein ClpB	199516725	G to A	chr5H_part1_199516725_A
HORVU5Hr1G031630	202056154	202057757	1604	40S ribosomal protein S19	202062593	G to C	chr5H_part1_202062593_C
HORVU5Hr1G032430	211283193	211283420	228	Non-specific serine/threonine protein kinase	211283531	G to A	chr5H_part1_211283531_A

Table S1. cont.

Gene ID	Mutation effect on transcript	Internal annotation of the mutant	Affected isoform	Position of mutation in cDNA	Position of Mutation in protein
HORVU5Hr1G027890	premature stop codon	EXON_5H_part1_160633192_160633623	HORVU5Hr1G027890.1	c.525	p.175
HORVU5Hr1G029670	downstream coding region	EXON_5H_part1_178370028_178370491	HORVU5Hr1G029670.1	c.*2517	
HORVU5Hr1G029910	upstream coding region	EXON_5H_part1_182793217_182793720	HORVU5Hr1G029910.8	c.-4159	
HORVU5Hr1G030940	downstream coding region	CDS_5H_part1_192355205_192355579	HORVU5Hr1G030940.1	c.*3956	
HORVU5Hr1G031470	upstream coding region	EXON_5H_part1_199378390_199378652	HORVU5Hr1G031470.8	c.-4996	
HORVU5Hr1G031630	upstream coding region	EXON_5H_part1_202056154_202056231	HORVU5Hr1G031630.1	c.-4838	
HORVU5Hr1G032430	upstream coding region	CDS_5H_part1_211283193_211283420	HORVU5Hr1G032430.1	c.-111	

Table S2. Overview of RNAseq reads and mapping results

Lane	Sample	PF Clusters	Yield (Mbases)	% >= Q30 bases	Mean Quality Score
1	107229	22,376,577	4,520	95.56	36.22
1	107231	21,932,224	4,430	95.24	36.1
1	107233	19,561,632	3,951	95.25	36.14
1	107235	20,630,560	4,167	95.71	36.24
1	107237	19,386,123	3,916	95.37	36.17
1	107239	20,053,643	4,051	95.72	36.23
1	107241	20,626,439	4,167	95.6	36.21
1	107243	20,166,570	4,074	95.61	36.2
1	107245	21,604,056	4,364	96.06	36.31
1	107247	18,975,817	3,833	95.71	36.22
1	107249	19,326,567	3,904	95.38	36.17
1	107251	19,635,769	3,966	94.26	35.98
1	107253	20,791,711	4,200	95.23	36.14
1	107255	21,350,631	4,313	95.93	36.26
1	107257	22,062,775	4,457	95.79	36.26
1	107259	21,507,018	4,344	95.87	36.25
1	107261	20,644,170	4,170	95.52	36.19
1	107263	22,681,047	4,582	95.2	36.13
1	107265	18,683,628	3,774	95.72	36.22
1	107267	24,278,896	4,904	96.05	36.3
1	107269	19,355,318	3,910	95.8	36.25
1	107271	21,218,515	4,286	95.53	36.2
1	107273	20,290,927	4,099	93.83	35.9
1	107275	18,430,934	3,723	95.64	36.22
2	107229	22,562,294	4,558	95.69	36.25
2	107231	22,189,773	4,482	95.36	36.12
2	107233	19,752,586	3,990	95.37	36.17
2	107235	20,904,791	4,223	95.83	36.26
2	107237	19,529,397	3,945	95.49	36.2
2	107239	20,310,327	4,103	95.84	36.25
2	107241	20,856,789	4,213	95.72	36.23
2	107243	20,436,490	4,128	95.73	36.23
2	107245	21,795,430	4,403	96.19	36.33
2	107247	19,111,224	3,860	95.81	36.24
2	107249	19,473,688	3,934	95.51	36.19
2	107251	19,846,346	4,009	94.36	36
2	107253	20,955,605	4,233	95.34	36.16
2	107255	21,594,671	4,362	96.03	36.28
2	107257	22,234,718	4,491	95.92	36.28
2	107259	21,711,249	4,386	95.98	36.27
2	107261	20,793,488	4,200	95.66	36.22
2	107263	22,956,790	4,637	95.33	36.16
2	107265	18,835,184	3,805	95.83	36.24
2	107267	24,545,072	4,958	96.18	36.32
2	107269	19,540,410	3,947	95.92	36.27
2	107271	21,405,829	4,324	95.65	36.22

Table S2. cont.

Lane	Sample	PF Clusters	Yield (Mbases)	% >= Q30 bases	Mean Quality Score
2	107273	20,532,358	4,148	93.92	35.92
2	107275	18,578,126	3,753	95.77	36.25

Table S3: Differentially expressed genes

	Elongation zone		**Meristem**		**Root_cap**		**Gene function**
Gene ID	**Log2FC**	**padj**	**Log2FC**	**padj**	**Log2FC**	**padj**	
HORVU0Hr1G000630	4.9	<0.001	6.2	<0.001	5.9	<0.001	NAC domain containing protein 103
HORVU0Hr1G000850	5.0	<0.001	8.2	<0.001	no DE	no DE	undescribed protein
HORVU0Hr1G000990	5.1	<0.001	7.1	<0.001	5.0	<0.001	undescribed protein
HORVU0Hr1G001190	no DE	no DE	6.3	0.005	no DE	no DE	Histone-lysine N-methyltransferase 2A
HORVU0Hr1G001230	6.7	0.002	5.5	0.027	6.9	0.002	myb domain protein 33
HORVU0Hr1G018690	7.0	<0.001	6.1	0.016	no DE	no DE	Disease resistance protein RPM1
HORVU0Hr1G025540	no DE	no DE	no DE	no DE	6.9	0.003	myb-like transcription factor family protein
HORVU0Hr1G025920	no DE	no DE	1.8	0.006	no DE	no DE	Zinc finger CCCH domain-containing protein 36
HORVU0Hr1G030440	1.7	0.013	2.0	<0.001	no DE	no DE	Endoplasmic reticulum-Golgi intermediate compartment protein 3
HORVU1Hr1G018770	-7.6	<0.001	no DE	no DE	no DE	no DE	Chymotrypsin inhibitor
HORVU1Hr1G065550	-5.8	<0.001	-3.5	<0.001	-4.6	0.014	TRICHOME BIREFRINGENCE-LIKE 7
HORVU1Hr1G065660	-6.4	<0.001	-6.7	0.003	no DE	no DE	undescribed protein
HORVU1Hr1G065710	-7.9	<0.001	no DE	no DE	no DE	no DE	undescribed protein
HORVU1Hr1G065770	-6.7	<0.001	-5.3	0.001	-5.7	<0.001	Sulfite reductase [NADPH] hemoprotein beta-component
HORVU1Hr1G067590	no DE	no DE	-6.4	0.001	no DE	no DE	SOSS complex subunit B homolog
HORVU1Hr1G067660	-1.9	<0.001	no DE	no DE	no DE	no DE	undescribed protein
HORVU1Hr1G067960	no DE	no DE	-6.8	<0.001	no DE	no DE	cytochrome c biogenesis protein family
HORVU1Hr1G067990	no DE	no DE	-6.0	0.001	-7.3	0.001	Nuclear transcription factor Y subunit C-3
HORVU1Hr1G068020	-6.4	<0.001	no DE	no DE	no DE	no DE	Aldehyde dehydrogenase family 2 member C4
HORVU1Hr1G068080	no DE	no DE	-5.2	0.046	no DE	no DE	Cyclin B1
HORVU1Hr1G068440	-8.7	<0.001	-7.8	<0.001	no DE	no DE	calmodulin 5
HORVU1Hr1G068580	-8.5	<0.001	-9.5	<0.001	no DE	no DE	Endoplasmic reticulum-Golgi intermediate compartment protein 3
HORVU1Hr1G068640	-3.2	<0.001	-3.6	<0.001	-3.9	<0.001	60S ribosomal protein L30
HORVU1Hr1G069420	no DE	no DE	-6.3	0.002	no DE	no DE	B3 domain-containing protein
HORVU1Hr1G078170	-2.8	<0.001	-2.4	<0.001	-3.5	<0.001	Meprin and TRAF (MATH) homology domain-containing protein
HORVU1Hr1G091830	3.5	0.043	no DE	no DE	no DE	no DE	Carbohydrate-binding X8 domain superfamily protein
HORVU1Hr1G093120	6.2	<0.001	3.4	0.005	no DE	no DE	Transducin/WD40 repeat-like superfamily protein
HORVU1Hr1G095270	3.5	0.012	no DE	no DE	no DE	no DE	Zinc finger CCCH domain-containing protein 37
HORVU2Hr1G026420	no DE	no DE	6.4	0.042	no DE	no DE	Peroxidase superfamily protein
HORVU2Hr1G064100	no DE	no DE	0.8	0.024	no DE	no DE	Disease resistance-responsive (dirigent-like protein) family protein
HORVU2Hr1G064330	-1.3	0.044	no DE	no DE	no DE	no DE	Peroxidase superfamily protein
HORVU2Hr1G085500	no DE	no DE	no DE	no DE	6.0	<0.001	Coffea canephora DH200=94 genomic scaffold, scaffold_890
HORVU2Hr1G107100	no DE	no DE	no DE	no DE	8.5	<0.001	Protein translation factor SUI1 homolog 1
HORVU2Hr1G111030	-1.1	0.026	no DE	no DE	no DE	no DE	xyloglucan endotransglucosylase/hydrolase 12
HORVU3Hr1G006440	no DE	no DE	no DE	no DE	-5.5	0.002	Xylanase inhibitor
HORVU3Hr1G019510	no DE	no DE	2.0	0.034	no DE	no DE	Zinc finger CCCH domain-containing protein 2
HORVU3Hr1G030770	-2.6	0.044	no DE	no DE	no DE	no DE	ATPase family gene 2 protein
HORVU3Hr1G036820	no DE	no DE	5.1	0.031	no DE	no DE	Peroxidase superfamily protein
HORVU3Hr1G076620	-3.7	<0.001	no DE	no DE	no DE	no DE	expansin 11
HORVU3Hr1G076640	-3.3	0.043	no DE	no DE	no DE	no DE	expansin 11
HORVU3Hr1G076650	-4.1	<0.001	no DE	no DE	no DE	no DE	expansin 11

Table S3: cont.

	Elongation zone		**Meristem**		**Root_cap**		**Gene function**
Gene ID	**Log2FC**	**padj**	**Log2FC**	**padj**	**Log2FC**	**padj**	
HORVU3Hr1G076660	-4.4	0.003	no DE	no DE	no DE	no DE	Expansin-A8
HORVU3Hr1G085990	-4.0	0.044	no DE	no DE	no DE	no DE	Chromosome 3B, genomic scaffold, cultivar Chinese Spring
HORVU3Hr1G089290	-2.1	0.003	no DE	no DE	no DE	no DE	Late embryogenesis abundant protein Lea5-A
HORVU4Hr1G031700	no DE	no DE	6.4	0.009	no DE	no DE	Exocyst complex component 7
HORVU4Hr1G051550	no DE	no DE	1.9	<0.001	no DE	no DE	Serine/threonine-protein kinase CTR1
HORVU4Hr1G053150	-1.0	0.002	no DE	no DE	no DE	no DE	Plant protein of unknown function (DUF247)
HORVU4Hr1G072270	-1.5	<0.001	no DE	no DE	no DE	no DE	unknown function
HORVU4Hr1G082900	-6.8	0.004	no DE	no DE	no DE	no DE	ESTs AU078251(R0889)
HORVU4Hr1G090090	no DE	no DE	no DE	no DE	7.4	0.009	Heat stress transcription factor C-2a
HORVU5Hr1G026160	no DE	no DE	1.6	0.029	no DE	no DE	Mitochondrial substrate carrier family protein
HORVU5Hr1G027890	-1.5	0.016	no DE	no DE	no DE	no DE	Sterile alpha motif (SAM) domain-containing protein
HORVU5Hr1G062610	-4.3	0.002	no DE	no DE	no DE	no DE	Disease resistance protein
HORVU5Hr1G066540	no DE	no DE	-3.8	0.028	no DE	no DE	unknown function
HORVU5Hr1G104680	7.6	0.036	no DE	no DE	no DE	no DE	Bifunctional inhibitor/lipid-transf. prot./seed storage 2S albumin prot.
HORVU5Hr1G119670	-3.8	<0.001	no DE	no DE	no DE	no DE	expansin 11
HORVU5Hr1G119680	-3.9	<0.001	no DE	no DE	no DE	no DE	expansin 11
HORVU5Hr1G119860	-3.3	0.019	no DE	no DE	no DE	no DE	expansin 11
HORVU6Hr1G011570	no DE	no DE	1.4	0.005	no DE	no DE	Chromosome 3B, genomic scaffold, cultivar Chinese Spring
HORVU6Hr1G013700	3.8	0.006	no DE	no DE	no DE	no DE	GDSL esterase/lipase
HORVU6Hr1G017950	1.5	0.036	no DE	no DE	no DE	no DE	unknown protein
HORVU7Hr1G006370	no DE	no DE	1.5	0.003	no DE	no DE	D-alanine--poly(phosphoribitol) ligase subunit 1
HORVU7Hr1G020300	3.3	0.026	no DE	no DE	no DE	no DE	Peroxidase superfamily protein
HORVU7Hr1G051810	2.2	0.013	no DE	no DE	no DE	no DE	methyl-CPG-binding domain protein 02
HORVU7Hr1G097070	no DE	no DE	no DE	no DE	6.3	0.047	Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16
HORVU7Hr1G120020	no DE	no DE	no DE	no DE	-7.5	0.005	Disease resistance protein
HORVU7Hr1G121530	-1.6	<0.001	no DE	no DE	no DE	no DE	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase prot.

Table S4: Oligonucleotide primer sequences

Name	**Purpose**	**Barley_identifier**	**Sequence 5´ - 3´**
αTub-F	qRT_PCR	HORVU1Hr1G081280	GAGGTTTGACGGTGCTCTGA
αTub-R	qRT_PCR	HORVU1Hr1G081280	GGTGATCTCGGCAACAGACA
GK-SAM-qRT-fw4	qRT_PCR	HORVU5Hr1G027890	ATTCTGCGGTTTATCAGGCG
GK-SAM-qRT-rv4	qRT_PCR	HORVU5Hr1G027890	AAACACCACCGATAGGCACG
HORVU3Hr1G076640-q-fw	qRT_PCR	HORVU3Hr1G076640	GGGATCGCCTATTTGTGC
HORVU3Hr1G076640-q-rv	qRT_PCR	HORVU3Hr1G076640	GTTGGAGGAGGAAGATGTCC
HORVU5Hr1G119670-q-fw	qRT_PCR	HORVU5Hr1G119670	TGGCAACAGTTCGACTACTAGC
HORVU5Hr1G119670-q-rv	qRT_PCR	HORVU5Hr1G119670	CGGGCAAGGTGATCATAATT
HORVU5Hr1G119680-q-fw	qRT_PCR	HORVU5Hr1G119680	GGCTGCCGGTCAGCTATACC
HORVU5Hr1G119680-q-rv	qRT_PCR	HORVU5Hr1G119680	AAATTCCGATGCTTGTCCG
HORVU5Hr1G119860-q-fw	qRT_PCR	HORVU5Hr1G119860	GGAAGTGCCCAGATGCATAC
HORVU5Hr1G119860-q-rv	qRT_PCR	HORVU5Hr1G119860	CCCGCTTCCAGCATATATTG
HORVU3Hr1G076660-q-fw	qRT_PCR	HORVU3Hr1G076660	CACGAACCGGGACAAATAAG
HORVU3Hr1G076660-q-rv	qRT_PCR	HORVU3Hr1G076660	GTTGAAAATGGAGCTCGGAG
GK-Hyg-fw	CRISPR validation (insertion)		ACTCACCGCGACGTCTGTCG
GK-Hyg-rv	CRISPR validation (insertion)		GCGCGTCTGCTGCTCCATA
GK_HvSAM_CRISPR_seq_fw	CRISPR validation (mutation)	HORVU5Hr1G027890	AGACGTGTTGGATACTATGTCG
GK-HvSAM_gDNA_rv1	CRISPR validation (mutation)	HORVU5Hr1G027890	GCA GAA ACC ACG ATC AAG CAT CAC C
GL-HvSAM-pGGC-fw-V2	EGT2 cloning (greengate plasmids)	HORVU5Hr1G027890	AAAGGTCTCAGGCTTAATGTCGGCTAAACGATCAC
GK-HvSAM-pGGC-rv	EGT2 cloning (greengate plasmids)	HORVU5Hr1G027890	AAAGGTCTCTCTGAAGGTTCCAGCTTTAGGGAGAC

Supporting Information Tables for Chapter 3

Title: ENHANCED GRAVITROPISM 2 coordinates molecular adaptations to gravistimulation in the elongation zone of barley roots

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Table S1 List of oligonucleotide primers.

Name	Purpose	Barley identifier	Sequence 5'-3'
EGT2-AD-fw (EcoRI)	EGT2 cloning (pGADT7/ pGBKT7 plasmids)	HORVU.MOREX.r3.5HG0447830.1	CGGAATTCATGTCGGCTAAACGATCACAG
EGT2-AD-rv (BamHI)			CGGGATCCTCAAGGTTCCAGCTTTAGG
EGT2-attB1-fw	EGT2 cloning (2in1 system)	HORVU.MOREX.r3.5HG0447830.1	GGGGACA AGT TTG TAC AAA AAA GCA GGC TTA ATGTCGGCTAAACGATCAC
EGT2-attB4-rv	EGT2 cloning (2in1 system, with stop codon)		GGGGAC AAC TTT GTA TAG AAA AGT TGG GTG AGGTTCCAGCTTTAGGGAG
EGT2-attB4-rv(n-tag)	EGT2 cloning (2in1 system, without stop codon)		GGGGACCACTTTGTACAAGAAAGCTGGGT TCAAGGCTTGAGAGCAATCG
OMT- attb3-fw	OMT cloning (2in1 system)	HORVU.MOREX.r3.3HG0330120.1	GGGGACA ACT TTG TAT AAT AAA GTT GGA ATGGGGTCCATCGCCGCC
OMT- attb2-rv	OMT cloning (2in1 system, with stop codon)		GGGGACCACTTTGTACAAGAAAGCTGGGT CTACTTGGTGAACTCGATG
GXM - attb3-fw	GXM cloning (2in1 system)	HORVU.MOREX.r3.7HG0749870.1	GGGGACA ACT TTG TAT AAT AAA GTT GGA ATGTCGAGCCCCGTGCAC
GXM - attb2-rv	GXM cloning (2in1 system, with stop codon)		GGGGACCACTTTGTACAAGAAAGCTGGGT CTAATTGAGAGGGCAGAA
PBP-attb3-fw	PBP cloning (2in1 system)	HORVU.MOREX.r3.7HG0709860.1	GGGGACA ACT TTG TAT AAT AAA GTT GGA ATGGTTGCCGTGGCGGCC
PBP-attb2-rv	PBP cloning (2in1 system, with stop codon)		GGGGACCACTTTGTACAAGAAAGCTGGGT TCAGTGCGACACCACACGAG
HMT-attb3-fw	HMT cloning (2in1 system)	HORVU.MOREX.r3.2HG0126380.1	GGGGACA ACT TTG TAT AAT AAA GTT GGA ATGGCGGACAAGATCTCCAC
HMT-attb2-rv	HMT cloning (2in1 system, with stop codon)		GGGGACCACTTTGTACAAGAAAGCTGGGT TCACATGACGCTGCACCCGG
HORVU.MOREX.r3.1HG0000050.1_attb3-fw	HORVU.MOREX.r3.1HG0000050.1 cloning (2in1 system)	HORVU.MOREX.r3.1HG0000050.1	GGGGACA ACT TTG TAT AAT AAA GTT GGA ATGGCGATGCGGGGCGTC
HORVU.MOREX.r3.1HG0000050.1 _attb2-rv (+TAG)	HORVU.MOREX.r3.1HG0000050.1 cloning (2in1 system, with stop codon)		GGGGACCACTTTGTACAAGAAAGCTGGGT TCAGCGATCCCGCAGCTCAT

Table SH Overview of differentially expressed genes (false discovery rate (FDR) <5%) in gravistimulated wild type roots.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0003270.1	2.823399	-2.89111	7.20642	2.10E-09	4.30E-05	-3.57691	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	root cap	3 h
HORVU.MOREX.r3.4HG0405330.1	1.798336	-1.47892	5.69161	5.58E-07	0.011441	5.598813	Cytochrome P450, putative	root cap	6 h
HORVU.MOREX.r3.4HG0402190.1	2.577422	-1.87054	5.34876	1.92E-06	0.01972	4.572588	Flavin-containing monooxygenase	root cap	6 h
HORVU.MOREX.r3.7HG0656980.1	1.490765	-1.98412	4.979942	7.12E-06	0.029524	3.341386	Transposon protein, putative, CACTA, En/Spm sub-class, expressed	root cap	6 h
HORVU.MOREX.r3.3HG0300110.1	1.511206	-2.56986	4.97713	7.19E-06	0.029524	2.824972	Acidic endochitinase	root cap	6 h
HORVU.MOREX.r3.3HG0276000.2	1.810064	-3.10951	5.10213	4.63E-06	0.029524	2.256709	GDSL esterase/lipase	root cap	6 h
HORVU.MOREX.r3.7HG0739570.1	2.549347	1.204008	4.862519	1.07E-05	0.03676	1.742172	cotton fiber protein	root cap	6 h
HORVU.MOREX.r3.2HG0125600.1	-1.28244	-0.84295	-6.38892	4.33E-08	0.000888	8.407785	DNA-directed RNA polymerase subunit alpha	root cap	12 h
HORVU.MOREX.r3.7HG0732860.1	-0.84978	6.992859	-6.07936	1.35E-07	0.001387	7.343196	Polyubiquitin	root cap	12 h
HORVU.MOREX.r3.7HG0702990.1	-0.54851	5.286374	-5.72619	4.92E-07	0.002233	6.156683	WD-repeat protein, putative	root cap	12 h
HORVU.MOREX.r3.6HG0552230.1	-0.8487	6.698601	-5.72377	4.96E-07	0.002233	6.12943	Polyubiquitin	root cap	12 h
HORVU.MOREX.r3.6HG0565880.1	-0.51588	6.39216	-5.69834	5.44E-07	0.002233	6.059052	Polyubiquitin	root cap	12 h
HORVU.MOREX.r3.6HG0553150.1	-0.81679	6.876917	-5.57225	8.59E-07	0.002396	5.612467	Polyubiquitin	root cap	12 h
HORVU.MOREX.r3.6HG0559390.1	-1.1202	4.844853	-5.53987	9.66E-07	0.002396	5.511704	Polyubiquitin protein	root cap	12 h
HORVU.MOREX.r3.7HG0724830.1	-0.68712	6.736593	-5.54022	9.65E-07	0.002396	5.470374	Zinc finger A20 and AN1 domain stress-associated protein	root cap	12 h
HORVU.MOREX.r3.1HG0093750.1	-1.02559	3.434371	-5.51661	1.05E-06	0.002396	5.423285	ATP-dependent zinc metalloprotease FtsH	root cap	12 h
HORVU.MOREX.r3.7HG0675390.1	-0.83136	3.34579	-5.47982	1.20E-06	0.002435	5.312858	Thioredoxin-like family protein	root cap	12 h
HORVU.MOREX.r3.6HG0565890.1	-0.81717	8.056863	-5.45027	1.33E-06	0.002435	5.156865	Polyubiquitin	root cap	12 h
HORVU.MOREX.r3.2HG0173440.1	-0.85101	3.881615	-5.41378	1.52E-06	0.002435	5.08651	AGAMOUS-like MADS-box transcription factor	root cap	12 h
HORVU.MOREX.r3.2HG0214820.1	-0.99075	3.095886	-5.41001	1.54E-06	0.002435	5.083794	Protein kinase, putative	root cap	12 h
HORVU.MOREX.r3.7HG0733110.1	-0.70107	6.267735	-5.24905	2.75E-06	0.004024	4.523263	Polyubiquitin	root cap	12 h
HORVU.MOREX.r3.3HG0299100.1	-0.54346	4.96179	-5.18945	3.39E-06	0.004274	4.346558	Zinc finger family protein	root cap	12 h
HORVU.MOREX.r3.2HG0203390.1	-1.08245	-1.42637	-5.08974	4.84E-06	0.004735	3.991515	Auxin-responsive protein	root cap	12 h
HORVU.MOREX.r3.1HG0081860.1	-0.87883	-0.61955	-5.07269	5.14E-06	0.004735	3.961192	Pollen Ole e 1 allergen/extensin	root cap	12 h
HORVU.MOREX.r3.7HG0709700.1	-1.08591	5.754852	-5.0935	4.77E-06	0.004735	3.949535	PENTATRICOPEPTIDE REPEAT 596	root cap	12 h
HORVU.MOREX.r3.1HG0057800.1	-1.34225	4.113561	-5.09894	4.68E-06	0.004735	3.916959	Protein BRANCHLESS TRICHOME	root cap	12 h
HORVU.MOREX.r3.3HG0244080.1	-0.96407	6.147357	-5.06947	5.20E-06	0.004735	3.888486	Homeobox leucine-zipper protein	root cap	12 h
HORVU.MOREX.r3.2HG0100060.1	-1.04214	3.172843	-5.0495	5.57E-06	0.004735	3.874201	Arginase	root cap	12 h
HORVU.MOREX.r3.1HG0051890.1	-0.87443	2.409167	-5.03979	5.77E-06	0.004735	3.854096	Glutathione S-transferase	root cap	12 h
HORVU.MOREX.r3.4HG0352420.1	-0.64137	4.361963	-5.0399	5.77E-06	0.004735	3.842691	MACPF domain protein	root cap	12 h
HORVU.MOREX.r3.6HG0614420.1	-0.70609	5.04629	-5.01674	6.26E-06	0.004939	3.778866	ethylene-responsive transcription factor	root cap	12 h
HORVU.MOREX.r3.6HG0621190.1	-1.04126	4.746594	-4.98162	7.08E-06	0.00519	3.662177	Chaperone protein dnaJ	root cap	12 h
HORVU.MOREX.r3.7HG0671720.1	-0.87912	4.165549	-4.9496	7.92E-06	0.005607	3.506882	Amino acid transporter, putative	root cap	12 h
HORVU.MOREX.r3.1HG0015430.1	-1.59517	0.318582	-5.19004	3.39E-06	0.004274	3.446159	Trihelix transcription factor GT-3b	root cap	12 h
HORVU.MOREX.r3.6HG0611930.1	-1.53928	-2.37556	-5.1776	3.54E-06	0.004274	3.42081	RING/U-box superfamily protein, putative	root cap	12 h
HORVU.MOREX.r3.4HG0403930.1	-1.02401	-0.63527	-4.92116	8.76E-06	0.005796	3.413686	Cysteine proteinase inhibitor	root cap	12 h
HORVU.MOREX.r3.2HG0097600.1	-0.52797	5.036264	-4.87356	1.03E-05	0.006632	3.31246	Protein DA1-related 1	root cap	12 h
HORVU.MOREX.r3.1HG0025520.1	-1.12521	2.003818	-4.99605	6.73E-06	0.005115	3.302967	RING/U-box superfamily protein	root cap	12 h
HORVU.MOREX.r3.6HG0568720.1	-0.81421	3.242843	-4.85594	1.10E-05	0.006839	3.256707	#N/A	root cap	12 h
HORVU.MOREX.r3.5HG0509060.1	-0.95964	4.702328	-4.83861	1.17E-05	0.006945	3.196184	Non-specific serine/threonine protein kinase	root cap	12 h
HORVU.MOREX.r3.3HG0256910.1	-0.82045	2.543019	-4.82557	1.22E-05	0.006945	3.154161	Ribonuclease I	root cap	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.6HG0607560.1	-0.80876	4.13176	-4.81846	1.25E-05	0.006945	3.127532	Adenine nucleotide alpha hydrolases-like superfamily protein	root cap	12 h
HORVU.MOREX.r3.6HG0568690.1	-1.03891	4.283634	-4.81101	1.29E-05	0.006945	3.104319	Cinnamoyl CoA reductase	root cap	12 h
HORVU.MOREX.r3.3HG0249970.1	-0.55296	3.802328	-4.80111	1.33E-05	0.007004	3.080605	Beta-amylase	root cap	12 h
HORVU.MOREX.r3.7HG0707460.1	-0.91662	2.531992	-4.79321	1.37E-05	0.007019	3.029348	Protein kinase, putative	root cap	12 h
HORVU.MOREX.r3.1HG0008890.1	-0.50372	5.398609	-4.78053	1.43E-05	0.007156	2.990593	Coiled-coil domain-containing protein, putative	root cap	12 h
HORVU.MOREX.r3.2HG0140970.1	-1.70457	2.378717	-4.92788	8.55E-06	0.005796	2.972836	Heat-shock protein, putative	root cap	12 h
HORVU.MOREX.r3.1HG0062480.1	0.848151	5.054697	4.747402	1.60E-05	0.007837	2.903511	1-deoxy-D-xylulose-5-phosphate synthase	root cap	12 h
HORVU.MOREX.r3.5HG0426180.1	-0.59936	4.726965	-4.72387	1.74E-05	0.008115	2.835302	Thioesterase family protein	root cap	12 h
HORVU.MOREX.r3.5HG0495770.1	-0.48077	4.845038	-4.7046	1.86E-05	0.008386	2.760621	RING/U-box superfamily protein	root cap	12 h
HORVU.MOREX.r3.2HG0130760.1	-0.6913	4.232936	-4.68621	1.98E-05	0.008472	2.715463	Protein yippee-like	root cap	12 h
HORVU.MOREX.r3.1HG0029270.1	-0.56384	4.599412	-4.64652	2.27E-05	0.008966	2.590698	Ubiquitin conjugating enzyme E2	root cap	12 h
HORVU.MOREX.r3.6HG0601740.1	-1.11478	-1.96393	-4.67705	2.05E-05	0.008566	2.554705	Formate-dependent nitrite reductase complex subunit NrfG	root cap	12 h
HORVU.MOREX.r3.3HG0251900.1	-0.58184	5.429565	-4.65874	2.18E-05	0.008941	2.553179	WRKY transcription factor	root cap	12 h
HORVU.MOREX.r3.7HG0659980.1	-0.75289	5.13795	-4.64851	2.26E-05	0.008966	2.54876	UAA transporter	root cap	12 h
HORVU.MOREX.r3.2HG0191150.1	0.987218	5.670797	4.624858	2.45E-05	0.00899	2.513627	Polygalacturonase QRT3	root cap	12 h
HORVU.MOREX.r3.3HG0281000.1	-1.13625	3.470695	-4.62746	2.43E-05	0.00899	2.513107	F-box protein	root cap	12 h
HORVU.MOREX.r3.4HG0332530.1	-0.56658	4.558532	-4.62005	2.49E-05	0.00899	2.504111	Aldo-keto reductase/ oxidoreductase	root cap	12 h
HORVU.MOREX.r3.1HG0075220.1	-1.01928	2.657679	-4.6239	2.46E-05	0.00899	2.497509	Actin	root cap	12 h
HORVU.MOREX.r3.5HG0487890.1	-0.81835	4.484514	-4.6133	2.55E-05	0.00901	2.478508	Protein DETOXIFICATION	root cap	12 h
HORVU.MOREX.r3.1HG0053120.1	-0.7353	4.408808	-4.619	2.50E-05	0.00899	2.467546	ADP-ribosylation factor GTPase-activating protein	root cap	12 h
HORVU.MOREX.r3.1HG0029060.1	0.331688	9.685002	4.688856	1.96E-05	0.008472	2.452944	70 kDa heat shock protein	root cap	12 h
HORVU.MOREX.r3.2HG0121950.1	-0.70691	3.757635	-4.59002	2.76E-05	0.009433	2.412075	RNA binding protein	root cap	12 h
HORVU.MOREX.r3.7HG0663550.1	-2.12756	0.155997	-4.72681	1.72E-05	0.008115	2.398947	Glycosyltransferase	root cap	12 h
HORVU.MOREX.r3.1HG0056360.1	-0.48733	6.496535	-4.60306	2.64E-05	0.009174	2.357061	Oxysterol-binding protein, expressed	root cap	12 h
HORVU.MOREX.r3.2HG0099980.1	-0.76137	2.832965	-4.56222	3.03E-05	0.009444	2.325886	Glyoxylate reductase/hydroxypyruvate reductase	root cap	12 h
HORVU.MOREX.r3.7HG0678530.1	-0.53528	5.729845	-4.56623	2.99E-05	0.009444	2.300151	Ubiquitin-associated domain-containing family protein	root cap	12 h
HORVU.MOREX.r3.6HG0557640.2	-0.85253	6.081969	-4.55992	3.06E-05	0.009444	2.284663	Polyubiquitin	root cap	12 h
HORVU.MOREX.r3.5HG0427690.1	-0.85507	0.757744	-4.56751	2.98E-05	0.009444	2.274183	Exostosin family protein	root cap	12 h
HORVU.MOREX.r3.1HG0058170.1	-0.49534	5.459776	-4.55165	3.14E-05	0.009444	2.266576	Autophagy-related protein 3	root cap	12 h
HORVU.MOREX.r3.3HG0231010.1	-0.48328	5.831789	-4.55366	3.12E-05	0.009444	2.260216	NH(3)-dependent NAD(+) synthetase	root cap	12 h
HORVU.MOREX.r3.5HG0501950.1	-1.18653	0.379734	-4.54541	3.21E-05	0.009444	2.228017	RNA-binding (RRM/RBD/RNP motifs) family protein	root cap	12 h
HORVU.MOREX.r3.7HG0703000.1	-0.71136	5.112448	-4.52506	3.44E-05	0.009522	2.194884	UDP-glucose 4-epimerase, putative	root cap	12 h
HORVU.MOREX.r3.3HG0227890.1	-1.18155	2.984434	-4.52994	3.39E-05	0.009522	2.183117	Lactation elevated protein 1	root cap	12 h
HORVU.MOREX.r3.2HG0201420.1	-1.09279	-0.04773	-4.51186	3.60E-05	0.009598	2.142929	Protein kinase	root cap	12 h
HORVU.MOREX.r3.2HG0173750.1	-0.50742	8.547687	-4.56753	2.98E-05	0.009444	2.124164	Aldehyde dehydrogenase	root cap	12 h
HORVU.MOREX.r3.3HG0329000.1	-0.54548	7.386719	-4.54458	3.22E-05	0.009444	2.112378	Haloacid dehalogenase-like hydrolase family protein, putative, expressed	root cap	12 h
HORVU.MOREX.r3.3HG0271550.1	-0.52196	6.477159	-4.5233	3.46E-05	0.009522	2.090392	Ubiquitin-like modifier-activating enzyme atg7	root cap	12 h
HORVU.MOREX.r3.4HG0348850.1	-0.69046	8.009697	-4.5358	3.32E-05	0.009522	2.084904	Neutral/alkaline invertase	root cap	12 h
HORVU.MOREX.r3.2HG0186670.1	-0.67647	4.974138	-4.48168	3.99E-05	0.010498	2.029023	3-oxo-5-alpha-steroid 4-dehydrogenase 3	root cap	12 h
HORVU.MOREX.r3.4HG0397570.1	-0.95641	4.104655	-4.47622	4.07E-05	0.010559	2.019113	Glucan endo-1,3-beta-glucosidase 3	root cap	12 h
HORVU.MOREX.r3.1HG0085780.1	-1.01066	2.653546	-4.4574	4.33E-05	0.010585	1.999303	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	root cap	12 h

Table Sн Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.7HG0749800.1	-0.77039	4.620717	-4.46721	4.19E-05	0.010585	1.989527	#N/A	root cap	12 h
HORVU.MOREX.r3.2HG0195580.1	-0.60678	7.713102	-4.52192	3.48E-05	0.009522	1.965649	UDP-glucose 4-epimerase, putative	root cap	12 h
HORVU.MOREX.r3.7HG0733070.1	-0.51348	6.760905	-4.47075	4.14E-05	0.010585	1.925919	Polyubiquitin	root cap	12 h
HORVU.MOREX.r3.3HG0228600.1	-0.80407	3.194099	-4.43292	4.71E-05	0.011232	1.920616	transmembrane protein, putative (DUF247)	root cap	12 h
HORVU.MOREX.r3.4HG0384590.1	-1.4357	1.137938	-4.46206	4.27E-05	0.010585	1.86961	Chaperone protein DnaJ	root cap	12 h
HORVU.MOREX.r3.5HG0481570.1	-0.8274	3.92217	-4.4383	4.62E-05	0.011159	1.809097	Inactive phospholipase C-like protein 1	root cap	12 h
HORVU.MOREX.r3.2HG0181380.1	0.784857	2.418376	4.420454	4.91E-05	0.01158	1.782252	Actin-related protein 2/3 complex subunit 2	root cap	12 h
HORVU.MOREX.r3.5HG0504720.1	0.464637	6.757338	4.410774	5.07E-05	0.011829	1.735987	Octicosapeptide/Phox/Bem1p domain-containing protein / tetratricopeptide repe	root cap	12 h
HORVU.MOREX.r3.7HG0713100.1	-0.72286	3.920881	-4.37511	5.72E-05	0.012723	1.72962	transmembrane protein, putative (DUF594)	root cap	12 h
HORVU.MOREX.r3.2HG0154110.1	-1.034	1.510407	-4.36463	5.93E-05	0.012723	1.717556	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	root cap	12 h
HORVU.MOREX.r3.2HG0175220.1	-0.43669	9.281963	-4.4605	4.29E-05	0.010585	1.70697	Amine oxidase	root cap	12 h
HORVU.MOREX.r3.2HG0117540.1	-0.56241	3.822761	-4.36329	5.95E-05	0.012723	1.703811	Methyltransferase-like protein	root cap	12 h
HORVU.MOREX.r3.7HG0685620.1	-0.38926	5.51038	-4.36564	5.91E-05	0.012723	1.695952	RING/U-box superfamily protein	root cap	12 h
HORVU.MOREX.r3.4HG0342860.1	-0.83523	3.568964	-4.35774	6.06E-05	0.012829	1.673634	Kinase family protein	root cap	12 h
HORVU.MOREX.r3.1HG0093880.1	-0.77277	4.163907	-4.36436	5.93E-05	0.012723	1.672783	Phosphoglucan phosphatase LSF1	root cap	12 h
HORVU.MOREX.r3.1HG0002330.1	-0.66462	5.33192	-4.36457	5.93E-05	0.012723	1.668277	Ras-like protein	root cap	12 h
HORVU.MOREX.r3.1HG0065120.1	-0.54994	3.907242	-4.35072	6.21E-05	0.013001	1.657088	Protein kinase superfamily protein	root cap	12 h
HORVU.MOREX.r3.4HG0391970.1	-1.21575	-1.7379	-4.37105	5.80E-05	0.012723	1.652152	LOB domain protein	root cap	12 h
HORVU.MOREX.r3.6HG0551620.1	-0.54924	5.566118	-4.33945	6.45E-05	0.013232	1.599519	BAX inhibitor 1	root cap	12 h
HORVU.MOREX.r3.7HG0668190.1	-0.58408	4.882662	-4.31675	6.96E-05	0.013841	1.53107	Phytochelatin synthase	root cap	12 h
HORVU.MOREX.r3.5HG0498320.1	0.429306	5.332211	4.314295	7.01E-05	0.013841	1.519631	Zinc finger, B-box	root cap	12 h
HORVU.MOREX.r3.3HG0271380.1	-0.54512	5.415877	-4.32755	6.71E-05	0.013533	1.511055	GDSL esterase/lipase	root cap	12 h
HORVU.MOREX.r3.3HG0291680.1	-0.97851	-0.37502	-4.29504	7.48E-05	0.01462	1.496854	Tubulin beta-2 chain	root cap	12 h
HORVU.MOREX.r3.6HG0561320.1	-1.28175	-0.01134	-4.28514	7.73E-05	0.014962	1.475521	RNA-directed RNA polymerase catalytic subunit	root cap	12 h
HORVU.MOREX.r3.1HG0051880.1	-0.82245	4.550064	-4.34334	6.36E-05	0.013192	1.467889	Glutathione S-transferase	root cap	12 h
HORVU.MOREX.r3.3HG0305540.1	-1.31675	-2.8839	-4.70151	1.88E-05	0.008386	1.459601	DUF1685 family protein	root cap	12 h
HORVU.MOREX.r3.6HG0626000.1	-1.08875	1.922137	-4.28247	7.80E-05	0.014962	1.36707	Calcineurin B-like protein	root cap	12 h
HORVU.MOREX.r3.4HG0382640.1	-1.38804	-2.50777	-4.51768	3.53E-05	0.009533	1.349406	Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 fa	root cap	12 h
HORVU.MOREX.r3.2HG0198000.1	0.300141	8.426845	4.32681	6.73E-05	0.013533	1.346151	RNA-binding family protein	root cap	12 h
HORVU.MOREX.r3.2HG0191970.1	-0.87526	3.27463	-4.23744	9.06E-05	0.016042	1.328992	Protein phosphatase 2c, putative	root cap	12 h
HORVU.MOREX.r3.1HG0069010.1	-0.8324	3.211686	-4.23768	9.06E-05	0.016042	1.312716	Glycerol-3-phosphate dehydrogenase [NAD(+)]	root cap	12 h
HORVU.MOREX.r3.2HG0147190.1	-0.72627	3.250226	-4.23757	9.06E-05	0.016042	1.291305	Zinc finger A20 and AN1 domain stress-associated protein	root cap	12 h
HORVU.MOREX.r3.1HG0027030.1	-0.75711	1.805042	-4.25354	8.59E-05	0.016026	1.284667	Mitochondrial carrier family	root cap	12 h
HORVU.MOREX.r3.5HG0529140.1	0.432548	10.3593	4.366513	5.89E-05	0.012723	1.284433	Elongation factor	root cap	12 h
HORVU.MOREX.r3.3HG0291590.1	-0.62888	5.468201	-4.23001	9.29E-05	0.016292	1.27413	Tunicamycin induced 1	root cap	12 h
HORVU.MOREX.r3.2HG0189190.1	-0.56412	5.637918	-4.23726	9.07E-05	0.016042	1.27098	Hexosyltransferase	root cap	12 h
HORVU.MOREX.r3.7HG0666350.1	-0.66019	2.690709	-4.22671	9.39E-05	0.016332	1.258411	FACT complex subunit SPT16	root cap	12 h
HORVU.MOREX.r3.4HG0336330.1	-0.82913	0.591327	-4.20935	9.95E-05	0.016843	1.246155	#N/A	root cap	12 h
HORVU.MOREX.r3.5HG0519200.1	-0.80827	2.210169	-4.21322	9.82E-05	0.016795	1.228799	DUF506 family protein	root cap	12 h
HORVU.MOREX.r3.5HG0501370.1	-0.90534	-0.59777	-4.20619	0.000101	0.016843	1.205796	Cytochrome P450, putative	root cap	12 h
HORVU.MOREX.r3.7HG0658130.1	-0.78542	4.23398	-4.20489	0.000101	0.016843	1.183352	Nodulin-like / Major Facilitator Superfamily protein	root cap	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.2HG0213480.1	-0.48207	8.002679	-4.24789	8.75E-05	0.016038	1.160298	Phosphomannomutase	root cap	12 h
HORVU.MOREX.r3.2HG0104110.1	-0.92422	3.073698	-4.21371	9.81E-05	0.016795	1.144121	CW7 protein, putative	root cap	12 h
HORVU.MOREX.r3.1HG0073140.1	-0.86351	1.311141	-4.1712	0.000113	0.018526	1.132761	Metal tolerance protein	root cap	12 h
HORVU.MOREX.r3.2HG0202110.1	-0.43979	8.934553	-4.26572	8.25E-05	0.01553	1.072325	Alpha-1,4-glucan-protein synthase [UDP-forming]	root cap	12 h
HORVU.MOREX.r3.2HG0099750.1	-0.55729	5.148054	-4.16018	0.000117	0.018909	1.04572	carbohydrate esterase, putative (DUF303)	root cap	12 h
HORVU.MOREX.r3.2HG0192960.1	-0.63914	3.213874	-4.16451	0.000115	0.018789	1.027258	Xyloglucan endotransglucosylase/hydrolase	root cap	12 h
HORVU.MOREX.r3.6HG0604990.1	-1.34952	1.556962	-4.2482	8.74E-05	0.016038	1.025382	senescence-associated family protein (DUF581)	root cap	12 h
HORVU.MOREX.r3.7HG0680170.1	-0.53226	4.825321	-4.15039	0.000121	0.019244	1.014283	mediator of RNA polymerase II transcription subunit	root cap	12 h
HORVU.MOREX.r3.4HG0411320.1	-0.49858	6.294368	-4.14747	0.000122	0.019262	0.994595	Appr-1-p processing enzyme family protein	root cap	12 h
HORVU.MOREX.r3.3HG0253860.1	-1.40922	-0.09276	-4.13021	0.000129	0.020232	0.988279	Rapid alkalinization factor (RALF) family protein	root cap	12 h
HORVU.MOREX.r3.6HG0598380.1	-1.04129	1.304428	-4.12426	0.000132	0.020321	0.974873	Expansin protein	root cap	12 h
HORVU.MOREX.r3.3HG0249710.1	-0.68048	2.92555	-4.12575	0.000131	0.020321	0.970391	Heme-binding protein, putative	root cap	12 h
HORVU.MOREX.r3.6HG0630410.1	-1.20626	-1.40652	-4.11023	0.000138	0.02066	0.957122	LOB domain protein-like	root cap	12 h
HORVU.MOREX.r3.3HG0250330.1	-0.55949	4.018268	-4.10577	0.00014	0.02066	0.910066	Phosphate translocator	root cap	12 h
HORVU.MOREX.r3.2HG0189340.1	-0.91308	1.373881	-4.19685	0.000104	0.017158	0.902253	#N/A	root cap	12 h
HORVU.MOREX.r3.7HG0668260.1	-1.47194	-0.18118	-4.10861	0.000139	0.02066	0.901284	Coiled-coil domain-containing protein 21, putative isoform 1	root cap	12 h
HORVU.MOREX.r3.2HG0151920.1	-0.85626	3.926991	-4.08544	0.00015	0.020899	0.88491	Retrovirus-related Pol polyprotein from transposon TNT 1-94	root cap	12 h
HORVU.MOREX.r3.3HG0308250.1	-0.53753	5.709159	-4.10929	0.000138	0.02066	0.882982	Telomere repeat-binding factor like-protein	root cap	12 h
HORVU.MOREX.r3.7HG0735280.1	-0.43439	7.186121	-4.1501	0.000121	0.019244	0.867029	Auxin response factor	root cap	12 h
HORVU.MOREX.r3.5HG0453430.1	-0.84985	3.783951	-4.07719	0.000154	0.020977	0.855892	Regulator of chromosome condensation (RCC1) family protein	root cap	12 h
HORVU.MOREX.r3.5HG0476220.1	-0.72929	2.950954	-4.09329	0.000146	0.020775	0.843927	Major facilitator superfamily transporter	root cap	12 h
HORVU.MOREX.r3.7HG0664810.1	-1.23154	2.590118	-4.07476	0.000155	0.020977	0.841051	Heat-shock protein, putative	root cap	12 h
HORVU.MOREX.r3.7HG0706090.1	-0.51791	5.276785	-4.08517	0.00015	0.020899	0.840887	methyl esterase 12	root cap	12 h
HORVU.MOREX.r3.3HG0234880.1	-0.78762	4.615778	-4.10121	0.000142	0.020673	0.831034	Guanine-nucleotide-exchange protein	root cap	12 h
HORVU.MOREX.r3.3HG0251700.1	-0.90786	5.703161	-4.07378	0.000155	0.020977	0.830229	Glucan endo-1,3-beta-glucosidase	root cap	12 h
HORVU.MOREX.r3.3HG0328340.1	-0.80723	4.602643	-4.07522	0.000155	0.020977	0.829255	Two-component response regulator	root cap	12 h
HORVU.MOREX.r3.5HG0458100.1	-0.80157	5.986393	-4.09586	0.000145	0.020749	0.820963	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	root cap	12 h
HORVU.MOREX.r3.6HG0565830.1	-0.70583	5.523345	-4.07154	0.000157	0.020994	0.815855	Polyubiquitin	root cap	12 h
HORVU.MOREX.r3.2HG0122840.1	-0.57117	5.447828	-4.10855	0.000139	0.02066	0.795163	4-alpha-glucanotransferase	root cap	12 h
HORVU.MOREX.r3.7HG0729010.1	-0.86518	-0.16187	-4.07422	0.000155	0.020977	0.774904	Peroxidase	root cap	12 h
HORVU.MOREX.r3.7HG0752830.1	-0.42282	6.536164	-4.08555	0.00015	0.020899	0.743067	Signal peptide peptidase-like protein	root cap	12 h
HORVU.MOREX.r3.3HG0284890.1	-0.69381	4.764663	-4.10614	0.00014	0.02066	0.733629	Alpha-amylase	root cap	12 h
HORVU.MOREX.r3.7HG0729510.1	-0.76062	4.709018	-4.03592	0.000176	0.022832	0.723945	WEB family protein, chloroplastic	root cap	12 h
HORVU.MOREX.r3.2HG0133060.1	-0.87061	2.031127	-4.03168	0.000178	0.022855	0.713484	Vacuole membrane-like protein	root cap	12 h
HORVU.MOREX.r3.5HG0511040.1	-0.94978	2.881944	-4.05589	0.000165	0.021808	0.693605	#N/A	root cap	12 h
HORVU.MOREX.r3.2HG0185660.1	-0.40954	4.65136	-4.03994	0.000174	0.022679	0.689467	Kinase family protein	root cap	12 h
HORVU.MOREX.r3.3HG0231330.1	-0.82403	4.950299	-4.02029	0.000185	0.023143	0.685121	Transferase family protein	root cap	12 h
HORVU.MOREX.r3.3HG0234890.1	-0.76907	3.013939	-4.00588	0.000194	0.023321	0.636478	ARF guanine-nucleotide exchange factor GNOM	root cap	12 h
HORVU.MOREX.r3.3HG0293570.1	-2.92576	-0.38794	-4.81622	1.26E-05	0.006945	0.629342	BTB/POZ domain-containing protein	root cap	12 h
HORVU.MOREX.r3.7HG0635050.1	-0.76481	0.346306	-4.00553	0.000194	0.023321	0.625437	NBS-LRR-like resistance protein	root cap	12 h
HORVU.MOREX.r3.5HG0517300.1	-1.09887	3.002936	-4.00488	0.000194	0.023321	0.624958	Aldehyde oxidase, putative	root cap	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.6HG0570660.1	-1.30055	3.599982	-3.99489	0.000201	0.023321	0.62235	DUF581 family protein	root cap	12 h
HORVU.MOREX.r3.3HG0252270.1	-0.96764	2.838807	-4.06773	0.000158	0.021119	0.618632	Germin-like protein 1	root cap	12 h
HORVU.MOREX.r3.5HG0480430.1	-0.75279	4.978135	-4.0126	0.00019	0.023321	0.604252	Aldehyde dehydrogenase	root cap	12 h
HORVU.MOREX.r3.2HG0119220.1	-0.69131	4.892203	-3.99638	0.0002	0.023321	0.60106	Gibberellin receptor GID1a	root cap	12 h
HORVU.MOREX.r3.5HG0446490.1	-0.80884	1.880935	-3.98706	0.000206	0.023449	0.593292	Syntaxin	root cap	12 h
HORVU.MOREX.r3.7HG0705240.1	-0.87314	0.811856	-4.01815	0.000186	0.023163	0.582854	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	root cap	12 h
HORVU.MOREX.r3.2HG0177780.1	-0.49352	3.700772	-3.98039	0.000211	0.023449	0.563349	Serine incorporator	root cap	12 h
HORVU.MOREX.r3.4HG0403910.1	-1.17259	-1.1504	-3.97882	0.000212	0.023449	0.533893	Cysteine proteinase inhibitor	root cap	12 h
HORVU.MOREX.r3.5HG0519030.1	-0.66053	3.970546	-3.9592	0.000225	0.0236	0.513875	Transmembrane protein 97	root cap	12 h
HORVU.MOREX.r3.3HG0275260.1	-0.75245	1.027903	-3.99991	0.000198	0.023321	0.513822	Mitogen-activated protein kinase	root cap	12 h
HORVU.MOREX.r3.6HG0607470.1	-0.45716	5.597761	-4.02674	0.000181	0.022855	0.513739	Inorganic pyrophosphatase, putative	root cap	12 h
HORVU.MOREX.r3.2HG0128490.1	-0.42898	4.434925	-3.95969	0.000225	0.0236	0.511137	#N/A	root cap	12 h
HORVU.MOREX.r3.2HG0205250.1	-0.78193	4.533688	-4.00004	0.000198	0.023321	0.510101	EamA-like transporter family	root cap	12 h
HORVU.MOREX.r3.5HG0471410.1	-0.46273	5.492756	-3.98531	0.000207	0.023449	0.509979	Sodium/hydrogen exchanger	root cap	12 h
HORVU.MOREX.r3.1HG0072100.1	-0.77492	4.063928	-3.97803	0.000212	0.023449	0.505805	2-oxoglutarate-dependent dioxygenase	root cap	12 h
HORVU.MOREX.r3.2HG0183730.1	-1.20226	3.434756	-3.9564	0.000227	0.023693	0.503296	Alpha 1,4-glycosyltransferase family protein, putative	root cap	12 h
HORVU.MOREX.r3.7HG0656980.1	1.220906	-1.98412	3.997931	0.000199	0.023321	0.496533	Transposon protein, putative, CACTA, En/Spm sub-class, expressed	root cap	12 h
HORVU.MOREX.r3.5HG0494890.1	-0.70304	5.120042	-3.9763	0.000213	0.023449	0.485422	Esterase/lipase/thioesterase family protein	root cap	12 h
HORVU.MOREX.r3.4HG0384300.1	-1.20119	-1.67949	-3.97879	0.000212	0.023449	0.466929	RING finger protein	root cap	12 h
HORVU.MOREX.r3.2HG0197550.1	-0.85929	-0.29036	-3.96233	0.000223	0.0236	0.459076	Transmembrane protein, putative	root cap	12 h
HORVU.MOREX.r3.4HG0378900.1	-0.52369	5.843019	-3.97574	0.000214	0.023449	0.454073	Kinase, putative	root cap	12 h
HORVU.MOREX.r3.3HG0266950.1	-0.69055	2.505445	-3.9373	0.000242	0.024573	0.438803	Calmodulin-binding protein	root cap	12 h
HORVU.MOREX.r3.6HG0608380.1	-0.47385	6.469706	-3.98334	0.000209	0.023449	0.436209	TBC domain containing protein	root cap	12 h
HORVU.MOREX.r3.3HG0286640.1	-0.92172	1.754903	-3.99441	0.000201	0.023321	0.431322	Chaperone protein dnaJ	root cap	12 h
HORVU.MOREX.r3.1HG0080260.1	-0.5082	3.804751	-3.9187	0.000257	0.025457	0.40421	Homogentisate phytyltransferase	root cap	12 h
HORVU.MOREX.r3.2HG0138270.1	-0.66143	3.593157	-3.91957	0.000256	0.025457	0.403701	Formin-like protein	root cap	12 h
HORVU.MOREX.r3.4HG0389860.1	-0.33912	6.138184	-3.96395	0.000222	0.0236	0.403149	S-ribonuclease binding protein	root cap	12 h
HORVU.MOREX.r3.7HG0646880.1	-0.48063	5.034739	-3.94552	0.000236	0.024313	0.402696	Hypersensitive-induced response protein	root cap	12 h
HORVU.MOREX.r3.4HG0385780.1	-0.53743	5.783595	-3.9437	0.000237	0.024313	0.369497	Mitogen-activated protein kinase	root cap	12 h
HORVU.MOREX.r3.3HG0227860.1	-0.38659	7.259658	-3.96709	0.00022	0.0236	0.366759	Katanin p60 ATPase-containing subunit, putative	root cap	12 h
HORVU.MOREX.r3.3HG0245010.1	-0.62494	4.432877	-3.91558	0.000259	0.025485	0.352221	Protein DJ-1	root cap	12 h
HORVU.MOREX.r3.7HG0733490.1	-0.68112	5.748977	-3.93253	0.000246	0.02483	0.339054	Carbonic anhydrase	root cap	12 h
HORVU.MOREX.r3.7HG0639840.1	-1.98752	-1.82989	-4.0958	0.000145	0.020749	0.336419	3-ketoacyl-CoA synthase	root cap	12 h
HORVU.MOREX.r3.7HG0743430.1	-1.27167	3.39891	-3.9427	0.000238	0.024313	0.333197	Aldehyde oxidase, putative	root cap	12 h
HORVU.MOREX.r3.6HG0577180.1	-1.00308	3.196769	-3.92969	0.000248	0.024934	0.333024	ADP,ATP carrier protein	root cap	12 h
HORVU.MOREX.r3.3HG0290130.1	-0.76123	3.667474	-3.92033	0.000255	0.025457	0.328571	arginine N-methyltransferase, putative (DUF688)	root cap	12 h
HORVU.MOREX.r3.3HG0220830.1	-1.40493	-0.11773	-4.02603	0.000182	0.022855	0.312429	Receptor-like kinase	root cap	12 h
HORVU.MOREX.r3.3HG0311480.1	-0.86407	2.639831	-3.97974	0.000211	0.023449	0.293133	Pollen Ole e 1 allergen/extensin	root cap	12 h
HORVU.MOREX.r3.3HG0231460.1	-0.77193	7.36546	-3.96088	0.000224	0.0236	0.289136	Endosomal targeting BRO1-like domain-containing protein	root cap	12 h
HORVU.MOREX.r3.1HG0057290.1	-0.74994	4.051245	-3.91475	0.00026	0.025485	0.284943	SBP (S-ribonuclease-binding protein) family protein	root cap	12 h
HORVU.MOREX.r3.7HG0670910.1	-0.42936	5.156942	-3.8955	0.000277	0.02665	0.28404	Aluminum activated malate transporter family protein	root cap	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.4HG0378750.1	-0.57172	3.963125	-3.88169	0.000289	0.027215	0.268539	Transmembrane protein 87A	root cap	12 h
HORVU.MOREX.r3.3HG0236350.1	-0.8717	2.304206	-3.89332	0.000279	0.026711	0.249493	F-box family protein	root cap	12 h
HORVU.MOREX.r3.5HG0455820.1	-0.96891	2.941847	-3.8853	0.000286	0.027027	0.244498	WD-repeat protein, putative	root cap	12 h
HORVU.MOREX.r3.2HG0211680.1	-1.01881	6.061784	-3.87344	0.000297	0.027661	0.238673	Amine oxidase family protein	root cap	12 h
HORVU.MOREX.r3.1HG0080790.1	-1.09909	0.911279	-3.95955	0.000225	0.0236	0.225685	Alpha/beta-Hydrolases superfamily protein	root cap	12 h
HORVU.MOREX.r3.1HG0014220.1	-0.85398	1.384051	-3.85311	0.000317	0.028759	0.218307	Nuclear pore complex protein Nup98	root cap	12 h
HORVU.MOREX.r3.3HG0293070.1	-0.63567	5.580025	-3.89651	0.000276	0.02665	0.217215	BnaA05g07570D protein	root cap	12 h
HORVU.MOREX.r3.6HG0548800.1	-1.17493	-1.57973	-3.85676	0.000313	0.028553	0.210522	transcription factor IIIA	root cap	12 h
HORVU.MOREX.r3.4HG0402190.1	1.926876	-1.87054	3.871156	0.000299	0.027661	0.208213	Flavin-containing monooxygenase	root cap	12 h
HORVU.MOREX.r3.7HG0736000.1	-0.74084	9.239643	-4.01129	0.00019	0.023321	0.208037	Chitinase	root cap	12 h
HORVU.MOREX.r3.4HG0381820.1	-0.61682	6.627467	-3.91387	0.000261	0.025485	0.207245	Fatty acid oxidation complex subunit alpha	root cap	12 h
HORVU.MOREX.r3.3HG0273730.1	-0.6509	6.291958	-3.88742	0.000284	0.026969	0.184385	Cytochrome P450	root cap	12 h
HORVU.MOREX.r3.4HG0413890.1	-0.42415	5.790126	-3.86633	0.000304	0.027944	0.155217	Alpha/beta-Hydrolases superfamily protein	root cap	12 h
HORVU.MOREX.r3.1HG0036390.1	-0.49067	4.682709	-3.84777	0.000322	0.029124	0.146666	ABC1-like kinase	root cap	12 h
HORVU.MOREX.r3.5HG0481030.1	-0.80032	4.153293	-3.83551	0.000335	0.02963	0.144373	Alpha/beta-Hydrolases superfamily protein, putative	root cap	12 h
HORVU.MOREX.r3.2HG0119150.1	-0.55047	4.618655	-3.83828	0.000332	0.029626	0.129811	Cytochrome P450, putative	root cap	12 h
HORVU.MOREX.r3.6HG0609220.1	-0.66757	5.489346	-3.86055	0.000309	0.028336	0.127946	Diacylglycerol O-acyltransferase 2	root cap	12 h
HORVU.MOREX.r3.3HG0277400.1	-0.60714	2.488136	-3.8213	0.00035	0.030345	0.122893	AMSH-like ubiquitin thioesterase 1	root cap	12 h
HORVU.MOREX.r3.5HG0462780.1	-0.53228	7.18947	-3.89016	0.000281	0.026857	0.121624	Transporter, putative, expressed	root cap	12 h
HORVU.MOREX.r3.5HG0468320.1	-0.84554	2.415447	-3.82534	0.000346	0.030163	0.107099	Inosine-5'-monophosphate dehydrogenase	root cap	12 h
HORVU.MOREX.r3.2HG0194790.1	-0.51495	6.395123	-3.87645	0.000294	0.027548	0.102939	Amine oxidase family protein	root cap	12 h
HORVU.MOREX.r3.7HG0708320.1	-0.6994	4.603991	-3.82453	0.000347	0.030163	0.093958	Stromal cell-derived factor 2-like protein	root cap	12 h
HORVU.MOREX.r3.1HG0059150.1	-0.75857	5.002155	-3.83296	0.000338	0.029743	0.091702	Annexin	root cap	12 h
HORVU.MOREX.r3.3HG0290180.1	-0.61166	3.615358	-3.842	0.000328	0.029534	0.084622	Non-specific serine/threonine protein kinase	root cap	12 h
HORVU.MOREX.r3.6HG0625490.1	-0.50042	3.526573	-3.79882	0.000376	0.031023	0.063541	Cytochrome b5 reductase 4	root cap	12 h
HORVU.MOREX.r3.2HG0165290.2	-0.78856	2.103536	-3.80715	0.000367	0.030889	0.055339	Initiation factor 4F subunit (DUF1350)	root cap	12 h
HORVU.MOREX.r3.6HG0623730.1	-0.9257	1.874032	-3.79536	0.000381	0.031023	0.054276	WEB family protein, chloroplastic	root cap	12 h
HORVU.MOREX.r3.5HG0513000.1	-0.45759	4.039212	-3.80798	0.000366	0.030889	0.051138	Transcription factor GTE1	root cap	12 h
HORVU.MOREX.r3.2HG0113590.1	-0.56087	3.800345	-3.79206	0.000385	0.031126	0.046603	Zinc finger CCCH domain protein, putative	root cap	12 h
HORVU.MOREX.r3.7HG0704050.1	-0.74666	2.331323	-3.7966	0.000379	0.031023	0.043818	Myeloid leukemia factor 1	root cap	12 h
HORVU.MOREX.r3.6HG0630690.1	-0.6132	3.335143	-3.78218	0.000397	0.031576	0.020939	Cyclin-dependent protein kinase inhibitor SMR9	root cap	12 h
HORVU.MOREX.r3.4HG0397280.1	-0.54432	4.108256	-3.79582	0.00038	0.031023	0.018921	Leucine-rich repeat (LRR) family protein	root cap	12 h
HORVU.MOREX.r3.3HG0275450.1	-0.92711	1.752203	-3.81151	0.000362	0.030802	0.011642	Elongation factor	root cap	12 h
HORVU.MOREX.r3.1HG0019440.1	-0.43384	5.729684	-3.83625	0.000334	0.02963	0.008411	Vegetative cell wall protein gp1	root cap	12 h
HORVU.MOREX.r3.2HG0096100.1	-0.86183	2.15401	-3.80558	0.000368	0.030889	-0.01152	3'-N-debenzoyl-2'-deoxytaxol N-benzoyltransferase	root cap	12 h
HORVU.MOREX.r3.7HG0725940.1	1.092577	-1.94583	3.774961	0.000406	0.031908	-0.01633	protein kinase family protein	root cap	12 h
HORVU.MOREX.r3.1HG0054960.1	-0.73435	4.410704	-3.80468	0.000369	0.030889	-0.02526	Adipocyte plasma membrane-associated protein	root cap	12 h
HORVU.MOREX.r3.7HG0702100.1	-0.85535	0.820309	-3.8289	0.000342	0.030001	-0.02696	Beta-1,3-N-acetylglucosaminyltransferase lunatic fringe	root cap	12 h
HORVU.MOREX.r3.7HG0713610.1	-0.48934	5.439775	-3.79867	0.000377	0.031023	-0.04321	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	root cap	12 h
HORVU.MOREX.r3.7HG0720730.1	-1.03623	0.190118	-3.7542	0.000433	0.032842	-0.0559	Fructose-bisphosphate aldolase	root cap	12 h
HORVU.MOREX.r3.7HG0682960.1	-0.70444	2.362947	-3.75725	0.000429	0.032842	-0.06307	Rhodanese/cell cycle control phosphatase superfamily protein	root cap	12 h

Table Sн Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.2HG0141900.1	0.671938	5.940265	3.790177	0.000387	0.031126	-0.06509	L-ascorbate oxidase-like protein	root cap	12 h
HORVU.MOREX.r3.7HG0669600.1	-0.64869	3.419699	-3.77659	0.000404	0.031908	-0.07011	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein, putativ	root cap	12 h
HORVU.MOREX.r3.4HG0406900.1	-0.57107	4.724038	-3.77093	0.000411	0.03207	-0.07189	Ubiquitin carboxyl-terminal hydrolase, putative	root cap	12 h
HORVU.MOREX.r3.3HG0219850.1	3.542475	-1.36231	4.032459	0.000178	0.022855	-0.07519	Teneurin-2	root cap	12 h
HORVU.MOREX.r3.5HG0459810.1	-0.56357	3.493172	-3.75449	0.000433	0.032842	-0.07563	Protein kinase like protein	root cap	12 h
HORVU.MOREX.r3.6HG0626330.1	-0.66717	3.928068	-3.81131	0.000362	0.030802	-0.08094	ENTH/ANTH/VHS superfamily protein	root cap	12 h
HORVU.MOREX.r3.7HG0700790.1	-0.61115	3.785936	-3.74813	0.000442	0.033181	-0.08254	Erythronate-4-phosphate dehydrogenase family protein	root cap	12 h
HORVU.MOREX.r3.4HG0340200.1	-0.67051	4.710006	-3.77511	0.000406	0.031908	-0.08545	RING finger and CHY zinc finger protein	root cap	12 h
HORVU.MOREX.r3.3HG0235800.1	-2.32714	-3.45011	-4.57065	2.95E-05	0.009444	-0.09519	E3 ubiquitin-protein ligase	root cap	12 h
HORVU.MOREX.r3.1HG0070670.1	-0.64127	4.791315	-3.75743	0.000429	0.032842	-0.09657	Protein kinase-like protein	root cap	12 h
HORVU.MOREX.r3.4HG0338810.1	-0.5886	4.132368	-3.77256	0.000409	0.032027	-0.10314	Inositol-tetrakisphosphate 1-kinase	root cap	12 h
HORVU.MOREX.r3.6HG0600190.1	-0.67023	3.392812	-3.74631	0.000444	0.033181	-0.10353	UPF0565 protein C2orf69	root cap	12 h
HORVU.MOREX.r3.4HG0393500.1	-0.83014	0.752818	-3.75422	0.000433	0.032842	-0.1104	#N/A	root cap	12 h
HORVU.MOREX.r3.1HG0019240.1	-0.9857	2.336885	-3.78663	0.000391	0.031354	-0.11077	N-acetyltransferase, putative	root cap	12 h
HORVU.MOREX.r3.2HG0128270.1	-0.77611	2.338352	-3.74365	0.000448	0.033181	-0.11265	Zinc finger family protein	root cap	12 h
HORVU.MOREX.r3.2HG0131330.1	-0.65025	7.99791	-3.83978	0.00033	0.029613	-0.12271	Transporter-related family protein	root cap	12 h
HORVU.MOREX.r3.6HG0591720.1	-0.48572	5.117239	-3.75186	0.000436	0.032929	-0.13432	Glucose-6-phosphate 1-dehydrogenase	root cap	12 h
HORVU.MOREX.r3.4HG0405830.1	-0.73613	2.230818	-3.729	0.000469	0.033952	-0.1371	cold regulated protein 27	root cap	12 h
HORVU.MOREX.r3.7HG0635410.1	-1.13571	0.730461	-3.79496	0.000381	0.031023	-0.15461	Protein yippee-like	root cap	12 h
HORVU.MOREX.r3.4HG0389580.1	-0.43409	5.135089	-3.74423	0.000447	0.033181	-0.15657	Mitochondrial carrier family	root cap	12 h
HORVU.MOREX.r3.3HG0242790.1	-0.49919	5.85397	-3.76035	0.000425	0.032842	-0.1629	Cell number regulator 8	root cap	12 h
HORVU.MOREX.r3.1HG0077710.1	-0.75035	-0.77894	-3.72225	0.000479	0.03425	-0.17275	Glycosyltransferase	root cap	12 h
HORVU.MOREX.r3.6HG0603150.1	-0.7566	4.113219	-3.75817	0.000428	0.032842	-0.18072	Argonaute	root cap	12 h
HORVU.MOREX.r3.3HG0295840.1	-0.58434	2.964243	-3.70959	0.000498	0.034906	-0.18264	Dehydrogenase-like protein	root cap	12 h
HORVU.MOREX.r3.1HG0077230.1	-0.7893	3.396902	-3.73992	0.000453	0.033451	-0.18389	VQ motif-containing protein	root cap	12 h
HORVU.MOREX.r3.5HG0516730.1	-0.80689	2.88293	-3.714	0.000492	0.034545	-0.18469	Peroxisomal membrane protein 13	root cap	12 h
HORVU.MOREX.r3.2HG0125510.1	-1.40719	0.997629	-3.71554	0.000489	0.034498	-0.18493	SPX domain-containing protein	root cap	12 h
HORVU.MOREX.r3.5HG0455240.1	-0.78574	2.696541	-3.74491	0.000446	0.033181	-0.18736	O-fucosyltransferase family protein	root cap	12 h
HORVU.MOREX.r3.4HG0390580.1	-0.73483	2.573232	-3.71765	0.000486	0.034388	-0.18741	#N/A	root cap	12 h
HORVU.MOREX.r3.7HG0725210.3	-0.69578	5.13305	-3.72919	0.000469	0.033952	-0.19062	Lysophosphatidylcholine acyltransferase 1	root cap	12 h
HORVU.MOREX.r3.1HG0081120.1	-1.44593	1.005477	-3.78193	0.000397	0.031576	-0.19634	DNA mismatch repair protein MutL	root cap	12 h
HORVU.MOREX.r3.4HG0392440.1	-0.6496	4.50652	-3.73128	0.000466	0.033952	-0.20368	Chaperone protein dnaJ	root cap	12 h
HORVU.MOREX.r3.2HG0174560.1	-0.50891	4.366463	-3.70462	0.000506	0.03504	-0.20716	Ras-related protein	root cap	12 h
HORVU.MOREX.r3.5HG0504340.1	-0.67217	3.865477	-3.69679	0.000519	0.035084	-0.21329	Mediator of RNA polymerase II transcription subunit 8	root cap	12 h
HORVU.MOREX.r3.3HG0295550.1	-0.51865	4.950607	-3.72839	0.00047	0.033952	-0.21562	Stomatal closure-related actin-binding protein 1	root cap	12 h
HORVU.MOREX.r3.1HG0062030.1	-1.45568	-2.69359	-3.96694	0.00022	0.0236	-0.22281	Dehydration responsive element binding transcription factor	root cap	12 h
HORVU.MOREX.r3.3HG0303670.1	-0.86762	1.411379	-3.69402	0.000523	0.035084	-0.22366	RNAse E/G-like protein	root cap	12 h
HORVU.MOREX.r3.5HG0445510.1	-0.47986	5.10535	-3.70146	0.000511	0.03504	-0.22612	Acyl-CoA-binding domain-containing protein 4	root cap	12 h
HORVU.MOREX.r3.5HG0520850.1	-0.54163	4.065206	-3.69593	0.00052	0.035084	-0.2347	Kinase, putative	root cap	12 h
HORVU.MOREX.r3.7HG0660830.1	-0.39304	5.341821	-3.72567	0.000474	0.034004	-0.24077	Ubiquitin-conjugating enzyme, E2	root cap	12 h
HORVU.MOREX.r3.5HG0464600.1	-0.6616	3.460343	-3.69436	0.000523	0.035084	-0.24739	Dual specificity protein phosphatase, putative	root cap	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.5HG0488620.1	-0.58424	3.531829	-3.73403	0.000462	0.033952	-0.25245	O-fucosyltransferase family protein	root cap	12 h
HORVU.MOREX.r3.2HG0181020.1	-0.60082	7.283571	-3.81338	0.000359	0.030802	-0.25633	#N/A	root cap	12 h
HORVU.MOREX.r3.2HG0168640.1	-0.49525	4.660135	-3.7204	0.000482	0.03433	-0.26514	F-box family protein	root cap	12 h
HORVU.MOREX.r3.5HG0497170.1	-0.56094	5.352547	-3.73035	0.000467	0.033952	-0.2746	Pimeloyl-[acyl-carrier protein] methyl ester esterase	root cap	12 h
HORVU.MOREX.r3.5HG0507370.1	-0.57749	4.402293	-3.68359	0.000541	0.035458	-0.27968	Protein kinase	root cap	12 h
HORVU.MOREX.r3.7HG0714350.1	-0.92413	3.30207	-3.67003	0.000564	0.036145	-0.28594	Acyl-[acyl-carrier-protein] hydrolase	root cap	12 h
HORVU.MOREX.r3.7HG0739570.1	2.162518	1.204008	4.026302	0.000181	0.022855	-0.30853	cotton fiber protein	root cap	12 h
HORVU.MOREX.r3.2HG0192920.1	-0.81411	0.782762	-3.68994	0.00053	0.035204	-0.31126	Xyloglucan endotransglucosylase/hydrolase	root cap	12 h
HORVU.MOREX.r3.5HG0463370.1	-1.10991	2.525221	-3.6797	0.000547	0.035604	-0.3205	Zinc finger family protein	root cap	12 h
HORVU.MOREX.r3.6HG0570850.1	-0.60087	5.628875	-3.70163	0.000511	0.03504	-0.32198	Protein kinase	root cap	12 h
HORVU.MOREX.r3.4HG0356780.1	-0.5458	4.400609	-3.66625	0.000571	0.036251	-0.32206	weak chloroplast movement under blue light protein (DUF827)	root cap	12 h
HORVU.MOREX.r3.4HG0353950.1	-1.63282	-1.81142	-3.80394	0.00037	0.030889	-0.3261	ubiquitin carboxyl-terminal hydrolase	root cap	12 h
HORVU.MOREX.r3.5HG0479000.1	-1.54475	3.962906	-3.66329	0.000576	0.036361	-0.32768	Alcohol dehydrogenase, putative	root cap	12 h
HORVU.MOREX.r3.5HG0471940.1	-0.36131	6.025728	-3.70816	0.000501	0.034928	-0.33146	Myb family transcription factor APL	root cap	12 h
HORVU.MOREX.r3.6HG0592790.1	-0.37766	4.902986	-3.69932	0.000515	0.03504	-0.33694	Nicotinamidase 1	root cap	12 h
HORVU.MOREX.r3.5HG0458770.1	0.716016	5.47733	3.671716	0.000561	0.036145	-0.34979	B3 domain-containing protein	root cap	12 h
HORVU.MOREX.r3.3HG0256430.1	-0.65593	4.497782	-3.69869	0.000516	0.03504	-0.35008	Hyp O-arabinosyltransferase-like protein	root cap	12 h
HORVU.MOREX.r3.4HG0406980.1	-0.91545	2.545348	-3.67033	0.000563	0.036145	-0.35059	Ras-related protein	root cap	12 h
HORVU.MOREX.r3.7HG0713160.1	-0.61179	6.232926	-3.69874	0.000516	0.03504	-0.35862	Acyl-coenzyme A oxidase	root cap	12 h
HORVU.MOREX.r3.3HG0275500.1	-1.65646	-1.87206	-3.75387	0.000434	0.032842	-0.36045	Flavin-containing monooxygenase	root cap	12 h
HORVU.MOREX.r3.3HG0288830.1	-0.33014	5.399232	-3.68242	0.000543	0.035458	-0.36367	MACPF domain protein	root cap	12 h
HORVU.MOREX.r3.5HG0496740.1	-1.66291	0.004024	-3.64074	0.000618	0.037835	-0.36974	Agmatine coumaroyltransferase-2	root cap	12 h
HORVU.MOREX.r3.5HG0471560.1	-0.59593	3.339465	-3.68612	0.000536	0.035389	-0.3867	Receptor kinase	root cap	12 h
HORVU.MOREX.r3.5HG0527770.1	-0.79643	1.038275	-3.72569	0.000474	0.034004	-0.39064	GDP-mannose transporter	root cap	12 h
HORVU.MOREX.r3.6HG0596240.1	-1.08231	0.960124	-3.69304	0.000525	0.035084	-0.39262	RNA-binding protein	root cap	12 h
HORVU.MOREX.r3.1HG0083840.1	-0.49752	3.99732	-3.63475	0.000629	0.037866	-0.39632	Serine-rich adhesin for platelets-like protein	root cap	12 h
HORVU.MOREX.r3.7HG0723770.1	-0.56504	6.493213	-3.68898	0.000532	0.035204	-0.39828	BZIP transcription factor protein	root cap	12 h
HORVU.MOREX.r3.3HG0281780.1	-0.66413	4.822877	-3.66202	0.000578	0.036393	-0.40001	Protein transport protein Sec61 subunit alpha	root cap	12 h
HORVU.MOREX.r3.2HG0172180.1	-0.79022	4.401326	-3.64374	0.000612	0.037598	-0.41143	Ring finger protein, putative	root cap	12 h
HORVU.MOREX.r3.4HG0395120.1	-0.65026	2.404038	-3.62219	0.000654	0.038466	-0.42205	Mitochondrial carrier family	root cap	12 h
HORVU.MOREX.r3.2HG0127370.1	-0.60917	7.932229	-3.81482	0.000358	0.030802	-0.42492	Alpha-1,4-glucan-protein synthase [UDP-forming] 1	root cap	12 h
HORVU.MOREX.r3.3HG0257120.1	-0.7598	1.984822	-3.62405	0.00065	0.038466	-0.42492	Histone-lysine N-methyltransferase	root cap	12 h
HORVU.MOREX.r3.4HG0343380.1	-0.43066	5.245167	-3.67433	0.000556	0.036019	-0.43512	ATP-dependent (S)-NAD(P)H-hydrate dehydratase	root cap	12 h
HORVU.MOREX.r3.1HG0071320.1	-1.03784	0.645871	-3.61032	0.000679	0.039422	-0.44663	Transcription elongation factor SPT5	root cap	12 h
HORVU.MOREX.r3.7HG0748320.1	-0.75144	3.37477	-3.60771	0.000684	0.039547	-0.4568	Receptor-like kinase	root cap	12 h
HORVU.MOREX.r3.2HG0184620.1	-0.78739	4.117573	-3.63498	0.000629	0.037866	-0.45774	Hsp70-Hsp90 organizing protein 1	root cap	12 h
HORVU.MOREX.r3.4HG0347330.1	-0.55857	6.923566	-3.70722	0.000502	0.034928	-0.46016	Aldehyde dehydrogenase	root cap	12 h
HORVU.MOREX.r3.2HG0180040.2	-1.10367	-2.17606	-3.68259	0.000542	0.035458	-0.46236	Trichome birefringence	root cap	12 h
HORVU.MOREX.r3.3HG0300080.1	-0.7491	5.888104	-3.66448	0.000574	0.036339	-0.46321	Kinase	root cap	12 h
HORVU.MOREX.r3.2HG0113410.1	-0.52509	4.641504	-3.6395	0.00062	0.037866	-0.46556	Protein AIG1	root cap	12 h
HORVU.MOREX.r3.2HG0113860.1	-1.20673	2.66732	-3.61625	0.000666	0.039067	-0.47095	Uveal autoantigen with coiled-coil domains and ankyrin repeats isoform 2	root cap	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.4HG0365970.1	-0.49877	5.950027	-3.65757	0.000586	0.036788	-0.47612	Phosphatidate phosphatase, Lipin	root cap	12 h
HORVU.MOREX.r3.4HG0417410.1	-1.34956	0.915973	-3.71816	0.000485	0.034388	-0.48195	Cold regulated protein 27	root cap	12 h
HORVU.MOREX.r3.7HG0677380.1	-0.55003	5.818397	-3.70162	0.000511	0.03504	-0.48413	Alpha-glucan water dikinase	root cap	12 h
HORVU.MOREX.r3.6HG0541580.1	0.269867	8.008196	3.688832	0.000532	0.035204	-0.49675	Aspartate aminotransferase	root cap	12 h
HORVU.MOREX.r3.7HG0733020.1	-0.53077	5.546828	-3.64445	0.000611	0.037598	-0.52062	Polyubiquitin	root cap	12 h
HORVU.MOREX.r3.2HG0135590.1	-0.63404	2.26601	-3.57977	0.000746	0.041215	-0.53028	Protein THYLAKOID FORMATION1, chloroplastic	root cap	12 h
HORVU.MOREX.r3.5HG0506790.1	-0.68378	5.002887	-3.6228	0.000653	0.038466	-0.53728	Calcineurin-like metallo-phosphoesterase superfamily	root cap	12 h
HORVU.MOREX.r3.1HG0051740.1	-0.98734	3.433417	-3.63114	0.000636	0.037993	-0.54521	Glutathione s-transferase, putative	root cap	12 h
HORVU.MOREX.r3.2HG0187980.1	-0.58131	2.469272	-3.57638	0.000754	0.041215	-0.54754	Transmembrane protein 184C	root cap	12 h
HORVU.MOREX.r3.4HG0407120.1	-0.57437	4.965682	-3.58914	0.000724	0.040619	-0.55774	methyl-coenzyme M reductase II subunit gamma, putative (DUF3741)	root cap	12 h
HORVU.MOREX.r3.1HG0092900.1	-1.54857	-2.96229	-3.99598	0.0002	0.023321	-0.55851	C3HC4-type RING finger-containing protein	root cap	12 h
HORVU.MOREX.r3.7HG0721080.1	-0.73373	4.617684	-3.60194	0.000696	0.039695	-0.56145	Zinc finger, B-box	root cap	12 h
HORVU.MOREX.r3.2HG0194600.1	-0.76373	1.177222	-3.56657	0.000777	0.041944	-0.56419	transmembrane protein, putative (DUF594)	root cap	12 h
HORVU.MOREX.r3.1HG0080420.1	-0.65181	3.160969	-3.60561	0.000689	0.039589	-0.56764	cotton fiber-like protein (DUF761)	root cap	12 h
HORVU.MOREX.r3.5HG0455770.1	-0.81391	0.761558	-3.64568	0.000608	0.037597	-0.57433	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	root cap	12 h
HORVU.MOREX.r3.4HG0391050.1	-0.67069	2.336797	-3.55928	0.000794	0.042658	-0.58446	Protein FAR1-RELATED SEQUENCE 7	root cap	12 h
HORVU.MOREX.r3.2HG0119920.1	-0.67111	6.226589	-3.62221	0.000654	0.038466	-0.58496	protein kinase family protein	root cap	12 h
HORVU.MOREX.r3.2HG0187170.1	-0.44887	6.368636	-3.63807	0.000623	0.037866	-0.59093	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	root cap	12 h
HORVU.MOREX.r3.2HG0163200.1	-0.52	5.22535	-3.60502	0.00069	0.039589	-0.59777	Yellow stripe-like transporter 12	root cap	12 h
HORVU.MOREX.r3.7HG0723280.1	-1.88397	-2.61155	-3.90003	0.000273	0.026515	-0.60034	PLATZ transcription factor family protein	root cap	12 h
HORVU.MOREX.r3.4HG0381750.1	-0.60952	5.381044	-3.63085	0.000637	0.037993	-0.60124	Calmodulin	root cap	12 h
HORVU.MOREX.r3.6HG0555250.1	-0.6987	0.376943	-3.55405	0.000807	0.042918	-0.60235	Esterase/lipase/thioesterase-like protein	root cap	12 h
HORVU.MOREX.r3.7HG0721660.1	-0.70582	4.153249	-3.61313	0.000673	0.039221	-0.60262	Serine/threonine-protein kinase mTOR	root cap	12 h
HORVU.MOREX.r3.5HG0440700.1	-0.44424	5.639406	-3.59786	0.000705	0.039869	-0.60436	Diacylglycerol kinase	root cap	12 h
HORVU.MOREX.r3.5HG0512430.1	-0.81029	3.653637	-3.57565	0.000755	0.041215	-0.60756	Phosphatase 2C family protein	root cap	12 h
HORVU.MOREX.r3.7HG0709580.1	-1.15886	-0.69882	-3.5547	0.000805	0.042918	-0.60793	ADP-ribosylation factor family protein	root cap	12 h
HORVU.MOREX.r3.7HG0676620.1	-1.44465	-0.20992	-3.65387	0.000593	0.0371	-0.61199	Mitogen activated protein kinase kinase kinase-like protein	root cap	12 h
HORVU.MOREX.r3.3HG0256160.1	-0.5031	4.949529	-3.61459	0.00067	0.039157	-0.61408	Cysteine proteinase inhibitor	root cap	12 h
HORVU.MOREX.r3.1HG0031820.1	-0.94472	1.763108	-3.54613	0.000827	0.04339	-0.61722	Calmodulin	root cap	12 h
HORVU.MOREX.r3.7HG0725140.1	0.628602	6.172211	3.561705	0.000788	0.042454	-0.63299	Lipid transfer protein	root cap	12 h
HORVU.MOREX.r3.3HG0235720.1	-1.47724	3.057636	-3.55366	0.000808	0.042918	-0.63522	FMN-dependent NADPH-azoreductase	root cap	12 h
HORVU.MOREX.r3.7HG0656220.1	-0.58305	4.216456	-3.60107	0.000698	0.039695	-0.63526	Protein DETOXIFICATION	root cap	12 h
HORVU.MOREX.r3.5HG0461790.1	-1.02717	-2.4609	-3.6297	0.000639	0.038018	-0.65122	Ring finger protein, putative	root cap	12 h
HORVU.MOREX.r3.7HG0635330.1	-1.73805	0.867741	-3.58994	0.000723	0.040619	-0.65181	Protein TolB	root cap	12 h
HORVU.MOREX.r3.2HG0168300.1	-1.16049	0.915123	-3.63276	0.000633	0.03799	-0.65266	Helicase/SANT-associated, putative isoform 5	root cap	12 h
HORVU.MOREX.r3.7HG0705130.1	1.008475	2.637633	3.536961	0.00085	0.043951	-0.65333	3'-N-debenzoyl-2'-deoxytaxol N-benzoyltransferase	root cap	12 h
HORVU.MOREX.r3.1HG0064310.1	-0.66177	4.083368	-3.55421	0.000807	0.042918	-0.65446	Ribosomal protein L34e superfamily protein	root cap	12 h
HORVU.MOREX.r3.2HG0169000.1	-1.43216	2.146274	-3.59491	0.000712	0.040123	-0.65812	arginine N-methyltransferase, putative (DUF688)	root cap	12 h
HORVU.MOREX.r3.5HG0481120.1	-0.98231	-1.50366	-3.53107	0.000866	0.043974	-0.66068	RING/U-box superfamily protein	root cap	12 h
HORVU.MOREX.r3.5HG0457960.1	-0.33819	5.424342	-3.57638	0.000754	0.041215	-0.66136	Tubby-like F-box protein	root cap	12 h
HORVU.MOREX.r3.4HG0400830.1	-2.27409	0.255399	-4.04009	0.000173	0.022679	-0.66164	ATP-dependent DNA helicase	root cap	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.UnG0753160.1	-0.61148	7.774397	-3.65234	0.000596	0.037163	-0.66494	Sucrose-phosphate synthase	root cap	12 h
HORVU.MOREX.r3.5HG0460300.1	-0.85938	4.047693	-3.52554	0.000881	0.044002	-0.67467	Rho GTPase-activating protein	root cap	12 h
HORVU.MOREX.r3.2HG0110640.1	-0.31371	5.40065	-3.57589	0.000755	0.041215	-0.68016	transcription factor-like protein	root cap	12 h
HORVU.MOREX.r3.7HG0719840.1	-0.68762	1.628095	-3.52688	0.000877	0.044002	-0.68261	DUF4050 family protein	root cap	12 h
HORVU.MOREX.r3.4HG0405330.1	1.16705	-1.47892	3.532493	0.000862	0.043974	-0.68428	Cytochrome P450, putative	root cap	12 h
HORVU.MOREX.r3.7HG0750850.1	3.805186	-0.5604	3.679068	0.000548	0.035604	-0.68574	Cellulose synthase-like protein	root cap	12 h
HORVU.MOREX.r3.5HG0496780.1	-0.51626	4.42219	-3.54809	0.000822	0.043324	-0.6911	C2 domain-containing protein / GRAM domain-containing protein	root cap	12 h
HORVU.MOREX.r3.7HG0682660.1	-1.93266	1.152818	-3.94214	0.000238	0.024313	-0.69152	Basic helix-loop-helix transcription factor	root cap	12 h
HORVU.MOREX.r3.2HG0164440.1	-0.62514	4.939875	-3.59874	0.000703	0.039869	-0.69202	glycosyltransferase family exostosin protein	root cap	12 h
HORVU.MOREX.r3.6HG0634140.1	-0.82326	2.257992	-3.51938	0.000897	0.044578	-0.6938	Disease resistance protein (NBS-LRR class) family	root cap	12 h
HORVU.MOREX.r3.7HG0677710.1	-1.33103	1.564676	-3.53791	0.000848	0.043951	-0.69393	BTB/POZ domain-containing protein	root cap	12 h
HORVU.MOREX.r3.1HG0056540.1	-0.97443	2.503604	-3.51859	0.000899	0.044578	-0.6947	Zinc finger family protein	root cap	12 h
HORVU.MOREX.r3.2HG0169420.1	-0.84193	4.736887	-3.57953	0.000746	0.041215	-0.71092	Regulator of chromosome condensation (RCC1) family protein	root cap	12 h
HORVU.MOREX.r3.1HG0003270.1	1.634235	-2.89111	3.870916	0.000299	0.027661	-0.71502	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	root cap	12 h
HORVU.MOREX.r3.2HG0162620.1	-1.58942	-1.43824	-3.66818	0.000567	0.036145	-0.71743	Auxin response factor	root cap	12 h
HORVU.MOREX.r3.1HG0089180.1	-0.60941	5.019103	-3.60369	0.000693	0.039595	-0.71796	Cold acclimation protein	root cap	12 h
HORVU.MOREX.r3.3HG0295500.2	-1.10063	1.304608	-3.54747	0.000823	0.043324	-0.72064	UDP-glycosyltransferase	root cap	12 h
HORVU.MOREX.r3.3HG0252100.1	-0.77278	1.973895	-3.64859	0.000603	0.037371	-0.72096	Stigma-specific Stig1 family protein, putative	root cap	12 h
HORVU.MOREX.r3.3HG0305840.1	-0.79566	0.764684	-3.50679	0.000932	0.045382	-0.72488	Calcium sensing receptor, chloroplastic	root cap	12 h
HORVU.MOREX.r3.4HG0394470.1	-1.1303	2.141349	-3.54143	0.000839	0.043796	-0.72507	Myb/SANT-like DNA-binding domain protein	root cap	12 h
HORVU.MOREX.r3.1HG0082670.1	-0.74133	1.71129	-3.51438	0.000911	0.044937	-0.7404	26S protease regulatory subunit 7	root cap	12 h
HORVU.MOREX.r3.3HG0320710.1	-0.57633	3.737114	-3.52803	0.000874	0.044002	-0.74378	SNF2 domain-containing protein / helicase domain-containing protein / F-box fam	root cap	12 h
HORVU.MOREX.r3.7HG0644160.1	-0.92814	-1.60125	-3.49636	0.000962	0.045846	-0.74775	GDSL esterase/lipase	root cap	12 h
HORVU.MOREX.r3.3HG0300580.1	-1.05615	5.442061	-3.50489	0.000938	0.045382	-0.74775	Glucan endo-1,3-beta-glucosidase, putative	root cap	12 h
HORVU.MOREX.r3.2HG0184350.1	-0.58181	3.027133	-3.49691	0.000961	0.045846	-0.74826	Cytochrome P450	root cap	12 h
HORVU.MOREX.r3.1HG0095220.1	-0.78131	2.300388	-3.53186	0.000864	0.043974	-0.74959	Pleckstrin-like (PH) domain protein	root cap	12 h
HORVU.MOREX.r3.3HG0231430.1	-0.37803	4.799815	-3.5253	0.000881	0.044002	-0.7522	#N/A	root cap	12 h
HORVU.MOREX.r3.5HG0517370.1	-2.33221	-3.29058	-4.10125	0.000142	0.020673	-0.76483	Zinc finger A20 and AN1 domain-containing stress-associated protein	root cap	12 h
HORVU.MOREX.r3.3HG0303190.1	-0.40578	8.19693	-3.60965	0.00068	0.039422	-0.76893	UDP-glucuronate decarboxylase protein 1	root cap	12 h
HORVU.MOREX.r3.6HG0560030.1	-0.5275	3.970473	-3.511	0.00092	0.045293	-0.76916	DUF1644 family protein	root cap	12 h
HORVU.MOREX.r3.7HG0700200.1	-0.45464	4.298926	-3.52818	0.000873	0.044002	-0.77372	Oxysterol-binding family protein	root cap	12 h
HORVU.MOREX.r3.5HG0494470.1	-0.46446	3.993787	-3.49723	0.00096	0.045846	-0.78799	Transmembrane emp24 domain-containing protein	root cap	12 h
HORVU.MOREX.r3.7HG0678310.1	-0.6653	3.452075	-3.55306	0.000809	0.042918	-0.79021	Protein DETOXIFICATION	root cap	12 h
HORVU.MOREX.r3.7HG0708910.1	-0.58414	-0.96712	-3.51695	0.000904	0.044693	-0.79655	NAC domain-containing protein, putative	root cap	12 h
HORVU.MOREX.r3.1HG0014560.1	-0.8326	3.027709	-3.49471	0.000967	0.045942	-0.79656	Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A	root cap	12 h
HORVU.MOREX.r3.6HG0550260.1	0.403208	5.617383	3.536	0.000853	0.04397	-0.79944	aminoalcoholphosphotransferase 1	root cap	12 h
HORVU.MOREX.r3.7HG0733550.1	1.58838	-0.67914	3.473047	0.001033	0.04717	-0.81074	Early nodulin-like protein	root cap	12 h
HORVU.MOREX.r3.2HG0141980.1	0.674343	5.307117	3.480704	0.001009	0.04706	-0.81299	Glucan endo-1,3-beta-glucosidase 3	root cap	12 h
HORVU.MOREX.r3.3HG0296420.1	-0.46375	7.295023	-3.57267	0.000762	0.041484	-0.8142	91A protein	root cap	12 h
HORVU.MOREX.r3.6HG0597880.1	-0.57049	4.866427	-3.52524	0.000881	0.044002	-0.81546	heat-inducible transcription repressor (DUF639)	root cap	12 h
HORVU.MOREX.r3.2HG0192180.1	0.227019	9.138579	3.636095	0.000627	0.037866	-0.8169	26S proteasome non-ATPase regulatory subunit 1	root cap	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.7HG0671350.1	-0.41595	4.825604	-3.50651	0.000933	0.045382	-0.81861	Potassium transporter	root cap	12 h
HORVU.MOREX.r3.6HG0617830.1	-0.90232	4.975661	-3.47789	0.001018	0.047149	-0.822	Cyclin-dependent kinase inhibitor	root cap	12 h
HORVU.MOREX.r3.7HG0648610.1	-0.29774	6.015867	-3.53799	0.000848	0.043951	-0.8275	Carboxypeptidase	root cap	12 h
HORVU.MOREX.r3.1HG0057610.1	-0.52206	4.023099	-3.50542	0.000936	0.045382	-0.8296	Peptide methionine sulfoxide reductase MsrA	root cap	12 h
HORVU.MOREX.r3.5HG0482710.1	0.623329	3.151378	3.482151	0.001005	0.046967	-0.82962	Hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyltransferase	root cap	12 h
HORVU.MOREX.r3.2HG0192860.1	-0.56244	6.583932	-3.5665	0.000777	0.041944	-0.85057	WRKY transcription factor	root cap	12 h
HORVU.MOREX.r3.2HG0124110.1	-0.73123	2.313092	-3.45546	0.001089	0.048807	-0.85464	GRAM domain protein/ABA-responsive-like protein	root cap	12 h
HORVU.MOREX.r3.3HG0309210.1	0.456235	5.46384	3.505194	0.000937	0.045382	-0.86181	Obg-like ATPase 1	root cap	12 h
HORVU.MOREX.r3.5HG0510240.1	4.866374	-2.27899	4.274457	8.01E-05	0.015225	-0.86404	Dirigent protein	root cap	12 h
HORVU.MOREX.r3.2HG0121380.1	-0.63645	6.42294	-3.53247	0.000862	0.043974	-0.86686	Cytochrome P450	root cap	12 h
HORVU.MOREX.r3.1HG0056810.1	0.578921	5.129894	3.480002	0.001011	0.04706	-0.86717	Haloacid dehalogenase-like hydrolase family protein, putative, expressed	root cap	12 h
HORVU.MOREX.r3.5HG0483810.1	-0.44894	4.62245	-3.479	0.001014	0.047096	-0.86849	Ubiquitin, putative	root cap	12 h
HORVU.MOREX.r3.7HG0740120.1	-0.86096	5.368158	-3.52063	0.000894	0.044517	-0.87049	Nodulin-like / Major Facilitator Superfamily protein	root cap	12 h
HORVU.MOREX.r3.3HG0306820.1	-0.59408	4.854402	-3.47278	0.001034	0.04717	-0.87212	ATP-dependent Clp protease ATP-binding subunit ClpX	root cap	12 h
HORVU.MOREX.r3.7HG0648140.1	-0.58291	6.798944	-3.54237	0.000836	0.043781	-0.87367	Homeobox leucine zipper protein	root cap	12 h
HORVU.MOREX.r3.6HG0622540.1	-0.58235	7.01829	-3.53697	0.00085	0.043951	-0.8768	Equilibrative nucleoside transporter	root cap	12 h
HORVU.MOREX.r3.5HG0436990.1	-0.63733	6.379696	-3.50664	0.000933	0.045382	-0.90139	SPX and EXS domain-containing protein 1	root cap	12 h
HORVU.MOREX.r3.2HG0109400.1	-1.26891	0.929608	-3.50359	0.000941	0.045454	-0.91098	D-alanine--D-alanine ligase	root cap	12 h
HORVU.MOREX.r3.7HG0728500.1	-0.92678	0.37984	-3.49259	0.000973	0.046043	-0.917	Protein phosphatase 2C	root cap	12 h
HORVU.MOREX.r3.2HG0100270.2	-0.59124	6.297507	-3.53236	0.000862	0.043974	-0.94183	Subtilisin-like protease	root cap	12 h
HORVU.MOREX.r3.5HG0517330.1	-0.50713	7.95292	-3.60464	0.000691	0.039589	-0.95431	Aldehyde oxidase, putative	root cap	12 h
HORVU.MOREX.r3.7HG0720980.1	-0.74282	1.598477	-3.45992	0.001075	0.048472	-0.96245	Glucan endo-1,3-beta-glucosidase 3	root cap	12 h
HORVU.MOREX.r3.5HG0439620.1	-0.48943	6.606388	-3.49247	0.000974	0.046043	-0.96398	Amino acid transporter, putative	root cap	12 h
HORVU.MOREX.r3.2HG0165780.1	-0.43394	6.457413	-3.50523	0.000937	0.045382	-0.9692	1,4-alpha-glucan-branching enzyme	root cap	12 h
HORVU.MOREX.r3.3HG0221140.1	-0.75898	2.320691	-3.48393	0.000999	0.046928	-0.97027	Glutathione S-transferase, putative, expressed	root cap	12 h
HORVU.MOREX.r3.6HG0631080.1	-0.49979	5.818779	-3.47025	0.001042	0.047291	-0.97246	Hydroxyproline-rich glycoprotein-like	root cap	12 h
HORVU.MOREX.r3.5HG0467230.2	-0.44861	5.749624	-3.47578	0.001024	0.04717	-0.98802	Alpha/beta-Hydrolases superfamily protein	root cap	12 h
HORVU.MOREX.r3.2HG0188070.1	-0.8323	0.589714	-3.50039	0.000951	0.045685	-0.98881	L-ascorbate oxidase-like protein	root cap	12 h
HORVU.MOREX.r3.1HG0068060.1	-0.35504	8.078852	-3.53276	0.000861	0.043974	-0.99456	DCD (Development and cell death) domain protein	root cap	12 h
HORVU.MOREX.r3.1HG0055320.1	-0.32104	5.996621	-3.45912	0.001077	0.048482	-0.99913	Protein phosphatase 2C	root cap	12 h
HORVU.MOREX.r3.5HG0456950.1	-0.42893	5.604947	-3.45707	0.001084	0.048677	-1.01074	Proteasome subunit alpha type	root cap	12 h
HORVU.MOREX.r3.3HG0273560.1	-1.30076	0.616289	-3.47359	0.001031	0.04717	-1.0412	2-oxoisovalerate dehydrogenase subunit beta	root cap	12 h
HORVU.MOREX.r3.2HG0133930.1	-2.10388	-2.62089	-3.79087	0.000386	0.031126	-1.04466	Cytochrome c6	root cap	12 h
HORVU.MOREX.r3.7HG0689920.1	1.352767	2.721231	3.496164	0.000963	0.045846	-1.05458	Carboxypeptidase	root cap	12 h
HORVU.MOREX.r3.3HG0232840.1	-0.46789	7.520309	-3.4733	0.001032	0.04717	-1.07205	Fatty acid oxidation complex subunit alpha	root cap	12 h
HORVU.MOREX.r3.6HG0615840.1	-1.86416	-2.2741	-3.66886	0.000566	0.036145	-1.10884	Metalloendoproteinase 1	root cap	12 h
HORVU.MOREX.r3.4HG0408300.1	-0.27223	7.884162	-3.47445	0.001029	0.04717	-1.12185	HR-like lesion-inducing protein-related protein	root cap	12 h
HORVU.MOREX.r3.4HG0406720.1	-1.74746	-1.7339	-3.46505	0.001058	0.04783	-1.12225	nuclear polyadenylated RNA-binding protein	root cap	12 h
HORVU.MOREX.r3.5HG0510700.1	-0.47072	7.762858	-3.50213	0.000946	0.04555	-1.12256	Beta-glucosidase	root cap	12 h
HORVU.MOREX.r3.4HG0340420.1	-0.48239	5.772276	-3.47194	0.001036	0.04717	-1.13182	GEM-like protein 1	root cap	12 h
HORVU.MOREX.r3.5HG0500130.1	-2.25541	-2.11769	-3.48947	0.000983	0.046251	-1.13427	Pathogenesis-related thaumatin-like protein	root cap	12 h

Table Sн Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0323410.1	-1.04908	-2.74988	-3.4826	0.001003	0.046967	-1.13714	TSA: Wollemia nobilis Ref_Wollemi_Transcript_14908_3298 transcribed RNA sequ	root cap	12 h
HORVU.MOREX.r3.3HG0315300.1	-0.86865	2.211349	-3.52527	0.000881	0.044002	-1.22958	Late embryogenesis abundant protein	root cap	12 h
HORVU.MOREX.r3.5HG0429390.1	3.178481	-0.95655	3.585647	0.000732	0.040947	-1.23874	Germin-like protein	root cap	12 h
HORVU.MOREX.r3.1HG0017350.1	-0.74546	4.123138	-3.4512	0.001103	0.049332	-1.27071	Peroxidase	root cap	12 h
HORVU.MOREX.r3.5HG0495750.1	-1.91447	-2.86879	-3.63564	0.000628	0.037866	-1.30772	B3 domain-containing protein	root cap	12 h
HORVU.MOREX.r3.2HG0207160.1	-0.72434	2.792582	-3.47183	0.001037	0.04717	-1.32139	Micronuclear linker histone polyprotein-like protein	root cap	12 h
HORVU.MOREX.r3.1HG0024440.1	1.761637	2.671204	3.566872	0.000776	0.041944	-1.36494	EGG APPARATUS-1 protein	root cap	12 h
HORVU.MOREX.r3.2HG0120640.1	-1.53762	0.112362	-3.57793	0.00075	0.041215	-1.39242	Protein root UVB sensitive 3	root cap	12 h
HORVU.MOREX.r3.1HG0072560.1	1.884607	-2.88695	3.490882	0.000979	0.046159	-1.40075	Chaperone protein dnaJ	root cap	12 h
HORVU.MOREX.r3.6HG0604200.1	2.948316	0.762306	3.965535	0.000221	0.0236	-1.45947	transcription repressor	root cap	12 h
HORVU.MOREX.r3.2HG0104400.1	2.849909	-1.01887	3.577137	0.000752	0.041215	-1.48818	Dirigent protein	root cap	12 h
HORVU.MOREX.r3.6HG0627900.1	2.447031	-3.19226	3.650641	0.000599	0.037246	-1.49886	Receptor-like protein kinase	root cap	12 h
HORVU.MOREX.r3.7HG0719310.1	-2.315	-2.19972	-3.4486	0.001112	0.049612	-1.59467	Cytoplasmic tRNA 2-thiolation protein 1	root cap	12 h
HORVU.MOREX.r3.4HG0399460.1	-2.11094	-1.4594	-3.46788	0.001049	0.047527	-1.6223	transcription repressor	root cap	12 h
HORVU.MOREX.r3.2HG0116730.1	3.253115	3.133763	3.54846	0.000821	0.043324	-1.66235	ABC transporter, putative	root cap	12 h
HORVU.MOREX.r3.4HG0402390.1	5.226258	-1.02408	3.576267	0.000754	0.041215	-1.80179	3-ketoacyl-CoA synthase	root cap	12 h
HORVU.MOREX.r3.3HG0328340.1	-1.45036	4.602643	-6.7403	1.18E-08	0.000242	9.530264	Two-component response regulator	meristem	12 h
HORVU.MOREX.r3.5HG0436920.1	-1.63437	1.708407	-5.87204	2.89E-07	0.002965	5.521741	RING/U-box superfamily protein	meristem	12 h
HORVU.MOREX.r3.6HG0605060.1	-0.8199	4.908798	-5.08838	4.86E-06	0.033236	4.011963	SBP (S-ribonuclease-binding protein) family protein	meristem	12 h
HORVU.MOREX.r3.1HG0089130.1	-0.46022	5.608758	-4.92789	8.55E-06	0.039818	3.468557	Serine/Threonine-kinase pakA-like protein	meristem	12 h
HORVU.MOREX.r3.1HG0073350.1	-1.26259	2.878989	-4.89183	9.70E-06	0.039818	3.351209	70 kDa heat shock protein	meristem	12 h
HORVU.MOREX.r3.5HG0517740.1	2.426466	-0.30721	6.112302	1.20E-07	0.002459	7.492382	Peroxidase	elongation zone	3 h
HORVU.MOREX.r3.4HG0395540.1	1.75487	4.838553	5.168475	3.66E-06	0.025019	4.096146	Glutamine synthetase	elongation zone	3 h
HORVU.MOREX.r3.6HG0623140.1	2.893193	-2.34532	5.333784	2.03E-06	0.020807	3.758867	#N/A	elongation zone	3 h
HORVU.MOREX.r3.5HG0527570.1	1.885468	4.789839	4.919898	8.79E-06	0.036487	3.460428	UDP-glycosyltransferase	elongation zone	3 h
HORVU.MOREX.r3.5HG0532150.1	2.523346	-2.26204	4.864651	1.07E-05	0.036487	3.135388	Expansin	elongation zone	3 h
HORVU.MOREX.r3.4HG0417920.1	2.669337	-1.69902	4.745546	1.61E-05	0.047323	2.848495	Peroxidase	elongation zone	3 h
HORVU.MOREX.r3.5HG0420460.1	3.093241	-1.03028	4.871991	1.04E-05	0.036487	1.921396	NBS-LRR-like resistance protein	elongation zone	3 h
HORVU.MOREX.r3.5HG0517740.1	2.679485	-0.30721	6.828114	8.52E-09	0.000175	10.01505	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.7HG0750000.1	2.377402	-2.12041	6.515961	2.71E-08	0.000207	8.667624	Disease resistance protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0663750.1	2.397222	3.681851	6.329002	5.40E-08	0.000207	8.23283	Galactoside 2-alpha-L-fucosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.1HG0010340.1	2.453683	-2.09413	6.363681	4.75E-08	0.000207	8.143603	Non-specific lipid-transfer protein-like protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0417920.1	3.451323	-1.69902	6.328486	5.41E-08	0.000207	8.079794	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.7HG0671470.1	-0.9246	4.81657	-6.28406	6.37E-08	0.000207	8.025028	Protein trichome birefringence	elongation zone	6 h
HORVU.MOREX.r3.4HG0395540.1	2.082668	4.838553	6.240994	7.46E-08	0.000207	7.797683	Glutamine synthetase	elongation zone	6 h
HORVU.MOREX.r3.4HG0408270.1	2.186194	-2.27119	6.22002	8.06E-08	0.000207	7.64336	LOB domain-containing protein, putative	elongation zone	6 h
HORVU.MOREX.r3.3HG0318590.1	2.82361	-1.25566	6.027641	1.63E-07	0.000373	7.197975	Endo-1,3-beta-glucanase	elongation zone	6 h
HORVU.MOREX.r3.5HG0518560.1	2.741276	2.148281	5.973574	1.99E-07	0.000409	6.987664	Leucine-rich repeat protein kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0415330.1	2.298155	3.57761	5.938845	2.26E-07	0.000422	6.838559	Cytochrome P450 family cinnamate 4-hydroxylase	elongation zone	6 h
HORVU.MOREX.r3.2HG0217090.1	2.254303	-0.85749	5.869515	2.92E-07	0.000499	6.646459	C2 calcium/lipid-binding and GRAM domain protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0527570.1	2.17181	4.789839	5.755027	4.43E-07	0.000649	6.256887	UDP-glycosyltransferase	elongation zone	6 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.5HG0429900.1	1.569007	4.093407	5.755871	4.41E-07	0.000649	6.254698	#N/A	elongation zone	6 h
HORVU.MOREX.r3.1HG0054190.1	2.243132	-0.12557	5.603621	7.67E-07	0.000984	5.682088	Expansin-like protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0080180.1	2.363438	-2.35246	5.610571	7.48E-07	0.000984	5.545157	Jacalin lectin family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0747230.1	0.983846	2.606945	5.493661	1.14E-06	0.001128	5.364691	Non-specific serine/threonine protein kinase	elongation zone	6 h
HORVU.MOREX.r3.6HG0550600.1	1.357649	1.720716	5.536978	9.76E-07	0.001113	5.309226	Protein ROOT HAIR DEFECTIVE 3 homolog	elongation zone	6 h
HORVU.MOREX.r3.3HG0329950.1	2.017307	1.75889	5.486008	1.17E-06	0.001128	5.243991	Pectin acetylesterase	elongation zone	6 h
HORVU.MOREX.r3.5HG0532140.1	2.101436	-1.00113	5.448458	1.34E-06	0.001128	5.182938	Expansin	elongation zone	6 h
HORVU.MOREX.r3.4HG0417010.1	1.926109	-1.71396	5.445447	1.36E-06	0.001128	5.130972	Receptor protein kinase, putative	elongation zone	6 h
HORVU.MOREX.r3.5HG0519120.1	1.78141	-0.8751	5.426543	1.45E-06	0.001128	5.124126	CASP-like protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0222830.1	-0.48403	7.515891	-5.5027	1.10E-06	0.001128	5.034028	Heavy metal transport/detoxification superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0054170.1	1.926734	0.15708	5.422633	1.47E-06	0.001128	5.005012	Expansin-like protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0234470.1	-0.56277	6.523252	-5.45501	1.31E-06	0.001128	4.997649	Kinase interacting (KIP1-like) family protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0297330.1	-0.63488	5.598322	-5.42073	1.48E-06	0.001128	4.95018	Receptor-like kinase	elongation zone	6 h
HORVU.MOREX.r3.6HG0626030.1	2.162985	-0.5621	5.368023	1.79E-06	0.001254	4.853647	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.4HG0413740.1	2.335849	-1.83472	5.349929	1.91E-06	0.001267	4.834231	12-oxophytodienoate reductase-like protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0413320.1	2.408495	2.316272	5.323825	2.10E-06	0.001348	4.757956	Subtilisin-like protease	elongation zone	6 h
HORVU.MOREX.r3.3HG0330220.1	1.170575	6.363412	5.363581	1.82E-06	0.001254	4.73745	GDSL esterase/lipase	elongation zone	6 h
HORVU.MOREX.r3.1HG0070340.1	1.597112	4.307027	5.361894	1.83E-06	0.001254	4.735557	Protein kinase-like protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0250060.1	2.548861	-2.50642	5.542587	9.57E-07	0.001113	4.691105	CASP-like protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0124850.1	1.751525	-0.21834	5.306118	2.24E-06	0.001351	4.672637	Dirigent protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0294960.1	1.785464	-1.29923	5.281463	2.45E-06	0.001352	4.64906	Eukaryotic translation initiation factor 3 subunit H	elongation zone	6 h
HORVU.MOREX.r3.5HG0535180.1	1.675045	-1.06768	5.267504	2.57E-06	0.001352	4.590332	#N/A	elongation zone	6 h
HORVU.MOREX.r3.3HG0329870.1	1.862808	-1.90322	5.259131	2.65E-06	0.001359	4.577099	Pectin acetylesterase	elongation zone	6 h
HORVU.MOREX.r3.4HG0351750.1	2.336208	-1.8238	5.248968	2.75E-06	0.001363	4.541046	BTB/POZ domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0199160.1	0.597614	6.474544	5.274269	2.51E-06	0.001352	4.465054	Kinesin-like protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0164020.1	1.16904	1.589544	5.204746	3.22E-06	0.001499	4.396228	E3 ubiquitin protein ligase drip2	elongation zone	6 h
HORVU.MOREX.r3.2HG0112690.1	1.313289	1.247173	5.274563	2.51E-06	0.001352	4.344444	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.5HG0488950.1	-1.08117	2.845933	-5.1895	3.39E-06	0.001514	4.342797	Cellulose synthase, putative	elongation zone	6 h
HORVU.MOREX.r3.7HG0642520.1	2.284003	-0.8717	5.204781	3.21E-06	0.001499	4.328546	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.2HG0195690.1	1.669205	-2.81043	5.312093	2.19E-06	0.001351	4.304607	filamentous hemagglutinin transporter	elongation zone	6 h
HORVU.MOREX.r3.1HG0072760.1	-0.81927	4.906091	-5.19219	3.36E-06	0.001514	4.19793	Serpin family protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0293310.1	1.921913	-2.57133	5.244511	2.79E-06	0.001363	4.191156	Protein upstream of flc	elongation zone	6 h
HORVU.MOREX.r3.2HG0112060.1	-0.78009	4.798982	-5.16625	3.69E-06	0.001583	4.186708	Transcription factor	elongation zone	6 h
HORVU.MOREX.r3.5HG0477750.1	2.461908	0.658352	5.165091	3.70E-06	0.001583	4.181246	Homeobox protein, putative	elongation zone	6 h
HORVU.MOREX.r3.3HG0235720.1	-2.2935	3.057636	-5.085	4.92E-06	0.001904	3.97504	FMN-dependent NADPH-azoreductase	elongation zone	6 h
HORVU.MOREX.r3.1HG0081950.1	3.02783	-2.05546	5.13377	4.14E-06	0.001733	3.96739	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.2HG0189670.1	1.586645	0.283223	5.104952	4.58E-06	0.001826	3.951537	Aquaporin-like protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0537150.1	1.4313	-2.24688	5.102156	4.63E-06	0.001826	3.933581	Protein DETOXIFICATION	elongation zone	6 h
HORVU.MOREX.r3.3HG0245250.1	4.001195	-1.64331	5.056812	5.43E-06	0.002019	3.858977	Cysteine protease, putative	elongation zone	6 h
HORVU.MOREX.r3.3HG0285440.1	1.714132	-1.28505	5.028484	6.00E-06	0.002019	3.810065	#N/A	elongation zone	6 h
HORVU.MOREX.r3.2HG0155750.1	1.817294	-0.29251	5.017459	6.24E-06	0.002019	3.775816	Ribonuclease	elongation zone	6 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.2HG0213020.1	1.669875	3.22145	5.018987	6.21E-06	0.002019	3.760502	Protein F12F1.11-, putative	elongation zone	6 h
HORVU.MOREX.r3.2HG0160560.1	-1.32161	2.799703	-5.01608	6.27E-06	0.002019	3.753458	Peptidylprolyl isomerase	elongation zone	6 h
HORVU.MOREX.r3.1HG0094110.1	2.621304	0.561027	4.997221	6.70E-06	0.002023	3.714629	Sigma factor sigB regulation protein rsbQ	elongation zone	6 h
HORVU.MOREX.r3.6HG0633900.1	2.250533	-0.51261	5.013382	6.33E-06	0.002019	3.671062	Calcium-dependent protein kinase	elongation zone	6 h
HORVU.MOREX.r3.2HG0192100.1	1.898231	1.501774	4.999422	6.65E-06	0.002023	3.660514	Serine/threonine-protein kinase	elongation zone	6 h
HORVU.MOREX.r3.1HG0006230.1	-0.62723	5.574	-5.03355	5.90E-06	0.002019	3.654349	Disease resistance protein RPM1	elongation zone	6 h
HORVU.MOREX.r3.2HG0112670.1	1.793326	0.989354	5.059305	5.39E-06	0.002019	3.636665	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.1HG0066610.1	1.140951	2.119827	5.021741	6.15E-06	0.002019	3.614935	Dirigent protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0156610.1	1.966857	-0.12875	4.978706	7.15E-06	0.002097	3.604955	ERD (Early-responsive to dehydration stress) family protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0325250.1	3.827258	-1.52184	5.115665	4.41E-06	0.001811	3.585871	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.5HG0527460.1	1.413704	1.065374	5.026848	6.04E-06	0.002019	3.571092	Pectin acetylesterase	elongation zone	6 h
HORVU.MOREX.r3.4HG0394330.1	1.298373	1.645952	4.982144	7.07E-06	0.002097	3.571046	Kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0312430.1	2.027052	-0.09459	4.940226	8.19E-06	0.002367	3.526814	E3 ubiquitin protein ligase drip2	elongation zone	6 h
HORVU.MOREX.r3.4HG0382620.1	0.645597	7.496381	5.005042	6.52E-06	0.002023	3.445143	Argininosuccinate lyase	elongation zone	6 h
HORVU.MOREX.r3.6HG0601830.1	1.688595	-2.05956	4.908467	9.15E-06	0.00245	3.421559	C2 calcium/lipid-binding and GRAM domain protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0350900.1	-0.44244	7.975994	-5.04518	5.66E-06	0.002019	3.409826	UDP-glucose 6-dehydrogenase	elongation zone	6 h
HORVU.MOREX.r3.1HG0005700.1	2.282402	-2.12158	4.90216	9.36E-06	0.00245	3.379499	#N/A	elongation zone	6 h
HORVU.MOREX.r3.5HG0470680.1	1.809572	-1.96407	4.892452	9.68E-06	0.00245	3.366296	Heavy metal transport/detoxification protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0047100.1	1.16872	4.15495	4.922399	8.72E-06	0.00245	3.363243	LanC-like protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0317780.1	1.348477	0.361248	4.88641	9.89E-06	0.00245	3.299334	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0329040.1	2.420593	-0.45471	4.866873	1.06E-05	0.002454	3.290501	Vacuolar-processing enzyme	elongation zone	6 h
HORVU.MOREX.r3.2HG0179560.1	1.265023	1.523229	4.892207	9.69E-06	0.00245	3.288011	Nodulin-like / Major Facilitator Superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0379660.1	1.488994	-1.00939	4.869022	1.05E-05	0.002454	3.26633	Transcription repressor OFP17	elongation zone	6 h
HORVU.MOREX.r3.3HG0237990.1	0.84265	4.191674	4.903838	9.30E-06	0.00245	3.257984	#N/A	elongation zone	6 h
HORVU.MOREX.r3.3HG0247440.1	-1.03879	2.109103	-4.8754	1.03E-05	0.002454	3.252388	Serine/threonine-protein kinase	elongation zone	6 h
HORVU.MOREX.r3.1HG0073390.1	1.680776	2.372781	4.856169	1.10E-05	0.002454	3.251725	Respiratory burst oxidase-like protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0472770.1	0.935693	4.331329	4.885725	9.91E-06	0.00245	3.251696	SIN3-like 2	elongation zone	6 h
HORVU.MOREX.r3.5HG0485940.1	2.28393	2.592249	4.852771	1.11E-05	0.002454	3.235626	Hexosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.7HG0747720.1	1.022779	3.70009	4.859879	1.08E-05	0.002454	3.23184	Cytokinin oxidase/dehydrogenase	elongation zone	6 h
HORVU.MOREX.r3.7HG0667060.1	1.645515	2.126304	4.85024	1.12E-05	0.002454	3.218683	target of early activation tagged (EAT) 2	elongation zone	6 h
HORVU.MOREX.r3.5HG0467870.1	1.235032	2.049337	4.846053	1.14E-05	0.002459	3.186763	Kynurenine formamidase	elongation zone	6 h
HORVU.MOREX.r3.4HG0400920.1	1.24527	4.093901	4.868231	1.05E-05	0.002454	3.144572	Kinesin-like protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0509120.1	1.329413	5.607225	4.909415	9.12E-06	0.00245	3.139496	Auxin-responsive protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0300950.1	-0.85585	3.921584	-4.85595	1.10E-05	0.002454	3.132576	Amino acid transporter, putative	elongation zone	6 h
HORVU.MOREX.r3.3HG0235350.1	2.5297	0.004514	4.837803	1.17E-05	0.002504	3.131832	Pollen Ole e 1 allergen and extensin family protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0346830.1	1.949416	-2.75621	4.903876	9.30E-06	0.00245	3.098291	WEB family protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0409230.1	2.214958	-0.03281	4.855714	1.10E-05	0.002454	3.09114	IQ domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0517760.1	2.078191	-2.35783	4.832731	1.19E-05	0.002523	3.064581	Zinc finger A20 and AN1 domain-containing stress-associated protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0470700.1	1.711283	-1.11013	4.803603	1.32E-05	0.002593	3.054163	Heavy metal transport/detoxification protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0405400.1	1.88462	2.976906	4.822336	1.24E-05	0.002589	3.048753	DUF936 family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0699010.1	1.37814	4.331849	4.802022	1.33E-05	0.002593	3.021367	LHY	elongation zone	6 h

Table Sʜ Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.4HG0415490.1	2.279941	-1.78464	4.787441	1.40E-05	0.002644	3.01628	14 kDa proline-rich protein DC2.15	elongation zone	6 h
HORVU.MOREX.r3.3HG0298080.1	1.206277	1.480621	4.806876	1.30E-05	0.002593	3.015565	Amino acid permease	elongation zone	6 h
HORVU.MOREX.r3.4HG0337110.1	-0.40188	7.514078	-4.90603	9.23E-06	0.00245	3.014211	Coatomer subunit alpha	elongation zone	6 h
HORVU.MOREX.r3.6HG0622250.1	1.439175	2.510596	4.792629	1.37E-05	0.002644	3.003956	Alpha/beta-hydrolase superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0524350.1	2.291352	-1.05304	4.781057	1.43E-05	0.002663	2.999931	Protein MIZU-KUSSEI 1	elongation zone	6 h
HORVU.MOREX.r3.6HG0600000.1	1.619501	-0.21905	4.80384	1.32E-05	0.002593	2.989788	Blue copper protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0748270.1	1.976082	0.645561	4.769564	1.49E-05	0.002721	2.972423	Blue copper protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0073550.1	2.083101	-1.6606	4.758755	1.54E-05	0.002728	2.939341	Laccase	elongation zone	6 h
HORVU.MOREX.r3.5HG0429180.1	1.588345	2.149739	4.762823	1.52E-05	0.002728	2.890774	Glycosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.3HG0254950.1	1.458454	1.01976	4.811486	1.28E-05	0.002593	2.888944	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.3HG0321700.1	0.826924	3.776226	4.755356	1.56E-05	0.002728	2.87577	FMN-dependent NADPH-azoreductase	elongation zone	6 h
HORVU.MOREX.r3.7HG0674720.1	2.213087	-1.46328	4.742885	1.63E-05	0.002754	2.866067	Epoxide hydrolase 2	elongation zone	6 h
HORVU.MOREX.r3.6HG0629520.1	1.814902	-0.9319	4.750709	1.59E-05	0.002734	2.863045	Ethylene-responsive transcription factor	elongation zone	6 h
HORVU.MOREX.r3.7HG0663920.1	2.620663	-0.12227	4.759457	1.54E-05	0.002728	2.850559	Alpha/beta-Hydrolases superfamily protein, putative	elongation zone	6 h
HORVU.MOREX.r3.7HG0739230.1	4.725231	-3.45098	5.275986	2.49E-06	0.001352	2.827608	Jacalin-like lectin	elongation zone	6 h
HORVU.MOREX.r3.2HG0180010.1	1.611356	1.125048	4.785735	1.40E-05	0.002644	2.826428	#N/A	elongation zone	6 h
HORVU.MOREX.r3.5HG0532150.1	2.45965	-2.26204	4.735246	1.67E-05	0.002754	2.819527	Expansin	elongation zone	6 h
HORVU.MOREX.r3.1HG0066800.1	1.452973	-2.50287	4.733908	1.68E-05	0.002754	2.806418	Potassium channel	elongation zone	6 h
HORVU.MOREX.r3.1HG0086370.1	2.439978	-3.20911	4.899111	9.46E-06	0.00245	2.79446	Glyoxal oxidase	elongation zone	6 h
HORVU.MOREX.r3.4HG0348800.1	1.299582	2.044228	4.709702	1.83E-05	0.002842	2.784431	TCP transcription factor	elongation zone	6 h
HORVU.MOREX.r3.5HG0537360.1	2.099833	-1.21127	4.707056	1.84E-05	0.002842	2.771019	transcription factor, putative (Protein of unknown function, DUF547)	elongation zone	6 h
HORVU.MOREX.r3.1HG0054180.1	1.743723	-0.6979	4.72537	1.73E-05	0.002797	2.768605	Expansin-like protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0541940.1	-0.45334	6.764259	-4.80795	1.30E-05	0.002593	2.751604	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0043520.1	-0.51948	4.227432	-4.7432	1.63E-05	0.002754	2.738959	F-box protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0730510.1	1.366303	-1.83116	4.694704	1.92E-05	0.002883	2.737722	Germin-like protein 1	elongation zone	6 h
HORVU.MOREX.r3.7HG0678160.1	-0.70262	6.566933	-4.76044	1.53E-05	0.002728	2.703576	Disease resistance protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0488050.1	1.895839	-2.9262	4.789925	1.38E-05	0.002644	2.688639	Blue copper protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0246540.1	-0.83451	4.407087	-4.70697	1.84E-05	0.002842	2.672307	Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A	elongation zone	6 h
HORVU.MOREX.r3.4HG0339890.1	1.693851	-1.1907	4.681314	2.02E-05	0.002975	2.671718	Pollen Ole e 1 allergen and extensin family protein, putative	elongation zone	6 h
HORVU.MOREX.r3.3HG0330200.1	1.317891	1.169812	4.753844	1.57E-05	0.002728	2.637862	Aquaporin	elongation zone	6 h
HORVU.MOREX.r3.4HG0405920.1	1.58089	0.085137	4.71022	1.82E-05	0.002842	2.637249	Hexosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.2HG0113990.1	2.278936	-2.49708	4.735486	1.67E-05	0.002754	2.631447	Calcium-dependent lipid-binding (CaLB domain) family protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0337950.1	2.55286	-0.29631	4.70456	1.86E-05	0.002842	2.604523	65-kDa microtubule-associated-like protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0275090.1	2.292549	-3.21251	4.849632	1.12E-05	0.002454	2.585923	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfar	elongation zone	6 h
HORVU.MOREX.r3.3HG0240310.1	-1.12244	6.614043	-4.73715	1.66E-05	0.002754	2.575514	DUF2921 family protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0613360.1	1.971445	-0.60847	4.698584	1.90E-05	0.002865	2.565885	Nucleotidylyl transferase superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0246670.1	1.674864	-1.91783	4.650851	2.24E-05	0.003069	2.542458	DUF4228 domain protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0527310.1	2.503643	-3.15598	4.817665	1.26E-05	0.002593	2.536395	Protein NRT1/ PTR FAMILY 5.5	elongation zone	6 h
HORVU.MOREX.r3.4HG0384620.1	1.046192	3.226323	4.654462	2.21E-05	0.003069	2.50729	Kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0196800.1	2.308663	-0.20994	4.682911	2.00E-05	0.002975	2.496555	Multidrug resistance protein ABC transporter family	elongation zone	6 h
HORVU.MOREX.r3.6HG0615840.1	3.029717	-2.2741	5.010543	6.40E-06	0.002019	2.495812	Metalloendoproteinase 1	elongation zone	6 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.2HG0097390.1	-0.67881	4.644505	-4.66435	2.14E-05	0.003066	2.461472	Inosine-5'-monophosphate dehydrogenase	elongation zone	6 h
HORVU.MOREX.r3.4HG0344370.1	1.666446	-2.72257	4.652708	2.22E-05	0.003069	2.449635	Glucuronoxylan 4-O-methyltransferase	elongation zone	6 h
HORVU.MOREX.r3.2HG0203070.1	1.028615	3.219858	4.654046	2.21E-05	0.003069	2.439331	Receptor-like kinase	elongation zone	6 h
HORVU.MOREX.r3.2HG0214070.1	2.22004	-2.62397	4.674435	2.06E-05	0.003023	2.41469	AT hook motif DNA-binding family protein, putative	elongation zone	6 h
HORVU.MOREX.r3.6HG0626020.1	1.599896	1.680187	4.703098	1.87E-05	0.002842	2.388228	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.1HG0087170.1	-0.54009	5.424188	-4.6476	2.26E-05	0.003076	2.368309	3-deoxy-manno-octulosonate cytidylyltransferase	elongation zone	6 h
HORVU.MOREX.r3.2HG0120830.1	2.427585	-3.15708	4.771755	1.47E-05	0.002721	2.358817	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.5HG0479500.1	1.485594	1.850868	4.617357	2.51E-05	0.003262	2.354289	Phosphonates import ATP-binding protein PhnC	elongation zone	6 h
HORVU.MOREX.r3.1HG0055240.1	2.238539	-3.1472	4.732093	1.69E-05	0.002754	2.352393	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	elongation zone	6 h
HORVU.MOREX.r3.3HG0234000.1	1.95946	-0.27443	4.644075	2.29E-05	0.003083	2.324145	Xyloglucan endotransglucosylase/hydrolase	elongation zone	6 h
HORVU.MOREX.r3.5HG0496980.1	-0.62711	5.215201	-4.65024	2.24E-05	0.003069	2.311565	Protein IQ-DOMAIN 1	elongation zone	6 h
HORVU.MOREX.r3.5HG0480980.1	2.820838	-1.63821	4.564578	3.01E-05	0.003715	2.310783	Spermidine/putrescine import ATP-binding protein PotA	elongation zone	6 h
HORVU.MOREX.r3.4HG0390770.1	1.127831	3.149264	4.561432	3.04E-05	0.003715	2.289506	Regulator of Vps4 activity in the MVB pathway protein, putative	elongation zone	6 h
HORVU.MOREX.r3.1HG0056620.1	1.936995	0.189162	4.652306	2.23E-05	0.003069	2.287993	Expansin protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0068010.1	1.638798	-0.26596	4.629764	2.41E-05	0.003207	2.270062	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.5HG0458890.1	0.613092	3.514885	4.587915	2.78E-05	0.003531	2.268363	senescence regulator (Protein of unknown function, DUF584)	elongation zone	6 h
HORVU.MOREX.r3.4HG0403620.1	1.680876	0.126435	4.643159	2.30E-05	0.003083	2.249992	#N/A	elongation zone	6 h
HORVU.MOREX.r3.4HG0409880.1	2.085554	-2.34755	4.623206	2.46E-05	0.003238	2.231724	Metal tolerance protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0027200.1	1.16177	4.502879	4.567182	2.98E-05	0.003709	2.210766	Auxin-responsive protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0728820.1	1.711457	1.672182	4.561878	3.04E-05	0.003715	2.203344	Xyloglucan endotransglucosylase/hydrolase	elongation zone	6 h
HORVU.MOREX.r3.7HG0739080.1	2.592859	-3.17965	4.716869	1.78E-05	0.002836	2.142108	Subtilisin-like protease	elongation zone	6 h
HORVU.MOREX.r3.1HG0075730.1	1.142807	1.539739	4.62608	2.44E-05	0.003227	2.105503	Subtilisin-like protease	elongation zone	6 h
HORVU.MOREX.r3.5HG0482670.1	1.369075	0.628979	4.584839	2.81E-05	0.003534	2.104686	Cellulose synthase	elongation zone	6 h
HORVU.MOREX.r3.3HG0307240.1	3.047396	-3.37688	4.719442	1.77E-05	0.002833	2.100061	Amino acid permease	elongation zone	6 h
HORVU.MOREX.r3.3HG0303410.1	0.766637	6.71103	4.658673	2.18E-05	0.003069	2.087438	Respiratory burst oxidase-like protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0210510.1	1.038663	-0.61919	4.526325	3.43E-05	0.004067	2.083709	Rapid alkalinization factor 1	elongation zone	6 h
HORVU.MOREX.r3.1HG0028320.1	-0.51736	6.850868	-4.60113	2.66E-05	0.003405	2.077768	70 kDa heat shock protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0600910.1	1.525494	1.060689	4.586951	2.79E-05	0.003531	2.077711	Aquaporin	elongation zone	6 h
HORVU.MOREX.r3.1HG0050700.1	1.470383	2.994863	4.544497	3.22E-05	0.00389	2.071266	ATP-dependent zinc metalloprotease FtsH	elongation zone	6 h
HORVU.MOREX.r3.5HG0512230.1	1.496443	2.04829	4.478337	4.04E-05	0.004424	2.062678	Protein ENHANCED DISEASE RESISTANCE 2-like	elongation zone	6 h
HORVU.MOREX.r3.5HG0470690.1	1.690588	-2.06961	4.480688	4.00E-05	0.004417	2.042055	Heavy metal transport/detoxification protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0345580.1	2.430549	-3.15122	4.669612	2.10E-05	0.003032	2.04184	Dirigent protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0402730.1	1.916573	-1.08162	4.494676	3.82E-05	0.004269	2.026897	Homeobox protein BEL1 like	elongation zone	6 h
HORVU.MOREX.r3.2HG0192410.1	1.946545	0.742041	4.555903	3.10E-05	0.003763	2.017531	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.7HG0722260.1	1.806626	-2.17609	4.464401	4.23E-05	0.004481	2.015299	RPM1-interacting protein 4	elongation zone	6 h
HORVU.MOREX.r3.1HG0066260.1	-0.44426	9.175242	-4.67254	2.08E-05	0.003023	1.9994	Tubulin beta chain	elongation zone	6 h
HORVU.MOREX.r3.7HG0742080.1	1.368426	-1.3261	4.46957	4.16E-05	0.004467	1.998271	Receptor-like kinase	elongation zone	6 h
HORVU.MOREX.r3.3HG0230870.1	1.663841	0.065486	4.457413	4.33E-05	0.004481	1.99767	Protein TRM32	elongation zone	6 h
HORVU.MOREX.r3.5HG0426110.1	2.400586	-3.22479	4.619901	2.49E-05	0.003254	1.979889	NBS-LRR class disease resistance protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0634520.1	1.552893	-2.23987	4.45638	4.35E-05	0.004481	1.978574	NBS-LRR-like resistance protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0065860.1	0.848897	4.236426	4.524346	3.45E-05	0.004071	1.97413	MLO-like protein	elongation zone	6 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0264650.1	1.800089	-2.1209	4.459394	4.30E-05	0.004481	1.973967	Retrovirus-related Pol polyprotein from transposon TNT 1-94	elongation zone	6 h
HORVU.MOREX.r3.3HG0309760.1	1.133557	3.402606	4.455882	4.36E-05	0.004481	1.966706	ROP-interactive CRIB motif protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0002960.1	1.189129	0.278873	4.514551	3.57E-05	0.004114	1.954537	NBS-LRR disease resistance protein, putative, expressed	elongation zone	6 h
HORVU.MOREX.r3.1HG0072910.2	-0.51436	4.342105	-4.47276	4.11E-05	0.004442	1.948413	Serine/threonine-protein kinase ATM	elongation zone	6 h
HORVU.MOREX.r3.7HG0641030.1	1.433632	-0.36725	4.497113	3.79E-05	0.004269	1.948011	Serpin family protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0622110.1	1.621992	2.81443	4.538426	3.29E-05	0.003948	1.947782	Pathogenesis-related protein 1	elongation zone	6 h
HORVU.MOREX.r3.4HG0400740.1	-0.30488	8.244974	-4.60131	2.65E-05	0.003405	1.933258	Cell division cycle protein 48-like protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0438460.1	1.637099	0.165145	4.474942	4.08E-05	0.004433	1.933105	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0636890.1	1.968408	0.940541	4.509718	3.63E-05	0.004159	1.84869	Expansin-like protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0576010.1	0.688546	4.663156	4.448925	4.46E-05	0.00453	1.844889	Protein kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0164850.1	-0.83779	4.574579	-4.45697	4.34E-05	0.004481	1.837023	SBP (S-ribonuclease binding protein) family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0666650.1	-1.74807	-0.31405	-4.40513	5.17E-05	0.00498	1.826821	Starch synthase, chloroplastic/amyloplastic	elongation zone	6 h
HORVU.MOREX.r3.1HG0057030.1	-0.85458	6.546046	-4.50545	3.68E-05	0.004196	1.82504	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.1HG0084970.1	1.228861	2.620282	4.439007	4.61E-05	0.004599	1.814145	Phosphatidylserine synthase 2	elongation zone	6 h
HORVU.MOREX.r3.6HG0550940.1	-0.3901	5.078026	-4.46072	4.28E-05	0.004481	1.799621	obscurin-like protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0454660.1	-0.40023	4.270815	-4.45065	4.43E-05	0.004526	1.782595	Alpha-(1,4)-fucosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.3HG0257680.1	-0.50697	4.018531	-4.41962	4.92E-05	0.004788	1.77026	GDSL esterase/lipase	elongation zone	6 h
HORVU.MOREX.r3.4HG0384390.1	1.194255	1.574903	4.39884	5.28E-05	0.00498	1.764321	Protein kinase family protein, putative, expressed	elongation zone	6 h
HORVU.MOREX.r3.3HG0238250.1	-0.98537	6.327265	-4.49393	3.83E-05	0.004269	1.759614	Gigantea-like protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0480130.1	2.755074	-2.63524	4.520606	3.50E-05	0.00408	1.754621	Kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0406670.1	0.896728	6.546221	4.529063	3.40E-05	0.004052	1.750733	Classical arabinogalactan protein 5	elongation zone	6 h
HORVU.MOREX.r3.3HG0253630.1	1.413934	3.730748	4.404741	5.18E-05	0.00498	1.738963	Late embryogenesis abundant protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0093050.1	1.093019	4.062497	4.43109	4.74E-05	0.004673	1.737545	Indole-3-acetic acid-amido synthetase GH3.3	elongation zone	6 h
HORVU.MOREX.r3.5HG0512210.1	3.384525	-2.87785	4.580288	2.85E-05	0.003568	1.728528	WRKY transcription factor	elongation zone	6 h
HORVU.MOREX.r3.5HG0520990.1	-0.74157	3.822638	-4.39069	5.43E-05	0.005017	1.728368	Kinase, putative	elongation zone	6 h
HORVU.MOREX.r3.7HG0751450.1	2.087902	0.190404	4.397294	5.31E-05	0.00498	1.72746	Glycosyltransferase family 92 protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0466440.1	-0.49623	4.963631	-4.44012	4.59E-05	0.004599	1.71567	Glucan endo-1,3-beta-glucosidase, putative	elongation zone	6 h
HORVU.MOREX.r3.6HG0576550.1	-0.54599	4.943295	-4.43697	4.64E-05	0.004603	1.693978	F-box protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0724140.1	1.052735	4.661226	4.426327	4.81E-05	0.004726	1.682048	FAD-binding Berberine family protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0489720.1	-0.43189	6.28355	-4.4771	4.05E-05	0.004424	1.675934	WPP domain-interacting protein 1	elongation zone	6 h
HORVU.MOREX.r3.2HG0178480.1	1.158204	-0.05624	4.39474	5.35E-05	0.004992	1.664541	RING/U-box superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0307250.1	2.116851	-2.48075	4.374902	5.72E-05	0.005129	1.661991	Amino acid permease	elongation zone	6 h
HORVU.MOREX.r3.2HG0115650.1	-1.04194	6.223826	-4.48697	3.92E-05	0.004347	1.660044	#N/A	elongation zone	6 h
HORVU.MOREX.r3.1HG0073330.1	-0.41018	5.588457	-4.44499	4.52E-05	0.004568	1.648802	Ubiquitin conjugating enzyme E2	elongation zone	6 h
HORVU.MOREX.r3.5HG0469300.1	1.837129	0.250216	4.348195	6.26E-05	0.00546	1.644784	CCCH-type zinc finger protein with ARM repeat domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0726170.1	-0.36883	7.833263	-4.5189	3.52E-05	0.00408	1.637807	Mitogen-activated protein kinase	elongation zone	6 h
HORVU.MOREX.r3.7HG0637030.1	1.199843	0.131716	4.383858	5.55E-05	0.005066	1.63244	Cytochrome P450 family protein, expressed	elongation zone	6 h
HORVU.MOREX.r3.5HG0490610.1	1.806309	-0.13337	4.337745	6.49E-05	0.005545	1.631143	Protein kinase	elongation zone	6 h
HORVU.MOREX.r3.5HG0497900.1	0.988943	3.680571	4.393535	5.38E-05	0.004992	1.566644	Rhomboid-like protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0670900.1	1.665796	2.29029	4.346402	6.30E-05	0.00546	1.563141	Aspartic proteinase Asp1	elongation zone	6 h
HORVU.MOREX.r3.5HG0488040.1	1.773284	-1.23014	4.344843	6.33E-05	0.00546	1.562854	Blue copper protein	elongation zone	6 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.2HG0175380.1	1.628515	3.452964	4.45505	4.37E-05	0.004481	1.55269	Sec14p-like phosphatidylinositol transfer family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0731560.1	1.82839	-0.87401	4.381706	5.59E-05	0.00508	1.546359	Regulator of Vps4 activity in the MVB pathway protein, putative	elongation zone	6 h
HORVU.MOREX.r3.7HG0661830.1	2.311953	-0.86487	4.303012	7.28E-05	0.005869	1.53054	GPI-anchored adhesin-like protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0017280.1	1.705673	-0.33011	4.345262	6.32E-05	0.00546	1.516513	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.4HG0394460.1	1.582218	0.734389	4.296061	7.46E-05	0.005869	1.500277	Protein DETOXIFICATION	elongation zone	6 h
HORVU.MOREX.r3.3HG0303210.1	1.045578	1.990963	4.38439	5.54E-05	0.005066	1.496242	Alpha/beta-Hydrolases superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0257840.1	1.382705	0.153713	4.378903	5.65E-05	0.005083	1.493426	S-acyltransferase	elongation zone	6 h
HORVU.MOREX.r3.3HG0267430.2	-0.70694	3.386958	-4.31704	6.95E-05	0.005693	1.486845	Receptor-like protein kinase	elongation zone	6 h
HORVU.MOREX.r3.2HG0127260.1	1.422613	-1.06197	4.333444	6.58E-05	0.005579	1.485352	COBRA-like protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0621170.1	2.497718	-0.64178	4.295036	7.48E-05	0.005869	1.48204	GPI-anchored adhesin-like protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0610980.1	1.484187	-1.88326	4.287107	7.68E-05	0.005948	1.471212	Nucleotide/sugar transporter family protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0548710.1	2.399406	-1.47311	4.281006	7.84E-05	0.00598	1.461884	Kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0310110.1	1.932063	0.692973	4.278796	7.90E-05	0.00598	1.458126	lysine ketoglutarate reductase trans-splicing-like protein, putative (DUF707)	elongation zone	6 h
HORVU.MOREX.r3.2HG0168700.1	-1.93174	0.035179	-4.46276	4.25E-05	0.004481	1.454954	ADP-ribosylation factor GTPase-activating protein AGD4	elongation zone	6 h
HORVU.MOREX.r3.7HG0715570.1	-0.48768	6.466383	-4.40172	5.23E-05	0.00498	1.454003	Transmembrane protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0228600.1	-0.83809	3.194099	-4.29945	7.37E-05	0.005869	1.451827	transmembrane protein, putative (DUF247)	elongation zone	6 h
HORVU.MOREX.r3.1HG0083250.1	-0.79226	3.094919	-4.27951	7.88E-05	0.00598	1.450196	Protein phosphatase 2c, putative	elongation zone	6 h
HORVU.MOREX.r3.2HG0112190.1	1.781051	-0.62536	4.305506	7.22E-05	0.005859	1.44703	Transcription repressor ofp17	elongation zone	6 h
HORVU.MOREX.r3.1HG0051110.1	-0.42943	4.84593	-4.35597	6.10E-05	0.005389	1.434594	Ankyrin repeat-containing protein, putative	elongation zone	6 h
HORVU.MOREX.r3.6HG0605120.1	-0.94165	2.469228	-4.28756	7.67E-05	0.005948	1.432225	RING/U-box superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0334360.1	1.012982	4.121321	4.37247	5.77E-05	0.005149	1.410669	Homeobox protein BEL1 like	elongation zone	6 h
HORVU.MOREX.r3.5HG0449620.1	0.680084	4.972296	4.345739	6.31E-05	0.00546	1.409923	weak chloroplast movement under blue light protein (DUF827)	elongation zone	6 h
HORVU.MOREX.r3.6HG0577040.1	2.174545	-1.97815	4.325824	6.75E-05	0.005655	1.409541	Ycf1	elongation zone	6 h
HORVU.MOREX.r3.2HG0144760.1	1.224079	-1.38996	4.267582	8.20E-05	0.006162	1.407	tRNA 5-methylaminomethyl-2-thiouridine biosynthesis bifunctional protein MnmC	elongation zone	6 h
HORVU.MOREX.r3.5HG0512490.1	1.796482	1.425049	4.384888	5.54E-05	0.005066	1.398205	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.3HG0330980.1	-0.38188	6.458067	-4.39777	5.30E-05	0.00498	1.38759	Protein IQ-DOMAIN 1	elongation zone	6 h
HORVU.MOREX.r3.2HG0157410.1	1.282714	2.254585	4.422845	4.87E-05	0.004759	1.379488	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.5HG0512710.1	1.953505	0.114178	4.252321	8.63E-05	0.006257	1.377069	N-acetyltransferase, putative, expressed	elongation zone	6 h
HORVU.MOREX.r3.3HG0310460.1	-0.8055	0.959034	-4.31324	7.04E-05	0.005732	1.371256	Glycosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.5HG0533760.1	1.286314	3.713664	4.402306	5.22E-05	0.00498	1.357668	Glycosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.7HG0721690.1	1.277014	0.537157	4.317998	6.93E-05	0.005693	1.356246	Endoglucanase	elongation zone	6 h
HORVU.MOREX.r3.2HG0214240.1	-0.72002	3.183258	-4.2562	8.52E-05	0.006257	1.350852	Disease resistance protein (NBS-LRR class) family	elongation zone	6 h
HORVU.MOREX.r3.3HG0306060.1	-0.40301	5.417997	-4.34218	6.39E-05	0.005486	1.345803	Thioredoxin-like protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0617970.1	1.743656	-1.86338	4.241216	8.95E-05	0.006432	1.345331	Glycosyltransferase family 92 protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0655210.1	1.73036	-1.68992	4.257075	8.49E-05	0.006257	1.330013	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.3HG0286100.1	2.060245	1.587249	4.272694	8.06E-05	0.006081	1.328105	CASP-like protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0412370.1	2.248347	-1.42512	4.232964	9.20E-05	0.006466	1.313575	Homeobox protein knotted-1, putative	elongation zone	6 h
HORVU.MOREX.r3.3HG0331030.1	-0.42461	7.059382	-4.37941	5.64E-05	0.005083	1.311415	Chaperone protein dnaJ, putative	elongation zone	6 h
HORVU.MOREX.r3.7HG0647950.1	2.328223	-1.042	4.247695	8.76E-05	0.006329	1.309073	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.5HG0485780.1	3.087395	-0.7336	4.235739	9.11E-05	0.006466	1.294071	1-aminocyclopropane-1-carboxylate oxidase	elongation zone	6 h
HORVU.MOREX.r3.3HG0233990.1	1.291557	1.603331	4.396975	5.31E-05	0.00498	1.287834	Xyloglucan endotransglucosylase/hydrolase	elongation zone	6 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.2HG0113720.1	1.376604	3.679958	4.330514	6.64E-05	0.005611	1.277074	Cytosolic Fe-S cluster assembly factor nbp35	elongation zone	6 h
HORVU.MOREX.r3.2HG0157710.1	-0.85214	2.534028	-4.25414	8.57E-05	0.006257	1.276901	actin cytoskeleton-regulatory complex pan-like protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0736150.1	1.217607	8.171407	4.43866	4.62E-05	0.004599	1.276341	Phosphatidylinositol transfer protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0208520.1	2.349203	-2.76284	4.323872	6.79E-05	0.005667	1.257069	Heavy metal transport/detoxification superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0612780.1	1.626017	1.073388	4.214609	9.78E-05	0.006777	1.247681	Dynein light chain	elongation zone	6 h
HORVU.MOREX.r3.3HG0303240.1	1.266074	2.978435	4.210707	9.90E-05	0.006797	1.228241	Ankyrin repeat-containing protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0382610.1	1.304492	0.223451	4.298199	7.40E-05	0.005869	1.227494	cytochrome P450, family 705, subfamily A, polypeptide 21	elongation zone	6 h
HORVU.MOREX.r3.6HG0585240.1	1.030864	0.751154	4.301068	7.33E-05	0.005869	1.224965	Kinase superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0696770.1	-0.32991	5.470938	-4.29995	7.36E-05	0.005869	1.224712	Protein kinase	elongation zone	6 h
HORVU.MOREX.r3.7HG0737340.1	1.656782	-0.10666	4.318196	6.92E-05	0.005693	1.224188	GDA1/CD39 nucleoside phosphatase family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0665040.1	3.136968	-3.45264	4.501356	3.73E-05	0.004232	1.220843	Protein EXORDIUM-like 1	elongation zone	6 h
HORVU.MOREX.r3.7HG0641750.1	2.886043	-2.73901	4.234967	9.14E-05	0.006466	1.212339	Aspartic proteinase nepenthesin-2	elongation zone	6 h
HORVU.MOREX.r3.5HG0533430.1	1.446154	0.093461	4.197599	0.000103	0.007027	1.211266	ROP-interactive CRIB motif protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0393870.1	1.509975	-1.59561	4.217434	9.69E-05	0.006737	1.20776	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.7HG0667610.1	1.533121	3.317002	4.316481	6.96E-05	0.005693	1.197908	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.2HG0161410.1	-0.33139	7.35188	-4.35509	6.12E-05	0.005389	1.179522	Acyl-[acyl-carrier-protein] desaturase	elongation zone	6 h
HORVU.MOREX.r3.7HG0640560.1	-3.05237	0.442209	-4.51862	3.52E-05	0.00408	1.178265	NBS-LRR disease resistance protein-like protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0721080.1	-0.88879	4.617684	-4.25844	8.45E-05	0.006257	1.177088	Zinc finger, B-box	elongation zone	6 h
HORVU.MOREX.r3.1HG0092010.1	0.723654	6.335202	4.318587	6.91E-05	0.005693	1.173644	#N/A	elongation zone	6 h
HORVU.MOREX.r3.6HG0613020.1	0.73279	4.924387	4.293425	7.52E-05	0.005869	1.17256	Caleosin	elongation zone	6 h
HORVU.MOREX.r3.3HG0280630.1	-0.41087	5.914468	-4.29776	7.41E-05	0.005869	1.172527	Glycosylphosphatidylinositol anchor attachment 1 protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0720100.1	0.785019	4.342288	4.228113	9.35E-05	0.006547	1.17236	Glucan endo-1,3-beta-glucosidase, putative	elongation zone	6 h
HORVU.MOREX.r3.7HG0722360.1	1.657991	0.664931	4.208263	9.98E-05	0.006829	1.171515	Receptor-like protein kinase	elongation zone	6 h
HORVU.MOREX.r3.7HG0707700.1	1.28134	-2.42617	4.188758	0.000106	0.007165	1.169507	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	elongation zone	6 h
HORVU.MOREX.r3.4HG0415420.1	-0.71383	6.947214	-4.32574	6.75E-05	0.005655	1.164807	Tubulin beta chain	elongation zone	6 h
HORVU.MOREX.r3.7HG0667620.1	1.390352	0.317173	4.282499	7.80E-05	0.005973	1.141699	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.3HG0218800.1	2.036577	-0.5154	4.174834	0.000112	0.007346	1.138679	hydroxyproline-rich glycoprotein family protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0215060.1	2.56843	-1.59998	4.239693	9.00E-05	0.006432	1.135309	WAT1-related protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0402030.1	-0.48854	5.321938	-4.25809	8.46E-05	0.006257	1.133581	Basic helix-loop-helix (BHLH) family transcription factor	elongation zone	6 h
HORVU.MOREX.r3.1HG0078970.1	1.606309	2.920959	4.286019	7.71E-05	0.005948	1.126937	Protein kinase, putative	elongation zone	6 h
HORVU.MOREX.r3.3HG0235320.1	2.090663	-0.14202	4.182294	0.000109	0.007272	1.124894	Pollen Ole e 1 allergen and extensin family protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0012340.1	1.341273	2.437594	4.258932	8.44E-05	0.006257	1.124798	Triose-phosphate transporter family protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0212860.1	1.881986	-1.30303	4.167517	0.000114	0.007387	1.119368	#N/A	elongation zone	6 h
HORVU.MOREX.r3.7HG0736960.1	-0.80623	3.87866	-4.18744	0.000107	0.007173	1.114131	BTB/POZ domain containing protein, expressed	elongation zone	6 h
HORVU.MOREX.r3.7HG0751300.1	1.431848	-1.39316	4.174339	0.000112	0.007346	1.103678	Phosphatidylinositol N-acetyglucosaminlytransferase subunit P-like protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0221180.1	1.198148	2.379805	4.335977	6.52E-05	0.005555	1.09362	Glycosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.1HG0094980.1	-0.59508	4.287159	-4.20004	0.000103	0.006994	1.082257	Mitochondrial outer membrane porin	elongation zone	6 h
HORVU.MOREX.r3.4HG0378580.1	-0.5394	5.353084	-4.25469	8.56E-05	0.006257	1.072092	Transcription factor	elongation zone	6 h
HORVU.MOREX.r3.7HG0724060.1	1.472051	0.588187	4.191324	0.000106	0.007128	1.06404	U-box domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0486660.1	1.327783	-2.06977	4.135973	0.000127	0.008027	1.031241	Calcium-binding protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0205990.1	2.277694	-2.55766	4.178281	0.00011	0.007321	1.007939	Glutaredoxin family protein, putative	elongation zone	6 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.6HG0623140.1	2.367924	-2.34532	4.233996	9.17E-05	0.006466	1.00097	#N/A	elongation zone	6 h
HORVU.MOREX.r3.7HG0647300.1	2.344324	-1.17681	4.128858	0.00013	0.008166	0.997754	AT hook motif DNA-binding family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0729000.1	1.037744	3.645636	4.176245	0.000111	0.007346	0.991496	RING/U-box superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0511450.1	0.425871	5.650127	4.239968	8.99E-05	0.006432	0.985226	ABC transporter B family protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0275060.1	1.379367	0.275212	4.171049	0.000113	0.007387	0.981393	Isoprenylcysteine alpha-carbonyl methylesterase ICME	elongation zone	6 h
HORVU.MOREX.r3.6HG0567780.1	-0.73168	3.016753	-4.12133	0.000133	0.008269	0.954213	disease resistance protein (TIR-NBS-LRR class)	elongation zone	6 h
HORVU.MOREX.r3.3HG0252960.1	1.52771	-1.0236	4.106352	0.00014	0.008505	0.944621	Calmodulin-binding protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0198870.1	1.180277	-0.51668	4.163197	0.000116	0.007453	0.943646	UPF0761 membrane protein Plut_1323	elongation zone	6 h
HORVU.MOREX.r3.6HG0570230.1	1.162509	0.733369	4.104145	0.000141	0.008516	0.927627	Aldose 1-epimerase family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0735700.1	1.751337	3.307934	4.114349	0.000136	0.00831	0.919377	Patatin	elongation zone	6 h
HORVU.MOREX.r3.1HG0077960.1	0.713733	7.898538	4.283421	7.78E-05	0.005973	0.872625	#N/A	elongation zone	6 h
HORVU.MOREX.r3.1HG0075260.1	3.591717	0.393741	4.218048	9.67E-05	0.006737	0.872368	Receptor kinase 2	elongation zone	6 h
HORVU.MOREX.r3.1HG0000050.1	-0.48669	5.048249	-4.16686	0.000114	0.007387	0.853426	RING-finger ubiquitin ligase	elongation zone	6 h
HORVU.MOREX.r3.4HG0412090.1	1.838635	-0.36354	4.072261	0.000156	0.009027	0.845801	C3HC4-type RING finger-containing protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0187450.1	1.502526	0.035956	4.167227	0.000114	0.007387	0.831957	Rhomboid-like protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0069570.1	-0.38714	8.695958	-4.29352	7.52E-05	0.005869	0.829353	Tubulin beta chain	elongation zone	6 h
HORVU.MOREX.r3.5HG0532120.1	1.958329	-1.75561	4.080201	0.000152	0.008905	0.828908	Expansin	elongation zone	6 h
HORVU.MOREX.r3.5HG0511820.1	2.863174	-3.38085	4.19273	0.000105	0.007118	0.826277	Cyclic nucleotide-gated channel	elongation zone	6 h
HORVU.MOREX.r3.3HG0319900.1	1.526392	-0.77823	4.087232	0.000149	0.008845	0.82349	Ankyrin repeat domain-containing protein 1	elongation zone	6 h
HORVU.MOREX.r3.2HG0164470.1	0.885954	3.24648	4.147607	0.000122	0.007749	0.81663	Nudix hydrolase	elongation zone	6 h
HORVU.MOREX.r3.5HG0457310.1	1.160147	0.314313	4.151574	0.00012	0.007696	0.802061	Exocyst complex component, putative	elongation zone	6 h
HORVU.MOREX.r3.7HG0680960.1	2.001292	0.611498	4.052042	0.000167	0.009235	0.786995	electron transporter, putative (Protein of unknown function, DUF547)	elongation zone	6 h
HORVU.MOREX.r3.5HG0494040.1	1.637166	-3.00086	4.080794	0.000152	0.008905	0.766255	Auxin efflux carrier component	elongation zone	6 h
HORVU.MOREX.r3.4HG0337720.1	2.735816	1.69822	4.357119	6.08E-05	0.005389	0.764459	PHD finger protein family	elongation zone	6 h
HORVU.MOREX.r3.7HG0730660.1	1.69589	-2.73673	4.079872	0.000152	0.008905	0.760753	#N/A	elongation zone	6 h
HORVU.MOREX.r3.5HG0500360.1	3.396968	1.290708	4.115784	0.000135	0.008295	0.753335	L-gulonolactone oxidase	elongation zone	6 h
HORVU.MOREX.r3.3HG0309780.1	3.054003	-2.21583	4.116906	0.000135	0.008295	0.743116	RING/U-box superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0723240.1	3.595489	-0.72296	4.211192	9.89E-05	0.006797	0.739836	TMV response-related protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0100750.1	1.493323	-1.62151	4.063312	0.000161	0.00914	0.730312	Dirigent protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0053060.1	1.094966	4.011378	4.091674	0.000147	0.008787	0.7239	PLATZ transcription factor	elongation zone	6 h
HORVU.MOREX.r3.6HG0593260.1	0.781168	5.929813	4.120134	0.000134	0.008277	0.722746	LETM1 and EF-hand domain-containing protein 1, mitochondrial	elongation zone	6 h
HORVU.MOREX.r3.5HG0500120.1	-1.06176	4.270851	-4.06631	0.000159	0.009076	0.719081	Thaumatin	elongation zone	6 h
HORVU.MOREX.r3.3HG0293570.1	-2.42284	-0.38794	-4.21086	9.90E-05	0.006797	0.718965	BTB/POZ domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0335450.1	2.849427	-2.95917	4.134345	0.000127	0.008045	0.713885	Nucleobase ascorbate transporter	elongation zone	6 h
HORVU.MOREX.r3.3HG0234970.1	0.680893	0.091122	4.101721	0.000142	0.008559	0.713597	6,7-dimethyl-8-ribityllumazine synthase	elongation zone	6 h
HORVU.MOREX.r3.2HG0102670.1	2.231459	-3.01135	4.122112	0.000133	0.008269	0.709464	Dirigent protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0521610.1	1.350561	0.681734	4.158361	0.000118	0.00755	0.706186	Protein kinase	elongation zone	6 h
HORVU.MOREX.r3.7HG0728480.1	1.577404	0.878141	4.180847	0.000109	0.007283	0.700674	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.4HG0333450.1	0.677657	3.618973	4.069688	0.000157	0.009044	0.697865	Type I inositol-1,4,5-trisphosphate 5-phosphatase CVP2	elongation zone	6 h
HORVU.MOREX.r3.2HG0118220.1	1.200541	1.251256	4.077872	0.000153	0.008933	0.693078	En/Spm-like transposon protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0205420.1	0.881002	-0.18096	4.077168	0.000154	0.008933	0.686703	#N/A	elongation zone	6 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0067720.1	1.31055	-2.10602	4.01713	0.000187	0.009858	0.680253	#N/A	elongation zone	6 h
HORVU.MOREX.r3.7HG0735840.1	-1.04726	4.848168	-4.07252	0.000156	0.009027	0.68008	serine/arginine repetitive matrix-like protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0641860.1	2.105613	0.566345	4.036788	0.000175	0.009467	0.670204	Ubiquitin carboxyl-terminal hydrolase 2	elongation zone	6 h
HORVU.MOREX.r3.2HG0181880.1	-0.34812	6.222963	-4.16736	0.000114	0.007387	0.666309	#N/A	elongation zone	6 h
HORVU.MOREX.r3.7HG0662370.1	1.725993	-1.65272	4.021453	0.000184	0.009796	0.660686	Pathogenesis-related protein 1	elongation zone	6 h
HORVU.MOREX.r3.3HG0298180.1	1.714999	-1.34466	4.009429	0.000192	0.009907	0.659972	#N/A	elongation zone	6 h
HORVU.MOREX.r3.3HG0252170.1	1.672983	-1.70754	4.004244	0.000195	0.009946	0.648623	DUF1685 family protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0509350.1	2.091009	-1.08767	4.08212	0.000151	0.008905	0.640197	Dirigent protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0673330.1	1.633347	-2.01567	3.998802	0.000198	0.010073	0.631308	Embryogenesis transmembrane protein-like	elongation zone	6 h
HORVU.MOREX.r3.4HG0412030.1	-0.5293	4.498999	-4.06149	0.000162	0.009144	0.630798	vacuolar sorting-associated protein (DUF946)	elongation zone	6 h
HORVU.MOREX.r3.4HG0342680.1	1.265446	-0.60974	4.057766	0.000164	0.009196	0.623076	Branchpoint-bridging protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0139810.1	1.024182	0.63654	4.119041	0.000134	0.008281	0.621047	Heavy metal transport/detoxification superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0483980.1	1.49107	-1.84454	3.992059	0.000203	0.010208	0.60216	Cinnamoyl CoA reductase	elongation zone	6 h
HORVU.MOREX.r3.3HG0281730.1	-1.52473	3.703997	-4.01298	0.000189	0.009875	0.597608	AP2/B3 transcription factor family protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0238180.1	-0.4947	4.144587	-4.0498	0.000168	0.009235	0.596744	#N/A	elongation zone	6 h
HORVU.MOREX.r3.4HG0380540.1	0.71167	3.365322	4.048467	0.000169	0.009235	0.594237	Aquaporin-1	elongation zone	6 h
HORVU.MOREX.r3.6HG0609680.1	1.5598	2.000697	3.987149	0.000206	0.010307	0.591637	Cobyric acid synthase	elongation zone	6 h
HORVU.MOREX.r3.3HG0234010.1	1.626236	-0.09759	4.116028	0.000135	0.008295	0.590752	Xyloglucan endotransglucosylase/hydrolase	elongation zone	6 h
HORVU.MOREX.r3.3HG0244000.1	2.012072	-2.4581	4.091016	0.000147	0.008787	0.581592	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0193170.1	5.202316	-0.2671	4.252191	8.63E-05	0.006257	0.578647	Pollen Ole e 1 allergen/extensin	elongation zone	6 h
HORVU.MOREX.r3.7HG0648620.1	1.334729	-1.54284	3.981217	0.00021	0.010399	0.567671	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0170230.1	0.620513	3.492538	4.005225	0.000194	0.009939	0.567565	Smr domain containing protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0255700.1	0.936777	1.416296	3.984093	0.000208	0.010359	0.561064	PQ-loop repeat family protein / transmembrane family protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0507680.1	1.509332	-1.22844	4.005809	0.000194	0.009939	0.557729	mitogen-activated protein kinase kinase kinase 6	elongation zone	6 h
HORVU.MOREX.r3.3HG0280060.1	1.897938	-2.86395	4.009069	0.000192	0.009907	0.545693	Heavy metal transport/detoxification superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0469340.1	1.364091	0.552227	4.003011	0.000196	0.009961	0.542595	Fasciclin-like arabinogalactan-protein-like	elongation zone	6 h
HORVU.MOREX.r3.6HG0553150.1	-0.59336	6.876917	-4.12536	0.000131	0.008235	0.534801	Polyubiquitin	elongation zone	6 h
HORVU.MOREX.r3.3HG0241320.1	-0.57499	3.585418	-4.01749	0.000187	0.009858	0.532925	Prolyl 4-hydroxylase alpha subunit, putative	elongation zone	6 h
HORVU.MOREX.r3.2HG0189530.1	1.502506	0.494093	4.084248	0.00015	0.00888	0.52337	Expansin protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0264640.1	1.450044	-2.14748	3.957494	0.000227	0.010873	0.513937	Retrotransposon protein, putative, unclassified	elongation zone	6 h
HORVU.MOREX.r3.3HG0288710.2	1.666455	-1.63853	3.960326	0.000225	0.010819	0.512944	GDSL esterase/lipase	elongation zone	6 h
HORVU.MOREX.r3.6HG0601670.1	-1.03885	2.45038	-3.9553	0.000228	0.010879	0.50788	Phosphatidic acid phosphatase	elongation zone	6 h
HORVU.MOREX.r3.5HG0464440.1	1.046278	0.420648	4.055712	0.000165	0.009196	0.500905	Kinase, putative	elongation zone	6 h
HORVU.MOREX.r3.2HG0178050.1	0.671937	4.229626	4.049295	0.000168	0.009235	0.498841	F-box protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0729510.1	-0.66076	4.709018	-4.05656	0.000164	0.009196	0.493535	WEB family protein, chloroplastic	elongation zone	6 h
HORVU.MOREX.r3.2HG0157450.1	1.0854	2.551061	4.14807	0.000122	0.007749	0.490267	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.3HG0319430.1	0.918067	2.262365	3.953545	0.00023	0.010879	0.482009	WD40-repeat protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0075320.1	1.179116	0.461847	4.057132	0.000164	0.009196	0.481515	Myb transcription factor	elongation zone	6 h
HORVU.MOREX.r3.2HG0181680.1	1.807609	-1.90882	3.965294	0.000221	0.010722	0.480716	CASP-like protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0090170.1	-0.58794	5.133692	-4.0215	0.000184	0.009796	0.473711	NBS-LRR-like resistance protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0410830.1	1.226737	1.674186	4.045177	0.000171	0.009285	0.473068	Transcription factor	elongation zone	6 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.7HG0727750.1	1.271368	5.212856	4.049506	0.000168	0.009235	0.460302	Zinc-transporting ATPase	elongation zone	6 h
HORVU.MOREX.r3.5HG0478450.1	-0.38866	5.597721	-4.05554	0.000165	0.009196	0.439217	AUGMIN subunit 5	elongation zone	6 h
HORVU.MOREX.r3.7HG0728870.1	-0.67588	6.913212	-4.16851	0.000114	0.007387	0.43008	Xyloglucan endotransglucosylase/hydrolase	elongation zone	6 h
HORVU.MOREX.r3.4HG0397010.1	1.588331	0.173587	3.955603	0.000228	0.010879	0.42269	Beta-glucosidase	elongation zone	6 h
HORVU.MOREX.r3.3HG0305150.1	-0.69222	4.756714	-4.0073	0.000193	0.009922	0.42243	Pectin lyase-like superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0186480.1	2.389649	-0.52788	3.930602	0.000247	0.011494	0.420658	1-aminocyclopropane-1-carboxylate synthase	elongation zone	6 h
HORVU.MOREX.r3.3HG0275490.1	1.905526	-2.47526	3.933074	0.000245	0.011462	0.420242	Zinc finger CCCH domain protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0558350.1	3.157234	-0.25422	4.069723	0.000157	0.009044	0.410293	#N/A	elongation zone	6 h
HORVU.MOREX.r3.4HG0335170.1	1.363685	1.390233	4.087215	0.000149	0.008845	0.400681	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0005730.1	2.121992	-3.38812	4.036771	0.000175	0.009467	0.398848	transcriptional factor B3 family protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0207720.1	0.911135	0.894337	3.981078	0.00021	0.010399	0.398137	Flavin-containing monooxygenase	elongation zone	6 h
HORVU.MOREX.r3.3HG0304780.1	-0.51325	4.983038	-4.02358	0.000183	0.009779	0.396785	Peptidyl serine alpha-galactosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.7HG0688870.1	0.781888	6.011072	4.084672	0.00015	0.00888	0.39521	Monodehydroascorbate reductase	elongation zone	6 h
HORVU.MOREX.r3.7HG0731490.1	-0.45292	4.892075	-4.00856	0.000192	0.009907	0.394041	Transmembrane protein, putative	elongation zone	6 h
HORVU.MOREX.r3.5HG0420460.1	2.673472	-1.03028	4.122825	0.000132	0.008269	0.390359	NBS-LRR-like resistance protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0242950.1	-0.43332	6.032036	-4.0472	0.000169	0.009249	0.389262	NF-X1 type zinc finger family protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0023200.1	1.268951	0.569684	3.911926	0.000262	0.011846	0.38519	LURP-one-like protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0412140.1	1.223956	2.514643	4.01206	0.00019	0.009875	0.381269	Zinc finger (C3HC4-type RING finger) protein family-like	elongation zone	6 h
HORVU.MOREX.r3.2HG0168070.1	1.302242	0.66133	4.068249	0.000158	0.009044	0.378793	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.4HG0400520.1	1.361771	-0.786	3.95733	0.000227	0.010873	0.374991	Lipid transfer protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0684180.1	0.646146	6.139387	4.100743	0.000142	0.008561	0.366996	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.4HG0412650.1	2.405969	1.247202	4.068558	0.000158	0.009044	0.365997	TVP38/TMEM64 family membrane protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0381790.1	1.152783	3.851367	4.049967	0.000168	0.009235	0.363944	transmembrane protein, putative (DUF247)	elongation zone	6 h
HORVU.MOREX.r3.3HG0326430.1	-0.3652	5.095188	-4.01458	0.000188	0.009875	0.363147	Diphosphomevalonate decarboxylase	elongation zone	6 h
HORVU.MOREX.r3.2HG0210610.1	0.90861	3.089943	3.971519	0.000217	0.010595	0.361942	Acetyl-coenzyme A synthetase	elongation zone	6 h
HORVU.MOREX.r3.3HG0322650.1	0.820926	3.559006	4.015792	0.000188	0.009875	0.36008	NAD kinase	elongation zone	6 h
HORVU.MOREX.r3.2HG0185600.1	1.219804	0.732582	4.02494	0.000182	0.009761	0.35993	TRIO and F-actin-binding protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0634130.1	-0.34476	5.21873	-4.02736	0.000181	0.009718	0.35688	Alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase	elongation zone	6 h
HORVU.MOREX.r3.7HG0649240.1	1.654371	-2.99572	3.995882	0.0002	0.010144	0.351149	protein kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0727650.1	2.785394	-1.35022	4.01979	0.000185	0.009823	0.338712	BTB/POZ domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0098090.1	-1.22748	-2.03609	-3.90116	0.000272	0.012171	0.328123	Translation initiation factor IF-2	elongation zone	6 h
HORVU.MOREX.r3.1HG0081620.1	-0.67083	3.155534	-3.91547	0.000259	0.01178	0.305948	Glycerophosphodiester phosphodiesterase	elongation zone	6 h
HORVU.MOREX.r3.7HG0739120.1	1.056623	2.007183	3.980317	0.000211	0.010399	0.280998	Receptor-like protein kinase	elongation zone	6 h
HORVU.MOREX.r3.2HG0214130.1	1.478431	3.799443	3.979911	0.000211	0.010399	0.279119	CoA ligase	elongation zone	6 h
HORVU.MOREX.r3.2HG0210500.1	1.440157	3.185342	4.104754	0.00014	0.008516	0.277495	Endoglucanase	elongation zone	6 h
HORVU.MOREX.r3.3HG0230640.1	2.149865	-1.25694	3.874376	0.000296	0.012756	0.276546	Thioesterase family protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0179790.1	1.090504	3.322266	3.890761	0.000281	0.012448	0.275276	Zinc finger ring-type protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0278170.1	1.707695	0.346839	3.872558	0.000298	0.01278	0.273946	CCCH-type zinc fingerfamily protein with RNA-binding domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0730530.1	1.30542	0.190357	3.91596	0.000259	0.01178	0.264659	Copper transport protein family	elongation zone	6 h
HORVU.MOREX.r3.2HG0192910.1	-0.7874	6.73787	-4.05151	0.000167	0.009235	0.262668	Xyloglucan endotransglucosylase/hydrolase	elongation zone	6 h
HORVU.MOREX.r3.2HG0140170.1	0.729722	2.981209	3.912956	0.000262	0.011846	0.262423	Ras-related protein Rab-21	elongation zone	6 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0294950.1	1.165905	-0.01143	3.947297	0.000234	0.011075	0.261902	Deubiquitinase SseL	elongation zone	6 h
HORVU.MOREX.r3.3HG0324180.1	-0.86838	4.528561	-3.92277	0.000253	0.011636	0.261303	#N/A	elongation zone	6 h
HORVU.MOREX.r3.4HG0401730.1	-0.71392	2.933703	-3.88505	0.000286	0.012542	0.259644	Pentatricopeptide repeat-containing protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0406060.1	2.287349	-1.45049	3.874045	0.000296	0.012756	0.250466	Agmatine coumaroyltransferase-2	elongation zone	6 h
HORVU.MOREX.r3.6HG0617750.1	-0.58528	4.935682	-3.99166	0.000203	0.010208	0.243819	Plant cadmium resistance 2	elongation zone	6 h
HORVU.MOREX.r3.4HG0407310.1	0.93114	3.764737	3.98741	0.000206	0.010307	0.236033	Xyloglucan galactosyltransferase KATAMARI1-like protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0059350.1	-0.58908	4.615638	-3.9447	0.000236	0.011121	0.234833	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0395940.1	1.431855	3.064976	3.893856	0.000278	0.012352	0.232016	Homocysteine S-methyltransferase family protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0349530.1	-0.39697	4.965038	-3.96357	0.000222	0.010731	0.225711	Tubby-like F-box protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0420480.1	2.172748	1.423525	3.855048	0.000315	0.013274	0.209779	BEL1-like homeodomain protein 6	elongation zone	6 h
HORVU.MOREX.r3.2HG0190260.1	1.048626	2.916863	3.857826	0.000312	0.013202	0.202002	SHR5-receptor-like kinase	elongation zone	6 h
HORVU.MOREX.r3.7HG0675770.1	-0.6	4.417254	-3.97472	0.000214	0.010525	0.196545	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0313900.1	1.79453	0.291481	3.844516	0.000326	0.013547	0.193434	Methyl esterase 1	elongation zone	6 h
HORVU.MOREX.r3.6HG0620520.1	0.766727	3.09452	3.977305	0.000213	0.010462	0.19341	Aminotransferase-related family protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0595190.1	1.697851	-2.07211	3.838398	0.000332	0.013678	0.167222	GDSL esterase/lipase	elongation zone	6 h
HORVU.MOREX.r3.3HG0293320.1	1.344097	0.363569	3.969018	0.000218	0.010619	0.166294	ALK tyrosine kinase receptor	elongation zone	6 h
HORVU.MOREX.r3.1HG0079020.1	2.109964	3.471696	3.859969	0.00031	0.013139	0.160129	Protein kinase, putative	elongation zone	6 h
HORVU.MOREX.r3.2HG0096230.1	1.3345	-2.9355	3.852368	0.000317	0.013296	0.156505	Phosphatidylinositol 3- and 4-kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0228940.1	1.160842	0.760498	3.884121	0.000287	0.012552	0.145085	Sulfate adenylyltransferase subunit 2	elongation zone	6 h
HORVU.MOREX.r3.3HG0256860.1	2.909361	-0.92611	4.253358	8.60E-05	0.006257	0.143357	Pentatricopeptide repeat-containing protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0298510.1	0.710619	4.425452	3.930013	0.000248	0.011494	0.142572	1-phosphatidylinositol-3-phosphate 5-kinase	elongation zone	6 h
HORVU.MOREX.r3.1HG0044290.1	0.806982	3.742696	3.847944	0.000322	0.013457	0.141382	electron protein, putative (Protein of unknown function, DUF547)	elongation zone	6 h
HORVU.MOREX.r3.4HG0355210.1	2.094068	-0.13769	3.830327	0.000341	0.013839	0.134843	transcription factor-like protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0255020.1	0.949433	3.48561	4.041865	0.000172	0.009361	0.121671	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.3HG0304490.1	1.083847	-1.40069	3.832099	0.000339	0.013839	0.117976	Myosin IC heavy chain	elongation zone	6 h
HORVU.MOREX.r3.3HG0254930.1	2.620343	-0.9917	3.816908	0.000355	0.014243	0.117873	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.4HG0380330.1	-0.49912	5.401503	-3.94057	0.000239	0.01124	0.117543	WRKY transcription factor	elongation zone	6 h
HORVU.MOREX.r3.4HG0349310.1	-0.411	5.375879	-3.9368	0.000242	0.011351	0.116605	Sec1 family domain-containing protein 2	elongation zone	6 h
HORVU.MOREX.r3.4HG0399970.1	1.108416	4.109756	3.954162	0.000229	0.010879	0.107234	Cytochrome b561 and DOMON domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0341050.1	1.365415	0.610576	3.863356	0.000307	0.013079	0.105564	Protein DETOXIFICATION	elongation zone	6 h
HORVU.MOREX.r3.5HG0436660.1	-0.47656	4.868326	-3.92783	0.000249	0.011499	0.103439	#N/A	elongation zone	6 h
HORVU.MOREX.r3.4HG0340030.1	1.905496	-1.31134	3.853895	0.000316	0.013286	0.099939	beta-fructofuranosidase 5	elongation zone	6 h
HORVU.MOREX.r3.1HG0050220.1	1.467589	-1.46767	3.814825	0.000358	0.01431	0.097532	Polyketide cyclase/dehydrase and lipid transport superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0606850.1	-0.45929	6.605397	-3.9712	0.000217	0.010595	0.096013	Methyltransferase	elongation zone	6 h
HORVU.MOREX.r3.3HG0293760.1	1.372775	3.466627	3.916563	0.000259	0.01178	0.092678	External alternative NAD(P)H-ubiquinone oxidoreductase B2, mitochondrial	elongation zone	6 h
HORVU.MOREX.r3.3HG0222130.1	-0.34138	8.795276	-4.06196	0.000162	0.009144	0.092182	Transmembrane protein 214	elongation zone	6 h
HORVU.MOREX.r3.2HG0207130.1	1.449031	1.218085	3.920773	0.000255	0.011684	0.088096	Acetyl-coenzyme A synthetase	elongation zone	6 h
HORVU.MOREX.r3.4HG0376720.1	2.748408	-0.40522	4.23288	9.20E-05	0.006466	0.077218	#N/A	elongation zone	6 h
HORVU.MOREX.r3.3HG0296120.1	1.531733	0.584762	3.862166	0.000308	0.013101	0.075777	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	elongation zone	6 h
HORVU.MOREX.r3.7HG0643260.1	-0.63975	3.282608	-3.83478	0.000336	0.013808	0.073857	BTB/POZ domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0631710.1	1.017095	2.878977	4.02712	0.000181	0.009718	0.065104	Aquaporin	elongation zone	6 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.4HG0331520.1	-0.58664	3.556196	-3.89973	0.000273	0.012201	0.063368	Protein UPSTREAM OF FLC	elongation zone	6 h
HORVU.MOREX.r3.2HG0209680.1	1.514912	0.534924	3.8234	0.000348	0.014059	0.0507	Isopropylmalate dehydrogenase	elongation zone	6 h
HORVU.MOREX.r3.2HG0164160.2	1.454876	-0.40053	3.790717	0.000386	0.014897	0.044823	Trihelix transcription factor	elongation zone	6 h
HORVU.MOREX.r3.7HG0747940.1	0.444076	7.327177	4.012837	0.000189	0.009875	0.029498	Polyamine oxidase	elongation zone	6 h
HORVU.MOREX.r3.6HG0573920.1	1.414493	-0.43481	3.793134	0.000383	0.014864	0.029255	Retrotransposon protein, putative, unclassified	elongation zone	6 h
HORVU.MOREX.r3.2HG0105830.1	0.792199	4.383346	3.852965	0.000317	0.013296	0.025007	#N/A	elongation zone	6 h
HORVU.MOREX.r3.5HG0519660.1	0.466698	3.342751	3.83078	0.00034	0.013839	0.021559	Basic helix-loop-helix transcription factor	elongation zone	6 h
HORVU.MOREX.r3.6HG0631600.1	1.116608	1.162908	3.92945	0.000248	0.011494	0.016681	Rop guanine nucleotide exchange factor, putative	elongation zone	6 h
HORVU.MOREX.r3.6HG0547660.1	2.243889	-1.78969	3.800782	0.000374	0.014703	0.011529	Copine-1	elongation zone	6 h
HORVU.MOREX.r3.2HG0207860.1	1.448619	-2.16402	3.778425	0.000401	0.015004	0.010905	Serine/threonine-protein kinase	elongation zone	6 h
HORVU.MOREX.r3.6HG0624390.1	1.263709	1.652699	3.778864	0.000401	0.015004	0.009373	Two-component response regulator	elongation zone	6 h
HORVU.MOREX.r3.3HG0285150.1	0.858919	1.826069	3.840902	0.000329	0.013651	0.008922	Tryptophan aminotransferase	elongation zone	6 h
HORVU.MOREX.r3.5HG0536200.1	1.101929	-0.5546	3.886604	0.000285	0.01251	0.004664	Xyloglucan endotransglucosylase/hydrolase	elongation zone	6 h
HORVU.MOREX.r3.4HG0405860.1	2.432806	1.28141	3.779565	0.0004	0.015004	0.001351	Protein WEAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT 1	elongation zone	6 h
HORVU.MOREX.r3.4HG0402000.1	-0.71102	8.180685	-3.99194	0.000203	0.010208	-0.00288	Kinase interacting (KIP1-like) family protein, putative	elongation zone	6 h
HORVU.MOREX.r3.2HG0111270.1	1.104611	-0.29425	3.788881	0.000388	0.014941	-0.00676	WUSCHEL-related homeobox	elongation zone	6 h
HORVU.MOREX.r3.4HG0338070.1	0.975103	1.603513	3.923496	0.000253	0.011634	-0.00773	Kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0057990.1	-0.60781	4.42891	-3.83889	0.000331	0.013678	-0.0088	O-fucosyltransferase family protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0454230.1	0.775647	2.88731	3.82286	0.000349	0.014059	-0.01562	Aminopeptidase	elongation zone	6 h
HORVU.MOREX.r3.1HG0052120.1	-0.62021	3.548831	-3.79064	0.000386	0.014897	-0.01867	GDP-mannose transporter	elongation zone	6 h
HORVU.MOREX.r3.5HG0461950.1	0.850185	2.97161	3.838985	0.000331	0.013678	-0.01903	2-isopropylmalate synthase 2	elongation zone	6 h
HORVU.MOREX.r3.7HG0741080.1	-0.79685	1.851569	-3.77862	0.000401	0.015004	-0.01948	Disease resistance protein RPM1	elongation zone	6 h
HORVU.MOREX.r3.4HG0335180.1	-0.62283	5.021928	-3.85483	0.000315	0.013274	-0.02139	Phosphatidylinositol N-acetyglucosaminlytransferase subunit P-like protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0604200.1	-1.00506	0.762306	-3.77857	0.000401	0.015004	-0.02657	transcription repressor	elongation zone	6 h
HORVU.MOREX.r3.1HG0051920.1	0.957177	2.286248	3.87961	0.000291	0.012681	-0.03212	Transcription factor	elongation zone	6 h
HORVU.MOREX.r3.3HG0327810.1	-0.48527	7.008521	-3.97021	0.000218	0.010603	-0.03357	Auxin efflux carrier protein-like	elongation zone	6 h
HORVU.MOREX.r3.5HG0486810.1	-1.00151	1.496685	-3.76948	0.000413	0.015322	-0.04016	Chaperone DnaJ	elongation zone	6 h
HORVU.MOREX.r3.6HG0555660.2	-0.4305	7.208638	-3.95416	0.000229	0.010879	-0.04056	Calreticulin/calnexin	elongation zone	6 h
HORVU.MOREX.r3.5HG0513780.1	0.602815	5.051864	3.905561	0.000268	0.012054	-0.04911	Kinesin-like protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0218010.1	-0.38361	8.228324	-3.98591	0.000207	0.010324	-0.04939	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	elongation zone	6 h
HORVU.MOREX.r3.4HG0417320.1	1.409745	1.098725	3.911669	0.000263	0.011846	-0.05517	Remorin	elongation zone	6 h
HORVU.MOREX.r3.3HG0305440.1	1.566672	-2.50175	3.755657	0.000431	0.015665	-0.05772	Late embryogenesis abundant protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0680410.1	-0.64709	4.544521	-3.86575	0.000304	0.013006	-0.058	Leucine-rich repeat (LRR) family protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0355460.1	-0.46368	4.5138	-3.8738	0.000297	0.012756	-0.06185	myosin-4 protein (DUF641)	elongation zone	6 h
HORVU.MOREX.r3.5HG0493080.1	0.649714	5.851163	3.88754	0.000284	0.01251	-0.06214	VWA domain containing protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0675310.1	1.456171	1.411092	3.886514	0.000285	0.01251	-0.06712	N-lysine methyltransferase	elongation zone	6 h
HORVU.MOREX.r3.1HG0079800.1	-0.50169	7.794068	-3.96403	0.000222	0.010731	-0.06984	Farnesyl diphosphate synthase	elongation zone	6 h
HORVU.MOREX.r3.7HG0707160.1	1.688228	-0.16087	3.745022	0.000446	0.015908	-0.08672	NAC domain-containing protein, putative	elongation zone	6 h
HORVU.MOREX.r3.6HG0588520.1	0.942761	2.56033	3.882779	0.000288	0.01258	-0.08795	Rop guanine nucleotide exchange factor	elongation zone	6 h
HORVU.MOREX.r3.6HG0557070.1	-0.56379	6.4953	-3.89578	0.000276	0.012309	-0.08865	Activator of heat shock protein ATPase	elongation zone	6 h
HORVU.MOREX.r3.4HG0383670.1	1.153631	2.012771	3.861216	0.000309	0.013114	-0.09291	Protein SCAR2	elongation zone	6 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0062110.1	1.355093	0.941667	3.746878	0.000443	0.015878	-0.09391	Pentatricopeptide repeat-containing protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0185370.1	2.612507	-1.4233	3.812331	0.000361	0.014368	-0.09839	Subtilisin-like protease	elongation zone	6 h
HORVU.MOREX.r3.7HG0704450.1	0.525161	5.126567	3.874262	0.000296	0.012756	-0.10426	Hexosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.5HG0481760.1	-0.29019	6.00272	-3.89561	0.000277	0.012309	-0.10428	Protein AUXIN RESPONSE 4	elongation zone	6 h
HORVU.MOREX.r3.6HG0559990.1	0.815896	5.045463	3.887002	0.000284	0.01251	-0.11135	Apoptosis-inducing factor-like protein A	elongation zone	6 h
HORVU.MOREX.r3.5HG0484660.1	1.489123	-0.23036	3.755081	0.000432	0.015665	-0.1296	Vacuolar-processing enzyme	elongation zone	6 h
HORVU.MOREX.r3.7HG0751340.1	1.044816	0.25739	3.843936	0.000326	0.013547	-0.13244	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0700270.1	-0.39241	7.724735	-3.94456	0.000236	0.011121	-0.13247	Transaldolase	elongation zone	6 h
HORVU.MOREX.r3.4HG0356860.1	0.993279	1.759753	3.751236	0.000437	0.01578	-0.1355	Ulp1 protease family, C-terminal catalytic domain containing protein, expressed	elongation zone	6 h
HORVU.MOREX.r3.7HG0671360.1	-0.33715	9.214028	-4.01186	0.00019	0.009875	-0.13979	Aldehyde dehydrogenase	elongation zone	6 h
HORVU.MOREX.r3.5HG0531070.1	3.405701	-3.02117	3.929373	0.000248	0.011494	-0.14075	Protein DETOXIFICATION	elongation zone	6 h
HORVU.MOREX.r3.4HG0340910.2	2.331663	-1.88941	3.793259	0.000383	0.014864	-0.14156	p-loop containing nucleoside triphosphate hydrolases superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0202250.1	1.350384	1.379273	3.74269	0.000449	0.01595	-0.14444	Kelch repeat-containing protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0177790.1	2.107683	-2.43363	3.764456	0.00042	0.0154	-0.14944	Methyl-CpG-binding domain protein 6	elongation zone	6 h
HORVU.MOREX.r3.4HG0342660.1	1.245412	1.013503	3.877014	0.000293	0.012756	-0.15427	Calcium-binding EF-hand family protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0014680.1	1.397217	-0.77974	3.710919	0.000496	0.017032	-0.17483	Tetraspanin family protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0469120.1	1.58902	-1.16488	3.740688	0.000452	0.016007	-0.18193	E3 ubiquitin-protein ligase SINA-like 10	elongation zone	6 h
HORVU.MOREX.r3.3HG0246300.1	0.485266	4.385187	3.808929	0.000364	0.014439	-0.20381	RNA-binding protein, putative	elongation zone	6 h
HORVU.MOREX.r3.7HG0653380.1	1.360238	1.304596	3.916315	0.000259	0.01178	-0.2097	GDSL esterase/lipase	elongation zone	6 h
HORVU.MOREX.r3.6HG0608960.1	0.675326	3.939137	3.781867	0.000397	0.015004	-0.21182	Galactan beta-1,4-galactosyltransferase GALS1	elongation zone	6 h
HORVU.MOREX.r3.4HG0386490.1	2.000337	-0.76068	3.731226	0.000466	0.016253	-0.21763	Receptor-like kinase, putative	elongation zone	6 h
HORVU.MOREX.r3.4HG0412790.1	0.657907	3.163327	3.779355	0.0004	0.015004	-0.22337	Remorin	elongation zone	6 h
HORVU.MOREX.r3.6HG0567150.1	1.074184	2.844231	3.694699	0.000522	0.017624	-0.22725	Exosome complex component	elongation zone	6 h
HORVU.MOREX.r3.3HG0299020.1	1.221284	-1.58695	3.692077	0.000526	0.01771	-0.22832	Protein NRT1/ PTR FAMILY 5.5	elongation zone	6 h
HORVU.MOREX.r3.6HG0609720.1	-0.70447	3.853974	-3.74045	0.000452	0.016007	-0.22834	Glucosamine 6-phosphate N-acetyltransferase	elongation zone	6 h
HORVU.MOREX.r3.4HG0416760.1	-0.58607	4.391267	-3.78399	0.000394	0.015004	-0.23116	Non-structural protein 1	elongation zone	6 h
HORVU.MOREX.r3.7HG0719830.1	-1.73302	0.487996	-3.69789	0.000517	0.017564	-0.23631	#N/A	elongation zone	6 h
HORVU.MOREX.r3.6HG0597590.1	-0.40757	6.568014	-3.86957	0.000301	0.012875	-0.2374	Protein disulfide-isomerase	elongation zone	6 h
HORVU.MOREX.r3.3HG0288710.1	1.482542	-1.93307	3.689136	0.000531	0.01781	-0.23991	GDSL esterase/lipase	elongation zone	6 h
HORVU.MOREX.r3.2HG0099900.1	0.580535	5.512063	3.81764	0.000355	0.014238	-0.24151	Glyoxylate reductase/hydroxypyruvate reductase	elongation zone	6 h
HORVU.MOREX.r3.4HG0332930.1	-1.6159	0.588838	-3.8102	0.000363	0.014437	-0.24713	Short-chain dehydrogenase/reductase family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0654480.1	-0.82074	4.98012	-3.79482	0.000381	0.014854	-0.25522	Histone H3	elongation zone	6 h
HORVU.MOREX.r3.5HG0529500.1	-0.31885	7.05237	-3.87496	0.000295	0.012756	-0.25544	Protein kinase	elongation zone	6 h
HORVU.MOREX.r3.3HG0276120.1	1.93491	-1.33075	3.685006	0.000538	0.017871	-0.25849	Phospholipase A1	elongation zone	6 h
HORVU.MOREX.r3.5HG0434380.1	-0.48255	4.006199	-3.75519	0.000432	0.015665	-0.25871	Receptor-like kinase	elongation zone	6 h
HORVU.MOREX.r3.3HG0287690.1	0.906034	2.646815	3.846112	0.000324	0.013509	-0.25885	Profilin	elongation zone	6 h
HORVU.MOREX.r3.7HG0668560.1	0.976069	0.264899	3.684469	0.000539	0.017872	-0.26132	Pyruvate dehydrogenase E1 component subunit alpha	elongation zone	6 h
HORVU.MOREX.r3.3HG0293130.1	1.061527	3.772343	3.782887	0.000396	0.015004	-0.26216	Eukaryotic aspartyl protease family protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0616450.1	1.387171	0.245809	3.737615	0.000456	0.016067	-0.26267	Na(+)/H(+) exchange regulatory cofactor NHE-RF3	elongation zone	6 h
HORVU.MOREX.r3.5HG0477180.1	-0.38979	5.597571	-3.82679	0.000344	0.01394	-0.26532	LAG1 longevity assurance-like protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0485220.1	-0.50725	5.159201	-3.79229	0.000384	0.014876	-0.26698	Gamma-tubulin complex component	elongation zone	6 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.7HG0712000.1	1.999225	-3.03639	3.732828	0.000463	0.016199	-0.27386	Transposon protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0038800.1	0.634516	2.879103	3.758877	0.000427	0.015589	-0.27694	Protein kinase	elongation zone	6 h
HORVU.MOREX.r3.2HG0204480.1	-0.63084	-0.53341	-3.73371	0.000462	0.016195	-0.28093	Cysteine protease	elongation zone	6 h
HORVU.MOREX.r3.5HG0508880.1	1.71581	-0.73312	3.671846	0.000561	0.018236	-0.28234	Leucine-rich repeat protein kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0211730.1	-0.50183	4.52794	-3.79723	0.000378	0.014813	-0.28439	Phosphoribosylformylglycinamidine synthase subunit PurQ	elongation zone	6 h
HORVU.MOREX.r3.5HG0420820.1	1.512927	-2.28387	3.670049	0.000564	0.01828	-0.28606	TIFY domain/Divergent CCT motif family protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0182990.1	-0.79277	2.816822	-3.74692	0.000443	0.015878	-0.29387	UDP-glycosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.1HG0026080.1	0.669772	4.010774	3.75311	0.000435	0.015735	-0.29681	RING finger protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0649950.1	0.604118	3.836695	3.775402	0.000405	0.015121	-0.29914	Nudix hydrolase	elongation zone	6 h
HORVU.MOREX.r3.4HG0417660.1	2.790655	-3.39591	3.832708	0.000338	0.013839	-0.30419	rRNA N-glycosidase	elongation zone	6 h
HORVU.MOREX.r3.1HG0090710.1	-0.39678	4.396711	-3.78302	0.000396	0.015004	-0.3071	transmembrane protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0714660.1	1.511632	-2.48817	3.67658	0.000553	0.018074	-0.31137	Retrovirus-related Pol polyprotein from transposon TNT 1-94	elongation zone	6 h
HORVU.MOREX.r3.1HG0069030.1	1.620953	1.48038	3.682516	0.000542	0.017926	-0.31488	Calcium-transporting ATPase	elongation zone	6 h
HORVU.MOREX.r3.3HG0298790.1	0.828883	4.93163	3.688708	0.000532	0.01781	-0.31866	Amidophosphoribosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.1HG0002570.1	1.329815	-1.7761	3.679139	0.000548	0.017997	-0.32178	GDSL esterase/lipase	elongation zone	6 h
HORVU.MOREX.r3.4HG0384230.1	-0.57981	3.949266	-3.73346	0.000462	0.016195	-0.32965	RING/U-box superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0126960.1	-0.56668	4.780474	-3.80139	0.000373	0.014703	-0.3311	Longifolia protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0671410.1	1.292059	-1.71062	3.652605	0.000595	0.01894	-0.3333	Glycosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.2HG0128490.1	-0.34746	4.434925	-3.77366	0.000408	0.015165	-0.33667	#N/A	elongation zone	6 h
HORVU.MOREX.r3.1HG0071420.1	0.917509	3.587411	3.69943	0.000515	0.017538	-0.33871	TOM1-like protein 2	elongation zone	6 h
HORVU.MOREX.r3.1HG0001010.1	-0.79498	4.233711	-3.72648	0.000473	0.016469	-0.33888	Pm3-like disease resistance protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0488200.1	1.124769	0.584662	3.65932	0.000583	0.018648	-0.34028	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.5HG0483860.1	-0.54771	3.316157	-3.68124	0.000545	0.017937	-0.34447	RING/U-box superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0533230.1	-0.52821	5.643177	-3.80229	0.000372	0.01469	-0.34779	Pirin-like protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0664720.1	1.172021	0.421259	3.809012	0.000364	0.014439	-0.35336	Blue copper protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0067980.1	1.480567	-1.60301	3.686909	0.000535	0.017814	-0.36761	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.3HG0246550.1	-0.79275	2.643364	-3.77987	0.0004	0.015004	-0.37021	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.2HG0184230.1	2.484088	-3.03591	3.686687	0.000535	0.017814	-0.37139	#N/A	elongation zone	6 h
HORVU.MOREX.r3.5HG0477220.1	1.014635	1.858254	3.668133	0.000567	0.018303	-0.37942	F-box protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0351290.1	1.050914	5.034448	3.806721	0.000367	0.014513	-0.39111	B3 domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0119080.1	0.820267	0.931759	3.67621	0.000553	0.018074	-0.39953	Endonuclease/exonuclease/phosphatase family protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0092860.1	1.378859	-1.39568	3.671	0.000562	0.018255	-0.40427	S-type anion channel	elongation zone	6 h
HORVU.MOREX.r3.5HG0461280.1	0.518097	6.01476	3.788538	0.000389	0.014941	-0.41204	Calcium-binding EF-hand protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0613430.1	1.926202	-1.24134	3.623302	0.000652	0.020088	-0.41209	RNA-dependent RNA polymerase	elongation zone	6 h
HORVU.MOREX.r3.2HG0129450.1	0.962481	1.029346	3.760547	0.000425	0.015563	-0.41329	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0742720.1	-0.35549	4.763908	-3.74818	0.000442	0.015869	-0.41389	Magnesium transporter MRS2-like protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0035400.1	0.540672	4.194434	3.759679	0.000426	0.015578	-0.41987	Ras-related protein, expressed	elongation zone	6 h
HORVU.MOREX.r3.5HG0460630.1	-0.98074	1.842017	-3.63182	0.000635	0.019743	-0.42185	DTW domain containing protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0493330.1	1.085278	0.977391	3.711273	0.000496	0.017032	-0.42506	UDP-glucuronate 4-epimerase 4	elongation zone	6 h
HORVU.MOREX.r3.1HG0006660.1	0.953973	5.455877	3.744067	0.000447	0.015908	-0.43968	Inorganic pyrophosphatase family protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0015750.1	1.767899	-2.91215	3.614636	0.00067	0.020541	-0.45028	transcription factor, putative (Protein of unknown function, DUF547)	elongation zone	6 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0323750.1	0.916829	2.450618	3.625955	0.000647	0.020044	-0.4527	bZIP transcription factor, putative (DUF630 and DUF632)	elongation zone	6 h
HORVU.MOREX.r3.5HG0430050.1	0.638041	4.495639	3.723105	0.000478	0.01656	-0.45876	Stomatal closure-related actin-binding protein 1	elongation zone	6 h
HORVU.MOREX.r3.1HG0087620.1	1.00565	3.06372	3.795221	0.000381	0.014854	-0.4615	Xyloglucan endotransglucosylase/hydrolase	elongation zone	6 h
HORVU.MOREX.r3.5HG0422080.1	0.422951	5.370925	3.768683	0.000414	0.015333	-0.46151	RING/U-box superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0203080.1	2.09661	0.039803	3.608613	0.000682	0.020703	-0.46359	NA	elongation zone	6 h
HORVU.MOREX.r3.4HG0382280.1	1.208932	2.916703	3.60375	0.000693	0.020828	-0.46421	Calcium-dependent phosphotriesterase superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0676570.1	-0.67091	6.054358	-3.75108	0.000438	0.01578	-0.46437	Deaminase-related family protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0088530.1	0.959256	0.052643	3.611159	0.000677	0.020693	-0.46732	Cytochrome b561 domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0553580.1	1.274208	-1.47778	3.633182	0.000632	0.019703	-0.47278	Methionine--tRNA ligase	elongation zone	6 h
HORVU.MOREX.r3.7HG0638340.1	1.291694	2.325425	3.606821	0.000686	0.020703	-0.47566	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0423790.1	-0.54515	1.914718	-3.66221	0.000578	0.018556	-0.48154	Casein kinase II subunit beta	elongation zone	6 h
HORVU.MOREX.r3.5HG0490800.1	1.247526	0.125384	3.601607	0.000697	0.020915	-0.48602	IRK-interacting protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0369880.1	-1.07041	2.555153	-3.60982	0.00068	0.020694	-0.49772	Flavin-binding kelch domain F box protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0728000.1	0.629734	5.007313	3.779383	0.0004	0.015004	-0.49935	Glycosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.2HG0174750.1	1.205453	1.498345	3.764811	0.000419	0.0154	-0.50093	Fasciclin-like arabinogalactan protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0075340.1	0.974552	1.815297	3.645735	0.000608	0.0192	-0.50159	Alpha/beta-Hydrolases superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0219380.1	1.046041	4.367645	3.799171	0.000376	0.01475	-0.50261	Glutamate receptor ionotropic, NMDA 3A	elongation zone	6 h
HORVU.MOREX.r3.5HG0447610.1	0.942992	3.765571	3.611691	0.000676	0.020693	-0.50509	#N/A	elongation zone	6 h
HORVU.MOREX.r3.6HG0557920.1	0.923139	4.693871	3.713366	0.000493	0.017016	-0.50783	Auxin response factor	elongation zone	6 h
HORVU.MOREX.r3.3HG0310390.1	1.633224	0.671699	3.646103	0.000607	0.0192	-0.51643	Transcription and mRNA export factor SUS1	elongation zone	6 h
HORVU.MOREX.r3.7HG0748070.1	1.352132	-0.49696	3.672831	0.000559	0.018209	-0.51803	Heavy metal transport/detoxification superfamily protein, putative	elongation zone	6 h
HORVU.MOREX.r3.3HG0218100.1	-0.33079	6.103028	-3.74992	0.000439	0.01581	-0.51969	Chaperone protein DnaJ	elongation zone	6 h
HORVU.MOREX.r3.7HG0746770.1	-0.49877	10.27031	-3.90228	0.000271	0.012154	-0.5232	Chaperone protein htpG family protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0041280.1	0.864441	4.323201	3.784782	0.000393	0.015004	-0.52324	Cellulose synthase	elongation zone	6 h
HORVU.MOREX.r3.2HG0140970.1	-0.80443	2.378717	-3.6533	0.000594	0.018929	-0.52666	Heat-shock protein, putative	elongation zone	6 h
HORVU.MOREX.r3.4HG0407230.1	1.421274	-0.9449	3.583553	0.000737	0.021545	-0.52796	Flowering-promoting factor 1-like protein 1	elongation zone	6 h
HORVU.MOREX.r3.1HG0015960.1	1.247268	-0.2749	3.591304	0.00072	0.021192	-0.52838	Protein kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0669590.1	1.463324	-0.99729	3.624475	0.00065	0.020075	-0.53524	Caleosin	elongation zone	6 h
HORVU.MOREX.r3.3HG0289020.1	1.176905	2.050529	3.703174	0.000509	0.017421	-0.53571	Receptor-like kinase	elongation zone	6 h
HORVU.MOREX.r3.3HG0307850.1	-0.69387	6.891759	-3.81341	0.000359	0.014346	-0.53617	Basic 7S globulin	elongation zone	6 h
HORVU.MOREX.r3.7HG0642940.1	1.901718	-1.68507	3.609264	0.000681	0.020699	-0.541	Tryptophan decarboxylase	elongation zone	6 h
HORVU.MOREX.r3.5HG0485800.1	-0.4179	8.255741	-3.82919	0.000342	0.013861	-0.54375	Protein disulfide isomerase	elongation zone	6 h
HORVU.MOREX.r3.1HG0089220.1	-0.84934	0.50855	-3.58229	0.00074	0.021553	-0.54644	Cell surface antigen I/II	elongation zone	6 h
HORVU.MOREX.r3.1HG0055500.1	1.205796	2.091951	3.773311	0.000408	0.015165	-0.54674	Pollen Ole e 1 allergen and extensin family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0661480.1	-0.29565	7.365152	-3.79455	0.000381	0.014854	-0.55229	Alpha-amylase 2	elongation zone	6 h
HORVU.MOREX.r3.6HG0619500.1	1.446488	-0.34034	3.593252	0.000715	0.021158	-0.55699	#N/A	elongation zone	6 h
HORVU.MOREX.r3.6HG0545620.1	-0.37959	11.02319	-3.92861	0.000249	0.011496	-0.55711	Heat shock 70 kDa protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0610500.1	0.95895	1.298618	3.767986	0.000415	0.015336	-0.57013	Eukaryotic aspartyl protease family protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0120490.1	1.315125	1.876399	3.76578	0.000418	0.015391	-0.57648	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.1HG0039370.1	-0.40294	4.945966	-3.68247	0.000542	0.017926	-0.57682	Leucine-rich repeat (LRR) family protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0512250.1	1.49733	-0.16991	3.689718	0.00053	0.01781	-0.57713	Receptor-like kinase, putative	elongation zone	6 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.4HG0391330.1	-0.4174	6.457456	-3.74568	0.000445	0.015908	-0.58242	Phosphomevalonate kinase	elongation zone	6 h
HORVU.MOREX.r3.4HG0392230.1	1.071412	0.189187	3.696101	0.00052	0.017591	-0.58442	RNA-binding family protein, putative	elongation zone	6 h
HORVU.MOREX.r3.6HG0549990.1	-0.91081	2.338996	-3.56085	0.00079	0.022277	-0.58738	Pentatricopeptide repeat-containing protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0601260.1	1.042577	3.050364	3.725452	0.000474	0.016494	-0.59399	Sulfotransferase	elongation zone	6 h
HORVU.MOREX.r3.4HG0353390.1	0.806003	1.790635	3.637572	0.000624	0.019542	-0.59562	Type I inositol-1,4,5-trisphosphate 5-phosphatase	elongation zone	6 h
HORVU.MOREX.r3.7HG0750170.1	1.280081	1.590474	3.575925	0.000755	0.021777	-0.59792	#N/A	elongation zone	6 h
HORVU.MOREX.r3.5HG0485790.1	0.767141	1.583435	3.69823	0.000516	0.017564	-0.60043	1-aminocyclopropane-1-carboxylate oxidase	elongation zone	6 h
HORVU.MOREX.r3.4HG0342480.1	0.99918	4.010766	3.702286	0.00051	0.017427	-0.60472	Subtilisin-like protease	elongation zone	6 h
HORVU.MOREX.r3.4HG0345840.1	1.474028	1.556535	3.551083	0.000814	0.022588	-0.60809	Receptor lectin kinase	elongation zone	6 h
HORVU.MOREX.r3.3HG0291040.1	0.761351	3.480757	3.607446	0.000685	0.020703	-0.60849	Glutathione S-transferase	elongation zone	6 h
HORVU.MOREX.r3.3HG0231000.1	0.97974	3.745714	3.723371	0.000477	0.01656	-0.60856	Gamma-glutamyltranspeptidase	elongation zone	6 h
HORVU.MOREX.r3.7HG0680990.1	-0.3482	5.931399	-3.73878	0.000455	0.016064	-0.61316	Laminin-like protein epi-1	elongation zone	6 h
HORVU.MOREX.r3.4HG0364050.1	0.755507	2.580176	3.591534	0.000719	0.021192	-0.61774	Sodium/hydrogen exchanger	elongation zone	6 h
HORVU.MOREX.r3.6HG0620200.1	1.402455	-0.686	3.560933	0.00079	0.022277	-0.61987	Kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0037910.1	-0.70404	4.060046	-3.59945	0.000702	0.020963	-0.62639	Starch synthase, chloroplastic/amyloplastic	elongation zone	6 h
HORVU.MOREX.r3.4HG0338290.1	0.836673	1.18244	3.564574	0.000781	0.02217	-0.62903	Glucan endo-1,3-beta-glucosidase	elongation zone	6 h
HORVU.MOREX.r3.2HG0124550.1	1.388435	2.362034	3.544183	0.000832	0.022817	-0.63085	Protein WEAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT 1	elongation zone	6 h
HORVU.MOREX.r3.2HG0158260.1	-0.99133	2.424618	-3.54054	0.000841	0.02292	-0.63896	Glycogen synthase	elongation zone	6 h
HORVU.MOREX.r3.5HG0477040.1	-0.40892	5.55814	-3.68124	0.000545	0.017937	-0.64307	MND1-interacting protein 1	elongation zone	6 h
HORVU.MOREX.r3.6HG0582480.1	0.74213	2.53548	3.577	0.000752	0.021767	-0.66403	Ethylene-responsive transcription factor-like protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0253860.1	2.235977	-0.09276	3.542259	0.000837	0.02283	-0.66418	Rapid alkalinization factor (RALF) family protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0314070.1	1.386924	-1.61281	3.534046	0.000858	0.023177	-0.66733	Protein kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0235030.1	-0.51603	3.06592	-3.56421	0.000782	0.02217	-0.66983	Dehydration-responsive element binding protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0620720.1	0.925278	0.656099	3.6936	0.000524	0.017655	-0.67209	Ribonuclease	elongation zone	6 h
HORVU.MOREX.r3.2HG0197540.1	1.248544	3.09996	3.570153	0.000768	0.022074	-0.67247	MYB protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0170210.1	1.703154	2.50277	3.530589	0.000867	0.023177	-0.67729	Pentatricopeptide repeat-containing protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0059340.1	-0.34212	6.875668	-3.74414	0.000447	0.015908	-0.67983	Conserved oligomeric Golgi complex subunit 5	elongation zone	6 h
HORVU.MOREX.r3.5HG0513980.1	1.257644	-0.36473	3.548567	0.000821	0.022653	-0.68289	Auxin-responsive protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0269130.1	1.229899	4.115188	3.78538	0.000393	0.015004	-0.68398	Leucine-rich repeat protein kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0024040.1	-0.35973	9.734968	-3.83314	0.000338	0.013839	-0.68892	Disulfide-isomerase	elongation zone	6 h
HORVU.MOREX.r3.2HG0117830.1	1.828193	-2.70524	3.521576	0.000891	0.023455	-0.69073	Protein trichome birefringence	elongation zone	6 h
HORVU.MOREX.r3.3HG0245120.1	3.008632	-2.69428	3.579122	0.000747	0.021656	-0.69076	Cysteine protease, putative	elongation zone	6 h
HORVU.MOREX.r3.7HG0634430.1	-0.82024	3.249235	-3.54489	0.00083	0.022798	-0.69287	NBS-LRR-like resistance protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0517190.1	0.612034	2.990144	3.562931	0.000785	0.022226	-0.69664	Calcium-dependent protein kinase	elongation zone	6 h
HORVU.MOREX.r3.4HG0405990.1	1.490237	0.091283	3.530995	0.000866	0.023177	-0.69696	Transmembrane protein, putative	elongation zone	6 h
HORVU.MOREX.r3.3HG0288700.1	-0.59049	3.838111	-3.59364	0.000715	0.021158	-0.69744	#N/A	elongation zone	6 h
HORVU.MOREX.r3.3HG0242150.1	2.816029	-3.21832	3.594624	0.000712	0.021154	-0.69914	Glycine-rich cell wall structural protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0293490.1	1.09879	-0.53962	3.630886	0.000637	0.01977	-0.70004	Expansin	elongation zone	6 h
HORVU.MOREX.r3.4HG0383530.1	1.160899	-0.0177	3.66083	0.00058	0.018607	-0.70623	Pathogenesis-related protein 1	elongation zone	6 h
HORVU.MOREX.r3.5HG0465810.1	2.584797	-0.29224	3.552432	0.000811	0.022568	-0.70879	Calcium-binding protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0265140.1	2.429957	-1.23714	3.568326	0.000772	0.022075	-0.71205	DUF3511 domain protein	elongation zone	6 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0241000.1	-1.14573	6.471225	-3.66746	0.000568	0.018312	-0.71256	HXXXD-type acyl-transferase-like protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0632270.1	-0.51155	3.993705	-3.59315	0.000716	0.021158	-0.72051	Leucine-rich repeat family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0636630.1	1.069984	-0.12855	3.596159	0.000709	0.021085	-0.72197	WAT1-related protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0391440.1	2.444945	2.5321	3.566854	0.000776	0.022144	-0.7237	Transcription initiation factor IIF subunit alpha	elongation zone	6 h
HORVU.MOREX.r3.3HG0328430.1	1.715402	-0.79684	3.504925	0.000938	0.024245	-0.728	Zinc transporter, putative	elongation zone	6 h
HORVU.MOREX.r3.4HG0354010.1	2.103758	-0.99752	3.50354	0.000942	0.024273	-0.72936	LURP-one-like protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0684880.1	0.720825	3.761267	3.610797	0.000678	0.020693	-0.72937	meiosis chromosome segregation family protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0520650.1	-0.68725	5.200623	-3.6436	0.000612	0.019279	-0.73148	Argonaute family protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0313020.1	-0.35711	5.21659	-3.65089	0.000599	0.018997	-0.73458	Alcohol dehydrogenase, putative	elongation zone	6 h
HORVU.MOREX.r3.2HG0184620.1	-1.00724	4.117573	-3.56447	0.000782	0.02217	-0.73656	Hsp70-Hsp90 organizing protein 1	elongation zone	6 h
HORVU.MOREX.r3.5HG0532560.1	1.841864	-0.15138	3.5015	0.000947	0.024363	-0.73656	Ras-related protein, expressed	elongation zone	6 h
HORVU.MOREX.r3.7HG0670690.1	0.617126	8.088776	3.819768	0.000352	0.01417	-0.7401	HIPL1 protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0721320.1	1.386436	-3.12942	3.518006	0.000901	0.023642	-0.74814	Auxin-responsive family protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0006400.1	0.703199	6.387241	3.757925	0.000428	0.015608	-0.75216	Beta-1,3-galactosyltransferase-like protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0212570.1	-0.40516	10.53927	-3.83098	0.00034	0.013839	-0.76313	Calreticulin	elongation zone	6 h
HORVU.MOREX.r3.3HG0288960.1	1.047837	4.129323	3.655136	0.000591	0.018851	-0.76325	Cellulose synthase	elongation zone	6 h
HORVU.MOREX.r3.7HG0725290.1	-0.60065	3.61352	-3.55994	0.000793	0.022309	-0.76686	YGL010w-like protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0124450.1	-0.54969	4.909528	-3.64212	0.000615	0.019328	-0.76896	calmodulin-binding protein (DUF1645)	elongation zone	6 h
HORVU.MOREX.r3.6HG0621190.1	-0.67317	4.746594	-3.63638	0.000626	0.019584	-0.76978	Chaperone protein dnaJ	elongation zone	6 h
HORVU.MOREX.r3.6HG0609830.1	0.771268	4.638207	3.737827	0.000456	0.016067	-0.77069	Pollen-specific arabinogalacta protein BAN102	elongation zone	6 h
HORVU.MOREX.r3.6HG0606530.1	0.657707	4.864638	3.677174	0.000552	0.018074	-0.77447	Myb family transcription factor APL	elongation zone	6 h
HORVU.MOREX.r3.2HG0096800.1	0.75183	4.6918	3.625038	0.000648	0.020071	-0.77531	Flavin-containing monooxygenase	elongation zone	6 h
HORVU.MOREX.r3.6HG0542640.1	1.2642	2.086759	3.581257	0.000742	0.021565	-0.77778	Plant/F1M20-13 protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0192270.1	2.365035	-2.74995	3.523578	0.000886	0.023423	-0.78273	Sodium transporter	elongation zone	6 h
HORVU.MOREX.r3.6HG0616880.1	-1.49604	-0.67725	-3.48233	0.001004	0.025247	-0.78438	Upf0503 protein, chloroplastic	elongation zone	6 h
HORVU.MOREX.r3.1HG0025320.1	1.216938	0.572545	3.487242	0.000989	0.025053	-0.78755	Receptor-like kinase, putative	elongation zone	6 h
HORVU.MOREX.r3.2HG0194620.1	2.066231	-2.14798	3.512418	0.000916	0.023957	-0.79004	F-box protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0644220.1	0.581232	8.36113	3.778945	0.000401	0.015004	-0.79369	Arginine decarboxylase	elongation zone	6 h
HORVU.MOREX.r3.1HG0087590.1	1.456679	-1.00814	3.493205	0.000972	0.024706	-0.79414	transmembrane protein, putative (DUF679 domain membrane protein 2)	elongation zone	6 h
HORVU.MOREX.r3.5HG0486960.1	-1.50136	2.507872	-3.47795	0.001018	0.025374	-0.79567	Alpha/beta-Hydrolases superfamily protein, putative	elongation zone	6 h
HORVU.MOREX.r3.1HG0002630.1	1.989681	4.599685	3.477997	0.001018	0.025374	-0.79615	Formin-like protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0707220.1	0.614353	4.707516	3.675721	0.000554	0.018074	-0.79734	#N/A	elongation zone	6 h
HORVU.MOREX.r3.4HG0400530.1	1.3693	0.815449	3.475798	0.001024	0.025509	-0.80126	#N/A	elongation zone	6 h
HORVU.MOREX.r3.6HG0542320.1	1.273934	2.291237	3.474933	0.001027	0.025525	-0.80567	Kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0295640.1	1.319709	-1.27257	3.533983	0.000858	0.023177	-0.80582	Protein MIZU-KUSSEI 1	elongation zone	6 h
HORVU.MOREX.r3.6HG0625570.1	0.571664	5.941941	3.701985	0.00051	0.017427	-0.81157	Transmembrane protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0055380.1	-0.47664	6.771434	-3.67949	0.000548	0.017997	-0.81415	Methylsterol monooxygenase 1-2	elongation zone	6 h
HORVU.MOREX.r3.2HG0216470.1	-0.58313	6.666412	-3.68778	0.000534	0.017814	-0.81435	Kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0570520.1	-0.25122	6.220455	-3.68654	0.000536	0.017814	-0.81499	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0225880.1	0.908065	4.380821	3.545766	0.000828	0.022768	-0.8166	Receptor-like kinase	elongation zone	6 h
HORVU.MOREX.r3.7HG0709270.1	0.887614	3.012432	3.588321	0.000726	0.021292	-0.82139	RING/U-box superfamily protein	elongation zone	6 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.6HG0589860.1	0.795652	4.121931	3.584453	0.000735	0.021516	-0.82207	Kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0063810.1	-0.41341	4.973905	-3.59673	0.000708	0.021078	-0.82523	Cyclin family protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0382550.1	0.659022	5.636635	3.64992	0.0006	0.019011	-0.83025	Xyloglucan 6-xylosyltransferase 1	elongation zone	6 h
HORVU.MOREX.r3.1HG0078750.1	-0.50118	3.941561	-3.53535	0.000855	0.023177	-0.83367	Tesmin/TSO1-like CXC domain containing protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0117030.1	0.624057	7.823219	3.710981	0.000496	0.017032	-0.84019	Glutamate synthase, putative	elongation zone	6 h
HORVU.MOREX.r3.2HG0120650.1	1.012572	1.67255	3.711013	0.000496	0.017032	-0.84356	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.1HG0049450.1	-0.45109	5.425708	-3.63297	0.000633	0.019703	-0.84449	#N/A	elongation zone	6 h
HORVU.MOREX.r3.7HG0658270.1	-0.60436	2.885178	-3.53702	0.00085	0.023137	-0.8503	Hyp O-arabinosyltransferase-like protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0294670.1	-1.5833	-0.36802	-3.52646	0.000878	0.023338	-0.85976	demeter-like protein 3	elongation zone	6 h
HORVU.MOREX.r3.5HG0528570.1	1.082949	0.170023	3.54314	0.000834	0.022819	-0.8704	Protein PLANT CADMIUM RESISTANCE 2	elongation zone	6 h
HORVU.MOREX.r3.6HG0542030.1	1.090227	1.995705	3.722414	0.000479	0.016568	-0.87062	Acid beta-fructofuranosidase	elongation zone	6 h
HORVU.MOREX.r3.4HG0343540.1	-1.86821	-0.26772	-3.551	0.000815	0.022588	-0.87555	BSD domain containing protein, expressed	elongation zone	6 h
HORVU.MOREX.r3.7HG0641180.1	0.477929	5.725264	3.633743	0.000631	0.019703	-0.87672	Protein ENHANCED DISEASE RESISTANCE 2-like	elongation zone	6 h
HORVU.MOREX.r3.5HG0537090.1	-0.3276	6.791678	-3.66542	0.000572	0.0184	-0.87699	WD40 repeat-containing protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0313090.1	0.808062	2.944421	3.521623	0.000891	0.023455	-0.8778	Thiamin pyrophosphokinase 1	elongation zone	6 h
HORVU.MOREX.r3.1HG0050440.1	1.630883	-1.13792	3.445783	0.001122	0.027022	-0.88028	DUF538 family protein (Protein of unknown function, DUF538)	elongation zone	6 h
HORVU.MOREX.r3.5HG0426280.1	0.802689	2.961285	3.450813	0.001105	0.026745	-0.88209	GTP binding protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0500180.1	-0.41309	4.872313	-3.58302	0.000738	0.02155	-0.88392	Peptidyl-prolyl cis-trans isomerase	elongation zone	6 h
HORVU.MOREX.r3.7HG0638940.1	2.403498	2.010885	3.533601	0.000859	0.023177	-0.88518	DnaJ domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0100900.2	1.466048	0.62711	3.445935	0.001121	0.027022	-0.89236	Phosphoglycerate mutase-like protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0527500.1	-0.51146	4.452639	-3.53065	0.000867	0.023177	-0.89468	Ribosomal L11 methyltransferase	elongation zone	6 h
HORVU.MOREX.r3.6HG0629810.2	1.014768	1.891863	3.442642	0.001132	0.027022	-0.89728	Auxin-responsive protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0083730.1	1.06344	0.340392	3.482628	0.001003	0.025247	-0.90119	Lipid transfer protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0000140.1	-0.36426	5.300482	-3.59039	0.000722	0.021192	-0.90275	Glycosyltransferase-like KOBITO 1	elongation zone	6 h
HORVU.MOREX.r3.4HG0356090.1	-0.62258	2.309877	-3.44397	0.001128	0.027022	-0.90891	DELLA domain GRAS family transcription factor GAI	elongation zone	6 h
HORVU.MOREX.r3.1HG0054510.1	1.021317	2.568148	3.494517	0.000968	0.024639	-0.91572	Protein PLASTID MOVEMENT IMPAIRED 1	elongation zone	6 h
HORVU.MOREX.r3.2HG0173960.1	0.683328	2.814915	3.479501	0.001013	0.025374	-0.9163	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.4HG0377070.1	-0.46487	5.867895	-3.59897	0.000703	0.020964	-0.91789	Kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0618760.1	-0.74765	4.331592	-3.52446	0.000883	0.023391	-0.91933	WRKY transcription factor, putative	elongation zone	6 h
HORVU.MOREX.r3.6HG0628410.1	-0.32229	8.572245	-3.76747	0.000416	0.015336	-0.91991	Germin-like protein 1-1	elongation zone	6 h
HORVU.MOREX.r3.6HG0626650.1	-0.26756	8.259289	-3.69582	0.00052	0.017591	-0.92463	26S protease regulatory subunit-like protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0651110.1	-0.35594	7.468711	-3.66923	0.000565	0.018298	-0.92934	AT4G29520-like protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0102600.1	-0.41046	5.97563	-3.60586	0.000688	0.020734	-0.92939	Peptidylprolyl isomerase	elongation zone	6 h
HORVU.MOREX.r3.4HG0354980.1	0.687205	2.412831	3.498746	0.000955	0.024445	-0.93222	#N/A	elongation zone	6 h
HORVU.MOREX.r3.4HG0331440.1	1.502997	-0.62465	3.435984	0.001155	0.027375	-0.93919	LOB domain-containing protein, putative	elongation zone	6 h
HORVU.MOREX.r3.2HG0152370.1	-0.42073	4.701662	-3.55696	0.0008	0.02239	-0.93946	MD-2-related lipid recognition domain-containing protein / ML domain-containing	elongation zone	6 h
HORVU.MOREX.r3.3HG0240350.1	0.666715	2.152333	3.491601	0.000976	0.024796	-0.94279	Two-component response regulator	elongation zone	6 h
HORVU.MOREX.r3.7HG0715170.1	1.505029	-0.05365	3.428796	0.001181	0.027814	-0.94361	Glycosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.4HG0348450.1	-1.24325	1.119942	-3.42634	0.001189	0.027891	-0.94508	O-fucosyltransferase family protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0331730.1	-0.30864	6.082061	-3.60717	0.000685	0.020703	-0.94565	Zinc finger, C2H2	elongation zone	6 h
HORVU.MOREX.r3.7HG0644540.1	0.755999	3.792744	3.463956	0.001062	0.026155	-0.96051	1-aminocyclopropane-1-carboxylate synthase	elongation zone	6 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.6HG0595580.1	2.387881	-0.31218	3.417633	0.001221	0.028437	-0.96489	Ammonium transporter	elongation zone	6 h
HORVU.MOREX.r3.6HG0633960.1	0.977583	2.11648	3.650654	0.000599	0.018997	-0.96976	Monosaccharide-sensing protein 2	elongation zone	6 h
HORVU.MOREX.r3.2HG0204340.1	-2.38704	-0.82148	-3.73562	0.000459	0.01614	-0.97123	ERD (early-responsive to dehydration stress) family protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0004560.1	0.877794	5.305216	3.530018	0.000869	0.023177	-0.97362	ERD (Early-responsive to dehydration stress) family protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0398550.1	0.95697	6.045114	3.697042	0.000518	0.017582	-0.97875	Calcium-transporting ATPase	elongation zone	6 h
HORVU.MOREX.r3.7HG0748670.1	2.330437	-1.85496	3.406744	0.001261	0.028987	-0.97913	GDSL esterase/lipase	elongation zone	6 h
HORVU.MOREX.r3.2HG0160130.1	0.595919	3.66281	3.603441	0.000693	0.020828	-0.98055	Basic helix-loop-helix transcription factor	elongation zone	6 h
HORVU.MOREX.r3.7HG0699020.1	1.492684	-0.26924	3.442819	0.001132	0.027022	-0.98574	Retrotransposon protein, putative, Ty3-gypsy subclass	elongation zone	6 h
HORVU.MOREX.r3.5HG0462200.1	1.66813	-0.85589	3.404127	0.001271	0.02915	-0.98797	Metacaspase	elongation zone	6 h
HORVU.MOREX.r3.1HG0061660.1	0.885936	3.333271	3.580949	0.000743	0.021565	-0.98837	RING/FYVE/PHD zinc finger superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0423820.1	0.952504	2.29448	3.412191	0.001241	0.028698	-0.99031	#N/A	elongation zone	6 h
HORVU.MOREX.r3.5HG0528520.1	-0.37801	4.086447	-3.52817	0.000873	0.023277	-0.99413	Epoxide hydrolase 2	elongation zone	6 h
HORVU.MOREX.r3.2HG0193000.1	-0.71756	5.418419	-3.53252	0.000862	0.023177	-0.99747	HTH-type transcriptional regulator YidZ	elongation zone	6 h
HORVU.MOREX.r3.6HG0606930.1	-0.37452	5.680326	-3.57274	0.000762	0.02193	-0.99998	3-ketodihydrosphingosine reductase	elongation zone	6 h
HORVU.MOREX.r3.7HG0669410.1	0.508302	3.917601	3.504741	0.000938	0.024245	-1.00593	Cytochrome P450	elongation zone	6 h
HORVU.MOREX.r3.1HG0032930.1	0.670299	5.503727	3.619237	0.00066	0.020312	-1.00638	lipase, putative (DUF620)	elongation zone	6 h
HORVU.MOREX.r3.3HG0288370.1	-0.97215	2.377529	-3.40334	0.001274	0.029154	-1.00691	Chaperone clpb, putative	elongation zone	6 h
HORVU.MOREX.r3.2HG0132590.1	-0.3315	6.039953	-3.61772	0.000663	0.020376	-1.01251	GDP-fucose protein O-fucosyltransferase 2	elongation zone	6 h
HORVU.MOREX.r3.3HG0292080.1	-0.49333	4.723449	-3.53021	0.000868	0.023177	-1.01265	F-box family protein-like	elongation zone	6 h
HORVU.MOREX.r3.6HG0622550.1	-0.34993	5.355981	-3.56854	0.000772	0.022075	-1.01301	Cyclic nucleotide-gated channel	elongation zone	6 h
HORVU.MOREX.r3.2HG0186750.1	2.919088	1.34332	3.638218	0.000623	0.019533	-1.01355	Growth-regulating factor	elongation zone	6 h
HORVU.MOREX.r3.7HG0747690.1	3.555856	0.558808	3.609986	0.000679	0.020694	-1.01965	Hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyltransferase	elongation zone	6 h
HORVU.MOREX.r3.3HG0280920.1	-0.734	3.219452	-3.55946	0.000794	0.022311	-1.01971	DUF4228 domain protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0620630.1	0.917238	3.35364	3.643419	0.000613	0.019279	-1.02228	Subtilisin-like protease	elongation zone	6 h
HORVU.MOREX.r3.4HG0391160.1	0.961782	4.078357	3.437601	0.00115	0.027274	-1.0225	Patatin	elongation zone	6 h
HORVU.MOREX.r3.7HG0726770.1	0.936261	2.29225	3.496706	0.000961	0.024536	-1.02467	Glycine-rich protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0341800.1	0.651379	2.209476	3.565182	0.00078	0.02217	-1.02687	Receptor-like kinase	elongation zone	6 h
HORVU.MOREX.r3.2HG0182400.1	0.787318	5.649464	3.606868	0.000686	0.020703	-1.03023	Aquaporin	elongation zone	6 h
HORVU.MOREX.r3.7HG0711890.1	1.034972	2.553034	3.524749	0.000883	0.023391	-1.03035	O-methyltransferase	elongation zone	6 h
HORVU.MOREX.r3.4HG0364210.1	2.506742	-2.34248	3.582055	0.00074	0.021553	-1.03304	#N/A	elongation zone	6 h
HORVU.MOREX.r3.6HG0577770.1	-1.91662	-0.27649	-3.52521	0.000881	0.023391	-1.03415	P-loop containing nucleoside triphosphate hydrolases superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0197230.1	1.239964	-1.20366	3.412461	0.00124	0.028698	-1.04106	disease resistance protein (TIR-NBS-LRR class)	elongation zone	6 h
HORVU.MOREX.r3.7HG0655170.1	1.356424	0.095219	3.426857	0.001187	0.027891	-1.04256	Late embryogenesis abundant protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0517640.1	-0.6841	6.451472	-3.57632	0.000754	0.021777	-1.04518	Glucan endo-1,3-beta-glucosidase, putative	elongation zone	6 h
HORVU.MOREX.r3.2HG0120470.1	1.316735	3.222129	3.668206	0.000567	0.018303	-1.05145	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.4HG0398090.1	0.671999	4.062819	3.552775	0.00081	0.022568	-1.05179	Syntaxin protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0388310.1	0.411842	3.870759	3.542848	0.000835	0.022819	-1.05405	Protein kinase	elongation zone	6 h
HORVU.MOREX.r3.3HG0244040.1	1.22859	-2.29384	3.390814	0.001323	0.029902	-1.05708	ethylene-responsive transcription factor	elongation zone	6 h
HORVU.MOREX.r3.4HG0355390.1	-0.74552	1.970371	-3.40081	0.001284	0.02931	-1.05918	RING/U-box superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0465400.1	1.191877	0.747502	3.548547	0.000821	0.022653	-1.07019	Trichome birefringence-like protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0674440.1	-0.45381	5.321799	-3.54829	0.000821	0.022653	-1.07201	Aluminum activated malate transporter family protein	elongation zone	6 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.6HG0572400.1	-0.41327	3.75498	-3.47036	0.001041	0.025776	-1.07302	F-box family protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0381150.1	2.074882	-0.56149	3.549958	0.000817	0.022629	-1.08111	nuclear pore complex protein (DUF3414)	elongation zone	6 h
HORVU.MOREX.r3.4HG0343710.1	-0.34929	4.292721	-3.50719	0.000931	0.024187	-1.08281	Calcineurin-like metallo-phosphoesterase superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0510160.1	-0.45995	4.316907	-3.46305	0.001065	0.026178	-1.08575	Myb/SANT-like DNA-binding domain protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0524060.1	1.293089	3.909294	3.498747	0.000955	0.024445	-1.08979	Remorin	elongation zone	6 h
HORVU.MOREX.r3.1HG0056240.1	0.671893	4.721848	3.552163	0.000812	0.022568	-1.09102	Trehalose 6-phosphate phosphatase	elongation zone	6 h
HORVU.MOREX.r3.3HG0278630.1	0.519308	5.03935	3.532936	0.000861	0.023177	-1.09385	Ras-related protein, expressed	elongation zone	6 h
HORVU.MOREX.r3.1HG0069380.1	0.824246	2.129643	3.486991	0.00099	0.025053	-1.09471	Cysteine proteinase inhibitor	elongation zone	6 h
HORVU.MOREX.r3.1HG0092200.1	1.364471	1.592343	3.361325	0.001445	0.031276	-1.09884	Solanesyl diphosphate synthase family protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0121570.1	-0.50747	4.65733	-3.48316	0.001002	0.025247	-1.10642	Protein LTV1	elongation zone	6 h
HORVU.MOREX.r3.2HG0182650.1	2.04427	-1.3514	3.370063	0.001408	0.030961	-1.10742	Cytokinin oxidase/dehydrogenase	elongation zone	6 h
HORVU.MOREX.r3.6HG0609520.1	-0.46892	8.966633	-3.65911	0.000583	0.018648	-1.10792	Fatty acid desaturase	elongation zone	6 h
HORVU.MOREX.r3.2HG0211880.1	-0.4562	4.077958	-3.45819	0.00108	0.026331	-1.10829	Exostosin family protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0373800.1	-1.0656	1.360295	-3.35658	0.001465	0.031424	-1.10939	helicase with zinc finger protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0044800.1	2.156857	-1.71771	3.359186	0.001454	0.031376	-1.11211	DnaJ heat shock amino-terminal domain protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0309410.1	-0.97268	3.365238	-3.38368	0.001352	0.03018	-1.11324	Subtilisin-like protease	elongation zone	6 h
HORVU.MOREX.r3.1HG0052250.1	1.481307	0.582616	3.358468	0.001457	0.031377	-1.11426	Membrane-associated kinase regulator-like protein, putative	elongation zone	6 h
HORVU.MOREX.r3.6HG0579050.1	1.256213	0.455547	3.356607	0.001465	0.031424	-1.11451	Pentatricopeptide repeat-containing protein At5g14820, mitochondrial	elongation zone	6 h
HORVU.MOREX.r3.3HG0308350.1	0.910081	4.926407	3.500607	0.00095	0.024398	-1.11725	Cysteine-rich receptor kinase	elongation zone	6 h
HORVU.MOREX.r3.1HG0051740.1	-1.90775	3.433417	-3.36841	0.001415	0.030961	-1.12137	Glutathione s-transferase, putative	elongation zone	6 h
HORVU.MOREX.r3.7HG0717610.1	0.589725	4.008622	3.510342	0.000922	0.024017	-1.12243	Pollen-specific protein SF21	elongation zone	6 h
HORVU.MOREX.r3.3HG0280960.1	0.713944	1.805356	3.462876	0.001065	0.026178	-1.12475	Glycosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.4HG0379290.1	-0.31691	5.28798	-3.51106	0.00092	0.024016	-1.12964	COP1-interacting-like protein, putative	elongation zone	6 h
HORVU.MOREX.r3.7HG0739910.1	-0.47919	4.210714	-3.4685	0.001047	0.025891	-1.1365	Disease resistance protein (NBS-LRR class) family	elongation zone	6 h
HORVU.MOREX.r3.5HG0508610.1	1.210921	3.825671	3.507445	0.00093	0.024187	-1.1369	Patatin	elongation zone	6 h
HORVU.MOREX.r3.1HG0072580.1	0.507449	5.490114	3.510775	0.000921	0.024016	-1.13814	Aminotransferase-related family protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0528310.1	0.571033	3.716139	3.482021	0.001005	0.025247	-1.13839	SPX domain-containing family protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0117100.1	0.914701	2.815111	3.344698	0.001518	0.031854	-1.13904	NHL repeat-containing protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0198320.1	1.713974	-0.19189	3.380128	0.001366	0.030437	-1.14285	Protein translation factor SUI1-like protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0558840.1	-0.26251	6.872948	-3.55747	0.000799	0.02239	-1.14679	Kinetochore protein nuf2, putative	elongation zone	6 h
HORVU.MOREX.r3.4HG0410910.1	2.274625	-2.20066	3.478218	0.001017	0.025374	-1.15344	Ubiquitin carboxyl-terminal hydrolase CYLD	elongation zone	6 h
HORVU.MOREX.r3.5HG0444060.1	-0.88566	1.863328	-3.35509	0.001472	0.031497	-1.15513	Calmodulin-binding family protein, putative, expressed	elongation zone	6 h
HORVU.MOREX.r3.3HG0276130.1	1.05447	-0.22255	3.388953	0.001331	0.029969	-1.15932	Phospholipase A1	elongation zone	6 h
HORVU.MOREX.r3.6HG0546160.1	0.788552	2.97611	3.513646	0.000913	0.023928	-1.16082	Acylamino-acid-releasing enzyme	elongation zone	6 h
HORVU.MOREX.r3.3HG0290300.1	2.995613	-2.72546	3.56112	0.00079	0.022277	-1.16252	Homeobox leucine zipper protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0171780.1	1.569453	-1.26245	3.335709	0.001559	0.032443	-1.16258	transcription repressor	elongation zone	6 h
HORVU.MOREX.r3.2HG0140700.1	-0.31445	5.904168	-3.53193	0.000864	0.023177	-1.16261	#N/A	elongation zone	6 h
HORVU.MOREX.r3.6HG0542050.1	1.293229	1.403897	3.600901	0.000699	0.02093	-1.16408	Acid beta-fructofuranosidase	elongation zone	6 h
HORVU.MOREX.r3.5HG0485960.1	1.767777	-2.16732	3.350303	0.001493	0.031694	-1.16548	Transmembrane emp24 domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0528280.1	0.424964	5.95615	3.546665	0.000825	0.022736	-1.16667	Organic solute transporter-like	elongation zone	6 h
HORVU.MOREX.r3.2HG0189780.1	1.683591	0.49991	3.368277	0.001415	0.030961	-1.17027	ethylene-responsive transcription factor	elongation zone	6 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0086480.1	1.367622	0.13169	3.358812	0.001456	0.031377	-1.17405	UV-B-induced protein, chloroplastic	elongation zone	6 h
HORVU.MOREX.r3.3HG0242870.1	-0.29248	7.618528	-3.59984	0.000701	0.020963	-1.17846	Carboxypeptidase	elongation zone	6 h
HORVU.MOREX.r3.6HG0627920.1	-0.28575	7.364979	-3.59031	0.000722	0.021192	-1.18198	Ankyrin repeat protein-like	elongation zone	6 h
HORVU.MOREX.r3.7HG0667180.1	-0.79845	1.133168	-3.32841	0.001593	0.03286	-1.19533	F-box protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0403370.1	-0.40266	4.841977	-3.46513	0.001058	0.026094	-1.19667	O-fucosyltransferase family protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0089130.1	-0.35304	5.608758	-3.47388	0.00103	0.025565	-1.20081	Serine/Threonine-kinase pakA-like protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0393520.1	0.781571	3.79819	3.422568	0.001203	0.028114	-1.20317	Microtubule associated protein family protein, putative, expressed	elongation zone	6 h
HORVU.MOREX.r3.2HG0172730.1	-0.43328	7.548613	-3.56918	0.00077	0.022075	-1.20709	Alpha-ketoglutarate-dependent dioxygenase alkB-like protein 2	elongation zone	6 h
HORVU.MOREX.r3.3HG0273730.1	-0.55109	6.291958	-3.53371	0.000859	0.023177	-1.20766	Cytochrome P450	elongation zone	6 h
HORVU.MOREX.r3.2HG0179320.1	0.799008	3.064606	3.430059	0.001176	0.02774	-1.21157	BTB/POZ domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0522630.1	0.721851	1.481024	3.521879	0.00089	0.023455	-1.21186	Blue copper protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0472810.1	0.883584	2.371978	3.554182	0.000807	0.022551	-1.21234	Aquaporin	elongation zone	6 h
HORVU.MOREX.r3.4HG0410640.1	-0.37826	8.151713	-3.59083	0.000721	0.021192	-1.21394	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	elongation zone	6 h
HORVU.MOREX.r3.2HG0109340.1	1.1237	0.874826	3.369099	0.001412	0.030961	-1.21485	Wound-induced protein 1, putative, expressed	elongation zone	6 h
HORVU.MOREX.r3.7HG0660720.1	1.67228	1.415323	3.352681	0.001483	0.031653	-1.22023	Ring finger protein, putative	elongation zone	6 h
HORVU.MOREX.r3.5HG0438280.1	-1.80554	0.696137	-3.35361	0.001478	0.031602	-1.22094	Protein translocase subunit SecA	elongation zone	6 h
HORVU.MOREX.r3.1HG0073010.1	0.83823	1.113004	3.520944	0.000893	0.023461	-1.22218	Kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0710170.1	-2.23823	0.072486	-3.45827	0.00108	0.026331	-1.22528	ATP-dependent DNA helicase 2 subunit KU70	elongation zone	6 h
HORVU.MOREX.r3.1HG0083040.1	-0.74817	1.526854	-3.39189	0.001319	0.029839	-1.22565	Retrovirus-related Pol polyprotein from transposon TNT 1-94	elongation zone	6 h
HORVU.MOREX.r3.7HG0667280.1	-0.43161	4.293106	-3.44295	0.001131	0.027022	-1.226	Hexosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.6HG0613230.1	-0.36781	6.009357	-3.52752	0.000875	0.023293	-1.23323	Allergen, putative	elongation zone	6 h
HORVU.MOREX.r3.6HG0566940.1	0.575621	4.632192	3.456992	0.001084	0.026395	-1.23533	Sulfurtransferase	elongation zone	6 h
HORVU.MOREX.r3.2HG0195600.1	-0.3589	4.30012	-3.44221	0.001134	0.027022	-1.23689	GPI mannosyltransferase 2	elongation zone	6 h
HORVU.MOREX.r3.3HG0322740.1	-0.90268	0.784975	-3.35622	0.001467	0.031424	-1.23717	transmembrane protein, putative (DUF247)	elongation zone	6 h
HORVU.MOREX.r3.7HG0751290.1	-0.90823	0.60944	-3.30604	0.001702	0.03438	-1.23788	Receptor-kinase, putative	elongation zone	6 h
HORVU.MOREX.r3.7HG0745700.1	-0.30534	5.461365	-3.49791	0.000958	0.024477	-1.23959	Phox (PX) domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0252250.1	1.398626	-1.6584	3.372568	0.001397	0.03093	-1.23999	Expansin	elongation zone	6 h
HORVU.MOREX.r3.7HG0656570.1	0.910474	1.40656	3.301451	0.001726	0.034545	-1.24512	Pentatricopeptide repeat-containing protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0120560.1	1.319028	3.65156	3.623809	0.000651	0.020087	-1.24529	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.5HG0474540.1	-0.36376	7.609556	-3.56527	0.00078	0.02217	-1.24578	Protein transport protein Sec61 subunit alpha	elongation zone	6 h
HORVU.MOREX.r3.7HG0722380.1	-0.50336	2.715102	-3.35625	0.001467	0.031424	-1.24987	Nudix hydrolase	elongation zone	6 h
HORVU.MOREX.r3.2HG0137140.1	-1.13362	0.734361	-3.30229	0.001721	0.034545	-1.25066	Acyl-CoA dehydrogenase family member 10	elongation zone	6 h
HORVU.MOREX.r3.7HG0679050.1	0.565689	4.002868	3.404806	0.001269	0.029123	-1.25557	Upstream activation factor subunit spp27	elongation zone	6 h
HORVU.MOREX.r3.6HG0593200.1	-0.87124	4.784544	-3.4036	0.001273	0.029154	-1.25682	Short-chain dehydrogenase/reductase family protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0030290.1	2.990007	-1.84835	3.512989	0.000915	0.023945	-1.25899	PRA1 family protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0488300.1	1.483763	2.76736	3.39983	0.001288	0.029352	-1.25958	ABC transporter G family member	elongation zone	6 h
HORVU.MOREX.r3.6HG0560140.1	2.173685	-1.9167	3.294894	0.001759	0.03479	-1.2647	Endoglucanase	elongation zone	6 h
HORVU.MOREX.r3.4HG0353120.1	1.422343	-2.86086	3.295926	0.001754	0.034787	-1.26878	Transposon protein, putative, CACTA, En/Spm sub-class	elongation zone	6 h
HORVU.MOREX.r3.3HG0239900.1	1.36656	3.375419	3.356822	0.001464	0.031424	-1.27127	Auxin-responsive protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0193510.2	-0.36012	3.804131	-3.41196	0.001242	0.028698	-1.276	Gpcr-type g protein 2	elongation zone	6 h
HORVU.MOREX.r3.6HG0611050.1	2.46585	-0.65229	3.569275	0.00077	0.022075	-1.27667	Rubisco methyltransferase family protein	elongation zone	6 h

Table Sн Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.5HG0473970.1	2.298764	-3.04844	3.330914	0.001582	0.032759	-1.27748	Glycosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.1HG0025870.1	0.56367	4.903164	3.453644	0.001095	0.026631	-1.27978	6,7-dimethyl-8-ribityllumazine synthase	elongation zone	6 h
HORVU.MOREX.r3.7HG0663940.1	0.835316	0.764913	3.444763	0.001125	0.027022	-1.28354	Alpha/beta-Hydrolases superfamily protein, putative	elongation zone	6 h
HORVU.MOREX.r3.4HG0396030.1	1.938505	0.582741	3.293492	0.001767	0.034855	-1.2851	Tubulin alpha chain	elongation zone	6 h
HORVU.MOREX.r3.7HG0636030.1	0.839192	-1.10938	3.386966	0.001338	0.030049	-1.28672	hydroxysteroid dehydrogenase 3	elongation zone	6 h
HORVU.MOREX.r3.7HG0728080.1	0.821239	4.103954	3.327381	0.001598	0.032894	-1.28779	Protein CHLOROPLAST IMPORT APPARATUS 2	elongation zone	6 h
HORVU.MOREX.r3.3HG0254940.1	0.860821	2.451212	3.543125	0.000834	0.022819	-1.28993	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.1HG0054010.1	0.571617	5.841657	3.535391	0.000854	0.023177	-1.29355	zinc finger B-box protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0701080.1	0.984388	-1.51889	3.304935	0.001708	0.034427	-1.29449	MYB transcription factor	elongation zone	6 h
HORVU.MOREX.r3.6HG0597320.1	-0.28729	6.618535	-3.50628	0.000934	0.024223	-1.29535	ATP-dependent Clp protease proteolytic subunit	elongation zone	6 h
HORVU.MOREX.r3.7HG0661490.1	-0.30737	6.094894	-3.49597	0.000964	0.024561	-1.29574	Stromal cell-derived factor 2	elongation zone	6 h
HORVU.MOREX.r3.2HG0171810.1	-0.48908	3.837575	-3.36737	0.001419	0.031012	-1.29725	DUF1644 family protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0075440.1	0.716354	1.650312	3.414336	0.001233	0.028622	-1.30319	Protein NRT1/ PTR FAMILY 5.5	elongation zone	6 h
HORVU.MOREX.r3.5HG0485610.1	1.185152	0.79472	3.335437	0.00156	0.032443	-1.30544	Cytochrome P450, putative	elongation zone	6 h
HORVU.MOREX.r3.3HG0258240.1	1.351762	1.126706	3.299747	0.001734	0.03465	-1.30547	Sacsin	elongation zone	6 h
HORVU.MOREX.r3.7HG0711230.1	0.58968	3.91603	3.376543	0.001381	0.030664	-1.3062	Auxin-responsive protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0714530.1	-1.36198	0.583064	-3.2808	0.001834	0.03577	-1.30637	F-box protein PP2	elongation zone	6 h
HORVU.MOREX.r3.3HG0307340.1	1.299012	1.041748	3.278696	0.001845	0.035889	-1.30674	Receptor-like kinase	elongation zone	6 h
HORVU.MOREX.r3.2HG0205200.1	-0.45711	4.551525	-3.41464	0.001232	0.028622	-1.30802	Ubiquitin carboxyl-terminal hydrolase	elongation zone	6 h
HORVU.MOREX.r3.3HG0257130.1	-0.50669	4.342452	-3.39935	0.00129	0.029352	-1.30857	Presenilin	elongation zone	6 h
HORVU.MOREX.r3.2HG0106260.1	2.138318	-2.23574	3.330361	0.001584	0.032759	-1.30885	F-box family protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0484180.1	0.408465	5.636527	3.473067	0.001033	0.025597	-1.3108	DUF868 family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0738770.1	0.926577	1.993948	3.272677	0.001878	0.036323	-1.31682	Receptor-like kinase	elongation zone	6 h
HORVU.MOREX.r3.2HG0121670.1	0.737294	2.510007	3.460128	0.001074	0.026284	-1.31969	Ribosome-releasing factor 2, mitochondrial	elongation zone	6 h
HORVU.MOREX.r3.1HG0046210.1	2.432764	-0.44242	3.311924	0.001673	0.034187	-1.32193	Receptor kinase	elongation zone	6 h
HORVU.MOREX.r3.3HG0236500.1	0.687458	5.370928	3.442402	0.001133	0.027022	-1.324	Pollen-specific protein SF21	elongation zone	6 h
HORVU.MOREX.r3.2HG0213250.1	-0.53848	6.347479	-3.50197	0.000946	0.024358	-1.3309	Choline transporter-related family protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0190300.1	0.597955	3.611092	3.425313	0.001193	0.027914	-1.33675	SHR5-receptor-like kinase	elongation zone	6 h
HORVU.MOREX.r3.3HG0307950.1	-0.303	6.122502	-3.48244	0.001004	0.025247	-1.34039	GPI transamidase component PIG-S	elongation zone	6 h
HORVU.MOREX.r3.7HG0706130.1	0.695062	4.046121	3.451295	0.001103	0.026745	-1.34131	Kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0403680.1	-1.26457	3.612484	-3.37319	0.001395	0.030906	-1.34211	#N/A	elongation zone	6 h
HORVU.MOREX.r3.4HG0396760.1	-0.40032	5.597414	-3.4748	0.001027	0.025525	-1.34253	Protein root UVB sensitive 3	elongation zone	6 h
HORVU.MOREX.r3.3HG0292490.1	0.897386	0.56764	3.443305	0.00113	0.027022	-1.34584	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein, putat	elongation zone	6 h
HORVU.MOREX.r3.1HG0040930.1	1.788286	-2.88506	3.306536	0.0017	0.03438	-1.34999	F-box family protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0062630.1	0.521188	5.379794	3.426236	0.00119	0.027891	-1.35007	#N/A	elongation zone	6 h
HORVU.MOREX.r3.5HG0495910.1	1.915482	-0.71833	3.2621	0.001937	0.036879	-1.35581	Respiratory burst oxidase homolog	elongation zone	6 h
HORVU.MOREX.r3.4HG0378080.1	2.8965	-1.12859	3.505461	0.000936	0.024245	-1.35662	#N/A	elongation zone	6 h
HORVU.MOREX.r3.4HG0383780.1	1.843386	-0.06269	3.333248	0.001571	0.032621	-1.36249	Laccase	elongation zone	6 h
HORVU.MOREX.r3.6HG0577220.1	1.847585	-2.2339	3.252914	0.00199	0.037535	-1.3659	Glycosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.7HG0662420.1	1.086645	1.123246	3.308235	0.001691	0.034363	-1.36782	Kinase-like protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0676690.1	0.802091	4.543618	3.557152	0.000799	0.02239	-1.36808	Receptor-like kinase	elongation zone	6 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0082630.1	-0.36116	5.023124	-3.42597	0.001191	0.027891	-1.36863	Glycosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.4HG0409180.1	-0.32848	6.8545	-3.49902	0.000955	0.024445	-1.36869	Glutathione S-transferase	elongation zone	6 h
HORVU.MOREX.r3.6HG0543540.1	1.505351	-0.02472	3.342677	0.001527	0.032013	-1.37011	Expansin protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0458440.1	-1.06742	1.256617	-3.24885	0.002014	0.037845	-1.3773	phosphoglycerate/bisphosphoglycerate mutase family protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0501200.1	-0.49089	4.695239	-3.40731	0.001259	0.028987	-1.37857	Thioredoxin superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0293010.1	-0.41184	4.239633	-3.40709	0.00126	0.028987	-1.37863	WD-repeat protein, putative	elongation zone	6 h
HORVU.MOREX.r3.2HG0168270.1	-0.53513	3.16772	-3.30572	0.001704	0.03438	-1.37984	Ubiquitin carboxyl-terminal hydrolase	elongation zone	6 h
HORVU.MOREX.r3.6HG0588350.1	-0.49933	4.125371	-3.34559	0.001514	0.031802	-1.38241	RING finger family protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0141140.1	1.060458	-2.85799	3.243919	0.002043	0.03815	-1.38719	DUF4228 domain protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0495730.1	0.985288	2.468419	3.381677	0.00136	0.030329	-1.38732	Kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0554050.1	0.865174	-1.56957	3.294882	0.001759	0.03479	-1.38751	cyclin-dependent kinase inhibitor	elongation zone	6 h
HORVU.MOREX.r3.4HG0342080.1	0.693973	4.067325	3.430642	0.001174	0.027723	-1.38771	Adenine/guanine permease	elongation zone	6 h
HORVU.MOREX.r3.7HG0749090.1	1.083227	-0.58865	3.369963	0.001408	0.030961	-1.38909	Expansin-like protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0582120.1	0.474716	3.287652	3.369458	0.00141	0.030961	-1.3893	magnesium transporter NIPA (DUF803)	elongation zone	6 h
HORVU.MOREX.r3.3HG0249640.1	0.598829	4.297068	3.434269	0.001161	0.027485	-1.39086	E3 ubiquitin-protein ligase	elongation zone	6 h
HORVU.MOREX.r3.6HG0555700.1	-0.36921	8.875975	-3.5732	0.000761	0.02193	-1.39114	Calreticulin/calnexin	elongation zone	6 h
HORVU.MOREX.r3.6HG0633650.1	-1.17282	0.935723	-3.24671	0.002027	0.037944	-1.39236	#N/A	elongation zone	6 h
HORVU.MOREX.r3.5HG0486750.1	0.734142	2.037011	3.384947	0.001347	0.030132	-1.39395	Phosphatase 2C family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0638850.1	-0.42458	7.446158	-3.53269	0.000861	0.023177	-1.3948	Cellulose synthase-like protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0057780.1	-0.40647	5.901425	-3.45204	0.001101	0.026729	-1.39646	bZIP transcription factor (DUF630 and DUF632)	elongation zone	6 h
HORVU.MOREX.r3.2HG0178160.1	-0.56924	7.879945	-3.5041	0.00094	0.024262	-1.39871	HTH-type transcriptional regulator YidZ	elongation zone	6 h
HORVU.MOREX.r3.6HG0607360.1	-0.55585	4.502873	-3.34854	0.001501	0.031694	-1.39955	WAT1-related protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0417670.1	1.218021	0.032065	3.409555	0.001251	0.028873	-1.40445	Lipid transfer protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0279100.1	1.189175	-1.86348	3.253361	0.001988	0.03752	-1.40817	Serine/threonine-protein kinase	elongation zone	6 h
HORVU.MOREX.r3.4HG0337870.1	0.822274	4.45297	3.420684	0.00121	0.028241	-1.4105	Homeobox-leucine zipper family protein / lipid-binding START domain-containing	elongation zone	6 h
HORVU.MOREX.r3.1HG0055320.1	-0.27754	5.996621	-3.45996	0.001075	0.026284	-1.4147	Protein phosphatase 2C	elongation zone	6 h
HORVU.MOREX.r3.1HG0073170.1	-0.61217	5.178736	-3.36559	0.001427	0.031106	-1.41553	F-box protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0631660.1	0.692153	5.110572	3.387391	0.001337	0.030044	-1.41608	RING/U-box superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0330040.1	-0.65876	2.332376	-3.25861	0.001957	0.037085	-1.4162	Kelch repeat-containing F-box family protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0122880.1	1.452158	1.048128	3.242228	0.002053	0.038269	-1.41718	Phytoene desaturase	elongation zone	6 h
HORVU.MOREX.r3.1HG0020270.1	-0.37999	5.457119	-3.39682	0.0013	0.029498	-1.41768	SAD1/UNC-84 domain protein, putative	elongation zone	6 h
HORVU.MOREX.r3.5HG0528910.1	0.915646	1.611089	3.365978	0.001425	0.031106	-1.41779	DUF3511 domain protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0468580.1	1.417051	-0.71714	3.307261	0.001696	0.03438	-1.41789	Cinnamoyl-CoA reductase	elongation zone	6 h
HORVU.MOREX.r3.3HG0288070.1	0.565253	0.496177	3.395473	0.001305	0.029585	-1.41861	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein, putati	elongation zone	6 h
HORVU.MOREX.r3.4HG0361680.1	-0.87521	4.471436	-3.33245	0.001574	0.032666	-1.42034	Nuclear distribution protein nudE-like 1	elongation zone	6 h
HORVU.MOREX.r3.5HG0420830.1	1.128876	-1.8789	3.239579	0.002069	0.038427	-1.42154	cycling DOF factor 1	elongation zone	6 h
HORVU.MOREX.r3.3HG0234030.1	0.932613	0.965447	3.438866	0.001145	0.027233	-1.42454	Xyloglucan galactosyltransferase KATAMARI1-like protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0025430.1	1.272739	0.604962	3.235551	0.002094	0.038776	-1.42521	WEB family protein (DUF827)	elongation zone	6 h
HORVU.MOREX.r3.7HG0648390.1	0.931378	-0.60992	3.3019	0.001723	0.034545	-1.4256	Protein casein kinase I-like 4	elongation zone	6 h
HORVU.MOREX.r3.1HG0003090.7	-1.19155	6.089425	-3.36909	0.001412	0.030961	-1.42645	Thionin-2.2	elongation zone	6 h
HORVU.MOREX.r3.5HG0448080.1	-0.55616	5.913862	-3.48048	0.00101	0.025334	-1.42749	Polyol transporter	elongation zone	6 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.7HG0676040.1	0.657176	-0.53383	3.301728	0.001724	0.034545	-1.43062	Decaprenyl-phosphate N-acetylglucosaminephosphotransferase	elongation zone	6 h
HORVU.MOREX.r3.7HG0650250.1	-0.51392	3.840838	-3.32591	0.001605	0.033004	-1.43066	Protein-O-fucosyltransferase 1	elongation zone	6 h
HORVU.MOREX.r3.6HG0613460.1	1.160272	2.574467	3.317967	0.001643	0.033722	-1.43285	MACPF domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0526200.1	-0.27222	5.485729	-3.4075	0.001259	0.028987	-1.43675	Sec14 cytosolic factor	elongation zone	6 h
HORVU.MOREX.r3.7HG0639930.1	-0.51382	3.436078	-3.29629	0.001752	0.034787	-1.43694	Protein FAR1-RELATED SEQUENCE 5	elongation zone	6 h
HORVU.MOREX.r3.2HG0161580.1	-0.55261	2.675596	-3.26116	0.001943	0.03691	-1.43772	Alpha/beta-Hydrolases superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0526160.1	-0.49719	4.252818	-3.3639	0.001434	0.031117	-1.44504	NBS-LRR resistance-like protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0650310.1	1.34066	2.884324	3.219994	0.002191	0.039786	-1.44519	RNA-binding family protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0417710.1	0.957589	0.768626	3.419588	0.001214	0.028302	-1.44627	Protease inhibitor/seed storage/lipid transfer protein family protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0326330.1	0.989929	0.282326	3.393048	0.001314	0.029768	-1.44669	Rho GTPase-activating protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0152430.1	-0.47782	6.139317	-3.45067	0.001105	0.026745	-1.44713	Ubiquitin carboxyl-terminal hydrolase, putative	elongation zone	6 h
HORVU.MOREX.r3.6HG0618180.1	1.443268	-2.40297	3.221915	0.002179	0.039605	-1.44815	Universal stress protein family protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0347840.1	0.48229	3.393693	3.305944	0.001703	0.03438	-1.44907	Receptor-type tyrosine-protein phosphatase	elongation zone	6 h
HORVU.MOREX.r3.2HG0121630.1	0.738785	3.093911	3.24361	0.002045	0.03815	-1.45083	Mitochondrial carrier family protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0511090.1	0.552882	5.583411	3.399218	0.00129	0.029352	-1.45167	Phytochrome	elongation zone	6 h
HORVU.MOREX.r3.2HG0117880.1	2.617431	-0.66123	3.231312	0.00212	0.039083	-1.46232	GDSL esterase/lipase	elongation zone	6 h
HORVU.MOREX.r3.3HG0218560.1	1.025919	0.309747	3.287218	0.001799	0.035369	-1.46421	Receptor-like protein kinase	elongation zone	6 h
HORVU.MOREX.r3.4HG0406600.1	0.744867	0.071867	3.384001	0.00135	0.03018	-1.46458	Heavy metal transport/detoxification superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0400990.1	-0.52699	5.330008	-3.39018	0.001326	0.029926	-1.46468	3-hydroxybenzoate 6-hydroxylase 1	elongation zone	6 h
HORVU.MOREX.r3.7HG0716640.1	0.831281	2.750789	3.478107	0.001017	0.025374	-1.465	Xyloglucan endotransglucosylase/hydrolase	elongation zone	6 h
HORVU.MOREX.r3.5HG0485410.1	2.23351	-0.44467	3.440032	0.001141	0.027169	-1.46659	#N/A	elongation zone	6 h
HORVU.MOREX.r3.5HG0441420.1	2.301652	-0.42861	3.33893	0.001544	0.032239	-1.46695	Ankyrin repeat-containing protein, putative	elongation zone	6 h
HORVU.MOREX.r3.3HG0309460.1	-0.28496	5.431182	-3.41381	0.001235	0.028635	-1.46731	Trichome birefringence-like protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0688730.1	0.515643	4.635127	3.339143	0.001543	0.032239	-1.47174	Myotubularin	elongation zone	6 h
HORVU.MOREX.r3.1HG0082770.1	-0.28673	7.702552	-3.48415	0.000999	0.025239	-1.47447	Reticulon-like protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0552230.1	-0.52885	6.698601	-3.44735	0.001116	0.026982	-1.47521	Polyubiquitin	elongation zone	6 h
HORVU.MOREX.r3.5HG0524800.1	-1.37206	1.969957	-3.20739	0.002273	0.040716	-1.47557	RNA polymerase II transcription mediator	elongation zone	6 h
HORVU.MOREX.r3.3HG0264440.1	-0.65319	2.161098	-3.22657	0.002149	0.039274	-1.47801	Condensin complex subunit 2	elongation zone	6 h
HORVU.MOREX.r3.2HG0145360.1	0.99074	3.483304	3.521457	0.000892	0.023455	-1.47842	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.7HG0731320.1	-0.34152	5.022738	-3.39779	0.001296	0.029445	-1.48169	O-fucosyltransferase family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0659040.1	0.83727	3.074402	3.25216	0.001995	0.037583	-1.48313	Formin-like protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0683600.1	1.85156	0.200809	3.222443	0.002175	0.039605	-1.48589	F-box protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0470170.1	-0.52632	3.126834	-3.2699	0.001893	0.036511	-1.48661	F-box family protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0055590.1	1.461738	-0.98036	3.207102	0.002275	0.040716	-1.48807	RING/U-box superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0389250.1	1.309859	3.018686	3.256512	0.001969	0.037279	-1.49206	lipase, putative (DUF620)	elongation zone	6 h
HORVU.MOREX.r3.6HG0607590.1	1.035755	1.682477	3.229268	0.002133	0.039141	-1.49349	U-box domain-containing family protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0335160.1	0.801062	3.629312	3.312649	0.001669	0.034187	-1.49638	Hedgehog-interacting-like protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0302340.1	-2.74254	-0.09437	-3.34737	0.001506	0.031731	-1.49728	Eukaryotic aspartyl protease family protein, expressed	elongation zone	6 h
HORVU.MOREX.r3.7HG0705500.1	1.092654	0.351075	3.19715	0.002341	0.041422	-1.50384	Non-lysosomal glucosylceramidase	elongation zone	6 h
HORVU.MOREX.r3.2HG0188490.1	-0.80805	2.129721	-3.22186	0.002179	0.039605	-1.51267	No-apical-meristem-associated carboxy-terminal domain protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0737470.1	1.027893	3.292476	3.553377	0.000809	0.022568	-1.51293	Peroxidase	elongation zone	6 h

Table Sн Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0296990.1	0.924845	-1.49078	3.224981	0.002159	0.039386	-1.51338	LURP-one-like protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0498240.1	2.677685	-1.97942	3.2285	0.002137	0.039149	-1.51359	Cytochrome P450, putative	elongation zone	6 h
HORVU.MOREX.r3.5HG0439190.1	-0.50769	2.950971	-3.31166	0.001674	0.034187	-1.5165	Cytochrome P450	elongation zone	6 h
HORVU.MOREX.r3.6HG0627570.1	-0.53916	4.766957	-3.34614	0.001512	0.031783	-1.51679	Immunoglobulin A1 protease autotransporter	elongation zone	6 h
HORVU.MOREX.r3.7HG0668820.1	0.563417	4.620228	3.468103	0.001049	0.025891	-1.52697	Endoglucanase	elongation zone	6 h
HORVU.MOREX.r3.7HG0720790.1	-0.87663	3.44449	-3.21698	0.00221	0.040038	-1.53092	Myb family transcription factor family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0738680.1	0.700665	3.55287	3.359412	0.001453	0.031376	-1.53145	Vacuolar sorting receptor family protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0132160.1	2.326143	-1.56452	3.29579	0.001755	0.034787	-1.53285	Ethylene-responsive transcription factor	elongation zone	6 h
HORVU.MOREX.r3.4HG0408780.1	2.085153	0.649042	3.362806	0.001439	0.031171	-1.53523	Pentatricopeptide repeat-containing protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0674990.1	-0.46509	3.286295	-3.27395	0.001871	0.036221	-1.53723	Mannan endo-1,4-beta-mannosidase-like protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0569610.1	-0.72343	5.321736	-3.41496	0.001231	0.028622	-1.54425	#N/A	elongation zone	6 h
HORVU.MOREX.r3.4HG0415590.1	-1.43555	-0.04239	-3.20186	0.00231	0.041032	-1.5512	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily p	elongation zone	6 h
HORVU.MOREX.r3.7HG0674320.1	-0.36868	4.709886	-3.3693	0.001411	0.030961	-1.55234	Vesicle transport protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0399530.1	1.75006	1.156384	3.180918	0.002454	0.042679	-1.55264	Zinc finger protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0667260.1	0.801391	2.036947	3.241502	0.002058	0.038281	-1.55386	Trichome birefringence-like protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0219750.1	-1.73555	-0.71619	-3.20495	0.002289	0.040793	-1.55811	Disease resistance protein (NBS-LRR class) family	elongation zone	6 h
HORVU.MOREX.r3.4HG0345610.1	-0.28595	8.214926	-3.49056	0.000979	0.024844	-1.55951	Protein transport protein Sec24-like family	elongation zone	6 h
HORVU.MOREX.r3.3HG0294390.1	0.716963	-1.06639	3.212456	0.00224	0.040418	-1.5635	Pectinesterase	elongation zone	6 h
HORVU.MOREX.r3.1HG0045770.1	1.745873	-2.26851	3.180885	0.002454	0.042679	-1.57286	GRAM domain-containing protein / ABA-responsive protein-related	elongation zone	6 h
HORVU.MOREX.r3.1HG0053450.1	0.857729	3.313219	3.444959	0.001124	0.027022	-1.57323	WEB family protein, chloroplastic	elongation zone	6 h
HORVU.MOREX.r3.5HG0459600.1	0.671997	3.96473	3.348872	0.001499	0.031694	-1.57442	Serine/threonine-protein kinase	elongation zone	6 h
HORVU.MOREX.r3.7HG0679760.1	-0.47293	6.056962	-3.38543	0.001345	0.030122	-1.57527	Basic helix-loop-helix transcription factor	elongation zone	6 h
HORVU.MOREX.r3.4HG0381620.1	1.270875	-2.76226	3.165465	0.002566	0.044285	-1.57728	Transcription factor, putative	elongation zone	6 h
HORVU.MOREX.r3.2HG0160700.1	2.049175	-0.50356	3.210289	0.002254	0.040566	-1.5801	L-threonine 3-dehydrogenase	elongation zone	6 h
HORVU.MOREX.r3.2HG0151790.1	2.587146	-1.72838	3.400937	0.001284	0.02931	-1.58237	Ankyrin repeat-containing protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0495860.1	0.777665	4.058331	3.351854	0.001486	0.031669	-1.58429	glycosyltransferase family exostosin protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0219410.1	0.753885	3.869903	3.330397	0.001584	0.032759	-1.58707	Hydroxyproline-rich glycoprotein family protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0307400.1	1.254974	1.770343	3.206033	0.002282	0.040785	-1.59143	GRAS family transcription factor	elongation zone	6 h
HORVU.MOREX.r3.6HG0617730.1	-0.33983	7.183954	-3.45838	0.00108	0.026331	-1.59159	Galactoside 2-alpha-L-fucosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.1HG0083550.1	2.808128	0.710912	3.348935	0.001499	0.031694	-1.59392	Pentatricopeptide repeat-containing protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0751060.1	-0.3863	4.948458	-3.3515	0.001488	0.031669	-1.59426	Disease resistance protein (NBS-LRR class) family	elongation zone	6 h
HORVU.MOREX.r3.6HG0581020.1	-0.32994	5.648771	-3.37037	0.001406	0.030961	-1.5956	Xyloglucan 6-xylosyltransferase 1	elongation zone	6 h
HORVU.MOREX.r3.1HG0047570.1	0.705153	2.998289	3.278716	0.001845	0.035889	-1.59895	Di-glucose binding protein with Kinesin motor domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0677510.1	-0.43265	5.971824	-3.37803	0.001375	0.030595	-1.60079	Glycosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.2HG0207790.1	1.182283	-2.59422	3.154097	0.002651	0.045332	-1.60406	Serine/threonine-protein kinase	elongation zone	6 h
HORVU.MOREX.r3.5HG0476690.1	-0.3216	5.143097	-3.33998	0.00154	0.032205	-1.60892	#N/A	elongation zone	6 h
HORVU.MOREX.r3.2HG0096520.1	1.579066	0.617281	3.160341	0.002604	0.044719	-1.60904	Pentatricopeptide repeat-containing protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0652820.1	-2.25153	-0.08916	-3.28557	0.001808	0.035474	-1.60999	Disease resistance protein (NBS-LRR class) family	elongation zone	6 h
HORVU.MOREX.r3.6HG0558430.1	2.253591	-1.96916	3.153871	0.002653	0.045332	-1.61194	SAUR-like auxin-responsive protein family, putative	elongation zone	6 h
HORVU.MOREX.r3.1HG0095170.1	1.583626	5.086192	3.298625	0.00174	0.03465	-1.61387	UDP-glucose-4-epimerase	elongation zone	6 h
HORVU.MOREX.r3.7HG0742370.1	1.338747	-1.39541	3.152168	0.002666	0.045479	-1.6143	Calmodulin	elongation zone	6 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.2HG0159540.1	-0.82915	3.353367	-3.22968	0.00213	0.039141	-1.6157	Glycosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.7HG0728060.1	0.478751	5.512337	3.348454	0.001501	0.031694	-1.6202	Aminodeoxychorismate synthase	elongation zone	6 h
HORVU.MOREX.r3.3HG0307310.1	-0.30788	5.321617	-3.34904	0.001499	0.031694	-1.62717	magnesium transporter, putative (DUF803)	elongation zone	6 h
HORVU.MOREX.r3.5HG0524120.1	-0.36691	5.963425	-3.3774	0.001377	0.030619	-1.62904	#N/A	elongation zone	6 h
HORVU.MOREX.r3.2HG0204940.1	-0.49608	6.058217	-3.34	0.00154	0.032205	-1.6315	Crossover junction endonuclease EME1	elongation zone	6 h
HORVU.MOREX.r3.3HG0295330.1	-0.40556	7.613979	-3.46125	0.00107	0.026245	-1.63226	Sugar phosphate/phosphate translocator	elongation zone	6 h
HORVU.MOREX.r3.3HG0288940.1	-0.48121	6.05706	-3.36492	0.001429	0.031106	-1.63319	WRKY transcription factor, putative, expressed	elongation zone	6 h
HORVU.MOREX.r3.1HG0056510.1	-1.46064	0.442591	-3.17049	0.002529	0.043758	-1.63686	Cytochrome P450, putative	elongation zone	6 h
HORVU.MOREX.r3.6HG0606360.1	2.08108	-2.06608	3.143467	0.002734	0.046171	-1.63714	Peptide transporter	elongation zone	6 h
HORVU.MOREX.r3.7HG0687630.1	-0.53741	7.969317	-3.43782	0.001149	0.027274	-1.64063	Acyl carrier protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0017770.1	0.751788	2.765713	3.302164	0.001722	0.034545	-1.64412	Germin-like protein 1	elongation zone	6 h
HORVU.MOREX.r3.5HG0525430.1	0.708665	4.268757	3.385954	0.001343	0.030107	-1.64467	Trichome birefringence-like protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0708080.1	1.686414	0.105537	3.149528	0.002687	0.045781	-1.64475	Molybdate transporter 1	elongation zone	6 h
HORVU.MOREX.r3.3HG0313320.1	1.501797	-2.45652	3.148285	0.002696	0.045838	-1.64695	Potassium transporter	elongation zone	6 h
HORVU.MOREX.r3.3HG0257310.1	-0.27332	7.693219	-3.43252	0.001167	0.027599	-1.64825	Glucosidase 2 subunit beta	elongation zone	6 h
HORVU.MOREX.r3.3HG0315130.1	-1.20057	1.022238	-3.16227	0.00259	0.044578	-1.64855	RING/U-box superfamily protein, putative	elongation zone	6 h
HORVU.MOREX.r3.7HG0735210.1	1.506838	-3.00596	3.173506	0.002507	0.043525	-1.65015	Peptide transporter	elongation zone	6 h
HORVU.MOREX.r3.4HG0391730.1	-0.31715	6.58587	-3.38974	0.001327	0.029931	-1.65606	UDP-glucuronate 4-epimerase 4	elongation zone	6 h
HORVU.MOREX.r3.5HG0432950.1	0.421233	5.320519	3.327414	0.001598	0.032894	-1.66302	L-galactose dehydrogenase	elongation zone	6 h
HORVU.MOREX.r3.1HG0051960.1	-1.091	1.903866	-3.13208	0.002825	0.047264	-1.66367	DNA topoisomerase 2	elongation zone	6 h
HORVU.MOREX.r3.6HG0607160.1	0.758549	2.134391	3.265697	0.001917	0.036694	-1.67238	chitin synthase, putative (DUF1218)	elongation zone	6 h
HORVU.MOREX.r3.1HG0073430.1	0.422695	3.344559	3.232771	0.002111	0.038952	-1.67374	O-fucosyltransferase family protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0522130.1	-0.48394	4.373396	-3.28454	0.001814	0.035513	-1.67841	#N/A	elongation zone	6 h
HORVU.MOREX.r3.5HG0473920.1	-0.46191	3.263199	-3.22935	0.002132	0.039141	-1.67891	OBP32pep, putative (DUF220)	elongation zone	6 h
HORVU.MOREX.r3.4HG0344550.1	1.692325	1.167724	3.123978	0.002891	0.047996	-1.68072	UPF0496 protein 4	elongation zone	6 h
HORVU.MOREX.r3.6HG0571750.1	1.142623	0.529808	3.125012	0.002882	0.047932	-1.68478	#N/A	elongation zone	6 h
HORVU.MOREX.r3.5HG0463550.1	0.847008	4.670129	3.230927	0.002122	0.039091	-1.68583	RNA-binding domain CCCH-type zinc finger protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0597620.1	-0.3814	5.241895	-3.33561	0.00156	0.032443	-1.68609	#N/A	elongation zone	6 h
HORVU.MOREX.r3.7HG0752940.1	-0.32484	6.359204	-3.34932	0.001497	0.031694	-1.68728	RING/FYVE/PHD zinc finger protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0210650.1	1.725412	0.042671	3.122555	0.002903	0.048115	-1.68841	BTB/POZ domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0121200.1	0.743407	0.643147	3.306121	0.001702	0.03438	-1.68962	Dirigent protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0693590.1	-0.40945	4.705719	-3.29854	0.00174	0.03465	-1.69015	Exocyst complex component, putative	elongation zone	6 h
HORVU.MOREX.r3.3HG0325670.1	-0.62185	3.462193	-3.17655	0.002485	0.04318	-1.69568	#N/A	elongation zone	6 h
HORVU.MOREX.r3.6HG0572960.1	-1.03781	1.634383	-3.11559	0.002961	0.048729	-1.69655	Chlorophyll a-b binding protein, chloroplastic	elongation zone	6 h
HORVU.MOREX.r3.3HG0239980.1	1.044211	1.292154	3.247599	0.002021	0.037914	-1.6971	Alpha/beta-Hydrolases superfamily protein, putative	elongation zone	6 h
HORVU.MOREX.r3.1HG0042120.1	-0.47008	4.166727	-3.2458	0.002032	0.03801	-1.69808	WD repeat protein, putative	elongation zone	6 h
HORVU.MOREX.r3.6HG0597770.1	-0.46077	4.348024	-3.24712	0.002024	0.037933	-1.69842	F-box/LRR protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0119800.1	1.49005	-1.32815	3.113822	0.002976	0.04885	-1.70002	GDSL esterase/lipase	elongation zone	6 h
HORVU.MOREX.r3.7HG0737890.1	1.01253	1.23238	3.371189	0.001403	0.030961	-1.70131	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.1HG0073460.1	0.458291	2.975475	3.215736	0.002218	0.040113	-1.70142	Microneme/rhoptry antigen	elongation zone	6 h
HORVU.MOREX.r3.3HG0253450.1	-0.369	5.357439	-3.30846	0.00169	0.034363	-1.70681	FHA domain containing protein, expressed	elongation zone	6 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0302230.1	0.611238	4.001482	3.306541	0.0017	0.03438	-1.70687	Avr9/Cf-9 rapidly elicited protein 137	elongation zone	6 h
HORVU.MOREX.r3.1HG0079920.1	0.617331	3.500385	3.299659	0.001735	0.03465	-1.71035	Disease resistance protein (NBS-LRR class) family	elongation zone	6 h
HORVU.MOREX.r3.1HG0069210.1	-0.70361	2.90701	-3.21437	0.002227	0.040229	-1.71171	LOW protein: E3 ubiquitin ligase-like protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0481580.1	0.763379	1.426704	3.268229	0.001903	0.036589	-1.71246	Hexosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.2HG0109580.1	-1.39181	-0.60672	-3.11359	0.002978	0.04885	-1.71271	Liprin-alpha-3	elongation zone	6 h
HORVU.MOREX.r3.5HG0532960.1	-0.40744	5.01578	-3.29445	0.001762	0.03479	-1.71704	ER lumen protein-retaining receptor	elongation zone	6 h
HORVU.MOREX.r3.2HG0213840.1	1.037211	-0.58232	3.191846	0.002378	0.041914	-1.72036	transcription repressor	elongation zone	6 h
HORVU.MOREX.r3.4HG0406140.1	0.462274	5.424725	3.317398	0.001646	0.033745	-1.7221	Transmembrane protein 131	elongation zone	6 h
HORVU.MOREX.r3.7HG0718190.1	0.690847	6.009061	3.426105	0.00119	0.027891	-1.72223	ABC transporter family protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0420630.1	-0.48088	3.720927	-3.24786	0.00202	0.037914	-1.72394	Ankyrin repeat family protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0256400.1	-0.49994	3.232954	-3.19112	0.002383	0.04193	-1.72736	rRNA N-glycosidase	elongation zone	6 h
HORVU.MOREX.r3.7HG0714400.1	0.87393	2.702391	3.1813	0.002451	0.042679	-1.73113	Auxin-responsive protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0499000.1	2.121898	-0.43495	3.225887	0.002154	0.039317	-1.73274	Purple acid phosphatase	elongation zone	6 h
HORVU.MOREX.r3.7HG0636540.1	1.968688	1.811078	3.12362	0.002894	0.048007	-1.73411	Pectin lyase-like superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0224440.1	0.810164	1.43625	3.262086	0.001937	0.036879	-1.73437	DUF4228 domain protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0540020.1	1.54027	-2.7011	3.11184	0.002993	0.048862	-1.73508	Ubiquitin carboxyl-terminal hydrolase 2	elongation zone	6 h
HORVU.MOREX.r3.7HG0704060.1	0.555967	4.974659	3.205005	0.002289	0.040793	-1.73709	AT hook motif DNA-binding family protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0193490.1	1.41193	-1.27815	3.102071	0.003078	0.049581	-1.73712	Growth-regulating factor	elongation zone	6 h
HORVU.MOREX.r3.4HG0352760.1	-0.34431	5.845969	-3.32978	0.001587	0.032759	-1.74084	GPI transamidase component PIG-T	elongation zone	6 h
HORVU.MOREX.r3.6HG0573290.1	0.315378	6.719302	3.365131	0.001429	0.031106	-1.744	Zinc finger A20 and AN1 domain stress-associated protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0156810.1	-1.60509	1.309434	-3.12132	0.002913	0.048242	-1.74517	Sodium/potassium/calcium exchanger 3	elongation zone	6 h
HORVU.MOREX.r3.2HG0196940.1	-0.3414	4.564537	-3.27171	0.001883	0.036357	-1.74837	Alpha-1,3-mannosyltransferase, putative	elongation zone	6 h
HORVU.MOREX.r3.6HG0609390.1	0.72323	5.890658	3.239785	0.002068	0.038427	-1.75154	Ribose-phosphate pyrophosphokinase, putative	elongation zone	6 h
HORVU.MOREX.r3.5HG0425880.1	-0.54849	2.819479	-3.15506	0.002644	0.045269	-1.7542	cDNA clone:J013058P10, full insert sequence	elongation zone	6 h
HORVU.MOREX.r3.2HG0162300.1	-0.43156	3.631707	-3.28496	0.001811	0.035503	-1.75461	Intracellular protein transporter USO1-like protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0410820.1	1.271354	3.960298	3.097813	0.003115	0.049823	-1.76431	SMAD/FHA domain-containing family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0637760.1	-0.42383	3.556847	-3.19914	0.002328	0.041321	-1.76811	#N/A	elongation zone	6 h
HORVU.MOREX.r3.7HG0682460.1	-0.35679	5.61607	-3.31115	0.001677	0.034204	-1.77171	ADP-ribosylation factor, putative	elongation zone	6 h
HORVU.MOREX.r3.4HG0394830.1	0.824201	0.997429	3.171291	0.002523	0.043737	-1.77635	Lecithin-cholesterol acyltransferase-like 1	elongation zone	6 h
HORVU.MOREX.r3.2HG0196520.1	0.736155	4.252659	3.26772	0.001906	0.036589	-1.77792	senescence-associated family protein (DUF581)	elongation zone	6 h
HORVU.MOREX.r3.1HG0079750.1	1.009409	-1.15538	3.135125	0.0028	0.046943	-1.77811	MYB transcription factor	elongation zone	6 h
HORVU.MOREX.r3.3HG0249430.1	-2.4815	-0.56924	-3.26405	0.001926	0.036837	-1.7817	Protein kinase	elongation zone	6 h
HORVU.MOREX.r3.7HG0658560.1	0.739428	3.664515	3.143569	0.002733	0.046171	-1.78172	Kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0493380.1	-0.32008	4.391009	-3.25104	0.002001	0.03764	-1.7826	Cyclin family protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0316640.1	-0.64098	4.162627	-3.28315	0.001821	0.035591	-1.78488	Pentatricopeptide repeat (PPR) superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0002340.1	-0.30519	6.091944	-3.30332	0.001716	0.034524	-1.78669	Tubulin-specific chaperone cofactor E-like protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0497490.1	1.347614	-1.08137	3.14929	0.002688	0.045781	-1.79059	SPX domain-like protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0309900.1	1.148609	-1.42396	3.11083	0.003002	0.048898	-1.79141	ROP-interactive CRIB motif protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0039670.1	-0.23814	7.408425	-3.36879	0.001413	0.030961	-1.79147	Calcium ion-binding protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0128240.1	-0.40735	5.300426	-3.26963	0.001895	0.036511	-1.79227	Aldose 1-epimerase	elongation zone	6 h
HORVU.MOREX.r3.6HG0602230.1	-0.51499	5.050411	-3.26216	0.001937	0.036879	-1.79255	Protein kinase	elongation zone	6 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0250940.1	-0.60542	3.302703	-3.18121	0.002452	0.042679	-1.79257	Polynucleotidyl transferase ribonuclease H-like superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0344830.1	-0.44922	4.535568	-3.23382	0.002104	0.038877	-1.79345	NBS-LRR disease resistance protein, putative, expressed	elongation zone	6 h
HORVU.MOREX.r3.1HG0090100.1	1.254066	1.392953	3.103352	0.003067	0.049561	-1.79688	DUF1645 family protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0243130.1	-0.75678	2.631713	-3.15594	0.002637	0.045214	-1.80082	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.2HG0208960.1	-0.8505	2.446722	-3.0987	0.003108	0.049818	-1.80373	Exocyst complex component EXO70B1	elongation zone	6 h
HORVU.MOREX.r3.2HG0165840.1	-0.55924	6.204491	-3.26593	0.001916	0.036694	-1.80573	Protein kinase	elongation zone	6 h
HORVU.MOREX.r3.2HG0117980.1	-0.35959	6.654309	-3.32984	0.001587	0.032759	-1.80714	Transmembrane protein 115	elongation zone	6 h
HORVU.MOREX.r3.5HG0531390.1	-0.29748	6.128355	-3.32464	0.001611	0.033096	-1.80992	Kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0466510.1	-0.96959	3.504705	-3.10606	0.003043	0.049244	-1.81025	Retrovirus-related Pol polyprotein from transposon TNT 1-94	elongation zone	6 h
HORVU.MOREX.r3.2HG0153420.1	0.741351	6.452276	3.352372	0.001484	0.031653	-1.81087	#N/A	elongation zone	6 h
HORVU.MOREX.r3.2HG0189010.1	1.011391	3.632309	3.197106	0.002342	0.041422	-1.81098	Glycerol-3-phosphate transporter, putative	elongation zone	6 h
HORVU.MOREX.r3.3HG0277100.1	-0.41939	4.350493	-3.22962	0.00213	0.039141	-1.81281	Calcium-dependent lipid-binding (CaLB domain) family protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0081220.1	-0.41721	5.709055	-3.29222	0.001773	0.034953	-1.81452	Galactose-6-phosphate isomerase subunit LacB	elongation zone	6 h
HORVU.MOREX.r3.1HG0051860.1	-0.64618	5.340638	-3.2371	0.002084	0.038637	-1.81616	Glutathione S-transferase	elongation zone	6 h
HORVU.MOREX.r3.2HG0169700.1	-0.42524	4.388016	-3.23374	0.002105	0.038877	-1.817	transmembrane protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0188300.1	-0.42572	4.693992	-3.21566	0.002219	0.040113	-1.81923	CsAtPR5	elongation zone	6 h
HORVU.MOREX.r3.4HG0348380.1	0.828904	1.737869	3.207005	0.002275	0.040716	-1.81929	phox (PX) domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0389200.1	0.700295	0.876157	3.143738	0.002732	0.046171	-1.81948	LIM domain-containing protein 1	elongation zone	6 h
HORVU.MOREX.r3.3HG0291030.1	0.614211	1.945138	3.312102	0.001672	0.034187	-1.82418	Glucan endo-1,3-beta-glucosidase 1	elongation zone	6 h
HORVU.MOREX.r3.3HG0292680.1	0.687349	2.459133	3.254365	0.001982	0.037445	-1.82681	Replicase polyprotein 1a	elongation zone	6 h
HORVU.MOREX.r3.5HG0488650.1	0.700777	4.071835	3.282384	0.001825	0.035637	-1.82711	Dof zinc finger protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0616240.1	0.837459	-0.52276	3.239264	0.002071	0.038428	-1.83191	Endoglucanase	elongation zone	6 h
HORVU.MOREX.r3.3HG0327170.1	-0.42388	7.966567	-3.35975	0.001452	0.031376	-1.83443	Bifunctional polymyxin resistance arnA protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0314240.1	-0.41732	5.164101	-3.25989	0.00195	0.03698	-1.83528	Potassium transporter	elongation zone	6 h
HORVU.MOREX.r3.7HG0665990.1	0.579124	6.156682	3.37477	0.001388	0.030794	-1.84092	Shikimate kinase	elongation zone	6 h
HORVU.MOREX.r3.3HG0246370.1	-0.4324	5.820127	-3.26366	0.001928	0.036846	-1.84285	Mannosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.4HG0379400.1	0.812035	1.850081	3.337366	0.001552	0.032356	-1.84646	Protein kinase-like protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0485760.1	1.397883	-1.3336	3.117853	0.002942	0.048492	-1.84867	65-kDa microtubule-associated-like protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0171550.1	-0.64018	4.111529	-3.15923	0.002613	0.044825	-1.84942	Major facilitator superfamily transporter	elongation zone	6 h
HORVU.MOREX.r3.7HG0680970.1	-0.79884	3.415292	-3.10299	0.00307	0.049561	-1.8564	Mitochondrial transcription termination factor family protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0477800.1	0.693459	5.596819	3.29854	0.00174	0.03465	-1.85777	Endo-1,3(4)-beta-glucanase 1	elongation zone	6 h
HORVU.MOREX.r3.1HG0076120.1	0.568455	7.792381	3.461231	0.001071	0.026245	-1.85944	Phosphatidylinositol transfer protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0230880.1	-0.2135	7.037661	-3.35025	0.001493	0.031694	-1.86093	Steroid 5-alpha reductase	elongation zone	6 h
HORVU.MOREX.r3.1HG0050920.1	0.834189	2.478719	3.277063	0.001854	0.03596	-1.86675	Trehalase	elongation zone	6 h
HORVU.MOREX.r3.1HG0090200.1	-0.51011	5.563212	-3.22797	0.002141	0.039149	-1.87046	NBS-LRR-like resistance protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0121830.1	-0.24655	7.00528	-3.34793	0.001504	0.031712	-1.87179	Calcium ion-binding protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0062450.1	-0.8201	7.022636	-3.27805	0.001849	0.035889	-1.87181	Pyrimidine-specific ribonucleoside hydrolase	elongation zone	6 h
HORVU.MOREX.r3.5HG0491250.1	-0.43929	3.850964	-3.14751	0.002702	0.045882	-1.87421	Cinnamoyl-CoA reductase 4	elongation zone	6 h
HORVU.MOREX.r3.2HG0134300.1	2.069302	1.307766	3.097573	0.003118	0.049823	-1.88001	Skp1, putative	elongation zone	6 h
HORVU.MOREX.r3.1HG0011820.1	0.973091	-1.28428	3.127317	0.002863	0.04772	-1.88002	Protein ABIL1	elongation zone	6 h
HORVU.MOREX.r3.2HG0141980.1	-0.40365	5.307117	-3.29845	0.001741	0.03465	-1.88139	Glucan endo-1,3-beta-glucosidase 3	elongation zone	6 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0258280.1	-0.28742	6.470164	-3.3035	0.001715	0.034524	-1.88715	Coatomer subunit beta	elongation zone	6 h
HORVU.MOREX.r3.3HG0298540.1	0.583325	7.885451	3.443447	0.00113	0.027022	-1.89307	Phosphatidylinositol transfer protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0390140.1	-0.26214	5.370404	-3.24183	0.002056	0.038279	-1.90153	Vacuolar protein sorting-associated protein 9A	elongation zone	6 h
HORVU.MOREX.r3.2HG0115930.1	-0.50204	9.174331	-3.38766	0.001336	0.030044	-1.90383	4-alpha-glucanotransferase	elongation zone	6 h
HORVU.MOREX.r3.2HG0168330.1	0.435261	5.088967	3.271911	0.001882	0.036357	-1.90456	Nicotinate phosphoribosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.5HG0444350.1	0.752919	2.597523	3.110473	0.003005	0.048898	-1.90532	Sn1-specific diacylglycerol lipase alpha	elongation zone	6 h
HORVU.MOREX.r3.2HG0160690.1	1.038193	-0.41896	3.13547	0.002797	0.046935	-1.90533	RALF	elongation zone	6 h
HORVU.MOREX.r3.1HG0003430.1	0.458613	4.894308	3.235062	0.002097	0.038797	-1.90577	TBC1 domain family member	elongation zone	6 h
HORVU.MOREX.r3.2HG0206920.1	0.937904	4.999661	3.102677	0.003073	0.049566	-1.90945	DNA polymerase I	elongation zone	6 h
HORVU.MOREX.r3.3HG0287000.1	0.778647	3.768611	3.206916	0.002276	0.040716	-1.90996	Respiratory burst oxidase	elongation zone	6 h
HORVU.MOREX.r3.1HG0072510.1	1.043202	-0.03799	3.111979	0.002992	0.048862	-1.91435	Protein-methionine-s-oxide reductase	elongation zone	6 h
HORVU.MOREX.r3.1HG0094770.1	-0.5512	3.670278	-3.10685	0.003036	0.049244	-1.91684	Transmembrane protein, putative	elongation zone	6 h
HORVU.MOREX.r3.3HG0316130.1	-0.69532	7.033938	-3.34656	0.00151	0.031775	-1.91747	Basic 7S globulin 2	elongation zone	6 h
HORVU.MOREX.r3.3HG0305800.1	0.724486	4.447	3.1809	0.002454	0.042679	-1.92296	Ribonuclease	elongation zone	6 h
HORVU.MOREX.r3.1HG0076060.1	-0.36366	6.353402	-3.29178	0.001775	0.034965	-1.92936	C2 calcium/lipid-binding and GRAM domain protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0575530.1	0.490052	6.1314	3.278125	0.001848	0.035889	-1.92997	Alcohol dehydrogenase, putative	elongation zone	6 h
HORVU.MOREX.r3.3HG0246500.1	0.768424	3.040522	3.289425	0.001788	0.035174	-1.93165	Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A	elongation zone	6 h
HORVU.MOREX.r3.2HG0152890.1	-0.65663	3.809628	-3.12706	0.002866	0.04772	-1.94191	TCP transcription factor	elongation zone	6 h
HORVU.MOREX.r3.3HG0284780.1	0.355958	5.323435	3.228951	0.002134	0.039142	-1.94987	Protein PLASTID MOVEMENT IMPAIRED 1-RELATED 1	elongation zone	6 h
HORVU.MOREX.r3.5HG0519810.1	-0.39195	7.617925	-3.31051	0.00168	0.034234	-1.95141	Diphosphomevalonate decarboxylase	elongation zone	6 h
HORVU.MOREX.r3.7HG0679350.1	-0.50858	3.668408	-3.22802	0.00214	0.039149	-1.95307	Leucine-rich repeat receptor-like protein kinase family	elongation zone	6 h
HORVU.MOREX.r3.5HG0527720.1	0.979501	0.951915	3.096354	0.003128	0.049957	-1.95442	Receptor protein kinase, putative,expressed	elongation zone	6 h
HORVU.MOREX.r3.5HG0493200.1	0.427709	8.020324	3.364467	0.001431	0.031116	-1.9545	Fasciclin-like arabinogalactan-protein-like	elongation zone	6 h
HORVU.MOREX.r3.4HG0384110.1	-0.30907	6.300031	-3.26797	0.001904	0.036589	-1.95779	RING/U-box superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0304710.1	-0.28797	8.270238	-3.36374	0.001435	0.031117	-1.95899	Fructose-bisphosphate aldolase	elongation zone	6 h
HORVU.MOREX.r3.7HG0651010.1	-0.85539	4.932391	-3.18358	0.002435	0.0426	-1.96309	Xyloglucan endotransglucosylase/hydrolase	elongation zone	6 h
HORVU.MOREX.r3.6HG0568170.1	0.852894	3.002871	3.15493	0.002645	0.045269	-1.96711	Transmembrane protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0042740.1	-0.29675	6.415285	-3.26637	0.001913	0.036691	-1.96834	Adaptin ear-binding coat-associated protein, putative	elongation zone	6 h
HORVU.MOREX.r3.1HG0086390.1	0.796769	-0.26089	3.121064	0.002915	0.048242	-1.97279	#N/A	elongation zone	6 h
HORVU.MOREX.r3.4HG0383400.1	-0.35575	5.833159	-3.28416	0.001816	0.035519	-1.97728	Protein COBRA, putative	elongation zone	6 h
HORVU.MOREX.r3.2HG0192000.1	0.786542	0.357064	3.204967	0.002289	0.040793	-1.97752	HXXXD-type acyl-transferase family protein, putative	elongation zone	6 h
HORVU.MOREX.r3.7HG0741640.1	-0.75666	4.20973	-3.12684	0.002867	0.04772	-1.97862	Histone H2A	elongation zone	6 h
HORVU.MOREX.r3.7HG0734380.1	-0.4554	4.659788	-3.16334	0.002582	0.044482	-1.97938	Mechanosensitive ion channel-like protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0058470.1	-0.37992	5.359187	-3.20794	0.002269	0.040716	-1.98097	RING/U-box superfamily protein, putative	elongation zone	6 h
HORVU.MOREX.r3.7HG0734670.1	-0.44022	6.626504	-3.27951	0.001841	0.035871	-1.98806	L-ascorbate oxidase	elongation zone	6 h
HORVU.MOREX.r3.4HG0377020.1	-0.29423	6.726202	-3.29446	0.001762	0.03479	-1.98904	Hexosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.6HG0616890.1	-0.91748	0.931971	-3.1074	0.003031	0.049213	-1.99113	UPF0503 protein, chloroplastic	elongation zone	6 h
HORVU.MOREX.r3.2HG0116990.1	0.555538	4.613527	3.212102	0.002242	0.040424	-1.99897	Phosphatidylinositol 4-phosphate 5-kinase 4	elongation zone	6 h
HORVU.MOREX.r3.6HG0543400.1	1.327886	-0.34964	3.140341	0.002758	0.046473	-2.00517	High affinity nitrate transporter	elongation zone	6 h
HORVU.MOREX.r3.1HG0021880.1	2.444903	0.747345	3.14276	0.002739	0.046227	-2.00635	SKP1-like protein 4	elongation zone	6 h
HORVU.MOREX.r3.3HG0271380.1	0.474111	5.415877	3.185576	0.002421	0.042416	-2.0065	GDSL esterase/lipase	elongation zone	6 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.6HG0615130.1	0.663016	3.141376	3.218471	0.002201	0.039927	-2.00906	TCP transcription factor	elongation zone	6 h
HORVU.MOREX.r3.2HG0197110.1	0.355576	6.332954	3.262124	0.001937	0.036879	-2.0123	AT hook motif DNA-binding family protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0331420.1	1.3604	6.431216	3.10655	0.003039	0.049244	-2.01882	Peptidyl-prolyl cis-trans isomerase	elongation zone	6 h
HORVU.MOREX.r3.1HG0042870.1	-0.24621	6.875706	-3.26763	0.001906	0.036589	-2.02184	Serine/threonine-protein phosphatase 2A regulatory subunit B'' subunit alpha	elongation zone	6 h
HORVU.MOREX.r3.7HG0745360.1	-0.31756	4.449287	-3.16202	0.002592	0.044578	-2.02431	Actin-related protein 2/3 complex subunit 3	elongation zone	6 h
HORVU.MOREX.r3.7HG0718830.1	0.72123	4.155941	3.285978	0.001806	0.035465	-2.03253	FAD-binding Berberine family protein, putative	elongation zone	6 h
HORVU.MOREX.r3.7HG0668440.1	0.559021	5.028289	3.196218	0.002348	0.041493	-2.03449	#N/A	elongation zone	6 h
HORVU.MOREX.r3.4HG0403510.1	-0.4133	4.248358	-3.14488	0.002723	0.046126	-2.0376	Protein kinase	elongation zone	6 h
HORVU.MOREX.r3.4HG0407470.1	0.865251	2.42529	3.223382	0.002169	0.039535	-2.04401	Serpin	elongation zone	6 h
HORVU.MOREX.r3.4HG0352200.1	0.624645	3.627838	3.139401	0.002766	0.046484	-2.04431	Methyltransferase-related protein, putative	elongation zone	6 h
HORVU.MOREX.r3.3HG0219860.1	-0.44448	3.216471	-3.10118	0.003086	0.049584	-2.0446	Disease resistance protein (NBS-LRR class) family	elongation zone	6 h
HORVU.MOREX.r3.7HG0687540.1	-0.31187	5.801521	-3.21049	0.002252	0.040566	-2.05101	Proteasome subunit alpha type	elongation zone	6 h
HORVU.MOREX.r3.1HG0003620.1	0.592803	2.573513	3.100608	0.003091	0.049625	-2.05571	Protein ZINC INDUCED FACILITATOR-LIKE 1	elongation zone	6 h
HORVU.MOREX.r3.7HG0718930.2	1.333753	-0.79034	3.145132	0.002721	0.046126	-2.05726	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.2HG0183780.1	-0.4371	5.376384	-3.18678	0.002413	0.042315	-2.05813	Sphingolipid delta-4 desaturase	elongation zone	6 h
HORVU.MOREX.r3.1HG0042290.1	0.406695	4.21134	3.17124	0.002524	0.043737	-2.06071	NBS-LRR disease resistance protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0168090.1	-0.33916	5.385495	-3.18295	0.00244	0.042629	-2.06769	Sphingomyelin synthase-like domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0554070.1	3.668711	1.92611	3.097922	0.003114	0.049823	-2.06807	HECT-like ubiquitin-conjugating enzyme (E2)-binding protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0242770.1	0.653721	1.656653	3.119969	0.002924	0.048315	-2.0787	Glycosyltransferases	elongation zone	6 h
HORVU.MOREX.r3.1HG0046180.1	0.409217	5.918665	3.244527	0.00204	0.038117	-2.07895	Ser/Thr protein phosphatase family protein, expressed	elongation zone	6 h
HORVU.MOREX.r3.1HG0069410.1	1.113651	3.463735	3.166476	0.002559	0.044197	-2.08305	Aldehyde dehydrogenase	elongation zone	6 h
HORVU.MOREX.r3.6HG0599080.1	-0.38683	8.233534	-3.27648	0.001857	0.035987	-2.08854	Hsp70-Hsp90 organizing protein 1	elongation zone	6 h
HORVU.MOREX.r3.7HG0730870.1	0.374378	7.493886	3.308519	0.00169	0.034363	-2.09011	Glycosyltransferases	elongation zone	6 h
HORVU.MOREX.r3.3HG0255040.1	-0.3733	4.904219	-3.12011	0.002923	0.048315	-2.09233	Mediator of RNA polymerase II transcription subunit 27	elongation zone	6 h
HORVU.MOREX.r3.1HG0053680.1	-0.30219	5.78418	-3.20829	0.002267	0.040716	-2.09586	Choline-phosphate cytidylyltransferase	elongation zone	6 h
HORVU.MOREX.r3.6HG0548360.1	-0.59509	3.627752	-3.11204	0.002991	0.048862	-2.09843	F-box family protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0221440.1	0.806842	2.700751	3.297347	0.001747	0.034729	-2.10235	Glycosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.1HG0079870.1	-0.82007	5.830169	-3.19521	0.002355	0.041579	-2.10358	Pectin lyase-like superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0058140.1	-0.40767	4.033555	-3.15332	0.002657	0.045366	-2.10444	ethylene-responsive transcription factor	elongation zone	6 h
HORVU.MOREX.r3.6HG0622740.1	0.452234	4.313476	3.182758	0.002441	0.042629	-2.11316	Protein DETOXIFICATION	elongation zone	6 h
HORVU.MOREX.r3.3HG0252610.1	-0.3373	7.233439	-3.21691	0.002211	0.040038	-2.11581	Protein kinase	elongation zone	6 h
HORVU.MOREX.r3.3HG0270910.1	-0.25347	6.963859	-3.25102	0.002001	0.03764	-2.1161	Protein YIPF	elongation zone	6 h
HORVU.MOREX.r3.2HG0119220.1	-0.46391	4.892203	-3.16335	0.002582	0.044482	-2.12344	Gibberellin receptor GID1a	elongation zone	6 h
HORVU.MOREX.r3.6HG0608780.1	-0.41697	7.822442	-3.26174	0.001939	0.036882	-2.1274	Heat shock 70 kDa protein, putative	elongation zone	6 h
HORVU.MOREX.r3.6HG0632320.1	-0.36064	5.523777	-3.14874	0.002693	0.045815	-2.16011	Leucine-rich repeat protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0501120.1	-0.26871	6.923122	-3.20468	0.002291	0.040793	-2.16127	26S proteasome regulatory subunit	elongation zone	6 h
HORVU.MOREX.r3.7HG0667630.1	1.074915	5.380802	3.186901	0.002412	0.042315	-2.16602	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.6HG0634200.1	0.950669	0.006824	3.112597	0.002987	0.048862	-2.17338	Syntaxin	elongation zone	6 h
HORVU.MOREX.r3.5HG0430940.1	0.928441	5.193365	3.187535	0.002407	0.042295	-2.17376	Glucan 1,3-beta-glucosidase	elongation zone	6 h
HORVU.MOREX.r3.7HG0711200.1	-0.38	5.29275	-3.18537	0.002423	0.042416	-2.19147	Hexosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.3HG0310540.1	-0.49862	5.764879	-3.13204	0.002825	0.047264	-2.19569	Mannosyl-oligosaccharide glucosidase	elongation zone	6 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.2HG0105990.1	-0.41256	6.154762	-3.19789	0.002336	0.041399	-2.19646	Cytochrome P450	elongation zone	6 h
HORVU.MOREX.r3.2HG0184180.1	0.884669	4.475955	3.19131	0.002381	0.04193	-2.20257	Remorin	elongation zone	6 h
HORVU.MOREX.r3.6HG0577360.1	-0.66197	5.665724	-3.26011	0.001949	0.03698	-2.20989	transmembrane protein, putative (Protein of unknown function, DUF642)	elongation zone	6 h
HORVU.MOREX.r3.5HG0454860.1	-0.3381	5.797971	-3.13975	0.002763	0.046475	-2.21359	Trehalose-6-phosphate synthase, putative	elongation zone	6 h
HORVU.MOREX.r3.4HG0342160.1	-0.36356	5.308472	-3.11332	0.002981	0.04885	-2.21486	Presenilin	elongation zone	6 h
HORVU.MOREX.r3.5HG0519040.1	-0.36819	4.736037	-3.11184	0.002993	0.048862	-2.21578	Serine/arginine repetitive matrix protein 2, putative isoform 1	elongation zone	6 h
HORVU.MOREX.r3.6HG0541250.1	-0.20957	7.143195	-3.18755	0.002407	0.042295	-2.24353	Acetate kinase	elongation zone	6 h
HORVU.MOREX.r3.1HG0026830.1	0.505722	3.566935	3.1115	0.002996	0.048871	-2.24463	Leucine-rich repeat receptor-like protein kinase family	elongation zone	6 h
HORVU.MOREX.r3.7HG0662650.1	-0.71282	6.460162	-3.13987	0.002762	0.046475	-2.24544	Histone H3	elongation zone	6 h
HORVU.MOREX.r3.1HG0022860.1	-0.3017	5.022173	-3.10159	0.003082	0.049584	-2.24629	Xylosyltransferase 1	elongation zone	6 h
HORVU.MOREX.r3.4HG0347400.1	-0.45285	6.883926	-3.19863	0.002331	0.041347	-2.2529	U-box domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0121410.1	0.925683	3.844656	3.127803	0.00286	0.04772	-2.25388	Cytochrome P450	elongation zone	6 h
HORVU.MOREX.r3.1HG0072840.1	-0.34283	5.890668	-3.12399	0.002891	0.047996	-2.27082	Ectonucleoside triphosphate diphosphohydrolase 1	elongation zone	6 h
HORVU.MOREX.r3.7HG0739180.1	-0.30909	7.099598	-3.20888	0.002263	0.040697	-2.28083	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0284100.1	0.38402	6.109021	3.16049	0.002603	0.044719	-2.29999	5'-nucleotidase SurE	elongation zone	6 h
HORVU.MOREX.r3.2HG0190290.1	0.601391	5.33841	3.110596	0.003004	0.048898	-2.30441	SHR5-receptor-like kinase	elongation zone	6 h
HORVU.MOREX.r3.3HG0262210.1	-0.28094	5.498655	-3.10775	0.003028	0.049213	-2.30876	Phosphatase 2C family protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0288360.1	-0.2874	5.883309	-3.11697	0.00295	0.048576	-2.31613	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	elongation zone	6 h
HORVU.MOREX.r3.5HG0463000.1	-0.44824	4.936645	-3.11969	0.002927	0.048315	-2.32535	Ulp1 protease family, C-terminal catalytic domain containing protein, expressed	elongation zone	6 h
HORVU.MOREX.r3.5HG0446900.1	-0.21894	6.633774	-3.14737	0.002703	0.045882	-2.32789	Dipeptidyl peptidase	elongation zone	6 h
HORVU.MOREX.r3.4HG0335700.1	-0.23936	5.55838	-3.09807	0.003113	0.049823	-2.33937	Alkaline ceramidase 3	elongation zone	6 h
HORVU.MOREX.r3.7HG0677940.1	-0.28967	7.210054	-3.16645	0.002559	0.044197	-2.34109	Transmembrane 9 superfamily member	elongation zone	6 h
HORVU.MOREX.r3.2HG0205750.1	-0.45601	6.410155	-3.11506	0.002966	0.048764	-2.34485	3-oxoacyl-[acyl-carrier-protein] synthase 3	elongation zone	6 h
HORVU.MOREX.r3.6HG0614100.1	0.831645	4.236522	3.103064	0.003069	0.049561	-2.35241	TPR repeat-containing thioredoxin TTL4	elongation zone	6 h
HORVU.MOREX.r3.5HG0527280.1	-0.25161	6.528337	-3.14466	0.002724	0.046126	-2.35717	Ras-related protein, expressed	elongation zone	6 h
HORVU.MOREX.r3.3HG0287070.1	-0.83892	6.192473	-3.10631	0.003041	0.049244	-2.37004	Glycosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.5HG0419520.1	-0.26213	7.603138	-3.20361	0.002298	0.040859	-2.37753	Microtubule-associated protein 70-2	elongation zone	6 h
HORVU.MOREX.r3.1HG0061710.1	0.424179	5.632386	3.130881	0.002834	0.047363	-2.39222	Trichome birefringence-like protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0529660.1	-0.27169	6.908166	-3.11468	0.002969	0.048778	-2.39388	Squamosa promoter-binding protein, putative	elongation zone	6 h
HORVU.MOREX.r3.3HG0301750.1	-0.45649	9.943131	-3.255	0.001978	0.037409	-2.39511	Alpha-1,4 glucan phosphorylase	elongation zone	6 h
HORVU.MOREX.r3.5HG0425680.1	-0.33898	7.233115	-3.13553	0.002797	0.046935	-2.39732	No exine formation 1	elongation zone	6 h
HORVU.MOREX.r3.7HG0726790.1	-0.30144	7.796481	-3.13189	0.002826	0.047264	-2.45362	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	elongation zone	6 h
HORVU.MOREX.r3.2HG0108780.1	-0.20548	8.923708	-3.19223	0.002375	0.041904	-2.45811	26S protease regulatory subunit	elongation zone	6 h
HORVU.MOREX.r3.5HG0430480.1	-0.27297	7.401068	-3.14184	0.002747	0.046311	-2.4776	Protein kinase	elongation zone	6 h
HORVU.MOREX.r3.4HG0381800.1	-0.27972	7.086406	-3.10202	0.003078	0.049581	-2.48719	AP-2 complex subunit mu	elongation zone	6 h
HORVU.MOREX.r3.6HG0539460.1	-0.22919	7.146504	-3.09918	0.003103	0.049789	-2.49466	FG-GAP repeat-containing protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0199550.1	-0.52199	7.232601	-3.10747	0.003031	0.049213	-2.50743	Glycosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.3HG0221490.1	-0.34942	7.438494	-3.12734	0.002863	0.04772	-2.50905	Sodium/hydrogen exchanger 1	elongation zone	6 h
HORVU.MOREX.r3.2HG0138540.1	0.579899	4.435354	3.170758	0.002527	0.043758	-2.52317	Blue copper protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0135210.1	0.672772	2.447492	3.101421	0.003084	0.049584	-2.53729	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	elongation zone	6 h
HORVU.MOREX.r3.5HG0470030.1	-0.40454	7.999201	-3.11882	0.002934	0.048397	-2.56747	3-ketoacyl-CoA thiolase	elongation zone	6 h

Table Sн Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.4HG0346720.1	-0.41162	10.60861	-3.20447	0.002292	0.040793	-2.5856	Protein disulfide-isomerase	elongation zone	6 h
HORVU.MOREX.r3.7HG0699010.1	2.219936	4.331849	8.039164	9.67E-11	1.99E-06	14.06542	LHY	elongation zone	12 h
HORVU.MOREX.r3.3HG0328340.1	-1.61312	4.602643	-7.59881	4.90E-10	5.03E-06	12.60193	Two-component response regulator	elongation zone	12 h
HORVU.MOREX.r3.6HG0550600.1	1.560832	1.720716	6.401342	4.13E-08	0.000274	8.492075	Protein ROOT HAIR DEFECTIVE 3 homolog	elongation zone	12 h
HORVU.MOREX.r3.6HG0609520.1	-0.83778	8.966633	-6.33217	5.33E-08	0.000274	8.133236	Fatty acid desaturase	elongation zone	12 h
HORVU.MOREX.r3.2HG0097390.1	-0.9076	4.644505	-6.05012	1.51E-07	0.000515	7.277088	Inosine-5'-monophosphate dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.5HG0517740.1	2.365849	-0.30721	5.929291	2.34E-07	0.000675	6.855633	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.5HG0537150.1	1.700402	-2.24688	6.145168	1.06E-07	0.000436	6.729744	Protein DETOXIFICATION	elongation zone	12 h
HORVU.MOREX.r3.7HG0636030.1	1.403702	-1.10938	5.84935	3.14E-07	0.000675	6.556341	hydroxysteroid dehydrogenase 3	elongation zone	12 h
HORVU.MOREX.r3.4HG0415420.1	-0.98235	6.947214	-5.80147	3.74E-07	0.000675	6.357551	Tubulin beta chain	elongation zone	12 h
HORVU.MOREX.r3.5HG0477040.1	-0.65743	5.55814	-5.75481	4.43E-07	0.000675	6.254191	MND1-interacting protein 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0715570.1	-0.64331	6.466383	-5.70699	5.27E-07	0.000675	6.044857	Transmembrane protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0072760.1	-0.91262	4.906091	-5.69425	5.52E-07	0.000675	6.040728	Serpin family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0065860.1	1.059627	4.236426	5.684903	5.71E-07	0.000675	6.007964	MLO-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0415330.1	2.206769	3.57761	5.655959	6.35E-07	0.000675	5.917139	Cytochrome P450 family cinnamate 4-hydroxylase	elongation zone	12 h
HORVU.MOREX.r3.3HG0329870.1	2.009599	-1.90322	5.688373	5.64E-07	0.000675	5.861495	Pectin acetylesterase	elongation zone	12 h
HORVU.MOREX.r3.7HG0736960.1	-1.15281	3.87866	-5.62384	7.13E-07	0.000675	5.692605	BTB/POZ domain containing protein, expressed	elongation zone	12 h
HORVU.MOREX.r3.6HG0541940.1	-0.53468	6.764259	-5.60401	7.66E-07	0.000675	5.659529	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0576550.1	-0.70013	4.943295	-5.57261	8.58E-07	0.000675	5.626732	F-box protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0477180.1	-0.57894	5.597571	-5.56653	8.77E-07	0.000675	5.589844	LAG1 longevity assurance-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0100750.1	2.000371	-1.62151	5.572159	8.60E-07	0.000675	5.583729	Dirigent protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0318590.1	2.636097	-1.25566	5.567612	8.74E-07	0.000675	5.555983	Endo-1,3-beta-glucanase	elongation zone	12 h
HORVU.MOREX.r3.6HG0545620.1	-0.55782	11.02319	-5.66803	6.07E-07	0.000675	5.544028	Heat shock 70 kDa protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0709860.1	-0.69289	6.368461	-5.55152	9.26E-07	0.000675	5.54022	Polyadenylate-binding protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0240640.1	-1.47936	5.859448	-5.5435	9.54E-07	0.000675	5.535402	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0750000.1	2.113151	-2.12041	5.672838	5.97E-07	0.000675	5.532886	Disease resistance protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0372280.1	-1.64456	3.216377	-5.67916	5.83E-07	0.000675	5.505877	xylulose kinase-2	elongation zone	12 h
HORVU.MOREX.r3.2HG0155750.1	2.014688	-0.29251	5.595662	7.90E-07	0.000675	5.478731	Ribonuclease	elongation zone	12 h
HORVU.MOREX.r3.2HG0205200.1	-0.76884	4.551525	-5.50324	1.10E-06	0.000754	5.397647	Ubiquitin carboxyl-terminal hydrolase	elongation zone	12 h
HORVU.MOREX.r3.1HG0010340.1	2.200324	-2.09413	5.595111	7.91E-07	0.000675	5.270722	Non-specific lipid-transfer protein-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0079800.1	-0.70852	7.794068	-5.48428	1.18E-06	0.000777	5.187997	Farnesyl diphosphate synthase	elongation zone	12 h
HORVU.MOREX.r3.4HG0395540.1	1.851854	4.838553	5.462982	1.27E-06	0.000793	5.187795	Glutamine synthetase	elongation zone	12 h
HORVU.MOREX.r3.2HG0169700.1	-0.74087	4.388016	-5.40701	1.56E-06	0.000889	5.074029	transmembrane protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0535180.1	1.724447	-1.06768	5.40731	1.56E-06	0.000889	5.051941	#N/A	elongation zone	12 h
HORVU.MOREX.r3.1HG0073390.1	1.866204	2.372781	5.420606	1.49E-06	0.000889	5.034035	Respiratory burst oxidase-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0078970.1	1.991718	2.920959	5.391788	1.65E-06	0.000913	4.962337	Protein kinase, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0417010.1	1.947177	-1.71396	5.47725	1.21E-06	0.000777	4.95958	Receptor protein kinase, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0160560.1	-1.46809	2.799703	-5.38108	1.71E-06	0.000924	4.945492	Peptidylprolyl isomerase	elongation zone	12 h
HORVU.MOREX.r3.5HG0527570.1	2.048334	4.789839	5.37112	1.77E-06	0.000933	4.925615	UDP-glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.1HG0059350.1	-0.82523	4.615638	-5.33851	1.99E-06	0.000974	4.843988	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0378580.1	-0.68702	5.353084	-5.31861	2.14E-06	0.001022	4.745139	Transcription factor	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0329040.1	2.624444	-0.45471	5.299649	2.29E-06	0.001061	4.620698	Vacuolar-processing enzyme	elongation zone	12 h
HORVU.MOREX.r3.6HG0555700.1	-0.56356	8.875975	-5.34932	1.92E-06	0.00097	4.609942	Calreticulin/calnexin	elongation zone	12 h
HORVU.MOREX.r3.3HG0305150.1	-0.94468	4.756714	-5.26829	2.56E-06	0.001143	4.609055	Pectin lyase-like superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0028320.1	-0.60288	6.850868	-5.29541	2.33E-06	0.001061	4.600616	70 kDa heat shock protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0746770.1	-0.69703	10.27031	-5.3463	1.94E-06	0.00097	4.505818	Chaperone protein htpG family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0070340.1	1.566317	4.307027	5.224526	3.00E-06	0.001254	4.403143	Protein kinase-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0482670.1	1.549392	0.628979	5.210589	3.15E-06	0.001254	4.35227	Cellulose synthase	elongation zone	12 h
HORVU.MOREX.r3.3HG0241000.1	-1.73226	6.471225	-5.19664	3.31E-06	0.001254	4.34874	HXXXD-type acyl-transferase-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0731490.1	-0.5994	4.892075	-5.18792	3.41E-06	0.001254	4.334328	Transmembrane protein, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0742080.1	1.576026	-1.3261	5.184107	3.46E-06	0.001254	4.296466	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.4HG0384390.1	1.395961	1.574903	5.179502	3.52E-06	0.001254	4.29185	Protein kinase family protein, putative, expressed	elongation zone	12 h
HORVU.MOREX.r3.1HG0081220.1	-0.67397	5.709055	-5.18155	3.49E-06	0.001254	4.270927	Galactose-6-phosphate isomerase subunit LacB	elongation zone	12 h
HORVU.MOREX.r3.1HG0006230.1	-0.65106	5.574	-5.17619	3.56E-06	0.001254	4.267941	Disease resistance protein RPM1	elongation zone	12 h
HORVU.MOREX.r3.2HG0097360.3	-1.1548	5.485237	-5.16189	3.74E-06	0.001254	4.22101	Laccase	elongation zone	12 h
HORVU.MOREX.r3.1HG0042740.1	-0.479	6.415285	-5.1747	3.58E-06	0.001254	4.202821	Adaptin ear-binding coat-associated protein, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0112670.1	1.837357	0.989354	5.170071	3.64E-06	0.001254	4.178453	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.3HG0237990.1	0.885957	4.191674	5.140066	4.05E-06	0.001254	4.164326	#N/A	elongation zone	12 h
HORVU.MOREX.r3.4HG0400920.1	1.313937	4.093901	5.128498	4.22E-06	0.001254	4.12767	Kinesin-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0067720.1	1.657385	-2.10602	5.177819	3.54E-06	0.001254	4.104761	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0730510.1	1.492597	-1.83116	5.13854	4.07E-06	0.001254	4.098203	Germin-like protein 1	elongation zone	12 h
HORVU.MOREX.r3.3HG0320840.1	-0.43634	7.266524	-5.15112	3.89E-06	0.001254	4.083994	Signal peptide peptidase family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0537360.1	2.289942	-1.21127	5.158664	3.79E-06	0.001254	3.999524	transcription factor, putative (Protein of unknown function, DUF547)	elongation zone	12 h
HORVU.MOREX.r3.2HG0153420.1	1.117386	6.452276	5.133567	4.14E-06	0.001254	3.993957	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0677230.1	-1.48294	4.893498	-5.14153	4.02E-06	0.001254	3.967566	Receptor protein kinase, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0346720.1	-0.684	10.60861	-5.1948	3.33E-06	0.001254	3.952302	Protein disulfide-isomerase	elongation zone	12 h
HORVU.MOREX.r3.2HG0207720.1	1.145726	0.894337	5.052416	5.52E-06	0.001514	3.89533	Flavin-containing monooxygenase	elongation zone	12 h
HORVU.MOREX.r3.4HG0354980.1	0.976228	2.412831	5.047897	5.61E-06	0.001514	3.872566	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0291490.1	-0.96114	7.190585	-5.08932	4.84E-06	0.00142	3.857396	#N/A	elongation zone	12 h
HORVU.MOREX.r3.4HG0402030.1	-0.58859	5.321938	-5.04782	5.61E-06	0.001514	3.852842	Basic helix-loop-helix (BHLH) family transcription factor	elongation zone	12 h
HORVU.MOREX.r3.6HG0550700.1	-2.29686	1.442253	-5.56153	8.93E-07	0.000675	3.844752	F-box family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0156610.1	1.995905	-0.12875	5.034818	5.87E-06	0.001545	3.837548	ERD (Early-responsive to dehydration stress) family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0601830.1	1.749784	-2.05956	5.070699	5.17E-06	0.001495	3.799878	C2 calcium/lipid-binding and GRAM domain protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0532140.1	1.958298	-1.00113	5.020638	6.17E-06	0.001545	3.791737	Expansin	elongation zone	12 h
HORVU.MOREX.r3.7HG0636370.1	1.410918	2.619393	5.030212	5.97E-06	0.001545	3.771879	MYB-related transcription factor	elongation zone	12 h
HORVU.MOREX.r3.2HG0152370.1	-0.60828	4.701662	-5.00819	6.45E-06	0.001557	3.73872	MD-2-related lipid recognition domain-containing protein / ML domain-containing	elongation zone	12 h
HORVU.MOREX.r3.3HG0257130.1	-0.77606	4.342452	-4.99665	6.72E-06	0.001584	3.713397	Presenilin	elongation zone	12 h
HORVU.MOREX.r3.3HG0295330.1	-0.60561	7.613979	-5.06587	5.26E-06	0.0015	3.69374	Sugar phosphate/phosphate translocator	elongation zone	12 h
HORVU.MOREX.r3.3HG0270400.1	-0.88988	4.405759	-4.99016	6.87E-06	0.001596	3.691468	Six-bladed beta-propeller, TolB-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0080180.1	2.199377	-2.35246	5.135327	4.11E-06	0.001254	3.68756	Jacalin lectin family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0479500.1	1.602566	1.850868	4.985214	6.99E-06	0.001596	3.665587	Phosphonates import ATP-binding protein PhnC	elongation zone	12 h
HORVU.MOREX.r3.2HG0112690.1	1.260737	1.247173	5.023686	6.11E-06	0.001545	3.658484	Peroxidase	elongation zone	12 h

Table Sн Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.2HG0124850.1	1.659319	-0.21834	4.978488	7.16E-06	0.001596	3.648927	Dirigent protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0055380.1	-0.6613	6.771434	-5.00868	6.44E-06	0.001557	3.627812	Methylsterol monooxygenase 1-2	elongation zone	12 h
HORVU.MOREX.r3.1HG0057990.1	-0.8162	4.42891	-4.96602	7.48E-06	0.001633	3.612353	O-fucosyltransferase family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0679350.1	-0.80904	3.668408	-4.97652	7.21E-06	0.001596	3.60021	Leucine-rich repeat receptor-like protein kinase family	elongation zone	12 h
HORVU.MOREX.r3.3HG0330980.1	-0.43852	6.458067	-4.99926	6.66E-06	0.001584	3.573263	Protein IQ-DOMAIN 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0218010.1	-0.49035	8.228324	-5.0271	6.03E-06	0.001545	3.57213	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	elongation zone	12 h
HORVU.MOREX.r3.3HG0240310.1	-1.19501	6.614043	-4.98186	7.08E-06	0.001596	3.565678	DUF2921 family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0394830.1	1.25434	0.997429	4.954452	7.79E-06	0.00167	3.560137	Lecithin-cholesterol acyltransferase-like 1	elongation zone	12 h
HORVU.MOREX.r3.5HG0527460.1	1.406926	1.065374	4.975588	7.23E-06	0.001596	3.554157	Pectin acetylesterase	elongation zone	12 h
HORVU.MOREX.r3.4HG0408270.1	1.826412	-2.27119	5.04187	5.73E-06	0.001526	3.551263	LOB domain-containing protein, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0002960.1	1.302114	0.278873	4.947682	7.98E-06	0.00167	3.513685	NBS-LRR disease resistance protein, putative, expressed	elongation zone	12 h
HORVU.MOREX.r3.2HG0112060.1	-0.75031	4.798982	-4.93592	8.31E-06	0.001723	3.505475	Transcription factor	elongation zone	12 h
HORVU.MOREX.r3.4HG0346830.1	2.077443	-2.75621	5.236067	2.88E-06	0.001254	3.501348	WEB family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0073330.1	-0.46147	5.588457	-4.94924	7.93E-06	0.00167	3.477857	Ubiquitin conjugating enzyme E2	elongation zone	12 h
HORVU.MOREX.r3.4HG0344370.1	1.830537	-2.72257	5.132489	4.16E-06	0.001254	3.420227	Glucuronoxylan 4-O-methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0303210.1	1.171749	1.990963	4.921456	8.75E-06	0.001789	3.405827	Alpha/beta-Hydrolases superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0612180.1	-0.82757	6.264663	-4.91289	9.01E-06	0.001809	3.378267	NHL repeat-containing protein-like	elongation zone	12 h
HORVU.MOREX.r3.7HG0726790.1	-0.48551	7.796481	-4.95152	7.87E-06	0.00167	3.368215	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	elongation zone	12 h
HORVU.MOREX.r3.1HG0066610.1	1.12183	2.119827	4.906046	9.23E-06	0.001821	3.363552	Dirigent protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0059790.1	-0.98655	4.636699	-4.88498	9.94E-06	0.001875	3.35111	Hydroxyproline-rich glycoprotein-like	elongation zone	12 h
HORVU.MOREX.r3.3HG0246540.1	-0.87824	4.407087	-4.87722	1.02E-05	0.001875	3.321623	Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A	elongation zone	12 h
HORVU.MOREX.r3.6HG0631400.1	1.211369	2.336066	4.878503	1.02E-05	0.001875	3.316019	Disease resistance protein RPM1	elongation zone	12 h
HORVU.MOREX.r3.4HG0397010.1	1.928371	0.173587	4.871128	1.04E-05	0.001875	3.292291	Beta-glucosidase	elongation zone	12 h
HORVU.MOREX.r3.4HG0400990.1	-0.78055	5.330008	-4.87219	1.04E-05	0.001875	3.272578	3-hydroxybenzoate 6-hydroxylase 1	elongation zone	12 h
HORVU.MOREX.r3.3HG0288940.1	-0.71571	6.05706	-4.88622	9.89E-06	0.001875	3.269132	WRKY transcription factor, putative, expressed	elongation zone	12 h
HORVU.MOREX.r3.6HG0631760.1	-0.53342	5.489051	-4.8577	1.09E-05	0.001875	3.210717	Signal peptide peptidase-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0350900.1	-0.4339	7.975994	-4.91958	8.80E-06	0.001789	3.186687	UDP-glucose 6-dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.3HG0246370.1	-0.65896	5.820127	-4.84876	1.13E-05	0.001897	3.180684	Mannosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.6HG0546160.1	1.077283	2.97611	4.853043	1.11E-05	0.001884	3.172305	Acylamino-acid-releasing enzyme	elongation zone	12 h
HORVU.MOREX.r3.6HG0604200.1	-1.39831	0.762306	-4.87926	1.01E-05	0.001875	3.170489	transcription repressor	elongation zone	12 h
HORVU.MOREX.r3.3HG0331030.1	-0.47748	7.059382	-4.8765	1.02E-05	0.001875	3.147658	Chaperone protein dnaJ, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0189670.1	1.512791	0.283223	4.823733	1.23E-05	0.001973	3.125547	Aquaporin-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0092010.1	0.814228	6.335202	4.858143	1.09E-05	0.001875	3.123286	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0168070.1	1.543833	0.66133	4.859148	1.09E-05	0.001875	3.120066	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.3HG0293310.1	1.870295	-2.57133	5.049878	5.57E-06	0.001514	3.113111	Protein upstream of flc	elongation zone	12 h
HORVU.MOREX.r3.3HG0299200.1	-0.66194	5.845565	-4.83275	1.19E-05	0.001973	3.105584	Ion channel DMI1	elongation zone	12 h
HORVU.MOREX.r3.1HG0003090.7	-1.88664	6.089425	-4.80881	1.30E-05	0.00203	3.105354	Thionin-2.2	elongation zone	12 h
HORVU.MOREX.r3.1HG0047100.1	1.150871	4.15495	4.81334	1.28E-05	0.002014	3.104576	LanC-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0392230.1	1.382213	0.189187	4.824216	1.23E-05	0.001973	3.102065	RNA-binding family protein, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0490800.1	1.646216	0.125384	4.865824	1.06E-05	0.001875	3.09782	IRK-interacting protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0327810.1	-0.60339	7.008521	-4.86578	1.06E-05	0.001875	3.076393	Auxin efflux carrier protein-like	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.2HG0160130.1	0.793328	3.66281	4.825686	1.22E-05	0.001973	3.037468	Basic helix-loop-helix transcription factor	elongation zone	12 h
HORVU.MOREX.r3.1HG0024040.1	-0.46705	9.734968	-4.91081	9.08E-06	0.001809	3.036831	Disulfide-isomerase	elongation zone	12 h
HORVU.MOREX.r3.5HG0536490.1	-1.51207	4.431144	-4.7867	1.40E-05	0.002142	3.031499	Acyl carrier protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0654480.1	-1.06939	4.98012	-4.7749	1.46E-05	0.002168	2.972611	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.7HG0719720.1	-0.71868	5.938268	-4.79057	1.38E-05	0.002131	2.971259	Phospholipase D	elongation zone	12 h
HORVU.MOREX.r3.1HG0073550.1	2.09899	-1.6606	4.772611	1.47E-05	0.002169	2.958888	Laccase	elongation zone	12 h
HORVU.MOREX.r3.5HG0517640.1	-0.94095	6.451472	-4.7923	1.37E-05	0.002131	2.952024	Glucan endo-1,3-beta-glucosidase, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0369880.1	-1.56807	2.555153	-4.81491	1.27E-05	0.002014	2.946173	Flavin-binding kelch domain F box protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0739910.1	-0.67872	4.210714	-4.7607	1.53E-05	0.002229	2.944522	Disease resistance protein (NBS-LRR class) family	elongation zone	12 h
HORVU.MOREX.r3.3HG0246670.1	1.756703	-1.91783	4.873725	1.03E-05	0.001875	2.940686	DUF4228 domain protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0334360.1	1.108594	4.121321	4.784683	1.41E-05	0.002142	2.923695	Homeobox protein BEL1 like	elongation zone	12 h
HORVU.MOREX.r3.2HG0217090.1	1.865928	-0.85749	4.748702	1.60E-05	0.00227	2.914013	C2 calcium/lipid-binding and GRAM domain protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0735840.1	-1.26875	4.848168	-4.73673	1.66E-05	0.002283	2.875179	serine/arginine repetitive matrix-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0518560.1	2.229337	2.148281	4.738783	1.65E-05	0.002283	2.869386	Leucine-rich repeat protein kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0066260.1	-0.46587	9.175242	-4.86211	1.08E-05	0.001875	2.865838	Tubulin beta chain	elongation zone	12 h
HORVU.MOREX.r3.3HG0275060.1	1.557367	0.275212	4.730526	1.70E-05	0.002284	2.850348	Isoprenylcysteine alpha-carbonyl methylesterase ICME	elongation zone	12 h
HORVU.MOREX.r3.5HG0528520.1	-0.51911	4.086447	-4.73398	1.68E-05	0.002283	2.849679	Epoxide hydrolase 2	elongation zone	12 h
HORVU.MOREX.r3.1HG0072580.1	0.682639	5.490114	4.745939	1.61E-05	0.00227	2.838814	Aminotransferase-related family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0073170.1	-0.89724	5.178736	-4.72631	1.73E-05	0.002284	2.837119	F-box protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0393870.1	1.684954	-1.59561	4.72629	1.73E-05	0.002284	2.837034	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.1HG0086090.1	1.04016	3.988991	4.737984	1.66E-05	0.002283	2.82294	Ubiquitin-conjugating enzyme E2	elongation zone	12 h
HORVU.MOREX.r3.2HG0172790.1	-0.81425	7.313554	-4.78148	1.43E-05	0.00215	2.80017	Lipoxygenase domain-containing 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0212570.1	-0.52089	10.53927	-4.85682	1.10E-05	0.001875	2.795552	Calreticulin	elongation zone	12 h
HORVU.MOREX.r3.7HG0736150.1	1.323904	8.171407	4.827574	1.21E-05	0.001973	2.788451	Phosphatidylinositol transfer protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0568390.1	0.653533	4.337129	4.734731	1.68E-05	0.002283	2.786735	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0597590.1	-0.50688	6.568014	-4.74996	1.59E-05	0.00227	2.765242	Protein disulfide-isomerase	elongation zone	12 h
HORVU.MOREX.r3.1HG0058390.1	-1.20169	4.869952	-4.70869	1.83E-05	0.002397	2.748496	GATA transcription factor	elongation zone	12 h
HORVU.MOREX.r3.5HG0508190.1	-0.71198	8.08234	-4.77714	1.45E-05	0.002167	2.747192	1-deoxy-D-xylulose 5-phosphate synthase 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0687630.1	-0.76226	7.969317	-4.77064	1.48E-05	0.002169	2.741723	Acyl carrier protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0235720.1	-2.07204	3.057636	-4.68947	1.96E-05	0.002467	2.725641	FMN-dependent NADPH-azoreductase	elongation zone	12 h
HORVU.MOREX.r3.7HG0706330.1	-0.52817	4.543867	-4.69332	1.93E-05	0.002465	2.722804	TOM1-like protein 2	elongation zone	12 h
HORVU.MOREX.r3.4HG0391330.1	-0.53457	6.457456	-4.7282	1.71E-05	0.002284	2.71273	Phosphomevalonate kinase	elongation zone	12 h
HORVU.MOREX.r3.4HG0405400.1	1.842353	2.976906	4.681294	2.02E-05	0.002487	2.686026	DUF936 family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0412030.1	-0.62225	4.498999	-4.67814	2.04E-05	0.002487	2.683197	vacuolar sorting-associated protein (DUF946)	elongation zone	12 h
HORVU.MOREX.r3.7HG0647520.1	-0.77042	6.632237	-4.701	1.88E-05	0.00243	2.679955	GDP-mannose 4,6 dehydratase-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0304490.1	1.3125	-1.40069	4.691007	1.95E-05	0.002467	2.678233	Myosin IC heavy chain	elongation zone	12 h
HORVU.MOREX.r3.6HG0621690.1	-0.74275	4.664753	-4.66821	2.11E-05	0.002487	2.655533	E3 ubiquitin-protein ligase	elongation zone	12 h
HORVU.MOREX.r3.3HG0222830.1	-0.41894	7.515891	-4.75409	1.57E-05	0.002265	2.654079	Heavy metal transport/detoxification superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0418530.1	-1.47421	4.704049	-4.6711	2.09E-05	0.002487	2.620025	ATP-dependent chaperone ClpB	elongation zone	12 h
HORVU.MOREX.r3.1HG0025870.1	0.758286	4.903164	4.674898	2.06E-05	0.002487	2.617095	6,7-dimethyl-8-ribityllumazine synthase	elongation zone	12 h
HORVU.MOREX.r3.7HG0667620.1	1.518926	0.317173	4.686416	1.98E-05	0.002478	2.612572	Peroxidase	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.4HG0394330.1	1.225618	1.645952	4.655838	2.20E-05	0.002522	2.600121	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0429900.1	1.296121	4.093407	4.647836	2.26E-05	0.002546	2.59445	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0728220.1	-0.52196	4.414112	-4.6502	2.24E-05	0.002546	2.594088	GATA transcription factor	elongation zone	12 h
HORVU.MOREX.r3.6HG0620520.1	0.900079	3.09452	4.678573	2.03E-05	0.002487	2.590735	Aminotransferase-related family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0303410.1	0.784391	6.71103	4.745354	1.62E-05	0.00227	2.589263	Respiratory burst oxidase-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0587140.1	-0.70674	4.797451	-4.64993	2.25E-05	0.002546	2.587235	Transmembrane 9 superfamily member	elongation zone	12 h
HORVU.MOREX.r3.2HG0200640.1	-0.52165	7.509809	-4.69925	1.89E-05	0.00243	2.578985	Carboxypeptidase	elongation zone	12 h
HORVU.MOREX.r3.3HG0330220.1	1.033583	6.363412	4.67461	2.06E-05	0.002487	2.566267	GDSL esterase/lipase	elongation zone	12 h
HORVU.MOREX.r3.2HG0199160.1	0.533679	6.474544	4.664283	2.14E-05	0.002506	2.56045	Kinesin-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0379660.1	1.430816	-1.00939	4.63139	2.39E-05	0.002546	2.542873	Transcription repressor OFP17	elongation zone	12 h
HORVU.MOREX.r3.1HG0044530.1	-0.47527	5.667948	-4.65952	2.17E-05	0.002513	2.539596	L-type lectin-domain containing receptor kinase VIII.2	elongation zone	12 h
HORVU.MOREX.r3.1HG0039670.1	-0.33646	7.408425	-4.6995	1.89E-05	0.00243	2.531827	Calcium ion-binding protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0226110.1	1.862092	-3.10127	5.008302	6.45E-06	0.001557	2.531262	Heat shock protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0339890.1	1.685825	-1.1907	4.628685	2.42E-05	0.002555	2.530358	Pollen Ole e 1 allergen and extensin family protein, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0218560.1	1.412843	0.309747	4.623788	2.46E-05	0.002585	2.514539	Receptor-like protein kinase	elongation zone	12 h
HORVU.MOREX.r3.1HG0087170.1	-0.54378	5.424188	-4.6443	2.29E-05	0.002546	2.508447	3-deoxy-manno-octulosonate cytidylyltransferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0449620.1	0.728408	4.972296	4.64018	2.32E-05	0.002546	2.506699	weak chloroplast movement under blue light protein (DUF827)	elongation zone	12 h
HORVU.MOREX.r3.2HG0178050.1	0.769183	4.229626	4.635321	2.36E-05	0.002546	2.500998	F-box protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0075320.1	1.343706	0.461847	4.639994	2.32E-05	0.002546	2.490724	Myb transcription factor	elongation zone	12 h
HORVU.MOREX.r3.3HG0294970.2	0.852795	2.769527	4.66849	2.11E-05	0.002487	2.488079	DNA-3-methyladenine glycosylase	elongation zone	12 h
HORVU.MOREX.r3.6HG0607360.1	-0.79761	4.502873	-4.61164	2.56E-05	0.002647	2.480611	WAT1-related protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0238180.1	-0.57461	4.144587	-4.6127	2.55E-05	0.002647	2.475081	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0720670.1	-0.88297	2.879624	-4.63468	2.37E-05	0.002546	2.471714	Nucleoside diphosphate kinase	elongation zone	12 h
HORVU.MOREX.r3.6HG0588350.1	-0.71335	4.125371	-4.60191	2.65E-05	0.002677	2.450539	RING finger family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0054190.1	1.88453	-0.12557	4.610995	2.57E-05	0.002647	2.449717	Expansin-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0085140.1	-0.54429	6.163123	-4.63673	2.35E-05	0.002546	2.446441	Serine/threonine protein phosphatase 2A regulatory subunit B	elongation zone	12 h
HORVU.MOREX.r3.4HG0380540.1	0.80901	3.365322	4.6036	2.63E-05	0.002677	2.442916	Aquaporin-1	elongation zone	12 h
HORVU.MOREX.r3.4HG0417920.1	2.624034	-1.69902	4.64325	2.30E-05	0.002546	2.440617	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.1HG0084970.1	1.277967	2.620282	4.602197	2.65E-05	0.002677	2.438186	Phosphatidylserine synthase 2	elongation zone	12 h
HORVU.MOREX.r3.7HG0637760.1	-0.63236	3.556847	-4.5978	2.69E-05	0.002684	2.437452	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0533760.1	1.365941	3.713664	4.670418	2.09E-05	0.002487	2.434186	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0717610.1	0.771857	4.008622	4.618543	2.50E-05	0.002619	2.433176	Pollen-specific protein SF21	elongation zone	12 h
HORVU.MOREX.r3.4HG0413740.1	2.066764	-1.83472	4.634178	2.37E-05	0.002546	2.421984	12-oxophytodienoate reductase-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0057780.1	-0.55468	5.901425	-4.63124	2.39E-05	0.002546	2.421229	bZIP transcription factor (DUF630 and DUF632)	elongation zone	12 h
HORVU.MOREX.r3.4HG0405780.1	0.639315	7.951421	4.713832	1.80E-05	0.00237	2.416231	Receptor-like protein kinase	elongation zone	12 h
HORVU.MOREX.r3.2HG0151920.1	-0.93756	3.926991	-4.5916	2.74E-05	0.002684	2.415362	Retrovirus-related Pol polyprotein from transposon TNT 1-94	elongation zone	12 h
HORVU.MOREX.r3.7HG0638850.1	-0.57145	7.446158	-4.6779	2.04E-05	0.002487	2.409563	Cellulose synthase-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0179560.1	1.197882	1.523229	4.585916	2.80E-05	0.00269	2.385472	Nodulin-like / Major Facilitator Superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0035400.1	0.66107	4.194434	4.603968	2.63E-05	0.002677	2.375066	Ras-related protein, expressed	elongation zone	12 h
HORVU.MOREX.r3.6HG0608780.1	-0.6072	7.822442	-4.65956	2.17E-05	0.002513	2.374493	Heat shock 70 kDa protein, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0454660.1	-0.41697	4.270815	-4.59161	2.74E-05	0.002684	2.373581	Alpha-(1,4)-fucosyltransferase	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.4HG0340200.1	-1.00517	4.710006	-4.5789	2.87E-05	0.002722	2.37174	RING finger and CHY zinc finger protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0300950.1	-0.81202	3.921584	-4.58506	2.81E-05	0.00269	2.362893	Amino acid transporter, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0333450.1	0.761677	3.618973	4.569582	2.96E-05	0.002794	2.34585	Type I inositol-1,4,5-trisphosphate 5-phosphatase CVP2	elongation zone	12 h
HORVU.MOREX.r3.1HG0031180.1	-0.48647	4.951	-4.58893	2.77E-05	0.002684	2.333401	Hexosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.4HG0341800.1	0.835853	2.209476	4.598434	2.68E-05	0.002684	2.332246	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.7HG0712850.1	-0.51263	4.698391	-4.56861	2.97E-05	0.002794	2.313984	Fiber protein Fb34	elongation zone	12 h
HORVU.MOREX.r3.4HG0361680.1	-1.28306	4.471436	-4.55765	3.08E-05	0.002848	2.311686	Nuclear distribution protein nudE-like 1	elongation zone	12 h
HORVU.MOREX.r3.3HG0254950.1	1.402237	1.01976	4.588473	2.77E-05	0.002684	2.311441	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.7HG0724060.1	1.597101	0.588187	4.553952	3.12E-05	0.002858	2.294427	U-box domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0677510.1	-0.59865	5.971824	-4.58905	2.77E-05	0.002684	2.28694	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0287070.1	-1.29173	6.192473	-4.58916	2.77E-05	0.002684	2.280294	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0312430.1	1.900038	-0.09459	4.565209	3.00E-05	0.0028	2.272136	E3 ubiquitin protein ligase drip2	elongation zone	12 h
HORVU.MOREX.r3.3HG0291030.1	0.844483	1.945138	4.589331	2.76E-05	0.002684	2.246325	Glucan endo-1,3-beta-glucosidase 1	elongation zone	12 h
HORVU.MOREX.r3.1HG0002570.1	1.619696	-1.7761	4.546267	3.20E-05	0.002921	2.243113	GDSL esterase/lipase	elongation zone	12 h
HORVU.MOREX.r3.4HG0349080.1	0.728322	3.881326	4.538024	3.29E-05	0.002965	2.242856	CBS domain containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0134700.1	-0.77196	2.881388	-4.53404	3.34E-05	0.002967	2.238545	Ras-related protein Rab-2	elongation zone	12 h
HORVU.MOREX.r3.3HG0230870.1	1.70205	0.065486	4.540328	3.27E-05	0.002958	2.211962	Protein TRM32	elongation zone	12 h
HORVU.MOREX.r3.5HG0470700.1	1.62798	-1.11013	4.522245	3.48E-05	0.003	2.202157	Heavy metal transport/detoxification protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0552860.1	-1.32499	6.65591	-4.54001	3.27E-05	0.002958	2.199129	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.1HG0043520.1	-0.50014	4.227432	-4.53601	3.32E-05	0.002967	2.195043	F-box protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0405920.1	1.531469	0.085137	4.527025	3.42E-05	0.002987	2.171278	Hexosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0429180.1	1.518471	2.149739	4.5098	3.63E-05	0.003013	2.15744	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0127530.1	-1.48823	2.912589	-4.52238	3.47E-05	0.003	2.152992	Glucan endo-1,3-beta-glucosidase 3	elongation zone	12 h
HORVU.MOREX.r3.7HG0726770.1	1.195641	2.29225	4.512265	3.60E-05	0.003013	2.152855	Glycine-rich protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0519810.1	-0.55181	7.617925	-4.58172	2.84E-05	0.002708	2.148553	Diphosphomevalonate decarboxylase	elongation zone	12 h
HORVU.MOREX.r3.1HG0052120.1	-0.76288	3.548831	-4.51071	3.62E-05	0.003013	2.132419	GDP-mannose transporter	elongation zone	12 h
HORVU.MOREX.r3.7HG0711890.1	1.311822	2.553034	4.513798	3.58E-05	0.003013	2.121476	O-methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.6HG0622250.1	1.387109	2.510596	4.566791	2.99E-05	0.002798	2.119721	Alpha/beta-hydrolase superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0175320.1	-0.85077	4.008441	-4.4887	3.90E-05	0.003173	2.091719	Protein FAR1-RELATED SEQUENCE 6	elongation zone	12 h
HORVU.MOREX.r3.6HG0548670.1	-1.16237	5.25208	-4.49163	3.86E-05	0.003167	2.082928	Histone H4	elongation zone	12 h
HORVU.MOREX.r3.6HG0582480.1	0.92359	2.53548	4.484342	3.95E-05	0.003202	2.081204	Ethylene-responsive transcription factor-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0068010.1	1.610494	-0.26596	4.520322	3.50E-05	0.003	2.079158	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.3HG0294960.1	1.551704	-1.29923	4.489588	3.88E-05	0.003173	2.069261	Eukaryotic translation initiation factor 3 subunit H	elongation zone	12 h
HORVU.MOREX.r3.6HG0627570.1	-0.74427	4.766957	-4.48357	3.96E-05	0.003202	2.045827	Immunoglobulin A1 protease autotransporter	elongation zone	12 h
HORVU.MOREX.r3.2HG0213250.1	-0.70922	6.347479	-4.53005	3.39E-05	0.002987	2.040743	Choline transporter-related family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0559990.1	0.945935	5.045463	4.514801	3.57E-05	0.003013	2.039135	Apoptosis-inducing factor-like protein A	elongation zone	12 h
HORVU.MOREX.r3.3HG0301000.1	0.916534	4.492782	4.47807	4.04E-05	0.003217	2.033298	ABC transporter B family-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0297330.1	-0.52724	5.598322	-4.50692	3.66E-05	0.00303	2.026252	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.7HG0665400.1	-0.78064	4.54259	-4.46267	4.26E-05	0.003301	2.012797	Mitochondrial 39S ribosomal protein L53	elongation zone	12 h
HORVU.MOREX.r3.7HG0724140.1	1.071058	4.661226	4.48254	3.98E-05	0.003202	2.009443	FAD-binding Berberine family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0438160.1	-0.54153	5.336636	-4.4766	4.06E-05	0.003217	2.008393	#N/A	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.2HG0136670.1	-1.9059	4.713901	-4.52731	3.42E-05	0.002987	2.001968	Cellulose synthase-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0494040.1	1.853113	-3.00086	4.658566	2.18E-05	0.002513	1.982849	Auxin efflux carrier component	elongation zone	12 h
HORVU.MOREX.r3.7HG0732290.1	-1.7091	2.965224	-4.5195	3.51E-05	0.003	1.981645	Dihydroflavonol-4-reductase	elongation zone	12 h
HORVU.MOREX.r3.5HG0485800.1	-0.5032	8.255741	-4.55542	3.10E-05	0.002857	1.981036	Protein disulfide isomerase	elongation zone	12 h
HORVU.MOREX.r3.1HG0055240.1	2.288179	-3.1472	4.824912	1.23E-05	0.001973	1.964779	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	elongation zone	12 h
HORVU.MOREX.r3.5HG0519120.1	1.491953	-0.8751	4.44632	4.50E-05	0.003412	1.964473	CASP-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0485220.1	-0.60757	5.159201	-4.46301	4.25E-05	0.003301	1.962926	Gamma-tubulin complex component	elongation zone	12 h
HORVU.MOREX.r3.3HG0269960.1	0.562759	4.098981	4.472878	4.11E-05	0.003241	1.959505	Protein kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0175380.1	1.656332	3.452964	4.514708	3.57E-05	0.003013	1.944856	Sec14p-like phosphatidylinositol transfer family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0661480.1	-0.35586	7.365152	-4.5208	3.49E-05	0.003	1.944699	Alpha-amylase 2	elongation zone	12 h
HORVU.MOREX.r3.6HG0574950.1	0.652988	6.289342	4.534867	3.33E-05	0.002967	1.940068	Receptor-like protein kinase	elongation zone	12 h
HORVU.MOREX.r3.2HG0113990.1	2.25069	-2.49708	4.63673	2.35E-05	0.002546	1.929458	Calcium-dependent lipid-binding (CaLB domain) family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0295020.1	-0.56766	4.746066	-4.45227	4.41E-05	0.003388	1.924047	Polyadenylate-binding protein 1-B-binding protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0351750.1	2.021135	-1.8238	4.440438	4.59E-05	0.003449	1.920398	BTB/POZ domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0181680.1	2.009347	-1.90882	4.432275	4.72E-05	0.003494	1.915151	CASP-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0674720.1	2.117226	-1.46328	4.479718	4.02E-05	0.003217	1.90847	Epoxide hydrolase 2	elongation zone	12 h
HORVU.MOREX.r3.3HG0293320.1	1.508086	0.363569	4.468004	4.18E-05	0.003274	1.907066	ALK tyrosine kinase receptor	elongation zone	12 h
HORVU.MOREX.r3.7HG0750170.1	1.566794	1.590474	4.43599	4.66E-05	0.003464	1.899452	#N/A	elongation zone	12 h
HORVU.MOREX.r3.1HG0051860.1	-0.9201	5.340638	-4.43662	4.65E-05	0.003464	1.89934	Glutathione S-transferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0121830.1	-0.33619	7.00528	-4.50983	3.63E-05	0.003013	1.89168	Calcium ion-binding protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0188300.1	-0.60263	4.693992	-4.42395	4.85E-05	0.003506	1.877333	CsAtPR5	elongation zone	12 h
HORVU.MOREX.r3.7HG0704450.1	0.603667	5.126567	4.44854	4.46E-05	0.003412	1.859229	Hexosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.1HG0082550.1	1.500181	-2.24502	4.445407	4.51E-05	0.003412	1.843821	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.1HG0079140.1	0.692729	4.435815	4.436066	4.66E-05	0.003464	1.822233	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0489720.1	-0.43318	6.28355	-4.46225	4.26E-05	0.003301	1.81881	WPP domain-interacting protein 1	elongation zone	12 h
HORVU.MOREX.r3.5HG0429930.1	-1.05885	4.099119	-4.39356	5.38E-05	0.003739	1.799766	Protein DEK	elongation zone	12 h
HORVU.MOREX.r3.2HG0104480.1	-0.79134	3.899784	-4.39202	5.40E-05	0.003746	1.799526	F-box protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0168090.1	-0.47994	5.385495	-4.42483	4.84E-05	0.003506	1.799282	Sphingomyelin synthase-like domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0643230.1	-0.7595	5.512465	-4.42855	4.78E-05	0.003501	1.791268	Transmembrane protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0660310.1	-0.64109	4.34026	-4.40531	5.17E-05	0.003656	1.787041	Protein kinase	elongation zone	12 h
HORVU.MOREX.r3.1HG0072910.2	-0.5099	4.342105	-4.38971	5.45E-05	0.003763	1.78251	Serine/threonine-protein kinase ATM	elongation zone	12 h
HORVU.MOREX.r3.6HG0542030.1	1.30864	1.995705	4.497603	3.78E-05	0.003115	1.772732	Acid beta-fructofuranosidase	elongation zone	12 h
HORVU.MOREX.r3.2HG0204940.1	-0.66903	6.058217	-4.41049	5.08E-05	0.00363	1.760745	Crossover junction endonuclease EME1	elongation zone	12 h
HORVU.MOREX.r3.3HG0307120.1	-0.63587	8.364634	-4.47696	4.06E-05	0.003217	1.752829	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0497900.1	0.996187	3.680571	4.402332	5.22E-05	0.00368	1.748422	Rhomboid-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0417320.1	1.588295	1.098725	4.424929	4.84E-05	0.003506	1.735275	Remorin	elongation zone	12 h
HORVU.MOREX.r3.1HG0082630.1	-0.47086	5.023124	-4.39468	5.36E-05	0.003738	1.722179	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0679050.1	0.722855	4.002868	4.371043	5.80E-05	0.003852	1.720978	Upstream activation factor subunit spp27	elongation zone	12 h
HORVU.MOREX.r3.4HG0385880.1	-0.93223	3.891411	-4.36053	6.01E-05	0.00391	1.695249	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0192100.1	1.683259	1.501774	4.362834	5.96E-05	0.003896	1.694509	Serine/threonine-protein kinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0330200.1	1.233486	1.169812	4.40707	5.14E-05	0.003647	1.68287	Aquaporin	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0309410.1	-1.35125	3.365238	-4.3764	5.70E-05	0.003832	1.672083	Subtilisin-like protease	elongation zone	12 h
HORVU.MOREX.r3.4HG0406060.1	2.606463	-1.45049	4.472125	4.12E-05	0.003241	1.662728	Agmatine coumaroyltransferase-2	elongation zone	12 h
HORVU.MOREX.r3.6HG0542040.1	1.328814	1.468748	4.444699	4.52E-05	0.003412	1.659916	Acid beta-fructofuranosidase	elongation zone	12 h
HORVU.MOREX.r3.3HG0257840.1	1.389722	0.153713	4.379772	5.63E-05	0.003829	1.658474	S-acyltransferase	elongation zone	12 h
HORVU.MOREX.r3.4HG0379400.1	1.067998	1.850081	4.428695	4.77E-05	0.003501	1.656569	Protein kinase-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0317780.1	1.216718	0.361248	4.345065	6.33E-05	0.00401	1.647161	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0696770.1	-0.33854	5.470938	-4.37909	5.64E-05	0.003829	1.646095	Protein kinase	elongation zone	12 h
HORVU.MOREX.r3.5HG0532960.1	-0.55076	5.01578	-4.36438	5.93E-05	0.003888	1.637258	ER lumen protein-retaining receptor	elongation zone	12 h
HORVU.MOREX.r3.5HG0447720.1	-0.63709	7.79832	-4.41897	4.93E-05	0.003553	1.628473	Dicarboxylate transporter 2.1, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.6HG0581010.1	-0.79523	4.49799	-4.33694	6.50E-05	0.004044	1.624034	Poly(A) polymerase	elongation zone	12 h
HORVU.MOREX.r3.4HG0411960.1	-0.9173	3.220574	-4.33341	6.58E-05	0.004054	1.622814	#N/A	elongation zone	12 h
HORVU.MOREX.r3.1HG0086010.1	-0.6194	5.131587	-4.3508	6.21E-05	0.003971	1.616267	TSA: Wollemia nobilis Ref_Wollemi_Transcript_14910_3291 transcribed RNA sequ	elongation zone	12 h
HORVU.MOREX.r3.4HG0390770.1	1.08226	3.149264	4.32974	6.66E-05	0.004056	1.611764	Regulator of Vps4 activity in the MVB pathway protein, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0107470.1	-0.65221	4.149979	-4.33169	6.62E-05	0.004054	1.609288	Pectate lyase	elongation zone	12 h
HORVU.MOREX.r3.7HG0651110.1	-0.43342	7.468711	-4.41758	4.96E-05	0.003557	1.607905	AT4G29520-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0600000.1	1.481651	-0.21905	4.338054	6.48E-05	0.004041	1.604949	Blue copper protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0288960.1	1.24567	4.129323	4.368993	5.84E-05	0.003853	1.597375	Cellulose synthase	elongation zone	12 h
HORVU.MOREX.r3.7HG0654410.1	-0.88402	6.620821	-4.37492	5.72E-05	0.003839	1.591348	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.4HG0349530.1	-0.44049	4.965038	-4.34796	6.27E-05	0.003993	1.5837	Tubby-like F-box protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0091870.1	-0.61113	5.262379	-4.34488	6.33E-05	0.00401	1.576011	Protein kinase superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0522060.1	-0.80368	4.084626	-4.31502	7.00E-05	0.004083	1.567232	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0678160.1	-0.64516	6.566933	-4.35952	6.03E-05	0.00391	1.563259	Disease resistance protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0383670.1	1.294062	2.012771	4.341282	6.41E-05	0.004025	1.550733	Protein SCAR2	elongation zone	12 h
HORVU.MOREX.r3.1HG0080760.1	-1.07021	7.93903	-4.3776	5.67E-05	0.003829	1.541427	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.1HG0050700.1	1.413469	2.994863	4.332111	6.61E-05	0.004054	1.540069	ATP-dependent zinc metalloprotease FtsH	elongation zone	12 h
HORVU.MOREX.r3.1HG0089220.1	-1.07794	0.50855	-4.341	6.41E-05	0.004025	1.531276	Cell surface antigen I/II	elongation zone	12 h
HORVU.MOREX.r3.6HG0543780.1	-0.94232	7.397821	-4.37157	5.79E-05	0.003852	1.525851	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.1HG0092810.1	-1.15487	7.116497	-4.33209	6.61E-05	0.004054	1.515014	Late embryogenesis abundant protein Lea14	elongation zone	12 h
HORVU.MOREX.r3.2HG0207790.1	1.619224	-2.59422	4.445222	4.52E-05	0.003412	1.508772	Serine/threonine-protein kinase	elongation zone	12 h
HORVU.MOREX.r3.5HG0489130.1	-1.38223	6.654428	-4.38072	5.61E-05	0.003829	1.506566	Receptor protein kinase, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0006400.1	0.823963	6.387241	4.409322	5.10E-05	0.003632	1.500205	Beta-1,3-galactosyltransferase-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0666340.1	-0.66114	4.728876	-4.3042	7.26E-05	0.004172	1.497311	Hexosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.6HG0609560.1	-1.12616	3.881425	-4.29089	7.59E-05	0.00423	1.493876	Alpha/beta hydrolase	elongation zone	12 h
HORVU.MOREX.r3.1HG0095210.1	-0.34876	8.682671	-4.42742	4.80E-05	0.003502	1.493832	Nucleoside diphosphate kinase	elongation zone	12 h
HORVU.MOREX.r3.7HG0751300.1	1.477716	-1.39316	4.291546	7.57E-05	0.00423	1.493222	Phosphatidylinositol N-acetyglucosaminlytransferase subunit P-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0056620.1	1.829984	0.189162	4.350602	6.21E-05	0.003971	1.493145	Expansin protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0047250.1	-0.86174	2.716377	-4.32164	6.84E-05	0.004083	1.490614	Major facilitator superfamily transporter	elongation zone	12 h
HORVU.MOREX.r3.3HG0280630.1	-0.41773	5.914468	-4.33891	6.46E-05	0.004041	1.484714	Glycosylphosphatidylinositol anchor attachment 1 protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0557920.1	1.069601	4.693871	4.314849	7.00E-05	0.004083	1.483056	Auxin response factor	elongation zone	12 h
HORVU.MOREX.r3.4HG0415720.1	-0.71083	4.208548	-4.30183	7.31E-05	0.00418	1.470103	Endoglucanase	elongation zone	12 h
HORVU.MOREX.r3.2HG0170560.1	-1.21823	3.704875	-4.32875	6.68E-05	0.004058	1.458503	Ras-like protein	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.5HG0420410.1	0.550715	5.049102	4.321666	6.84E-05	0.004083	1.448437	Ubiquitin-conjugating enzyme E2	elongation zone	12 h
HORVU.MOREX.r3.3HG0305270.1	-0.62745	5.993243	-4.31568	6.98E-05	0.004083	1.445082	U-box domain-containing family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0398090.1	0.814604	4.062819	4.318349	6.92E-05	0.004083	1.444254	Syntaxin protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0478450.1	-0.41743	5.597721	-4.31729	6.94E-05	0.004083	1.438873	AUGMIN subunit 5	elongation zone	12 h
HORVU.MOREX.r3.4HG0341050.1	1.507336	0.610576	4.2742	8.02E-05	0.004331	1.437845	Protein DETOXIFICATION	elongation zone	12 h
HORVU.MOREX.r3.6HG0542970.1	-1.09532	4.467056	-4.27183	8.08E-05	0.004342	1.42845	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.7HG0662650.1	-1.00965	6.460162	-4.3167	6.96E-05	0.004083	1.42349	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.4HG0402730.1	1.837201	-1.08162	4.268691	8.17E-05	0.004344	1.413591	Homeobox protein BEL1 like	elongation zone	12 h
HORVU.MOREX.r3.1HG0054170.1	1.561465	0.15708	4.295755	7.46E-05	0.004207	1.411281	Expansin-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0338070.1	1.073526	1.603513	4.319566	6.89E-05	0.004083	1.410607	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0461280.1	0.591328	6.01476	4.318145	6.93E-05	0.004083	1.409356	Calcium-binding EF-hand protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0247440.1	-0.91441	2.109103	-4.31397	7.02E-05	0.004083	1.407777	Serine/threonine-protein kinase	elongation zone	12 h
HORVU.MOREX.r3.6HG0542050.1	1.554948	1.403897	4.367007	5.88E-05	0.003866	1.402642	Acid beta-fructofuranosidase	elongation zone	12 h
HORVU.MOREX.r3.5HG0511090.1	0.696828	5.583411	4.297216	7.43E-05	0.004198	1.400671	Phytochrome	elongation zone	12 h
HORVU.MOREX.r3.7HG0738770.1	1.211448	1.993948	4.358917	6.04E-05	0.00391	1.400567	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0285440.1	1.491529	-1.28505	4.272794	8.06E-05	0.00434	1.400422	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0298080.1	1.086173	1.480621	4.268551	8.17E-05	0.004344	1.400229	Amino acid permease	elongation zone	12 h
HORVU.MOREX.r3.3HG0280060.1	2.094624	-2.86395	4.45809	4.32E-05	0.003335	1.388218	Heavy metal transport/detoxification superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0110840.1	-0.62257	6.010911	-4.28947	7.62E-05	0.004238	1.38683	2-dehydro-3-deoxyphosphooctonate aldolase	elongation zone	12 h
HORVU.MOREX.r3.7HG0709110.1	-1.56963	3.79338	-4.25991	8.41E-05	0.004437	1.380343	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.3HG0329950.1	1.631461	1.75889	4.291207	7.58E-05	0.00423	1.378215	Pectin acetylesterase	elongation zone	12 h
HORVU.MOREX.r3.1HG0019410.1	-0.96466	2.787892	-4.28398	7.76E-05	0.004293	1.372074	Transducin/WD-like repeat-protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0403070.1	-0.672	6.7424	-4.30813	7.16E-05	0.004139	1.366264	Serine/threonine-protein phosphatase	elongation zone	12 h
HORVU.MOREX.r3.2HG0205750.1	-0.64261	6.410155	-4.30409	7.26E-05	0.004172	1.354776	3-oxoacyl-[acyl-carrier-protein] synthase 3	elongation zone	12 h
HORVU.MOREX.r3.5HG0511450.1	0.434001	5.650127	4.298297	7.40E-05	0.004195	1.352635	ABC transporter B family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0172730.1	-0.53292	7.548613	-4.33352	6.58E-05	0.004054	1.351163	Alpha-ketoglutarate-dependent dioxygenase alkB-like protein 2	elongation zone	12 h
HORVU.MOREX.r3.1HG0072540.1	-1.20754	5.751313	-4.2615	8.37E-05	0.004425	1.349429	Histone H4	elongation zone	12 h
HORVU.MOREX.r3.6HG0585240.1	1.031982	0.751154	4.282334	7.81E-05	0.004294	1.337296	Kinase superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0674440.1	-0.55543	5.321799	-4.28011	7.86E-05	0.004314	1.328447	Aluminum activated malate transporter family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0221180.1	1.205783	2.379805	4.342396	6.38E-05	0.004025	1.327074	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0209300.1	-1.18247	4.575756	-4.23881	9.02E-05	0.00464	1.324291	Sugar transporter, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0068370.1	-1.27704	4.947166	-4.23626	9.10E-05	0.004668	1.313667	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0718190.1	0.873213	6.009061	4.35186	6.19E-05	0.003971	1.310351	ABC transporter family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0634200.1	1.283575	0.006824	4.259056	8.43E-05	0.004438	1.309729	Syntaxin	elongation zone	12 h
HORVU.MOREX.r3.2HG0183740.1	-1.21852	5.211569	-4.23012	9.29E-05	0.004702	1.309581	Sugar transporter, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0677580.1	-1.49919	5.782253	-4.23991	8.99E-05	0.004635	1.30143	Protein O-linked-mannose beta-1,4-N-acetylglucosaminyltransferase 2	elongation zone	12 h
HORVU.MOREX.r3.1HG0079870.1	-1.13274	5.830169	-4.27854	7.90E-05	0.004314	1.299823	Pectin lyase-like superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0497490.1	1.76946	-1.08137	4.224964	9.45E-05	0.004721	1.29578	SPX domain-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0210420.1	-0.57174	7.910637	-4.322	6.84E-05	0.004083	1.29342	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3	elongation zone	12 h
HORVU.MOREX.r3.7HG0648620.1	1.421385	-1.54284	4.233649	9.18E-05	0.004697	1.288073	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0417410.1	-1.68956	0.915973	-4.3783	5.66E-05	0.003829	1.283171	Cold regulated protein 27	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.6HG0610500.1	1.092672	1.298618	4.302095	7.31E-05	0.00418	1.281725	Eukaryotic aspartyl protease family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0667610.1	1.529334	3.317002	4.283131	7.78E-05	0.004294	1.279977	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.5HG0524350.1	2.055719	-1.05304	4.218576	9.65E-05	0.004752	1.277835	Protein MIZU-KUSSEI 1	elongation zone	12 h
HORVU.MOREX.r3.1HG0041280.1	0.980912	4.323201	4.299521	7.37E-05	0.004195	1.271428	Cellulose synthase	elongation zone	12 h
HORVU.MOREX.r3.7HG0641750.1	2.979122	-2.73901	4.369425	5.83E-05	0.003853	1.265579	Aspartic proteinase nepenthesin-2	elongation zone	12 h
HORVU.MOREX.r3.3HG0327170.1	-0.55247	7.966567	-4.31388	7.02E-05	0.004083	1.265145	Bifunctional polymyxin resistance arnA protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0528280.1	0.512705	5.95615	4.276712	7.95E-05	0.004329	1.244628	Organic solute transporter-like	elongation zone	12 h
HORVU.MOREX.r3.5HG0459270.1	-0.84855	3.649219	-4.20887	9.96E-05	0.004816	1.241247	Cation calcium exchanger	elongation zone	12 h
HORVU.MOREX.r3.6HG0572960.1	-1.57567	1.634383	-4.38224	5.58E-05	0.003829	1.23804	Chlorophyll a-b binding protein, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.1HG0018810.1	-0.96919	5.360039	-4.2115	9.88E-05	0.004807	1.232275	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0157260.1	1.445115	-0.94189	4.207568	0.0001	0.004816	1.230818	NAD(P)H dehydrogenase (Quinone)	elongation zone	12 h
HORVU.MOREX.r3.7HG0667280.1	-0.53944	4.293106	-4.21833	9.66E-05	0.004752	1.225249	Hexosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0301750.1	-0.62386	9.943131	-4.37094	5.80E-05	0.003852	1.220849	Alpha-1,4 glucan phosphorylase	elongation zone	12 h
HORVU.MOREX.r3.4HG0400740.1	-0.28746	8.244974	-4.31653	6.96E-05	0.004083	1.218679	Cell division cycle protein 48-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0721690.1	1.257552	0.537157	4.224495	9.46E-05	0.004721	1.213527	Endoglucanase	elongation zone	12 h
HORVU.MOREX.r3.4HG0412790.1	0.733626	3.163327	4.207108	0.0001	0.004816	1.202035	Remorin	elongation zone	12 h
HORVU.MOREX.r3.1HG0053530.1	-1.45226	2.523226	-4.38005	5.63E-05	0.003829	1.197995	Glycerol-3-phosphate acyltransferase, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.2HG0115930.1	-0.65234	9.174331	-4.32974	6.66E-05	0.004056	1.193772	4-alpha-glucanotransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0662160.1	-0.58652	5.721315	-4.22042	9.59E-05	0.004752	1.191973	Phosphopantothenoylcysteine decarboxylase	elongation zone	12 h
HORVU.MOREX.r3.2HG0117030.1	0.722651	7.823219	4.298367	7.40E-05	0.004195	1.188672	Glutamate synthase, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0249400.1	1.212766	4.937663	4.310132	7.11E-05	0.004123	1.184833	Plasma membrane-associated cation-binding protein 1	elongation zone	12 h
HORVU.MOREX.r3.5HG0530750.1	-0.4972	5.706474	-4.22831	9.34E-05	0.004702	1.182274	Post-GPI attachment to proteins factor 3	elongation zone	12 h
HORVU.MOREX.r3.5HG0498320.1	0.421419	5.332211	4.228061	9.35E-05	0.004702	1.180629	Zinc finger, B-box	elongation zone	12 h
HORVU.MOREX.r3.5HG0432360.1	0.637144	6.047915	4.269128	8.16E-05	0.004344	1.170388	Inter-alpha-trypsin inhibitor heavy chain, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0420150.1	-0.441	6.344897	-4.24068	8.97E-05	0.004634	1.158981	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0609720.1	-0.80756	3.853974	-4.17823	0.00011	0.005113	1.156809	Glucosamine 6-phosphate N-acetyltransferase	elongation zone	12 h
HORVU.MOREX.r3.1HG0036370.1	-0.39076	6.141758	-4.24102	8.96E-05	0.004634	1.150968	Ras-related protein, expressed	elongation zone	12 h
HORVU.MOREX.r3.5HG0466010.1	-0.66964	3.637084	-4.17721	0.000111	0.005113	1.150669	Glutaredoxin	elongation zone	12 h
HORVU.MOREX.r3.3HG0302140.1	-0.4769	5.575661	-4.21705	9.70E-05	0.004761	1.147805	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0082770.1	-0.3557	7.702552	-4.27588	7.98E-05	0.004329	1.147785	Reticulon-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0161410.1	-0.32757	7.35188	-4.27923	7.89E-05	0.004314	1.147354	Acyl-[acyl-carrier-protein] desaturase	elongation zone	12 h
HORVU.MOREX.r3.6HG0625570.1	0.659825	5.941941	4.27068	8.11E-05	0.004344	1.147226	Transmembrane protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0498150.1	-1.28562	5.56412	-4.1845	0.000108	0.005063	1.141376	2-keto-3-deoxy-L-rhamnonate aldolase	elongation zone	12 h
HORVU.MOREX.r3.2HG0174820.1	-0.49585	6.649571	-4.22977	9.30E-05	0.004702	1.141142	F-box family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0080370.1	-0.48419	5.91275	-4.22394	9.48E-05	0.004721	1.134648	F-box family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0064740.1	0.757373	3.101051	4.184285	0.000108	0.005063	1.125888	Phospholipase A1	elongation zone	12 h
HORVU.MOREX.r3.4HG0392160.1	-1.26162	6.711088	-4.20599	0.000101	0.004823	1.125839	Glucan endo-1,3-beta-glucosidase, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0240710.1	-1.40334	3.472687	-4.17606	0.000111	0.005113	1.120306	Boron transporter	elongation zone	12 h
HORVU.MOREX.r3.1HG0057900.1	-0.66246	4.053556	-4.17406	0.000112	0.005113	1.118737	MYB-related transcription factor	elongation zone	12 h
HORVU.MOREX.r3.7HG0641030.1	1.349055	-0.36725	4.188688	0.000107	0.005013	1.11698	Serpin family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0727750.1	1.323645	5.212856	4.204674	0.000101	0.004833	1.111823	Zinc-transporting ATPase	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.2HG0182400.1	0.924203	5.649464	4.243957	8.87E-05	0.004634	1.10986	Aquaporin	elongation zone	12 h
HORVU.MOREX.r3.3HG0325250.1	3.373214	-1.52184	4.40057	5.25E-05	0.00369	1.094327	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.7HG0707700.1	1.299693	-2.42617	4.218608	9.65E-05	0.004752	1.088988	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	elongation zone	12 h
HORVU.MOREX.r3.7HG0635320.1	-0.59826	8.584452	-4.27486	8.00E-05	0.004331	1.083184	BAG family molecular chaperone regulator 7	elongation zone	12 h
HORVU.MOREX.r3.5HG0500120.1	-1.105	4.270851	-4.15476	0.000119	0.005253	1.081867	Thaumatin	elongation zone	12 h
HORVU.MOREX.r3.3HG0304780.1	-0.53973	4.983038	-4.18997	0.000106	0.005013	1.081655	Peptidyl serine alpha-galactosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0636630.1	1.233529	-0.12855	4.161349	0.000117	0.005234	1.076926	WAT1-related protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0433570.1	-0.5807	4.985176	-4.15947	0.000117	0.005234	1.076758	E3 ubiquitin protein ligase DRIP2	elongation zone	12 h
HORVU.MOREX.r3.5HG0504710.1	-0.3963	6.006762	-4.21054	9.91E-05	0.004807	1.06976	Signal peptidase subunit	elongation zone	12 h
HORVU.MOREX.r3.1HG0081950.1	2.576402	-2.05546	4.242161	8.92E-05	0.004634	1.064484	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.3HG0288710.2	1.75276	-1.63853	4.159693	0.000117	0.005234	1.063382	GDSL esterase/lipase	elongation zone	12 h
HORVU.MOREX.r3.3HG0287000.1	1.00542	3.768611	4.173841	0.000112	0.005113	1.056305	Respiratory burst oxidase	elongation zone	12 h
HORVU.MOREX.r3.3HG0251830.1	-1.12154	3.41269	-4.15745	0.000118	0.005245	1.055573	Plant regulator RWP-RK	elongation zone	12 h
HORVU.MOREX.r3.3HG0294950.1	1.231536	-0.01143	4.160938	0.000117	0.005234	1.052113	Deubiquitinase SseL	elongation zone	12 h
HORVU.MOREX.r3.6HG0626030.1	1.722439	-0.5621	4.168357	0.000114	0.005183	1.051979	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.2HG0210510.1	0.964903	-0.61919	4.15782	0.000118	0.005245	1.051041	Rapid alkalinization factor 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0737870.1	-1.71847	1.699649	-4.25021	8.69E-05	0.004559	1.040195	E3 ubiquitin-protein ligase RNF12-A	elongation zone	12 h
HORVU.MOREX.r3.3HG0230090.1	0.940606	1.525122	4.228639	9.33E-05	0.004702	1.037877	Cysteine protease, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0600500.1	-0.86376	3.118887	-4.13759	0.000126	0.0054	1.032825	Ceramide kinase	elongation zone	12 h
HORVU.MOREX.r3.6HG0539460.1	-0.31637	7.146504	-4.22727	9.37E-05	0.004703	1.026815	FG-GAP repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0234210.1	0.989786	3.873833	4.159386	0.000117	0.005234	1.022203	Receptor protein kinase, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0739120.1	1.108937	2.007183	4.16673	0.000115	0.005199	1.017973	Receptor-like protein kinase	elongation zone	12 h
HORVU.MOREX.r3.5HG0513780.1	0.648523	5.051864	4.189825	0.000106	0.005013	1.01478	Kinesin-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0204920.1	-1.38459	3.638603	-4.16375	0.000116	0.005234	1.012207	Crossover junction endonuclease EME1B	elongation zone	12 h
HORVU.MOREX.r3.2HG0102670.1	2.391367	-3.01135	4.431283	4.73E-05	0.003494	1.009149	Dirigent protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0038800.1	0.700493	2.879103	4.140907	0.000125	0.005398	1.003947	Protein kinase	elongation zone	12 h
HORVU.MOREX.r3.2HG0120650.1	1.154291	1.67255	4.241326	8.95E-05	0.004634	1.002559	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.4HG0357230.1	-1.22682	5.256363	-4.13104	0.000129	0.005458	1.001035	Pyridoxal 5'-phosphate synthase subunit PdxS	elongation zone	12 h
HORVU.MOREX.r3.5HG0529500.1	-0.34939	7.05237	-4.21102	9.89E-05	0.004807	0.994542	Protein kinase	elongation zone	12 h
HORVU.MOREX.r3.5HG0446210.1	-1.06958	3.497682	-4.13087	0.000129	0.005458	0.994488	Agenet domain, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0403620.1	1.536981	0.126435	4.192795	0.000105	0.004991	0.990315	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0543800.1	-0.92812	7.420452	-4.20718	0.0001	0.004816	0.990216	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.7HG0722360.1	1.636206	0.664931	4.12172	0.000133	0.005517	0.986935	Receptor-like protein kinase	elongation zone	12 h
HORVU.MOREX.r3.7HG0700270.1	-0.42456	7.724735	-4.23203	9.23E-05	0.004702	0.985323	Transaldolase	elongation zone	12 h
HORVU.MOREX.r3.2HG0165840.1	-0.72761	6.204491	-4.15667	0.000118	0.005247	0.984828	Protein kinase	elongation zone	12 h
HORVU.MOREX.r3.7HG0676570.1	-0.75448	6.054358	-4.16064	0.000117	0.005234	0.966551	Deaminase-related family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0739400.1	-1.21056	4.93511	-4.124	0.000132	0.005517	0.963995	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.2HG0198870.1	1.177674	-0.51668	4.127474	0.00013	0.005469	0.963587	UPF0761 membrane protein Plut_1323	elongation zone	12 h
HORVU.MOREX.r3.6HG0568880.1	-1.26447	5.953717	-4.13798	0.000126	0.0054	0.961847	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0110580.1	-0.55957	3.365388	-4.11625	0.000135	0.005554	0.961828	Ras-responsive element-binding protein 1	elongation zone	12 h
HORVU.MOREX.r3.3HG0306420.1	-1.04302	3.782406	-4.11041	0.000138	0.005596	0.951762	TPR repeat-containing protein ZIP4	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0293760.1	1.453863	3.466627	4.143802	0.000124	0.005393	0.950534	External alternative NAD(P)H-ubiquinone oxidoreductase B2, mitochondrial	elongation zone	12 h
HORVU.MOREX.r3.2HG0207130.1	1.534229	1.218085	4.147631	0.000122	0.005349	0.95016	Acetyl-coenzyme A synthetase	elongation zone	12 h
HORVU.MOREX.r3.7HG0663920.1	2.354114	-0.12227	4.181561	0.000109	0.005098	0.947156	Alpha/beta-Hydrolases superfamily protein, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0207860.1	1.587118	-2.16402	4.154338	0.000119	0.005253	0.943939	Serine/threonine-protein kinase	elongation zone	12 h
HORVU.MOREX.r3.4HG0337110.1	-0.34603	7.514078	-4.21378	9.80E-05	0.004801	0.943096	Coatomer subunit alpha	elongation zone	12 h
HORVU.MOREX.r3.7HG0729150.1	1.260149	-2.07184	4.107247	0.000139	0.005596	0.943004	GDSL esterase/lipase	elongation zone	12 h
HORVU.MOREX.r3.2HG0199560.1	-1.82807	5.029114	-4.10998	0.000138	0.005596	0.942071	Organic cation transporter-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0275770.1	0.728263	5.894882	4.201195	0.000102	0.004877	0.938511	Alpha/beta hydrolase-like	elongation zone	12 h
HORVU.MOREX.r3.5HG0469120.1	1.737777	-1.16488	4.102936	0.000141	0.005625	0.936066	E3 ubiquitin-protein ligase SINA-like 10	elongation zone	12 h
HORVU.MOREX.r3.1HG0075730.1	1.047776	1.539739	4.196987	0.000104	0.004934	0.924583	Subtilisin-like protease	elongation zone	12 h
HORVU.MOREX.r3.7HG0676350.1	-0.60217	4.38572	-4.12953	0.000129	0.005466	0.920845	Maternal effect embryo arrest protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0305500.1	-1.31455	2.378582	-4.17435	0.000112	0.005113	0.914269	50S ribosomal protein-related, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0648460.1	0.620827	2.500172	4.111429	0.000137	0.005593	0.912195	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0720100.1	0.768927	4.342288	4.105142	0.00014	0.005599	0.912009	Glucan endo-1,3-beta-glucosidase, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0051740.1	-2.71044	3.433417	-4.14521	0.000123	0.005379	0.908551	Glutathione s-transferase, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0190230.1	-1.47377	4.385744	-4.09308	0.000146	0.005731	0.906254	Histone H4	elongation zone	12 h
HORVU.MOREX.r3.7HG0660760.1	-1.15356	5.301372	-4.10691	0.000139	0.005596	0.904214	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.1HG0054180.1	1.538617	-0.6979	4.100335	0.000142	0.005654	0.903462	Expansin-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0380330.1	-0.52912	5.401503	-4.138	0.000126	0.0054	0.90305	WRKY transcription factor	elongation zone	12 h
HORVU.MOREX.r3.4HG0395220.1	-0.65223	6.119297	-4.1417	0.000124	0.005398	0.902652	Trehalose-6-phosphate synthase	elongation zone	12 h
HORVU.MOREX.r3.5HG0517190.1	0.702954	2.990144	4.089167	0.000148	0.005751	0.89564	Calcium-dependent protein kinase	elongation zone	12 h
HORVU.MOREX.r3.4HG0337950.1	2.271565	-0.29631	4.119137	0.000134	0.00553	0.89075	65-kDa microtubule-associated-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0458890.1	0.554844	3.514885	4.105111	0.00014	0.005599	0.880751	senescence regulator (Protein of unknown function, DUF584)	elongation zone	12 h
HORVU.MOREX.r3.6HG0552800.1	-1.13398	7.010449	-4.13639	0.000127	0.005411	0.874778	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.1HG0089130.1	-0.4243	5.608758	-4.11581	0.000135	0.005554	0.873458	Serine/Threonine-kinase pakA-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0748270.1	1.725878	0.645561	4.081136	0.000152	0.005814	0.872048	Blue copper protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0289020.1	1.305574	2.050529	4.11506	0.000136	0.005554	0.866394	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0304370.1	0.608195	4.367817	4.12174	0.000133	0.005517	0.863869	Glutamyl-tRNA(Gln) amidotransferase subunit A	elongation zone	12 h
HORVU.MOREX.r3.3HG0319900.1	1.531919	-0.77823	4.07715	0.000154	0.005819	0.859784	Ankyrin repeat domain-containing protein 1	elongation zone	12 h
HORVU.MOREX.r3.5HG0481440.1	-0.47662	4.469677	-4.10645	0.00014	0.005596	0.859431	glucan synthase-like 10	elongation zone	12 h
HORVU.MOREX.r3.3HG0264650.1	1.692176	-2.1209	4.127697	0.00013	0.005469	0.857287	Retrovirus-related Pol polyprotein from transposon TNT 1-94	elongation zone	12 h
HORVU.MOREX.r3.5HG0510940.1	-1.46151	5.282693	-4.0755	0.000155	0.005829	0.850169	HMG-Y-related protein A	elongation zone	12 h
HORVU.MOREX.r3.3HG0244690.1	-0.83906	4.95279	-4.08165	0.000151	0.005814	0.839301	Tubulin alpha chain	elongation zone	12 h
HORVU.MOREX.r3.3HG0233990.1	1.24044	1.603331	4.189007	0.000106	0.005013	0.838882	Xyloglucan endotransglucosylase/hydrolase	elongation zone	12 h
HORVU.MOREX.r3.2HG0097950.1	-0.87049	10.61692	-4.24093	8.96E-05	0.004634	0.836316	Apyrase	elongation zone	12 h
HORVU.MOREX.r3.3HG0297180.1	-1.7609	2.307652	-4.21181	9.87E-05	0.004807	0.833175	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0490610.1	1.717845	-0.13337	4.073125	0.000156	0.005863	0.833139	Protein kinase	elongation zone	12 h
HORVU.MOREX.r3.7HG0699020.1	1.85112	-0.26924	4.351227	6.20E-05	0.003971	0.831186	Retrotransposon protein, putative, Ty3-gypsy subclass	elongation zone	12 h
HORVU.MOREX.r3.3HG0222130.1	-0.3574	8.795276	-4.22182	9.55E-05	0.004743	0.828263	Transmembrane protein 214	elongation zone	12 h
HORVU.MOREX.r3.7HG0709270.1	1.010671	3.012432	4.092512	0.000146	0.005731	0.828025	RING/U-box superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0120320.1	0.824766	1.685244	4.169557	0.000113	0.005174	0.823334	Peroxidase	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.4HG0385780.1	-0.56087	5.783595	-4.12205	0.000133	0.005517	0.822654	Mitogen-activated protein kinase	elongation zone	12 h
HORVU.MOREX.r3.1HG0023610.1	-1.32683	5.369444	-4.0785	0.000153	0.005814	0.821833	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0551740.1	-0.70258	5.295694	-4.08498	0.00015	0.0058	0.821437	Early light-inducible protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0050920.1	1.043125	2.478719	4.123174	0.000132	0.005517	0.803006	Trehalase	elongation zone	12 h
HORVU.MOREX.r3.5HG0425680.1	-0.45559	7.233115	-4.15499	0.000119	0.005253	0.801983	No exine formation 1	elongation zone	12 h
HORVU.MOREX.r3.1HG0005700.1	1.949907	-2.12158	4.078759	0.000153	0.005814	0.798959	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0558800.1	-0.64398	5.008691	-4.0695	0.000158	0.00589	0.79346	DNA-binding protein BIN4	elongation zone	12 h
HORVU.MOREX.r3.4HG0404750.1	-2.00695	2.885556	-4.05386	0.000166	0.006055	0.787843	Hydrolase, alpha/beta fold family protein, expressed	elongation zone	12 h
HORVU.MOREX.r3.3HG0271380.1	0.607629	5.415877	4.092597	0.000146	0.005731	0.785605	GDSL esterase/lipase	elongation zone	12 h
HORVU.MOREX.r3.3HG0295680.1	0.616236	4.416665	4.113964	0.000136	0.005558	0.785088	Dihydropyrimidinase	elongation zone	12 h
HORVU.MOREX.r3.7HG0720790.1	-1.17463	3.44449	-4.06893	0.000158	0.00589	0.781788	Myb family transcription factor family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0626020.1	1.428647	1.680187	4.141812	0.000124	0.005398	0.778046	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.1HG0008200.1	-2.45219	1.354368	-4.05613	0.000165	0.006032	0.775839	Cytochrome P450	elongation zone	12 h
HORVU.MOREX.r3.2HG0184180.1	1.137619	4.475955	4.139182	0.000125	0.0054	0.77234	Remorin	elongation zone	12 h
HORVU.MOREX.r3.7HG0670900.1	1.570995	2.29029	4.054332	0.000166	0.006055	0.771381	Aspartic proteinase Asp1	elongation zone	12 h
HORVU.MOREX.r3.7HG0642520.1	1.830252	-0.8717	4.065528	0.00016	0.005945	0.770686	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.1HG0060320.1	-1.05585	7.084889	-4.10794	0.000139	0.005596	0.769387	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.7HG0747230.1	0.746133	2.606945	4.044909	0.000171	0.006089	0.766735	Non-specific serine/threonine protein kinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0255020.1	0.984176	3.48561	4.17494	0.000111	0.005113	0.759937	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.5HG0513740.1	1.598995	-3.01674	4.231653	9.24E-05	0.004702	0.758283	Alpha/beta-Hydrolases superfamily protein, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0084540.1	-0.51556	4.682873	-4.06461	0.00016	0.005948	0.757601	F-box family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0308420.1	-0.8279	3.844691	-4.04158	0.000173	0.00612	0.757262	Integrator complex subunit	elongation zone	12 h
HORVU.MOREX.r3.3HG0246560.1	-0.76999	5.025368	-4.04832	0.000169	0.006075	0.756947	Multiprotein-bridging factor, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0666650.1	-1.60043	-0.31405	-4.0693	0.000158	0.00589	0.752726	Starch synthase, chloroplastic/amyloplastic	elongation zone	12 h
HORVU.MOREX.r3.6HG0631710.1	1.057823	2.878977	4.175195	0.000111	0.005113	0.750974	Aquaporin	elongation zone	12 h
HORVU.MOREX.r3.1HG0001010.1	-0.88425	4.233711	-4.04897	0.000168	0.006075	0.750273	Pm3-like disease resistance protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0586850.1	-1.26756	0.435847	-4.10252	0.000141	0.005625	0.746832	Replication-associated protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0139910.1	-1.00909	2.439496	-4.04606	0.00017	0.006081	0.744843	RNA-binding CRS1 / YhbY (CRM) domain protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0377070.1	-0.53464	5.867895	-4.08874	0.000148	0.005751	0.738742	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0661060.1	-0.44743	6.051504	-4.08894	0.000148	0.005751	0.736993	Ethylene-responsive transcription factor	elongation zone	12 h
HORVU.MOREX.r3.6HG0614840.1	0.569248	5.33259	4.114761	0.000136	0.005554	0.732255	Shikimate kinase	elongation zone	12 h
HORVU.MOREX.r3.4HG0384620.1	0.92359	3.226323	4.047899	0.000169	0.006075	0.725588	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0282170.1	-1.82596	6.992997	-4.09211	0.000146	0.005731	0.712133	Methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0463760.1	-0.74771	3.113818	-4.02506	0.000182	0.00626	0.709355	Ethanolamine-phosphate cytidylyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0309900.1	1.463688	-1.42396	4.034118	0.000177	0.006165	0.706816	ROP-interactive CRIB motif protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0734670.1	-0.5608	6.626504	-4.11818	0.000134	0.005536	0.702896	L-ascorbate oxidase	elongation zone	12 h
HORVU.MOREX.r3.4HG0384230.1	-0.63771	3.949266	-4.03514	0.000176	0.006165	0.702046	RING/U-box superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0661830.1	2.193351	-0.86487	4.032858	0.000178	0.006165	0.70134	GPI-anchored adhesin-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0194840.1	-1.85975	3.704881	-4.02801	0.00018	0.006231	0.701099	Glucans biosynthesis glucosyltransferase H	elongation zone	12 h
HORVU.MOREX.r3.2HG0157410.1	1.212013	2.254585	4.141316	0.000125	0.005398	0.696567	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.7HG0653380.1	1.439011	1.304596	4.138632	0.000126	0.0054	0.693981	GDSL esterase/lipase	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.5HG0485860.1	-0.6617	3.795871	-4.04914	0.000168	0.006075	0.685731	LysM domain-containing GPI-anchored protein 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0164160.2	1.553915	-0.40053	4.049615	0.000168	0.006075	0.682135	Trihelix transcription factor	elongation zone	12 h
HORVU.MOREX.r3.3HG0238250.1	-0.89848	6.327265	-4.09553	0.000145	0.005722	0.680184	Gigantea-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0164650.1	-0.47352	5.166801	-4.0469	0.00017	0.006075	0.680128	Sucrose nonfermenting 4-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0404740.1	0.80758	2.889075	4.079976	0.000152	0.005814	0.67668	Hydrolase, alpha/beta fold family protein, expressed	elongation zone	12 h
HORVU.MOREX.r3.5HG0486750.1	0.873877	2.037011	4.040656	0.000173	0.006125	0.671235	Phosphatase 2C family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0146580.1	-0.5505	4.815547	-4.03643	0.000176	0.006165	0.668194	PHD finger alfin-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0382610.1	1.243522	0.223451	4.062262	0.000161	0.005955	0.666417	cytochrome P450, family 705, subfamily A, polypeptide 21	elongation zone	12 h
HORVU.MOREX.r3.4HG0348800.1	1.130201	2.044228	4.010239	0.000191	0.006387	0.665813	TCP transcription factor	elongation zone	12 h
HORVU.MOREX.r3.7HG0650970.1	-1.17613	7.468679	-4.07605	0.000154	0.005829	0.661654	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.3HG0319960.1	-0.94542	2.661966	-4.03427	0.000177	0.006165	0.658603	F-box-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0255700.1	0.949034	1.416296	4.007633	0.000193	0.006402	0.653542	PQ-loop repeat family protein / transmembrane family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0017280.1	1.59651	-0.33011	4.022299	0.000184	0.006278	0.650143	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.2HG0210610.1	0.925465	3.089943	4.022117	0.000184	0.006278	0.650022	Acetyl-coenzyme A synthetase	elongation zone	12 h
HORVU.MOREX.r3.7HG0749170.1	-1.3517	5.305591	-4.02946	0.00018	0.006217	0.649194	DUF241 domain protein (DUF241)	elongation zone	12 h
HORVU.MOREX.r3.4HG0406600.1	0.888365	0.071867	4.046912	0.00017	0.006075	0.646893	Heavy metal transport/detoxification superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0597620.1	-0.47097	5.241895	-4.0637	0.000161	0.005948	0.646402	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0218100.1	-0.36221	6.103028	-4.0702	0.000157	0.00589	0.646235	Chaperone protein DnaJ	elongation zone	12 h
HORVU.MOREX.r3.5HG0463550.1	1.043959	4.670129	4.01103	0.000191	0.006387	0.64457	RNA-binding domain CCCH-type zinc finger protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0598750.1	1.171516	0.858146	4.097067	0.000144	0.005704	0.644096	Remorin	elongation zone	12 h
HORVU.MOREX.r3.6HG0627920.1	-0.3309	7.364979	-4.1197	0.000134	0.00553	0.642997	Ankyrin repeat protein-like	elongation zone	12 h
HORVU.MOREX.r3.3HG0272160.2	-0.706	3.90619	-4.007	0.000193	0.006402	0.640427	Aldo/keto reductase family oxidoreductase	elongation zone	12 h
HORVU.MOREX.r3.5HG0461830.1	-1.41496	1.937434	-4.1337	0.000128	0.005436	0.638145	F-box/kelch-repeat protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0649950.1	0.647727	3.836695	4.033277	0.000177	0.006165	0.636184	Nudix hydrolase	elongation zone	12 h
HORVU.MOREX.r3.4HG0342160.1	-0.48024	5.308472	-4.04338	0.000172	0.006102	0.635113	Presenilin	elongation zone	12 h
HORVU.MOREX.r3.1HG0069570.1	-0.37717	8.695958	-4.15957	0.000117	0.005234	0.631104	Tubulin beta chain	elongation zone	12 h
HORVU.MOREX.r3.1HG0052810.1	-0.66093	7.005109	-4.07861	0.000153	0.005814	0.62667	Mitochondrial carrier protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0586290.1	-0.87785	2.563314	-4.00053	0.000197	0.006444	0.62289	CDT1-like protein a, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.3HG0218800.1	1.971084	-0.5154	3.999058	0.000198	0.006444	0.621042	hydroxyproline-rich glycoprotein family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0497360.1	-0.56078	3.787521	-3.9983	0.000199	0.006448	0.619229	Bile acid sodium symporter	elongation zone	12 h
HORVU.MOREX.r3.2HG0099010.1	1.17563	-2.64978	4.082181	0.000151	0.005814	0.616661	Glutamyl-tRNA (Gln) amidotransferase subunit A	elongation zone	12 h
HORVU.MOREX.r3.7HG0747940.1	0.459113	7.327177	4.128528	0.00013	0.005469	0.613541	Polyamine oxidase	elongation zone	12 h
HORVU.MOREX.r3.1HG0026430.1	-0.41505	4.788835	-4.03732	0.000175	0.00616	0.604281	Proline-rich receptor-like kinase, putative (DUF1421)	elongation zone	12 h
HORVU.MOREX.r3.4HG0335690.1	-0.64334	6.238374	-4.05177	0.000167	0.006064	0.602143	Zinc finger CCCH domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0008510.2	0.543767	3.338317	3.999991	0.000198	0.006444	0.597615	Beta-hexosaminidase	elongation zone	12 h
HORVU.MOREX.r3.3HG0288700.1	-0.67011	3.838111	-3.99334	0.000202	0.006513	0.595243	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0242950.1	-0.4367	6.032036	-4.0512	0.000167	0.006064	0.591728	NF-X1 type zinc finger family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0307850.1	-0.75535	6.891759	-4.10701	0.000139	0.005596	0.590726	Basic 7S globulin	elongation zone	12 h
HORVU.MOREX.r3.2HG0121200.1	0.902639	0.643147	4.029244	0.00018	0.006217	0.585822	Dirigent protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0477750.1	1.981434	0.658352	4.013485	0.000189	0.006367	0.576746	Homeobox protein, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0401730.1	-0.7434	2.933703	-3.97939	0.000211	0.006618	0.575755	Pentatricopeptide repeat-containing protein	elongation zone	12 h

Table Sн Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.4HG0413320.1	1.859757	2.316272	3.991716	0.000203	0.006534	0.574251	Subtilisin-like protease	elongation zone	12 h
HORVU.MOREX.r3.1HG0018190.2	-1.18149	3.737279	-3.97592	0.000214	0.00667	0.561255	Aspartic proteinase	elongation zone	12 h
HORVU.MOREX.r3.7HG0684880.1	0.79924	3.761267	3.997829	0.000199	0.006448	0.560572	meiosis chromosome segregation family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0091330.1	-0.97883	4.42056	-3.97754	0.000212	0.006645	0.560416	Flavin-containing monooxygenase	elongation zone	12 h
HORVU.MOREX.r3.7HG0669580.1	0.7114	1.551164	4.041416	0.000173	0.00612	0.559434	Caleosin	elongation zone	12 h
HORVU.MOREX.r3.4HG0412090.1	1.817709	-0.36354	3.988402	0.000205	0.006554	0.557106	C3HC4-type RING finger-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0454720.1	0.569329	5.752069	4.01507	0.000188	0.006364	0.555617	Filament-like plant protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0142740.1	0.365846	6.623245	4.091156	0.000147	0.005738	0.554294	Protein phosphatase 2c	elongation zone	12 h
HORVU.MOREX.r3.5HG0514950.1	-0.5784	5.805968	-4.0236	0.000183	0.006269	0.54917	Actin-depolymerizing factor	elongation zone	12 h
HORVU.MOREX.r3.7HG0730840.1	-1.08969	4.5286	-3.98201	0.000209	0.0066	0.548401	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.1HG0076120.1	0.68528	7.792381	4.177781	0.00011	0.005113	0.546564	Phosphatidylinositol transfer protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0650250.1	-0.62992	3.840838	-3.9741	0.000215	0.006679	0.54407	Protein-O-fucosyltransferase 1	elongation zone	12 h
HORVU.MOREX.r3.3HG0245250.1	3.239054	-1.64331	3.988561	0.000205	0.006554	0.537673	Cysteine protease, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0110130.1	-1.02012	3.822081	-4.00269	0.000196	0.00643	0.534689	Transcription factor protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0180010.1	1.375117	1.125048	4.01451	0.000188	0.006364	0.533217	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0313900.1	1.873062	0.291481	4.005222	0.000194	0.006419	0.526921	Methyl esterase 1	elongation zone	12 h
HORVU.MOREX.r3.3HG0296010.1	1.968773	-0.38601	3.961341	0.000224	0.006805	0.525691	WAT1-related protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0543770.1	-0.9087	7.792354	-4.06286	0.000161	0.005954	0.52526	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.6HG0567150.1	1.159328	2.844231	3.979896	0.000211	0.006618	0.523284	Exosome complex component	elongation zone	12 h
HORVU.MOREX.r3.5HG0464440.1	1.039304	0.420648	4.004921	0.000194	0.006419	0.517211	Kinase, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0590430.1	-0.41192	5.249518	-4.00282	0.000196	0.00643	0.513924	Multidrug resistance protein MdtC	elongation zone	12 h
HORVU.MOREX.r3.3HG0308350.1	1.03734	4.926407	3.997424	0.000199	0.006448	0.511026	Cysteine-rich receptor kinase	elongation zone	12 h
HORVU.MOREX.r3.5HG0457310.1	1.126551	0.314313	4.001557	0.000197	0.006443	0.510447	Exocyst complex component, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0096600.1	-0.59642	8.083915	-4.08285	0.000151	0.005814	0.508985	Pyruvate dehydrogenase E1 component subunit alpha	elongation zone	12 h
HORVU.MOREX.r3.1HG0075650.1	1.18635	4.442331	4.080471	0.000152	0.005814	0.506425	transmembrane protein, putative (DUF1218)	elongation zone	12 h
HORVU.MOREX.r3.1HG0073010.1	0.958928	1.113004	4.033381	0.000177	0.006165	0.500115	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0722260.1	1.63999	-2.17609	3.973294	0.000215	0.006686	0.499731	RPM1-interacting protein 4	elongation zone	12 h
HORVU.MOREX.r3.3HG0314270.1	-0.78876	2.38297	-3.96934	0.000218	0.006691	0.498499	F-box-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0112030.1	0.516722	5.79888	4.034679	0.000177	0.006165	0.498297	B3 domain-containing transcription factor VAL3	elongation zone	12 h
HORVU.MOREX.r3.6HG0615840.1	2.786594	-2.2741	4.528701	3.40E-05	0.002987	0.496025	Metalloendoproteinase 1	elongation zone	12 h
HORVU.MOREX.r3.4HG0406670.1	0.814044	6.546221	4.069503	0.000158	0.00589	0.495065	Classical arabinogalactan protein 5	elongation zone	12 h
HORVU.MOREX.r3.3HG0255220.1	-0.99854	5.459644	-3.9754	0.000214	0.006671	0.493668	Geranylgeranyl reductase	elongation zone	12 h
HORVU.MOREX.r3.6HG0545970.1	-0.48011	5.654969	-4.01071	0.000191	0.006387	0.491545	Short-chain dehydrogenase/reductase family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0186680.1	-0.69402	7.556619	-4.06168	0.000162	0.005955	0.489932	Histone H1	elongation zone	12 h
HORVU.MOREX.r3.2HG0165920.1	1.323692	1.852926	3.95265	0.00023	0.006891	0.489524	Purple acid phosphatase	elongation zone	12 h
HORVU.MOREX.r3.7HG0661450.1	0.669138	6.337893	4.07787	0.000153	0.005816	0.487059	Phosphoinositide phosphatase family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0409230.1	1.858508	-0.03281	3.989212	0.000205	0.006554	0.486208	IQ domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0524010.1	-1.3108	6.200507	-3.98427	0.000208	0.006583	0.48512	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0495730.1	1.153289	2.468419	3.974701	0.000214	0.006676	0.482125	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0306060.1	-0.3737	5.417997	-4.00749	0.000193	0.006402	0.47904	Thioredoxin-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0183780.1	-0.55786	5.376384	-4.00045	0.000197	0.006444	0.478889	Sphingolipid delta-4 desaturase	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.5HG0532150.1	2.123181	-2.26204	3.983079	0.000209	0.006588	0.478194	Expansin	elongation zone	12 h
HORVU.MOREX.r3.6HG0633900.1	1.826189	-0.51261	3.970636	0.000217	0.006691	0.477093	Calcium-dependent protein kinase	elongation zone	12 h
HORVU.MOREX.r3.7HG0679760.1	-0.56827	6.056962	-4.01322	0.000189	0.006367	0.471735	Basic helix-loop-helix transcription factor	elongation zone	12 h
HORVU.MOREX.r3.6HG0618630.1	-0.60317	6.66233	-4.06035	0.000162	0.00597	0.467752	Glucan endo-1,3-beta-glucosidase 3	elongation zone	12 h
HORVU.MOREX.r3.1HG0075440.1	0.832065	1.650312	3.970108	0.000218	0.006691	0.465883	Protein NRT1/ PTR FAMILY 5.5	elongation zone	12 h
HORVU.MOREX.r3.6HG0609100.1	-1.11456	1.570415	-3.99474	0.000201	0.006494	0.464721	3-hydroxy-3-methylglutaryl coenzyme A reductase	elongation zone	12 h
HORVU.MOREX.r3.4HG0383870.1	-0.79619	7.088832	-4.01989	0.000185	0.006303	0.463059	Malonyl CoA-acyl carrier protein transacylase containing protein, expressed	elongation zone	12 h
HORVU.MOREX.r3.4HG0395940.1	1.45687	3.064976	3.941134	0.000239	0.006937	0.460473	Homocysteine S-methyltransferase family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0543740.1	-0.9818	7.842285	-4.0446	0.000171	0.006089	0.460458	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.2HG0140170.1	0.740702	2.981209	3.944158	0.000237	0.006926	0.459744	Ras-related protein Rab-21	elongation zone	12 h
HORVU.MOREX.r3.6HG0568910.1	0.82335	3.99892	4.025904	0.000182	0.00626	0.455537	L-gulonolactone oxidase	elongation zone	12 h
HORVU.MOREX.r3.2HG0214090.1	-1.07901	7.152075	-3.98803	0.000205	0.006554	0.450429	C2 calcium/lipid-binding and GRAM domain protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0056280.1	-1.05304	3.39368	-3.93948	0.00024	0.006944	0.449166	Xyloglucan galactosyltransferase KATAMARI1	elongation zone	12 h
HORVU.MOREX.r3.6HG0547660.1	2.391812	-1.78969	4.063885	0.00016	0.005948	0.440347	Copine-1	elongation zone	12 h
HORVU.MOREX.r3.2HG0127260.1	1.313234	-1.06197	3.949596	0.000233	0.006891	0.438906	COBRA-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0415490.1	1.916614	-1.78464	3.931274	0.000247	0.007038	0.434288	14 kDa proline-rich protein DC2.15	elongation zone	12 h
HORVU.MOREX.r3.2HG0192900.1	-1.32098	6.268762	-3.95666	0.000227	0.006853	0.432205	Xyloglucan endotransglucosylase/hydrolase	elongation zone	12 h
HORVU.MOREX.r3.7HG0714910.1	-0.70352	7.21685	-4.02456	0.000182	0.00626	0.426256	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0512490.1	1.663332	1.425049	4.01258	0.00019	0.006369	0.426193	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.3HG0242150.1	3.271829	-3.21832	4.261719	8.36E-05	0.004425	0.422949	Glycine-rich cell wall structural protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0495840.1	-0.39103	5.657016	-3.98949	0.000204	0.006554	0.422198	Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha	elongation zone	12 h
HORVU.MOREX.r3.7HG0714930.1	-0.39796	7.749002	-4.05239	0.000167	0.006062	0.420028	UDP-galactose transporter, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0064220.1	-0.75906	4.418073	-3.92612	0.000251	0.007078	0.416623	Isoamylase-like glucan debranching enzyme	elongation zone	12 h
HORVU.MOREX.r3.6HG0575690.1	-0.85327	3.926859	-3.92597	0.000251	0.007078	0.415734	Exostosin-like	elongation zone	12 h
HORVU.MOREX.r3.6HG0588520.1	0.971566	2.56033	3.985751	0.000207	0.006561	0.411471	Rop guanine nucleotide exchange factor	elongation zone	12 h
HORVU.MOREX.r3.6HG0595860.1	-0.45682	5.620865	-3.9715	0.000217	0.006691	0.409036	E3 ubiquitin-protein ligase	elongation zone	12 h
HORVU.MOREX.r3.1HG0085420.1	-0.75789	3.718027	-3.92016	0.000256	0.007125	0.407661	DNA replication complex GINS protein PSF2	elongation zone	12 h
HORVU.MOREX.r3.1HG0061660.1	0.986173	3.333271	3.986796	0.000206	0.006561	0.406461	RING/FYVE/PHD zinc finger superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0206470.1	0.55066	6.2777	4.039803	0.000174	0.006131	0.401113	Loricrin-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0444060.1	-1.08418	1.863328	-3.93464	0.000244	0.007006	0.399591	Calmodulin-binding family protein, putative, expressed	elongation zone	12 h
HORVU.MOREX.r3.5HG0465690.1	0.828296	3.37211	3.945746	0.000235	0.006919	0.398279	Phytol kinase	elongation zone	12 h
HORVU.MOREX.r3.6HG0626070.1	0.569575	3.613021	3.954274	0.000229	0.006881	0.393097	UDP-N-acetylglucosamine--N-acetylmuramyl-(Pentapeptide) pyrophosphoryl-unde	elongation zone	12 h
HORVU.MOREX.r3.7HG0739480.1	-0.88395	7.565794	-4.00421	0.000195	0.006419	0.392692	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.3HG0252170.1	1.656456	-1.70754	3.930232	0.000247	0.007043	0.390328	DUF1685 family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0511860.1	-0.92938	6.516686	-3.98609	0.000207	0.006561	0.384364	Blue copper protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0488040.1	1.623253	-1.23014	3.921476	0.000255	0.007125	0.383407	Blue copper protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0674750.1	-0.4465	5.335659	-3.96543	0.000221	0.006756	0.383282	Dual specificity protein phosphatase, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0225610.1	-0.86364	2.476199	-3.93357	0.000245	0.007006	0.382941	Mediator of RNA polymerase II transcription subunit 22	elongation zone	12 h
HORVU.MOREX.r3.4HG0345990.1	0.511432	6.344145	4.00819	0.000192	0.006402	0.380012	GDP-L-galactose phosphorylase 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0650300.1	0.67397	3.514135	3.942036	0.000238	0.006937	0.37908	Protein kinase	elongation zone	12 h
HORVU.MOREX.r3.2HG0182020.2	-1.34584	3.196873	-3.90942	0.000265	0.00721	0.378139	Phenylalanine ammonia-lyase	elongation zone	12 h

Table Sн Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.4HG0381990.1	1.46516	1.592907	3.972147	0.000216	0.006691	0.377003	Pre-mRNA splicing factor, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0426280.1	0.913367	2.961285	3.930876	0.000247	0.007038	0.375538	GTP binding protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0606140.1	2.005058	-0.36014	3.958801	0.000226	0.006833	0.375461	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0531450.1	0.914179	-1.15012	3.925691	0.000251	0.007078	0.373971	Speckle-type POZ protein-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0056560.1	-0.39174	5.466997	-3.96952	0.000218	0.006691	0.373742	AP-3 complex subunit delta	elongation zone	12 h
HORVU.MOREX.r3.1HG0048030.1	-0.46033	7.472589	-4.01437	0.000189	0.006364	0.372158	Membrane steroid-binding protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0721760.1	-0.3845	8.4211	-4.05685	0.000164	0.006028	0.368885	Translocon-associated protein subunit alpha	elongation zone	12 h
HORVU.MOREX.r3.6HG0629520.1	1.528497	-0.9319	3.915365	0.00026	0.007125	0.365732	Ethylene-responsive transcription factor	elongation zone	12 h
HORVU.MOREX.r3.1HG0074500.1	-1.07864	7.370525	-3.98045	0.00021	0.006618	0.360713	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.2HG0128890.1	-0.68362	5.994209	-3.95872	0.000226	0.006833	0.360124	RAN GTPASE ACTIVATING protein 2	elongation zone	12 h
HORVU.MOREX.r3.1HG0077880.1	-1.07543	3.552074	-3.91005	0.000264	0.007205	0.358976	BAG family molecular chaperone regulator 7	elongation zone	12 h
HORVU.MOREX.r3.7HG0705700.1	-0.6989	3.946655	-3.91098	0.000263	0.007193	0.35868	Calcium ion-binding protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0438750.1	-0.72831	5.420678	-3.94797	0.000234	0.006891	0.357	Disease resistance protein (NBS-LRR class) family	elongation zone	12 h
HORVU.MOREX.r3.1HG0054500.1	-0.97984	5.920469	-3.9493	0.000233	0.006891	0.353256	#N/A	elongation zone	12 h
HORVU.MOREX.r3.1HG0078750.1	-0.56448	3.941561	-3.90589	0.000268	0.007263	0.350547	Tesmin/TSO1-like CXC domain containing protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0354970.1	-0.68025	6.732308	-3.98592	0.000207	0.006561	0.350426	Omega-3 fatty acid desaturase	elongation zone	12 h
HORVU.MOREX.r3.3HG0299010.1	-1.07148	2.065005	-3.91814	0.000257	0.007125	0.346533	Protein NRT1/ PTR FAMILY 5.5	elongation zone	12 h
HORVU.MOREX.r3.7HG0650980.1	-0.9585	5.5668	-3.93719	0.000242	0.006974	0.343837	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.4HG0340920.1	-0.43794	4.789685	-3.9192	0.000256	0.007125	0.341981	RNA-binding KH domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0741080.1	-0.83663	1.851569	-3.90006	0.000273	0.007364	0.340277	Disease resistance protein RPM1	elongation zone	12 h
HORVU.MOREX.r3.3HG0250060.1	1.991888	-2.50642	4.147566	0.000122	0.005349	0.338129	CASP-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0074260.1	-0.40016	7.572556	-4.01556	0.000188	0.006364	0.335415	Beta-glucosidase	elongation zone	12 h
HORVU.MOREX.r3.4HG0370520.1	-0.74284	3.910658	-3.89647	0.000276	0.007381	0.335302	inactive purple acid phosphatase-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0378330.1	1.261165	0.037978	3.920412	0.000255	0.007125	0.331573	transcription repressor	elongation zone	12 h
HORVU.MOREX.r3.6HG0620630.1	1.012137	3.35364	4.02034	0.000185	0.006303	0.331391	Subtilisin-like protease	elongation zone	12 h
HORVU.MOREX.r3.3HG0244240.1	1.222215	3.630904	3.914963	0.00026	0.007125	0.330616	Alpha/beta-Hydrolases superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0398550.1	1.049275	6.045114	4.052829	0.000166	0.006062	0.330555	Calcium-transporting ATPase	elongation zone	12 h
HORVU.MOREX.r3.1HG0055230.1	-0.88924	7.590256	-4.00424	0.000195	0.006419	0.330418	Methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0513810.1	0.629718	4.245645	3.952317	0.00023	0.006891	0.330305	Malate dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.5HG0460160.1	0.430942	6.54551	4.024865	0.000182	0.00626	0.330281	Bifunctional uridylyltransferase/uridylyl-removing enzyme	elongation zone	12 h
HORVU.MOREX.r3.5HG0533230.1	-0.55534	5.643177	-3.96252	0.000223	0.00679	0.330258	Pirin-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0230190.1	-1.17966	2.957931	-3.94024	0.00024	0.006944	0.32855	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0309460.1	-0.33386	5.431182	-3.95887	0.000226	0.006833	0.326114	Trichome birefringence-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0016810.1	-0.81163	5.521689	-3.91477	0.00026	0.007125	0.320822	Agenet domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0730070.1	-1.33555	6.723992	-3.94509	0.000236	0.006919	0.318158	Thaumatin-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0252250.1	1.603359	-1.6584	3.891444	0.00028	0.007449	0.318073	Expansin	elongation zone	12 h
HORVU.MOREX.r3.4HG0335180.1	-0.63969	5.021928	-3.91484	0.00026	0.007125	0.31323	Phosphatidylinositol N-acetyglucosaminlytransferase subunit P-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0012340.1	1.253337	2.437594	3.939378	0.00024	0.006944	0.312979	Triose-phosphate transporter family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0197560.1	-0.76776	5.104956	-3.89722	0.000275	0.00738	0.303155	RNA-binding protein 39	elongation zone	12 h
HORVU.MOREX.r3.3HG0254930.1	2.689498	-0.9917	3.908716	0.000265	0.007214	0.300402	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.2HG0196800.1	2.024398	-0.20994	3.999539	0.000198	0.006444	0.298898	Multidrug resistance protein ABC transporter family	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.5HG0490830.1	-0.41664	5.180095	-3.92195	0.000254	0.007125	0.296014	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0340910.2	2.527565	-1.88941	4.135578	0.000127	0.005414	0.292021	p-loop containing nucleoside triphosphate hydrolases superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0016710.2	1.755892	-3.14485	4.085564	0.00015	0.0058	0.290984	Annexin	elongation zone	12 h
HORVU.MOREX.r3.1HG0067980.1	1.560748	-1.60301	3.881814	0.000289	0.007575	0.289972	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.7HG0746230.1	-0.60374	6.353103	-3.95642	0.000227	0.006853	0.28833	Receptor protein kinase-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0612780.1	1.533597	1.073388	3.917698	0.000258	0.007125	0.287468	Dynein light chain	elongation zone	12 h
HORVU.MOREX.r3.3HG0256580.1	-0.49073	6.795309	-3.95493	0.000229	0.006876	0.285959	NEDD8-activating enzyme E1 catalytic subunit	elongation zone	12 h
HORVU.MOREX.r3.7HG0729000.1	0.979307	3.645636	3.898164	0.000274	0.007375	0.285877	RING/U-box superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0606940.1	-3.08142	2.180677	-4.39605	5.33E-05	0.003734	0.281793	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0480980.1	2.465734	-1.63821	3.899867	0.000273	0.007364	0.279174	Spermidine/putrescine import ATP-binding protein PotA	elongation zone	12 h
HORVU.MOREX.r3.3HG0288240.1	-0.69902	5.202677	-3.89632	0.000276	0.007381	0.274004	ubiquitin fusion degradation 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0171550.1	-0.81251	4.111529	-3.87687	0.000294	0.007636	0.271834	Major facilitator superfamily transporter	elongation zone	12 h
HORVU.MOREX.r3.5HG0520990.1	-0.65535	3.822638	-3.8797	0.000291	0.007597	0.270986	Kinase, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0601260.1	1.107052	3.050364	3.948217	0.000234	0.006891	0.268642	Sulfotransferase	elongation zone	12 h
HORVU.MOREX.r3.6HG0624630.1	-0.44344	6.985603	-3.97928	0.000211	0.006618	0.264482	Aspartate aminotransferase	elongation zone	12 h
HORVU.MOREX.r3.4HG0342850.1	-0.4054	5.711387	-3.92415	0.000252	0.007103	0.262195	Serpin family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0604860.1	-1.09537	1.903058	-3.93412	0.000244	0.007006	0.258698	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.1HG0069290.1	-0.33331	8.209881	-4.01783	0.000186	0.006334	0.257858	Nucleotide-sugar transporter family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0573920.1	1.475431	-0.43481	3.944927	0.000236	0.006919	0.252712	Retrotransposon protein, putative, unclassified	elongation zone	12 h
HORVU.MOREX.r3.6HG0603530.1	-1.09117	2.451293	-3.87968	0.000291	0.007597	0.252432	Protein DETOXIFICATION	elongation zone	12 h
HORVU.MOREX.r3.1HG0087620.1	1.053131	3.06372	3.962767	0.000223	0.00679	0.251206	Xyloglucan endotransglucosylase/hydrolase	elongation zone	12 h
HORVU.MOREX.r3.2HG0115780.1	-1.18166	6.198436	-3.95077	0.000232	0.006891	0.247731	FAD-binding Berberine family protein, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0187440.1	-0.53745	5.452931	-3.91678	0.000258	0.007125	0.241392	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0631600.1	1.124704	1.162908	3.938525	0.000241	0.006954	0.23913	Rop guanine nucleotide exchange factor, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0155810.1	-0.94308	3.567204	-3.86139	0.000309	0.007759	0.238582	Replication protein A 70 kDa DNA-binding subunit A	elongation zone	12 h
HORVU.MOREX.r3.1HG0023200.1	1.271124	0.569684	3.884635	0.000286	0.007556	0.23679	LURP-one-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0287690.1	0.932619	2.646815	3.943227	0.000237	0.006937	0.234015	Profilin	elongation zone	12 h
HORVU.MOREX.r3.1HG0001510.1	-1.06579	3.140127	-3.86222	0.000308	0.007759	0.230565	NBS-LRR-like resistance protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0384110.1	-0.37757	6.300031	-3.94887	0.000233	0.006891	0.229437	RING/U-box superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0097360.1	-0.82577	5.914899	-3.90289	0.00027	0.007323	0.22628	Laccase	elongation zone	12 h
HORVU.MOREX.r3.3HG0286160.1	-1.74814	6.290215	-3.88114	0.00029	0.007581	0.226209	Pollen Ole e 1 allergen/extensin	elongation zone	12 h
HORVU.MOREX.r3.3HG0242030.1	-1.66538	2.331268	-3.94825	0.000234	0.006891	0.222702	Alpha/beta-Hydrolases superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0555660.2	-0.43508	7.208638	-3.96976	0.000218	0.006691	0.221947	Calreticulin/calnexin	elongation zone	12 h
HORVU.MOREX.r3.2HG0113880.1	0.62138	4.823614	3.908391	0.000265	0.007214	0.220577	Heavy metal transport/detoxification superfamily protein, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0426210.3	0.861042	1.98152	3.861529	0.000308	0.007759	0.219907	Protein IQ-DOMAIN 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0192400.1	0.785664	3.506293	3.862664	0.000307	0.007759	0.20101	Receptor protein kinase, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0622110.1	1.423774	2.81443	3.922937	0.000253	0.007121	0.200877	Pathogenesis-related protein 1	elongation zone	12 h
HORVU.MOREX.r3.6HG0593200.1	-1.018	4.784544	-3.86135	0.000309	0.007759	0.200011	Short-chain dehydrogenase/reductase family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0157290.1	-1.07392	3.397681	-3.85029	0.00032	0.007921	0.198771	Calcineurin-like metallo-phosphoesterase superfamily	elongation zone	12 h
HORVU.MOREX.r3.1HG0086370.1	2.105225	-3.20911	4.108594	0.000139	0.005596	0.198412	Glyoxal oxidase	elongation zone	12 h
HORVU.MOREX.r3.4HG0342660.1	1.266999	1.013503	3.92803	0.000249	0.007073	0.19738	Calcium-binding EF-hand family protein	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.5HG0485610.1	1.357976	0.79472	3.845829	0.000324	0.007986	0.195993	Cytochrome P450, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0420460.1	2.796521	-1.03028	4.319064	6.90E-05	0.004083	0.195936	NBS-LRR-like resistance protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0256380.1	-0.85666	6.689113	-3.91745	0.000258	0.007125	0.193908	Ubiquitin-conjugating enzyme E2	elongation zone	12 h
HORVU.MOREX.r3.2HG0139370.1	-0.79417	6.338385	-3.92966	0.000248	0.007046	0.188684	Xyloglucan endotransglucosylase/hydrolase	elongation zone	12 h
HORVU.MOREX.r3.2HG0203070.1	0.872154	3.219858	3.885153	0.000286	0.007556	0.186942	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.5HG0489840.1	-1.11502	2.789323	-3.88458	0.000286	0.007556	0.186721	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0304710.1	-0.34666	8.270238	-4.0082	0.000192	0.006402	0.184934	Fructose-bisphosphate aldolase	elongation zone	12 h
HORVU.MOREX.r3.3HG0321700.1	0.683543	3.776226	3.853653	0.000316	0.007898	0.183987	FMN-dependent NADPH-azoreductase	elongation zone	12 h
HORVU.MOREX.r3.7HG0739080.1	2.344023	-3.17965	4.174016	0.000112	0.005113	0.182638	Subtilisin-like protease	elongation zone	12 h
HORVU.MOREX.r3.2HG0128840.1	-0.59474	4.89057	-3.89289	0.000279	0.007434	0.179281	Son of sevenless	elongation zone	12 h
HORVU.MOREX.r3.3HG0248440.1	0.696104	4.338634	3.945978	0.000235	0.006919	0.179012	Ras-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0056240.1	0.741885	4.721848	3.916231	0.000259	0.007125	0.178954	Trehalose 6-phosphate phosphatase	elongation zone	12 h
HORVU.MOREX.r3.4HG0337040.1	0.991278	2.764027	3.867206	0.000303	0.007757	0.17738	Accelerated cell death 11 family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0190680.1	-0.48109	6.930995	-3.92636	0.000251	0.007078	0.173461	Aminotransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0178160.1	-0.65043	7.879945	-3.95685	0.000227	0.006853	0.169735	HTH-type transcriptional regulator YidZ	elongation zone	12 h
HORVU.MOREX.r3.6HG0600910.1	1.324317	1.060689	3.919899	0.000256	0.007125	0.165547	Aquaporin	elongation zone	12 h
HORVU.MOREX.r3.2HG0182010.1	-0.852	6.691165	-3.93288	0.000245	0.007012	0.164458	Phenylalanine ammonia-lyase	elongation zone	12 h
HORVU.MOREX.r3.3HG0283080.2	1.024447	1.384373	3.879057	0.000292	0.007602	0.160765	suppressor	elongation zone	12 h
HORVU.MOREX.r3.6HG0632020.2	1.448126	-2.23983	3.869996	0.0003	0.007754	0.160369	Photosystem II 22 kDa, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.7HG0685970.1	0.769168	4.80192	3.969522	0.000218	0.006691	0.157807	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0299280.1	-0.73257	4.635338	-3.85836	0.000311	0.007805	0.155665	WD-repeat protein, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0486660.1	1.249554	-2.06977	3.836147	0.000334	0.008157	0.151516	Calcium-binding protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0053060.1	1.041453	4.011378	3.852947	0.000317	0.007902	0.148877	PLATZ transcription factor	elongation zone	12 h
HORVU.MOREX.r3.5HG0432640.1	-0.38942	5.94978	-3.89248	0.000279	0.007434	0.139617	Protein O-linked-mannose beta-1,4-N-acetylglucosaminyltransferase 2	elongation zone	12 h
HORVU.MOREX.r3.5HG0469300.1	1.644501	0.250216	3.824648	0.000347	0.008288	0.138985	CCCH-type zinc finger protein with ARM repeat domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0622300.1	-0.79426	7.348551	-3.92727	0.00025	0.007078	0.134636	Pathogenesis-related protein 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0741640.1	-0.96463	4.20973	-3.83382	0.000337	0.008177	0.133135	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.1HG0065520.1	0.525843	5.125584	3.915944	0.000259	0.007125	0.132262	KH domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0293130.1	1.088174	3.772343	3.860562	0.000309	0.007759	0.131482	Eukaryotic aspartyl protease family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0558840.1	-0.29144	6.872948	-3.91756	0.000258	0.007125	0.130073	Kinetochore protein nuf2, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0548710.1	2.180602	-1.47311	3.823767	0.000348	0.008288	0.128125	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0193930.1	-0.69923	3.655261	-3.83366	0.000337	0.008177	0.126367	ATP synthase epsilon chain	elongation zone	12 h
HORVU.MOREX.r3.2HG0122080.1	0.592342	3.732882	3.899137	0.000273	0.007364	0.123185	DUF630 family protein, putative (DUF630 and DUF632)	elongation zone	12 h
HORVU.MOREX.r3.5HG0513440.1	-0.40915	5.701505	-3.89517	0.000277	0.007399	0.122818	#N/A	elongation zone	12 h
HORVU.MOREX.r3.1HG0026830.1	0.629926	3.566935	3.881972	0.000289	0.007575	0.121332	Leucine-rich repeat receptor-like protein kinase family	elongation zone	12 h
HORVU.MOREX.r3.4HG0337120.1	-0.65051	5.989451	-3.88586	0.000285	0.007554	0.116931	Histone H1, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0485940.1	1.857338	2.592249	3.824069	0.000347	0.008288	0.116865	Hexosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0278170.1	1.706706	0.346839	3.840083	0.00033	0.008104	0.116858	CCCH-type zinc fingerfamily protein with RNA-binding domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0510590.4	-1.47342	4.084011	-3.8693	0.000301	0.007754	0.11046	Beta-glucosidase	elongation zone	12 h
HORVU.MOREX.r3.7HG0686000.1	-0.65705	5.976004	-3.87175	0.000298	0.007733	0.106776	Biotin synthase	elongation zone	12 h
HORVU.MOREX.r3.4HG0377020.1	-0.35522	6.726202	-3.93658	0.000242	0.006978	0.106333	Hexosyltransferase	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.7HG0656750.1	-0.78725	3.218229	-3.81435	0.000358	0.008428	0.105458	Exocyst complex component, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0231780.1	-1.06119	5.499284	-3.82742	0.000344	0.008287	0.103727	Charged multivesicular body protein 5	elongation zone	12 h
HORVU.MOREX.r3.2HG0140970.1	-0.85919	2.378717	-3.82426	0.000347	0.008288	0.102609	Heat-shock protein, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0244010.1	-0.66104	4.561972	-3.81872	0.000353	0.008389	0.101781	Kinase superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0212860.1	1.760564	-1.30303	3.834701	0.000336	0.008176	0.094258	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0242870.1	-0.32352	7.618528	-3.94909	0.000233	0.006891	0.09409	Carboxypeptidase	elongation zone	12 h
HORVU.MOREX.r3.3HG0298390.1	-1.15585	3.722188	-3.81008	0.000363	0.008498	0.092909	Adenine nucleotide alpha hydrolases-like superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0054510.1	1.113899	2.568148	3.81085	0.000362	0.008498	0.085359	Protein PLASTID MOVEMENT IMPAIRED 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0118580.1	-1.06141	4.186861	-3.81487	0.000358	0.008427	0.084972	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0182210.2	0.863928	0.342142	3.869403	0.000301	0.007754	0.084239	Transporter-related family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0402600.2	-1.22584	2.451456	-3.87387	0.000296	0.0077	0.083807	5-dehydro-2-deoxygluconokinase	elongation zone	12 h
HORVU.MOREX.r3.2HG0197680.1	-0.39683	7.691665	-3.91983	0.000256	0.007125	0.083345	actin cytoskeleton-regulatory complex pan-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0124450.1	-0.58966	4.909528	-3.86569	0.000304	0.007757	0.081338	calmodulin-binding protein (DUF1645)	elongation zone	12 h
HORVU.MOREX.r3.6HG0597640.1	0.766519	3.081429	3.823937	0.000348	0.008288	0.079915	Nitrilase	elongation zone	12 h
HORVU.MOREX.r3.5HG0420970.1	0.891505	2.170731	3.817384	0.000355	0.008389	0.074953	ERD (Early-responsive to dehydration stress) family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0514110.1	-0.6477	6.24431	-3.86686	0.000303	0.007757	0.071163	#N/A	elongation zone	12 h
HORVU.MOREX.r3.1HG0050440.1	1.805239	-1.13792	3.838733	0.000332	0.00812	0.071021	DUF538 family protein (Protein of unknown function, DUF538)	elongation zone	12 h
HORVU.MOREX.r3.2HG0180090.1	-0.59663	3.817498	-3.80935	0.000364	0.008498	0.070296	F-box protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0098090.1	-1.23275	-2.03609	-3.86936	0.000301	0.007754	0.070028	Translation initiation factor IF-2	elongation zone	12 h
HORVU.MOREX.r3.6HG0577040.1	2.017784	-1.97815	3.9414	0.000239	0.006937	0.069154	Ycf1	elongation zone	12 h
HORVU.MOREX.r3.6HG0581020.1	-0.38317	5.648771	-3.87321	0.000297	0.007707	0.063591	Xyloglucan 6-xylosyltransferase 1	elongation zone	12 h
HORVU.MOREX.r3.1HG0047130.1	-0.50123	5.781989	-3.85025	0.00032	0.007921	0.060804	Pre-mRNA splicing factor-related	elongation zone	12 h
HORVU.MOREX.r3.4HG0353390.1	0.849076	1.790635	3.815567	0.000357	0.008418	0.059068	Type I inositol-1,4,5-trisphosphate 5-phosphatase	elongation zone	12 h
HORVU.MOREX.r3.6HG0543250.1	-0.79371	6.018336	-3.96496	0.000221	0.006756	0.05802	Receptor-like protein kinase	elongation zone	12 h
HORVU.MOREX.r3.4HG0407990.1	0.870734	3.438278	3.867611	0.000302	0.007757	0.056614	C2 calcium/lipid-binding and GRAM domain protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0467870.1	0.993588	2.049337	3.804563	0.00037	0.00855	0.055267	Kynurenine formamidase	elongation zone	12 h
HORVU.MOREX.r3.2HG0144760.1	1.107751	-1.38996	3.793804	0.000382	0.008703	0.053624	tRNA 5-methylaminomethyl-2-thiouridine biosynthesis bifunctional protein MnmC	elongation zone	12 h
HORVU.MOREX.r3.3HG0310110.1	1.750342	0.692973	3.800338	0.000375	0.008587	0.049864	lysine ketoglutarate reductase trans-splicing-like protein, putative (DUF707)	elongation zone	12 h
HORVU.MOREX.r3.6HG0560290.1	-2.45486	-0.18724	-4.29478	7.49E-05	0.00421	0.049857	Cyclin	elongation zone	12 h
HORVU.MOREX.r3.2HG0159540.1	-1.01294	3.353367	-3.79365	0.000383	0.008703	0.048468	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.6HG0603410.1	-0.76039	6.46923	-3.85117	0.000319	0.007921	0.046696	Homeobox-leucine zipper protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0382760.1	-0.93305	4.231724	-3.80304	0.000371	0.008553	0.045854	CoA ligase	elongation zone	12 h
HORVU.MOREX.r3.2HG0192410.1	1.68137	0.742041	3.865903	0.000304	0.007757	0.042609	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.2HG0158620.1	-0.42124	4.942048	-3.84544	0.000325	0.007986	0.04228	Hydroxyproline-rich glycoprotein-like	elongation zone	12 h
HORVU.MOREX.r3.1HG0090170.1	-0.56275	5.133692	-3.82451	0.000347	0.008288	0.039166	NBS-LRR-like resistance protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0054010.1	0.633748	5.841657	3.91165	0.000263	0.007187	0.037799	zinc finger B-box protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0106260.1	2.573854	-2.23574	4.093316	0.000146	0.005731	0.037307	F-box family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0085700.1	-0.96337	4.979026	-3.7999	0.000375	0.008587	0.036446	Sodium Bile acid symporter family	elongation zone	12 h
HORVU.MOREX.r3.1HG0072510.1	1.259198	-0.03799	3.790654	0.000386	0.008739	0.034658	Protein-methionine-s-oxide reductase	elongation zone	12 h
HORVU.MOREX.r3.3HG0283990.1	-0.52523	7.009142	-3.88298	0.000288	0.007575	0.030692	Glycylpeptide N-tetradecanoyltransferase	elongation zone	12 h
HORVU.MOREX.r3.1HG0046180.1	0.492342	5.918665	3.900792	0.000272	0.007363	0.029938	Ser/Thr protein phosphatase family protein, expressed	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0024140.1	-1.02861	6.990532	-3.8978	0.000275	0.007375	0.02989	Cellulose synthase-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0477220.1	1.053019	1.858254	3.785855	0.000392	0.008794	0.029522	F-box protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0739460.1	-1.04859	6.558798	-3.8487	0.000321	0.007942	0.025994	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.5HG0509390.1	1.095672	0.147864	3.81986	0.000352	0.008372	0.023972	LEM3 (Ligand-effect modulator 3)-like	elongation zone	12 h
HORVU.MOREX.r3.6HG0616130.1	0.588645	6.04228	3.933843	0.000245	0.007006	0.02372	Hexosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0673610.1	-0.55871	3.691119	-3.79665	0.000379	0.00865	0.022371	CONSTANS-like zinc finger protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0199520.1	-1.66919	1.070689	-3.98346	0.000208	0.006588	0.022084	mechanosensitive channel of small conductance-like 5	elongation zone	12 h
HORVU.MOREX.r3.6HG0606930.1	-0.40773	5.680326	-3.85348	0.000316	0.007898	0.021112	3-ketodihydrosphingosine reductase	elongation zone	12 h
HORVU.MOREX.r3.1HG0038960.1	-1.03759	2.949857	-3.7923	0.000384	0.008721	0.020549	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0501980.1	-0.44855	5.561069	-3.84225	0.000328	0.008058	0.01989	Rop guanine nucleotide exchange factor, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0283740.1	0.545755	5.066973	3.850321	0.00032	0.007921	0.017527	Anoctamin-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0066530.1	-1.19262	4.906097	-3.78038	0.000399	0.008889	0.014176	DUF630 family protein, putative (DUF630 and DUF632)	elongation zone	12 h
HORVU.MOREX.r3.5HG0513980.1	1.341517	-0.36473	3.778592	0.000401	0.00891	0.011307	Auxin-responsive protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0531070.1	3.684604	-3.02117	4.284451	7.75E-05	0.004293	0.009433	Protein DETOXIFICATION	elongation zone	12 h
HORVU.MOREX.r3.5HG0461170.1	-0.68308	4.201237	-3.7825	0.000396	0.008859	0.00682	Protein FAR1-RELATED SEQUENCE 5	elongation zone	12 h
HORVU.MOREX.r3.3HG0266960.1	-0.6095	4.636036	-3.80266	0.000372	0.008553	0.003626	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0204020.1	0.741716	1.435954	3.833165	0.000338	0.008177	0.001965	Sulfate transporter	elongation zone	12 h
HORVU.MOREX.r3.2HG0107740.1	-0.56434	9.485909	-3.95132	0.000231	0.006891	-0.00255	Ascorbate peroxidase	elongation zone	12 h
HORVU.MOREX.r3.5HG0533430.1	1.330724	0.093461	3.792933	0.000383	0.008713	-0.0028	ROP-interactive CRIB motif protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0533630.1	-1.44445	5.193358	-3.84687	0.000323	0.007978	-0.00521	Expansin	elongation zone	12 h
HORVU.MOREX.r3.5HG0421310.1	1.073256	0.680461	3.818482	0.000354	0.008389	-0.00908	Receptor protein kinase, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0250630.1	-0.69859	3.543167	-3.77211	0.00041	0.008991	-0.01311	tRNA(His) guanylyltransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0688870.1	0.748556	6.011072	3.881764	0.000289	0.007575	-0.01714	Monodehydroascorbate reductase	elongation zone	12 h
HORVU.MOREX.r3.4HG0339750.1	-0.61166	7.537128	-3.88796	0.000283	0.007523	-0.02015	Cathepsin B-like cysteine protease	elongation zone	12 h
HORVU.MOREX.r3.3HG0289970.1	-0.60452	4.641812	-3.78611	0.000392	0.008794	-0.02199	Riboflavin kinase/fmn hydrolase	elongation zone	12 h
HORVU.MOREX.r3.2HG0110060.1	-0.57746	6.526409	-3.85064	0.000319	0.007921	-0.02366	Aldehyde dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.6HG0555500.1	-0.61887	5.078092	-3.83348	0.000337	0.008177	-0.03804	Subtilisin-like protease	elongation zone	12 h
HORVU.MOREX.r3.6HG0550940.1	-0.33463	5.078026	-3.81411	0.000359	0.008428	-0.0383	obscurin-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0045770.1	2.120943	-2.26851	3.941014	0.000239	0.006937	-0.04256	GRAM domain-containing protein / ABA-responsive protein-related	elongation zone	12 h
HORVU.MOREX.r3.5HG0517760.1	1.696398	-2.35783	3.809692	0.000364	0.008498	-0.04465	Zinc finger A20 and AN1 domain-containing stress-associated protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0661890.1	-0.57398	7.916049	-3.89911	0.000273	0.007364	-0.04657	3-oxoacyl-[acyl-carrier-protein] synthase	elongation zone	12 h
HORVU.MOREX.r3.1HG0081620.1	-0.65092	3.155534	-3.76157	0.000423	0.009125	-0.04755	Glycerophosphodiester phosphodiesterase	elongation zone	12 h
HORVU.MOREX.r3.3HG0236000.1	-0.44653	6.001989	-3.8213	0.00035	0.008343	-0.0506	Ectonucleotide pyrophosphatase/phosphodiesterase, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0231880.1	-1.08129	2.985187	-3.77529	0.000405	0.008965	-0.05068	Leucine-rich repeat (LRR) family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0617970.1	1.5786	-1.86338	3.765043	0.000419	0.009082	-0.05076	Glycosyltransferase family 92 protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0052080.1	-0.45021	6.314334	-3.83259	0.000338	0.008182	-0.05111	C-terminal binding protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0633160.1	-0.77726	3.333953	-3.75595	0.000431	0.00924	-0.05698	U-box domain-containing protein 62	elongation zone	12 h
HORVU.MOREX.r3.5HG0485760.1	1.663329	-1.3336	3.753877	0.000434	0.009279	-0.05826	65-kDa microtubule-associated-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0128230.1	-0.94154	5.522587	-3.78823	0.000389	0.008785	-0.05836	Thaumatin	elongation zone	12 h
HORVU.MOREX.r3.1HG0073050.1	-1.46272	3.873682	-3.75239	0.000436	0.009279	-0.06085	Histone H4	elongation zone	12 h
HORVU.MOREX.r3.7HG0636660.1	-0.40995	6.587599	-3.86332	0.000307	0.007759	-0.06167	SKP1-like protein	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.2HG0148170.1	-1.31696	0.675747	-3.86147	0.000308	0.007759	-0.06802	transmembrane protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0307240.1	2.701127	-3.37688	4.083101	0.000151	0.005814	-0.07366	Amino acid permease	elongation zone	12 h
HORVU.MOREX.r3.3HG0231050.1	-0.88093	7.166338	-3.8456	0.000324	0.007986	-0.07371	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.4HG0412370.1	2.027924	-1.42512	3.74849	0.000441	0.009306	-0.07444	Homeobox protein knotted-1, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0122510.1	0.706896	2.203854	3.829761	0.000341	0.008246	-0.07524	Sphingoid base hydroxylase 2	elongation zone	12 h
HORVU.MOREX.r3.7HG0718540.1	0.78858	3.335782	3.752632	0.000435	0.009279	-0.07805	Heat shock transcription factor	elongation zone	12 h
HORVU.MOREX.r3.2HG0168010.1	-0.55596	4.55186	-3.77198	0.00041	0.008991	-0.08103	Aldo-keto reductase	elongation zone	12 h
HORVU.MOREX.r3.3HG0276160.2	1.557918	-3.02913	3.948098	0.000234	0.006891	-0.08266	GDSL esterase/lipase	elongation zone	12 h
HORVU.MOREX.r3.5HG0420980.1	0.791941	2.046048	3.750927	0.000438	0.009279	-0.0855	ERD (Early-responsive to dehydration stress) family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0061390.1	0.721862	1.721091	3.866324	0.000304	0.007757	-0.08796	Trichome birefringence-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0065370.1	-0.77917	5.483156	-3.78667	0.000391	0.008794	-0.08809	TPX2 (Targeting protein for Xklp2) family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0659040.1	0.960934	3.074402	3.741749	0.000451	0.009442	-0.09014	Formin-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0466190.1	-0.70948	5.829313	-3.83487	0.000336	0.008176	-0.0939	Protein transport protein Sec61 subunit beta, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0157450.1	1.025741	2.551061	3.886335	0.000285	0.007552	-0.09658	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.2HG0124130.1	-0.72369	4.407551	-3.76214	0.000423	0.009118	-0.0974	Cyclin family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0000050.1	-0.44534	5.048249	-3.79621	0.000379	0.008652	-0.10018	RING-finger ubiquitin ligase	elongation zone	12 h
HORVU.MOREX.r3.6HG0608180.1	1.109853	0.307405	3.73753	0.000457	0.009532	-0.10373	Protein MIZU-KUSSEI 1	elongation zone	12 h
HORVU.MOREX.r3.1HG0065020.1	-1.1703	5.184531	-3.74213	0.00045	0.009442	-0.10509	BZIP transcription factor	elongation zone	12 h
HORVU.MOREX.r3.2HG0185370.1	2.719499	-1.4233	3.968401	0.000219	0.006702	-0.10599	Subtilisin-like protease	elongation zone	12 h
HORVU.MOREX.r3.2HG0205420.1	0.822282	-0.18096	3.762954	0.000422	0.009111	-0.10643	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0097010.1	0.397998	5.998881	3.849915	0.00032	0.007921	-0.10649	Sterol 3-beta-glucosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0677940.1	-0.35754	7.210054	-3.86706	0.000303	0.007757	-0.10717	Transmembrane 9 superfamily member	elongation zone	12 h
HORVU.MOREX.r3.2HG0168330.1	0.509769	5.088967	3.827093	0.000344	0.008287	-0.10947	Nicotinate phosphoribosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.4HG0415600.1	-1.68475	5.888147	-3.75847	0.000428	0.009191	-0.11147	HXXXD-type acyl-transferase family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0484660.1	1.491417	-0.23036	3.732868	0.000463	0.009604	-0.11754	Vacuolar-processing enzyme	elongation zone	12 h
HORVU.MOREX.r3.2HG0181660.1	-0.83461	5.953972	-3.78834	0.000389	0.008785	-0.12216	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	elongation zone	12 h
HORVU.MOREX.r3.1HG0024900.1	0.348583	5.998911	3.839151	0.000331	0.008118	-0.12418	Macrophage erythroblast attacher	elongation zone	12 h
HORVU.MOREX.r3.2HG0214240.1	-0.63166	3.183258	-3.73123	0.000466	0.009644	-0.12751	Disease resistance protein (NBS-LRR class) family	elongation zone	12 h
HORVU.MOREX.r3.5HG0469340.1	1.288979	0.552227	3.736539	0.000458	0.009546	-0.12937	Fasciclin-like arabinogalactan-protein-like	elongation zone	12 h
HORVU.MOREX.r3.1HG0072110.1	-0.814	5.194691	-3.7796	0.0004	0.008901	-0.131	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0620650.1	-0.57696	7.259903	-3.86063	0.000309	0.007759	-0.13238	Subtilisin protease	elongation zone	12 h
HORVU.MOREX.r3.7HG0684180.1	0.613883	6.139387	3.866545	0.000303	0.007757	-0.1337	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.6HG0549810.1	0.522353	6.037644	3.856865	0.000313	0.007832	-0.13693	Rac-like GTP binding protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0045490.1	-0.4149	5.161254	-3.77338	0.000408	0.008984	-0.13865	RING/U-box superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0484180.1	0.449292	5.636527	3.807438	0.000366	0.00853	-0.13976	DUF868 family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0400040.1	0.603727	1.083906	3.804939	0.000369	0.00855	-0.14096	Cytochrome b561 and DOMON domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0051920.1	0.939664	2.286248	3.78247	0.000396	0.008859	-0.14117	Transcription factor	elongation zone	12 h
HORVU.MOREX.r3.4HG0418640.1	-0.69142	4.260686	-3.72788	0.000471	0.009706	-0.14227	C2 domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0182280.1	-0.72761	6.433901	-3.80187	0.000373	0.008557	-0.14387	Auxin response factor	elongation zone	12 h
HORVU.MOREX.r3.7HG0654510.1	-1.34959	5.364113	-3.7472	0.000443	0.009332	-0.14645	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.5HG0537090.1	-0.34553	6.791678	-3.83786	0.000333	0.008132	-0.14818	WD40 repeat-containing protein	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.7HG0718830.1	0.846116	4.155941	3.86129	0.000309	0.007759	-0.14822	FAD-binding Berberine family protein, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0526250.1	-0.32537	12.03818	-3.99139	0.000203	0.006534	-0.14836	70 kDa heat shock protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0534340.1	-1.05251	3.235501	-3.72043	0.000482	0.009857	-0.15343	Transferase, transferring glycosyl groups	elongation zone	12 h
HORVU.MOREX.r3.7HG0720130.1	-0.59159	6.1996	-3.80356	0.000371	0.008553	-0.1553	Phosphatidylcholine:diacylglycerol cholinephosphotransferase 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0168730.1	-0.52815	7.047952	-3.80181	0.000373	0.008557	-0.15926	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0620720.1	0.955463	0.656099	3.799664	0.000375	0.008587	-0.16162	Ribonuclease	elongation zone	12 h
HORVU.MOREX.r3.4HG0351440.1	0.460798	5.31189	3.816949	0.000355	0.008391	-0.16217	Rho GTPase-activating protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0376720.1	2.944864	-0.40522	4.559089	3.07E-05	0.002847	-0.16243	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0536200.1	1.076437	-0.5546	3.769039	0.000413	0.009031	-0.16782	Xyloglucan endotransglucosylase/hydrolase	elongation zone	12 h
HORVU.MOREX.r3.1HG0067410.1	-0.41497	5.646383	-3.77791	0.000402	0.00892	-0.17055	1-acyl-sn-glycerol-3-phosphate acyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0235350.1	2.006446	0.004514	3.733848	0.000462	0.009584	-0.17067	Pollen Ole e 1 allergen and extensin family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0288420.1	-0.92497	7.285552	-3.78607	0.000392	0.008794	-0.17552	Mannan endo-1,4-beta-mannosidase-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0184620.1	-1.07628	4.117573	-3.71607	0.000488	0.009916	-0.18349	Hsp70-Hsp90 organizing protein 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0679060.1	0.797325	1.156649	3.728877	0.000469	0.009696	-0.18381	Nuclear transport factor 2 family protein, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0221240.1	0.781353	1.030061	3.791279	0.000385	0.008739	-0.1908	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0285780.1	1.031952	1.233022	3.803871	0.00037	0.008553	-0.19082	Protein kinase, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0342080.1	0.765648	4.067325	3.778952	0.000401	0.00891	-0.1911	Adenine/guanine permease	elongation zone	12 h
HORVU.MOREX.r3.6HG0543730.1	-0.85299	7.651801	-3.81804	0.000354	0.008389	-0.19365	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.1HG0072530.1	-1.14492	4.730817	-3.72543	0.000474	0.009762	-0.19607	Histone H4	elongation zone	12 h
HORVU.MOREX.r3.6HG0616480.1	-0.60564	5.832986	-3.76911	0.000413	0.009031	-0.19632	#N/A	elongation zone	12 h
HORVU.MOREX.r3.1HG0094110.1	2.009173	0.561027	3.703053	0.000509	0.010183	-0.19812	Sigma factor sigB regulation protein rsbQ	elongation zone	12 h
HORVU.MOREX.r3.5HG0420830.1	1.288318	-1.8789	3.717478	0.000486	0.009899	-0.20402	cycling DOF factor 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0192910.1	-0.7466	6.73787	-3.82888	0.000342	0.00826	-0.20522	Xyloglucan endotransglucosylase/hydrolase	elongation zone	12 h
HORVU.MOREX.r3.1HG0077950.1	-0.3894	4.840037	-3.75103	0.000438	0.009279	-0.21039	BSD domain containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0168270.1	-0.61213	3.16772	-3.69799	0.000517	0.010257	-0.21314	Ubiquitin carboxyl-terminal hydrolase	elongation zone	12 h
HORVU.MOREX.r3.7HG0685920.1	0.53821	4.571683	3.787257	0.00039	0.008794	-0.21325	Solute carrier family 35 protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0079020.1	2.039497	3.471696	3.699655	0.000514	0.010233	-0.21388	Protein kinase, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0510160.1	-0.50168	4.316907	-3.71785	0.000486	0.009897	-0.2143	Myb/SANT-like DNA-binding domain protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0010470.1	-0.58354	5.658792	-3.75063	0.000438	0.009279	-0.21643	Arginine/serine-rich splicing factor, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0560930.1	0.640376	5.592543	3.808424	0.000365	0.008513	-0.21881	ternary complex factor MIP1 leucine-zipper protein (Protein of unknown function,	elongation zone	12 h
HORVU.MOREX.r3.3HG0241630.1	-0.65151	5.456663	-3.80494	0.000369	0.00855	-0.21969	Embryo-specific 3	elongation zone	12 h
HORVU.MOREX.r3.2HG0190620.1	0.959315	0.132535	3.700251	0.000513	0.010224	-0.21982	Ceramide kinase	elongation zone	12 h
HORVU.MOREX.r3.4HG0381790.1	1.08853	3.851367	3.790603	0.000386	0.008739	-0.22082	transmembrane protein, putative (DUF247)	elongation zone	12 h
HORVU.MOREX.r3.7HG0728820.1	1.427083	1.672182	3.725005	0.000475	0.009765	-0.22165	Xyloglucan endotransglucosylase/hydrolase	elongation zone	12 h
HORVU.MOREX.r3.3HG0318400.1	-0.96279	6.359366	-3.74014	0.000453	0.009464	-0.22238	S-formylglutathione hydrolase	elongation zone	12 h
HORVU.MOREX.r3.1HG0018590.1	0.841734	2.172649	3.804832	0.000369	0.00855	-0.22336	MYB transcription factor	elongation zone	12 h
HORVU.MOREX.r3.5HG0422080.1	0.426725	5.370925	3.780828	0.000398	0.008886	-0.22584	RING/U-box superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0501120.1	-0.32218	6.923122	-3.80519	0.000369	0.00855	-0.22891	26S proteasome regulatory subunit	elongation zone	12 h
HORVU.MOREX.r3.5HG0493850.1	-0.52792	7.419096	-3.81748	0.000355	0.008389	-0.22991	Acyl-[acyl-carrier-protein] hydrolase	elongation zone	12 h
HORVU.MOREX.r3.4HG0396710.1	-1.15706	6.334866	-3.75229	0.000436	0.009279	-0.23058	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.7HG0662210.1	-0.57909	8.387754	-3.82453	0.000347	0.008288	-0.23366	T-complex protein 1 subunit delta	elongation zone	12 h

Table Sн Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0291040.1	0.785987	3.480757	3.698682	0.000516	0.010244	-0.23402	Glutathione S-transferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0228940.1	1.119244	0.760498	3.708278	0.0005	0.010068	-0.23468	Sulfate adenylyltransferase subunit 2	elongation zone	12 h
HORVU.MOREX.r3.4HG0350800.1	-2.538	1.29696	-4.03893	0.000174	0.006138	-0.23574	FBD-associated F-box protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0398900.1	-1.04009	8.042635	-3.80941	0.000364	0.008498	-0.23689	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.1HG0066800.1	1.176372	-2.50287	3.714313	0.000491	0.009948	-0.23997	Potassium channel	elongation zone	12 h
HORVU.MOREX.r3.5HG0512350.1	-1.1281	7.007306	-3.75658	0.00043	0.009231	-0.24167	Cytochrome P450	elongation zone	12 h
HORVU.MOREX.r3.7HG0636890.1	1.679045	0.940541	3.774152	0.000407	0.008984	-0.24497	Expansin-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0488950.1	-0.74427	2.845933	-3.69656	0.000519	0.010292	-0.24581	Cellulose synthase, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0619500.1	1.490131	-0.34034	3.684658	0.000539	0.01044	-0.24618	#N/A	elongation zone	12 h
HORVU.MOREX.r3.1HG0091240.1	0.568875	4.910104	3.787215	0.00039	0.008794	-0.24724	Mitogen-activated protein kinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0275090.1	1.921845	-3.21251	3.942268	0.000238	0.006937	-0.24893	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfa	elongation zone	12 h
HORVU.MOREX.r3.1HG0090760.1	-0.60365	3.106359	-3.68826	0.000533	0.010373	-0.24914	Nuclear transcription factor Y subunit B	elongation zone	12 h
HORVU.MOREX.r3.2HG0187640.1	-0.79541	2.595046	-3.69064	0.000529	0.010355	-0.24963	Gamma-tubulin complex component	elongation zone	12 h
HORVU.MOREX.r3.5HG0454860.1	-0.41026	5.797971	-3.76474	0.000419	0.009082	-0.24986	Trehalose-6-phosphate synthase, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0107820.1	-0.6777	4.968047	-3.74132	0.000451	0.009442	-0.25135	Glycosyltransferases	elongation zone	12 h
HORVU.MOREX.r3.2HG0099900.1	0.574116	5.512063	3.751124	0.000438	0.009279	-0.2518	Glyoxylate reductase/hydroxypyruvate reductase	elongation zone	12 h
HORVU.MOREX.r3.2HG0100900.2	1.598476	0.62711	3.76838	0.000414	0.009031	-0.25697	Phosphoglycerate mutase-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0389200.1	0.819065	0.876157	3.683972	0.00054	0.010443	-0.25872	LIM domain-containing protein 1	elongation zone	12 h
HORVU.MOREX.r3.1HG0055400.1	-0.50514	5.192784	-3.71993	0.000483	0.009862	-0.26034	Gag polyprotein	elongation zone	12 h
HORVU.MOREX.r3.4HG0401720.1	-1.12859	7.267357	-3.76644	0.000417	0.009058	-0.26139	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.7HG0714510.1	-1.15591	5.004338	-3.68279	0.000542	0.010462	-0.2656	Protein phosphatase 2C	elongation zone	12 h
HORVU.MOREX.r3.3HG0224680.1	-0.41086	5.580543	-3.75075	0.000438	0.009279	-0.27335	Ferredoxin reductase-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0046650.1	-0.60389	6.618439	-3.80584	0.000368	0.00855	-0.2757	Carboxypeptidase	elongation zone	12 h
HORVU.MOREX.r3.7HG0708320.1	-0.67687	4.603991	-3.72159	0.00048	0.009831	-0.27764	Stromal cell-derived factor 2-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0358310.1	-0.7158	4.422454	-3.69606	0.00052	0.010292	-0.2795	Scarecrow transcription factor family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0430940.1	1.096859	5.193365	3.781257	0.000398	0.008884	-0.28226	Glucan 1,3-beta-glucosidase	elongation zone	12 h
HORVU.MOREX.r3.2HG0112190.1	1.553885	-0.62536	3.686549	0.000536	0.010399	-0.28382	Transcription repressor ofp17	elongation zone	12 h
HORVU.MOREX.r3.2HG0189940.1	-1.32041	5.951644	-3.71266	0.000494	0.00998	-0.28399	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0151910.1	-1.0244	2.112464	-3.67767	0.000551	0.010541	-0.28525	Retrovirus-related Pol polyprotein from transposon TNT 1-94	elongation zone	12 h
HORVU.MOREX.r3.2HG0199600.1	-2.21726	2.139352	-3.77558	0.000405	0.008965	-0.28719	Organic cation transporter protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0285840.1	0.989928	-0.69484	3.681722	0.000544	0.010463	-0.28777	Senescence/dehydration-associated protein-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0190220.1	-0.99801	6.32386	-3.74121	0.000451	0.009442	-0.288	#N/A	elongation zone	12 h
HORVU.MOREX.r3.1HG0089750.1	-1.13685	2.726337	-3.71159	0.000495	0.009994	-0.28966	DNA-3-methyladenine glycosylase 1	elongation zone	12 h
HORVU.MOREX.r3.3HG0324180.1	-0.82122	4.528561	-3.68775	0.000534	0.010379	-0.29375	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0510320.1	0.722219	5.613209	3.862994	0.000307	0.007759	-0.29404	Myosin family protein, putative, expressed	elongation zone	12 h
HORVU.MOREX.r3.6HG0618760.1	-0.79667	4.331592	-3.69076	0.000529	0.010355	-0.29407	WRKY transcription factor, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0001460.1	-0.83629	5.414195	-3.73424	0.000461	0.009584	-0.29623	Transmembrane protein, putative (DUF247)	elongation zone	12 h
HORVU.MOREX.r3.7HG0737890.1	1.135165	1.23238	3.78358	0.000395	0.008847	-0.2992	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.3HG0299820.1	-1.06121	7.690345	-3.77117	0.000411	0.009004	-0.29949	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.5HG0436660.1	-0.45509	4.868326	-3.73039	0.000467	0.009659	-0.30247	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0306840.1	0.55811	5.072726	3.770131	0.000412	0.009024	-0.30293	KH domain-containing protein	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0062110.1	1.357883	0.941667	3.722814	0.000478	0.009812	-0.3052	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0663150.1	-0.39192	4.624346	-3.71596	0.000489	0.009916	-0.30995	Protein trichome birefringence	elongation zone	12 h
HORVU.MOREX.r3.6HG0543720.1	-0.90855	2.548383	-3.67052	0.000563	0.01063	-0.31027	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.4HG0381310.1	-1.02883	-0.06914	-3.67211	0.00056	0.010623	-0.31068	Cell surface antigen I/II	elongation zone	12 h
HORVU.MOREX.r3.4HG0399970.1	1.059518	4.109756	3.748828	0.000441	0.009306	-0.31111	Cytochrome b561 and DOMON domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0521610.1	1.234662	0.681734	3.758285	0.000428	0.009191	-0.31131	Protein kinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0320040.1	-1.47022	0.715118	-3.87817	0.000292	0.007614	-0.31505	Phytochromobilin:ferredoxin oxidoreductase	elongation zone	12 h
HORVU.MOREX.r3.6HG0597320.1	-0.31118	6.618535	-3.7682	0.000415	0.009031	-0.31802	ATP-dependent Clp protease proteolytic subunit	elongation zone	12 h
HORVU.MOREX.r3.2HG0129450.1	0.959651	1.029346	3.72803	0.00047	0.009706	-0.32099	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0150450.1	-0.6592	7.245664	-3.77386	0.000407	0.008984	-0.32102	Pyruvate kinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0314070.1	1.444048	-1.61281	3.663376	0.000576	0.010779	-0.32441	Protein kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0221460.1	-0.59807	7.255591	-3.76626	0.000417	0.009058	-0.32665	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0187450.1	1.359735	0.035956	3.723143	0.000478	0.009812	-0.32773	Rhomboid-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0610980.1	1.293514	-1.88326	3.653501	0.000594	0.011015	-0.3306	Nucleotide/sugar transporter family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0751340.1	1.017261	0.25739	3.715102	0.00049	0.009933	-0.33169	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0323530.1	-0.76598	3.205547	-3.65464	0.000592	0.010996	-0.33233	cysteine-rich RLK (RECEPTOR-like protein kinase) 30	elongation zone	12 h
HORVU.MOREX.r3.2HG0170230.1	0.574424	3.492538	3.658786	0.000584	0.010905	-0.33679	Smr domain containing protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0354010.1	2.217604	-0.99752	3.692471	0.000526	0.010342	-0.33698	LURP-one-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0527500.1	-0.53972	4.452639	-3.67417	0.000557	0.010588	-0.33813	Ribosomal L11 methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0190470.1	-0.58734	4.623548	-3.68135	0.000544	0.010463	-0.3434	Argonaute family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0541250.1	-0.25052	7.143195	-3.77686	0.000403	0.00894	-0.34402	Acetate kinase	elongation zone	12 h
HORVU.MOREX.r3.1HG0076060.1	-0.42041	6.353402	-3.76748	0.000416	0.009042	-0.3454	C2 calcium/lipid-binding and GRAM domain protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0454230.1	0.751017	2.88731	3.664062	0.000575	0.010776	-0.34639	Aminopeptidase	elongation zone	12 h
HORVU.MOREX.r3.4HG0396220.1	-0.38499	8.114652	-3.8104	0.000363	0.008498	-0.34877	Alpha-glucosidase like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0501200.1	-0.54024	4.695239	-3.70311	0.000509	0.010183	-0.34917	Thioredoxin superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0707160.1	1.662232	-0.16087	3.654331	0.000592	0.010997	-0.35173	NAC domain-containing protein, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0509120.1	1.036665	5.607225	3.74911	0.00044	0.009306	-0.35427	Auxin-responsive protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0026010.1	0.648876	4.391694	3.688693	0.000532	0.010373	-0.35443	Kinase interacting (KIP1-like) family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0394870.1	1.106204	-0.77161	3.658296	0.000585	0.010911	-0.35459	Formin-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0298540.1	0.658454	7.885451	3.881932	0.000289	0.007575	-0.35631	Phosphatidylinositol transfer protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0039370.1	-0.40796	4.945966	-3.69566	0.000521	0.010292	-0.36083	Leucine-rich repeat (LRR) family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0476380.1	-0.66147	4.634573	-3.66663	0.00057	0.010701	-0.36397	Major facilitator superfamily transporter	elongation zone	12 h
HORVU.MOREX.r3.5HG0512210.1	2.998356	-2.87785	3.952795	0.00023	0.006891	-0.36414	WRKY transcription factor	elongation zone	12 h
HORVU.MOREX.r3.1HG0005750.1	-0.44392	7.06453	-3.76884	0.000414	0.009031	-0.36662	Ankyrin repeat family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0192270.1	2.550248	-2.74995	3.825406	0.000346	0.008288	-0.36918	Sodium transporter	elongation zone	12 h
HORVU.MOREX.r3.7HG0749090.1	1.181462	-0.58865	3.674674	0.000556	0.010588	-0.37218	Expansin-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0416070.1	-2.14611	7.030234	-3.69419	0.000523	0.010309	-0.37402	GATA transcription factor	elongation zone	12 h
HORVU.MOREX.r3.1HG0079810.1	-0.54028	3.696599	-3.64346	0.000612	0.011222	-0.37467	WD repeat protein-like	elongation zone	12 h
HORVU.MOREX.r3.2HG0172580.1	1.652595	-0.45214	3.674805	0.000556	0.010588	-0.38097	Sugar transporter, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0247250.1	-1.32408	3.952989	-3.63603	0.000627	0.011422	-0.38407	V-type proton ATPase subunit E	elongation zone	12 h
HORVU.MOREX.r3.3HG0303240.1	1.11421	2.978435	3.632505	0.000634	0.01149	-0.38983	Ankyrin repeat-containing protein	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.2HG0160550.1	-2.71679	2.252308	-3.86636	0.000304	0.007757	-0.39115	At4g33800-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0641860.1	1.969302	0.566345	3.710691	0.000497	0.010012	-0.39221	Ubiquitin carboxyl-terminal hydrolase 2	elongation zone	12 h
HORVU.MOREX.r3.1HG0090710.1	-0.39015	4.396711	-3.69213	0.000526	0.010342	-0.39238	transmembrane protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0425250.1	1.550422	-1.96474	3.633741	0.000631	0.011477	-0.39559	Disease resistance protein RPH8A	elongation zone	12 h
HORVU.MOREX.r3.6HG0597400.2	1.318778	3.448997	3.674268	0.000557	0.010588	-0.39827	Carboxypeptidase	elongation zone	12 h
HORVU.MOREX.r3.7HG0639360.1	0.74913	7.224542	3.751994	0.000436	0.009279	-0.40094	Autophagy-related protein 22-1	elongation zone	12 h
HORVU.MOREX.r3.6HG0545630.1	-1.49407	3.70973	-3.62804	0.000642	0.011595	-0.40303	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.1HG0076800.1	0.647108	5.255637	3.750939	0.000438	0.009279	-0.41338	Kinesin-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0465520.1	-1.86399	0.949637	-3.86064	0.000309	0.007759	-0.41439	Transposon protein, putative, CACTA, En/Spm sub-class, expressed	elongation zone	12 h
HORVU.MOREX.r3.6HG0612070.1	-0.52599	5.864582	-3.69081	0.000529	0.010355	-0.41489	RNA-binding family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0281730.1	-1.36518	3.703997	-3.63133	0.000636	0.011508	-0.41507	AP2/B3 transcription factor family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0751030.1	1.318873	2.711562	3.621869	0.000655	0.011707	-0.42333	MYB-related protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0079950.1	0.311174	5.644065	3.718651	0.000484	0.009892	-0.42777	Lys-63-specific deubiquitinase BRCC36	elongation zone	12 h
HORVU.MOREX.r3.6HG0606990.1	1.427945	-0.1834	3.799081	0.000376	0.008593	-0.42865	RNA-binding protein Nova-1	elongation zone	12 h
HORVU.MOREX.r3.5HG0528310.1	0.604431	3.716139	3.669076	0.000566	0.010658	-0.4291	SPX domain-containing family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0303970.1	-0.67794	5.51606	-3.6709	0.000562	0.01063	-0.42917	Internal alternative NAD(P)H-ubiquinone oxidoreductase A1, mitochondrial	elongation zone	12 h
HORVU.MOREX.r3.1HG0068710.1	-1.07378	4.871841	-3.67635	0.000553	0.010558	-0.42968	Ethylene-responsive factor-like transcription factor	elongation zone	12 h
HORVU.MOREX.r3.7HG0685360.1	0.604994	4.544409	3.70219	0.00051	0.010189	-0.43073	Receptor protein kinase, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0057610.1	0.698136	4.023099	3.633624	0.000631	0.011477	-0.43241	Peptide methionine sulfoxide reductase MsrA	elongation zone	12 h
HORVU.MOREX.r3.3HG0270910.1	-0.29532	6.963859	-3.75394	0.000434	0.009279	-0.45039	Protein YIPF	elongation zone	12 h
HORVU.MOREX.r3.1HG0006660.1	0.94286	5.455877	3.676244	0.000553	0.010558	-0.45247	Inorganic pyrophosphatase family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0060340.1	-1.41274	6.073412	-3.6478	0.000604	0.011171	-0.45447	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.7HG0667730.1	0.459143	5.429237	3.713196	0.000493	0.009973	-0.45624	Chaperone protein dnaJ	elongation zone	12 h
HORVU.MOREX.r3.7HG0739640.1	-0.96227	8.298465	-3.73639	0.000458	0.009546	-0.45636	Auxin efflux carrier component	elongation zone	12 h
HORVU.MOREX.r3.2HG0174750.1	1.195019	1.498345	3.709999	0.000498	0.010024	-0.45749	Fasciclin-like arabinogalactan protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0664720.1	1.147644	0.421259	3.70465	0.000506	0.010163	-0.45932	Blue copper protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0616710.1	-0.98545	5.40807	-3.64205	0.000615	0.011251	-0.45937	Cyclin family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0554840.1	0.877771	2.671575	3.622247	0.000654	0.011707	-0.46238	Phosphopantetheine adenylyltransferase	elongation zone	12 h
HORVU.MOREX.r3.4HG0400520.1	1.263484	-0.786	3.623587	0.000651	0.011674	-0.46458	Lipid transfer protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0169720.1	-0.49615	4.773186	-3.6329	0.000633	0.01149	-0.46727	Zinc finger CCCH domain-containing protein 28	elongation zone	12 h
HORVU.MOREX.r3.1HG0014680.1	1.378384	-0.77974	3.624964	0.000649	0.011649	-0.4716	Tetraspanin family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0607960.1	0.530257	6.253417	3.763963	0.00042	0.009095	-0.47449	Protein KINESIN LIGHT CHAIN-RELATED 3	elongation zone	12 h
HORVU.MOREX.r3.2HG0109340.1	1.204394	0.874826	3.603828	0.000692	0.012162	-0.47543	Wound-induced protein 1, putative, expressed	elongation zone	12 h
HORVU.MOREX.r3.1HG0050220.1	1.403533	-1.46767	3.601413	0.000698	0.012162	-0.47556	Polyketide cyclase/dehydrase and lipid transport superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0470030.1	-0.4954	7.999201	-3.77223	0.000409	0.008991	-0.47611	3-ketoacyl-CoA thiolase	elongation zone	12 h
HORVU.MOREX.r3.5HG0465260.1	-0.77701	2.270829	-3.61344	0.000672	0.011932	-0.47707	Zinc finger HIT domain-containing protein 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0119360.1	-2.1031	-1.10965	-3.83677	0.000334	0.008151	-0.47711	Gibberellin receptor GID1A	elongation zone	12 h
HORVU.MOREX.r3.3HG0246030.1	1.088338	0.793866	3.609912	0.00068	0.012034	-0.47865	Blue copper protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0139810.1	0.927478	0.63654	3.689556	0.000531	0.01036	-0.47904	Heavy metal transport/detoxification superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0105050.1	1.856826	0.102901	3.802656	0.000372	0.008553	-0.48014	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0470170.1	-0.59204	3.126834	-3.60155	0.000697	0.012162	-0.48019	F-box family protein	elongation zone	12 h

Table Sʜ Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0057030.1	-0.69874	6.546046	-3.70199	0.00051	0.010189	-0.48257	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.4HG0414000.1	0.769809	1.7924	3.626084	0.000646	0.011635	-0.4838	Short-chain dehydrogenase/reductase family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0510500.1	0.463597	5.572952	3.700993	0.000512	0.01021	-0.48473	RNA binding family protein isoform 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0670690.1	0.621261	8.088776	3.824432	0.000347	0.008288	-0.48534	HIPL1 protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0295450.1	-0.82213	2.043228	-3.60571	0.000688	0.01213	-0.48624	Cytochrome P450 family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0470940.1	0.50071	5.957094	3.71712	0.000487	0.0099	-0.48669	Protein ENHANCED DISEASE RESISTANCE 2-like	elongation zone	12 h
HORVU.MOREX.r3.2HG0118220.1	1.083065	1.251256	3.627374	0.000644	0.011609	-0.48824	En/Spm-like transposon protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0400800.1	-0.42632	4.757552	-3.64677	0.000606	0.011192	-0.48902	Transcription factor	elongation zone	12 h
HORVU.MOREX.r3.2HG0194450.1	-0.38186	5.508153	-3.65006	0.0006	0.011123	-0.49132	Secretory carrier-associated membrane protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0285150.1	0.817734	1.826069	3.617495	0.000664	0.011834	-0.49522	Tryptophan aminotransferase	elongation zone	12 h
HORVU.MOREX.r3.4HG0394690.1	-0.32971	5.03075	-3.65977	0.000582	0.010887	-0.49828	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0749150.1	-2.05551	3.418595	-3.6497	0.000601	0.011126	-0.49894	DUF241 domain protein (DUF241)	elongation zone	12 h
HORVU.MOREX.r3.3HG0309780.1	2.840115	-2.21583	3.759706	0.000426	0.009169	-0.49927	RING/U-box superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0012170.1	-0.84196	3.51455	-3.59266	0.000717	0.012358	-0.49982	Disease resistance protein RPM1	elongation zone	12 h
HORVU.MOREX.r3.2HG0119220.1	-0.54563	4.892203	-3.67081	0.000563	0.01063	-0.50163	Gibberellin receptor GID1a	elongation zone	12 h
HORVU.MOREX.r3.3HG0287800.1	-0.68859	4.734584	-3.61619	0.000666	0.011861	-0.50487	6-phosphogluconate dehydrogenase family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0074600.1	-1.22446	3.896702	-3.58829	0.000726	0.012414	-0.50703	Cytochrome P450	elongation zone	12 h
HORVU.MOREX.r3.3HG0251950.1	-0.69158	3.77745	-3.60677	0.000686	0.012117	-0.50932	Polynucleotidyl transferase, ribonuclease H-like superfamily protein, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0364050.1	0.761651	2.580176	3.593111	0.000716	0.012358	-0.50985	Sodium/hydrogen exchanger	elongation zone	12 h
HORVU.MOREX.r3.1HG0006650.1	-0.87831	8.905369	-3.74455	0.000447	0.00939	-0.51025	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.4HG0386000.2	-0.51779	3.642466	-3.60281	0.000695	0.012162	-0.51296	Transthyretin-like S-allantoin synthase protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0318700.1	0.508878	6.088388	3.727488	0.000471	0.009709	-0.51805	Phosphotransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0285570.1	-0.72853	3.375913	-3.60943	0.000681	0.012039	-0.51832	Serine acetyltransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0129200.1	-0.58836	5.391664	-3.64399	0.000611	0.011213	-0.51916	glutamyl-tRNA (Gln) amidotransferase subunit A (DUF620)	elongation zone	12 h
HORVU.MOREX.r3.7HG0674590.1	1.129929	1.003958	3.591586	0.000719	0.012373	-0.52179	Retrovirus-related Pol polyprotein from transposon TNT 1-94	elongation zone	12 h
HORVU.MOREX.r3.7HG0707220.1	0.621046	4.707516	3.695759	0.00052	0.010292	-0.52764	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0683940.1	0.891844	2.232556	3.58418	0.000736	0.012507	-0.52933	65-kDa microtubule-associated-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0522090.1	0.601137	2.891849	3.614038	0.000671	0.011927	-0.53187	Exocyst complex component EXO84B	elongation zone	12 h
HORVU.MOREX.r3.1HG0049550.1	0.399156	3.543555	3.594221	0.000713	0.01234	-0.53676	Protein BPS1, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.6HG0570960.1	-1.1965	6.423531	-3.63423	0.00063	0.011476	-0.5393	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.4HG0410640.1	-0.39703	8.151713	-3.74119	0.000451	0.009442	-0.54112	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	elongation zone	12 h
HORVU.MOREX.r3.5HG0532560.1	1.897846	-0.15138	3.59502	0.000711	0.012335	-0.54124	Ras-related protein, expressed	elongation zone	12 h
HORVU.MOREX.r3.4HG0335170.1	1.250295	1.390233	3.7052	0.000505	0.010156	-0.54189	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0723730.1	0.903529	2.888777	3.644966	0.00061	0.011213	-0.54216	RNA binding protein, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0656430.1	-0.37147	6.915192	-3.67976	0.000547	0.010502	-0.54297	Zinc finger CCCH domain protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0731950.1	0.785413	3.076597	3.684006	0.00054	0.010443	-0.54671	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0616300.1	0.550224	5.182691	3.695279	0.000521	0.010294	-0.54724	Histidine kinase	elongation zone	12 h
HORVU.MOREX.r3.5HG0482360.1	-0.78437	2.02018	-3.63944	0.00062	0.011322	-0.54849	WAT1-related protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0687080.1	-0.55476	4.583869	-3.60789	0.000684	0.012086	-0.54971	RNA-binding family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0248280.1	-0.39368	8.50615	-3.7484	0.000441	0.009306	-0.54999	Reticulon-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0524800.1	-1.62524	1.969957	-3.64575	0.000608	0.011202	-0.55103	RNA polymerase II transcription mediator	elongation zone	12 h

Table Sн Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.6HG0567330.1	-1.2531	5.748869	-3.60195	0.000696	0.012162	-0.55194	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit	elongation zone	12 h
HORVU.MOREX.r3.1HG0023620.1	-0.9138	6.596829	-3.66366	0.000575	0.010779	-0.55195	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.1HG0072520.1	-1.06453	4.709601	-3.60084	0.000699	0.012173	-0.55386	#N/A	elongation zone	12 h
HORVU.MOREX.r3.1HG0064610.1	-0.97295	5.770306	-3.60178	0.000697	0.012162	-0.5576	membrane-associated kinase regulator	elongation zone	12 h
HORVU.MOREX.r3.3HG0280310.1	-0.68124	2.629974	-3.56879	0.000771	0.012872	-0.55765	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0480130.1	2.366623	-2.63524	3.773247	0.000408	0.008984	-0.55856	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0718200.1	0.854267	3.590015	3.67245	0.00056	0.010623	-0.56015	Kinesin-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0036930.1	-1.08193	6.161598	-3.61623	0.000666	0.011861	-0.56334	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.1HG0061710.1	0.502223	5.632386	3.702871	0.000509	0.010183	-0.5659	Trichome birefringence-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0407560.1	0.414982	3.734856	3.630866	0.000637	0.011514	-0.56594	Ras family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0650210.1	-0.41276	6.623351	-3.68352	0.000541	0.010448	-0.56774	Oligosaccharyltransferase complex subunit ostc	elongation zone	12 h
HORVU.MOREX.r3.3HG0246500.1	0.862979	3.040522	3.693171	0.000525	0.010332	-0.56803	Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A	elongation zone	12 h
HORVU.MOREX.r3.3HG0319760.1	-0.45627	3.423519	-3.58045	0.000744	0.012578	-0.57121	Alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0706140.1	-0.56111	4.415559	-3.58963	0.000723	0.012401	-0.57234	Bromodomain-containing factor 2	elongation zone	12 h
HORVU.MOREX.r3.5HG0420670.1	-0.7737	3.163154	-3.56246	0.000786	0.013014	-0.57409	Translation elongation factor EF1A/initiation factor IF2gamma family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0553150.1	-0.53218	6.876917	-3.69196	0.000527	0.010342	-0.57422	Polyubiquitin	elongation zone	12 h
HORVU.MOREX.r3.4HG0344990.1	-1.23095	2.816049	-3.58428	0.000735	0.012507	-0.57447	NBS-LRR disease resistance protein family-1	elongation zone	12 h
HORVU.MOREX.r3.5HG0462450.1	1.304696	-0.84666	3.594265	0.000713	0.01234	-0.57629	S-acyltransferase	elongation zone	12 h
HORVU.MOREX.r3.1HG0053450.1	0.925669	3.313219	3.711733	0.000495	0.009994	-0.57879	WEB family protein, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.7HG0752370.1	0.765482	2.088249	3.667256	0.000569	0.010699	-0.58343	NBS-LRR-like resistance protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0388310.1	0.425172	3.870759	3.638158	0.000623	0.011357	-0.58599	Protein kinase	elongation zone	12 h
HORVU.MOREX.r3.7HG0728910.1	-0.83454	4.539344	-3.58285	0.000739	0.012516	-0.58664	Ring finger protein, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0130180.1	-0.30301	5.922255	-3.65611	0.000589	0.010966	-0.58836	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0234010.1	1.464655	-0.09759	3.657394	0.000587	0.010932	-0.58922	Xyloglucan endotransglucosylase/hydrolase	elongation zone	12 h
HORVU.MOREX.r3.2HG0116540.1	-0.59965	3.495583	-3.58655	0.00073	0.012447	-0.58968	5-aminolevulinate synthase, mitochondrial	elongation zone	12 h
HORVU.MOREX.r3.3HG0288710.1	1.449009	-1.93307	3.563459	0.000784	0.012995	-0.59141	GDSL esterase/lipase	elongation zone	12 h
HORVU.MOREX.r3.3HG0279760.1	-0.78786	3.223061	-3.57086	0.000766	0.012828	-0.59223	NAC domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0093750.1	-0.93936	3.434371	-3.56017	0.000792	0.013047	-0.59257	ATP-dependent zinc metalloprotease FtsH	elongation zone	12 h
HORVU.MOREX.r3.7HG0663750.1	1.429923	3.681851	3.560953	0.00079	0.013047	-0.59285	Galactoside 2-alpha-L-fucosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0461950.1	0.803167	2.97161	3.588095	0.000727	0.012414	-0.59325	2-isopropylmalate synthase 2	elongation zone	12 h
HORVU.MOREX.r3.6HG0601680.1	0.862149	2.148004	3.588378	0.000726	0.012414	-0.59343	Vesicle-associated 1-1-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0316110.1	-1.05048	5.235108	-3.6431	0.000613	0.011224	-0.59368	Basic 7S globulin 2	elongation zone	12 h
HORVU.MOREX.r3.5HG0527650.1	-0.69457	4.818573	-3.59969	0.000701	0.012206	-0.59387	Succinate--CoA ligase [ADP-forming] subunit alpha-1, mitochondrial	elongation zone	12 h
HORVU.MOREX.r3.5HG0490720.1	-3.94475	0.668588	-4.11974	0.000134	0.00553	-0.5982	Retrovirus-related Pol polyprotein from transposon TNT 1-94	elongation zone	12 h
HORVU.MOREX.r3.4HG0403680.1	-1.38283	3.612484	-3.58074	0.000743	0.012578	-0.59901	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0164850.1	-0.67246	4.574579	-3.60552	0.000689	0.01213	-0.60202	SBP (S-ribonuclease binding protein) family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0063430.1	0.395673	7.658435	3.745901	0.000445	0.00936	-0.60257	Oxidoreductase, 2OG-Fe(II) oxygenase family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0382620.1	0.481021	7.496381	3.671908	0.000561	0.010623	-0.60364	Argininosuccinate lyase	elongation zone	12 h
HORVU.MOREX.r3.4HG0386830.1	-1.04086	3.806924	-3.54789	0.000822	0.01322	-0.61257	UDP-glucuronate decarboxylase protein 1	elongation zone	12 h
HORVU.MOREX.r3.3HG0231240.1	1.05285	0.82508	3.571363	0.000765	0.012828	-0.61354	Short-chain dehydrogenase/reductase family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0115480.1	-0.69267	3.022508	-3.5479	0.000822	0.01322	-0.61643	Tesmin/TSO1-like CXC domain protein	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0087150.1	-0.87603	6.174716	-3.68177	0.000544	0.010463	-0.62285	Purple acid phosphatase	elongation zone	12 h
HORVU.MOREX.r3.3HG0310540.1	-0.58524	5.764879	-3.62503	0.000648	0.011649	-0.62468	Mannosyl-oligosaccharide glucosidase	elongation zone	12 h
HORVU.MOREX.r3.4HG0410090.1	0.598135	5.519883	3.646626	0.000607	0.011192	-0.62652	Hypersensitive-induced response protein 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0202250.1	1.294398	1.379273	3.543478	0.000834	0.013311	-0.62724	Kelch repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0718170.1	1.022393	1.273375	3.546403	0.000826	0.013244	-0.62731	Pleiotropic drug resistance ABC transporter	elongation zone	12 h
HORVU.MOREX.r3.7HG0751290.1	-1.01768	0.60944	-3.62183	0.000655	0.011707	-0.62765	Receptor-kinase, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0398420.1	-0.55096	3.560721	-3.55753	0.000798	0.013094	-0.62797	Membrane steroid-binding protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0054070.1	1.20247	0.426324	3.554136	0.000807	0.01314	-0.62927	CASP-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0290510.1	-0.89133	3.665191	-3.54157	0.000838	0.013368	-0.6311	Tesmin/TSO1-like CXC domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0026080.1	0.644875	4.010774	3.579919	0.000745	0.012588	-0.63456	RING finger protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0737440.1	-1.17613	5.648436	-3.56962	0.000769	0.012856	-0.63481	carboxyl-terminal peptidase (DUF239)	elongation zone	12 h
HORVU.MOREX.r3.7HG0702660.1	1.161249	1.220256	3.554263	0.000806	0.01314	-0.63575	CoA ligase	elongation zone	12 h
HORVU.MOREX.r3.5HG0508870.1	0.75041	4.361487	3.673465	0.000558	0.010601	-0.63619	Kinase interacting (KIP1-like) family protein, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0155450.1	-0.85433	3.209398	-3.5534	0.000809	0.01314	-0.64026	Major facilitator superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0050990.1	-2.28703	2.072399	-3.8939	0.000278	0.00742	-0.64109	Membrane protein insertase YidC	elongation zone	12 h
HORVU.MOREX.r3.5HG0426060.1	-0.62578	3.90766	-3.54972	0.000818	0.013192	-0.64352	Protein FAR1-RELATED SEQUENCE 3	elongation zone	12 h
HORVU.MOREX.r3.7HG0739380.1	-0.94239	6.500354	-3.62628	0.000646	0.011635	-0.64457	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.7HG0728480.1	1.403506	0.878141	3.667433	0.000569	0.010699	-0.6451	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.6HG0616790.1	-0.5905	7.277735	-3.65503	0.000591	0.010993	-0.64552	Transport inhibitor response 1-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0072680.1	0.905093	1.174684	3.542965	0.000835	0.013321	-0.64731	Respiratory burst oxidase-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0161670.1	-0.52234	5.960687	-3.60984	0.00068	0.012034	-0.6477	SWI/SNF complex component SNF12-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0024280.1	-0.71937	7.969902	-3.68535	0.000538	0.010428	-0.64898	Dihydrolipoyl dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.1HG0095440.1	-0.34329	7.430324	-3.67131	0.000562	0.01063	-0.64946	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0219410.1	0.816398	3.869903	3.5989	0.000703	0.012226	-0.65044	Hydroxyproline-rich glycoprotein family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0261980.1	-0.59022	3.054779	-3.53553	0.000854	0.013502	-0.65065	Serine/threonine-protein phosphatase	elongation zone	12 h
HORVU.MOREX.r3.7HG0687050.1	-0.46362	5.185144	-3.64444	0.000611	0.011213	-0.65323	NC domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0313490.1	-0.90704	3.185804	-3.55614	0.000802	0.013121	-0.65434	Rapid alkalinization factor (RALF) family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0057620.1	-0.74779	6.017316	-3.60344	0.000693	0.012162	-0.65494	Kinase like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0277330.1	-0.62245	4.294396	-3.55351	0.000808	0.01314	-0.66099	CASP-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0253440.1	-0.832	1.953551	-3.54775	0.000823	0.01322	-0.66142	Protein RETICULATA, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.6HG0629220.1	-0.75231	5.709587	-3.58779	0.000728	0.012414	-0.66925	methyl-coenzyme M reductase II subunit gamma, putative (DUF3741)	elongation zone	12 h
HORVU.MOREX.r3.2HG0161020.1	-0.86615	7.262436	-3.64116	0.000617	0.011272	-0.6702	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0640560.1	-2.53466	0.442209	-3.91514	0.00026	0.007125	-0.6742	NBS-LRR disease resistance protein-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0554790.1	-0.3005	7.933943	-3.68963	0.000531	0.01036	-0.67552	Proteasome subunit alpha type	elongation zone	12 h
HORVU.MOREX.r3.5HG0504670.1	-1.30216	3.865033	-3.53927	0.000844	0.01341	-0.67563	Acetyl-coenzyme A synthetase	elongation zone	12 h
HORVU.MOREX.r3.5HG0527670.1	-1.94866	3.348267	-3.54701	0.000825	0.013239	-0.68071	Cytochrome P450	elongation zone	12 h
HORVU.MOREX.r3.4HG0394980.1	-0.83162	8.862444	-3.68138	0.000544	0.010463	-0.68237	Allene oxide synthase	elongation zone	12 h
HORVU.MOREX.r3.2HG0209810.1	0.432063	6.643137	3.66659	0.00057	0.010701	-0.68602	Katanin p80 WD40 repeat-containing subunit B1 homolog	elongation zone	12 h
HORVU.MOREX.r3.5HG0532120.1	1.726027	-1.75561	3.522887	0.000888	0.013841	-0.68705	Expansin	elongation zone	12 h
HORVU.MOREX.r3.2HG0099740.1	-0.39325	5.374952	-3.58363	0.000737	0.012516	-0.68991	Zinc finger family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0179410.1	-0.56969	2.81034	-3.53231	0.000862	0.013594	-0.69063	transmembrane protein, putative (DUF1068)	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0245400.1	0.618669	5.359013	3.722118	0.000479	0.009824	-0.69191	GDSL esterase/lipase	elongation zone	12 h
HORVU.MOREX.r3.6HG0605130.1	1.024442	-2.05206	3.529754	0.000869	0.013618	-0.69271	Invertase inhibitor	elongation zone	12 h
HORVU.MOREX.r3.3HG0293490.1	1.087833	-0.53962	3.570972	0.000766	0.012828	-0.69674	Expansin	elongation zone	12 h
HORVU.MOREX.r3.7HG0730820.1	-0.96964	5.001622	-3.55021	0.000817	0.013183	-0.69858	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.7HG0748070.1	1.319155	-0.49696	3.553542	0.000808	0.01314	-0.6992	Heavy metal transport/detoxification superfamily protein, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0419590.1	0.511222	6.133126	3.678625	0.000549	0.010519	-0.7007	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0297000.1	1.160655	-0.77719	3.515845	0.000907	0.013962	-0.7012	LURP-one-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0324070.1	1.763822	4.131542	3.529704	0.000869	0.013618	-0.70858	Beta-1,3-glucanase	elongation zone	12 h
HORVU.MOREX.r3.1HG0062980.1	1.0336	1.135611	3.528358	0.000873	0.013663	-0.71081	L-gulonolactone oxidase	elongation zone	12 h
HORVU.MOREX.r3.5HG0517490.1	0.764187	1.614895	3.550775	0.000815	0.01317	-0.71093	Protein kinase	elongation zone	12 h
HORVU.MOREX.r3.4HG0348380.1	0.918556	1.737869	3.551674	0.000813	0.013153	-0.71126	phox (PX) domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0521630.1	0.66458	4.704079	3.590578	0.000721	0.012386	-0.71491	Beta-1,3-galactosyltransferase-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0482590.1	-0.92635	4.122873	-3.51587	0.000907	0.013962	-0.71602	Major facilitator superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0308820.1	-0.36137	9.031851	-3.71794	0.000486	0.009897	-0.71727	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	elongation zone	12 h
HORVU.MOREX.r3.6HG0634130.1	-0.30969	5.21873	-3.60215	0.000696	0.012162	-0.71755	Alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0695500.1	-0.44661	6.592723	-3.61823	0.000662	0.011818	-0.72822	Transmembrane 9 superfamily member	elongation zone	12 h
HORVU.MOREX.r3.6HG0593050.1	0.910784	0.467029	3.540487	0.000841	0.013377	-0.72958	C2 domain-containing protein / GRAM domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0465400.1	1.213326	0.747502	3.597097	0.000707	0.012273	-0.73118	Trichome birefringence-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0252380.1	1.021872	2.240647	3.50746	0.00093	0.014174	-0.73463	DNA-binding storekeeper protein-related transcriptional regulator	elongation zone	12 h
HORVU.MOREX.r3.3HG0276130.1	1.096246	-0.22255	3.507177	0.000931	0.014175	-0.73559	Phospholipase A1	elongation zone	12 h
HORVU.MOREX.r3.2HG0113720.1	1.164831	3.679958	3.603302	0.000694	0.012162	-0.73623	Cytosolic Fe-S cluster assembly factor nbp35	elongation zone	12 h
HORVU.MOREX.r3.6HG0570430.1	0.374683	5.175773	3.592767	0.000716	0.012358	-0.74176	Ubiquitin-conjugating enzyme E2	elongation zone	12 h
HORVU.MOREX.r3.3HG0288370.1	-1.02207	2.377529	-3.50667	0.000933	0.014176	-0.74243	Chaperone clpb, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0262210.1	-0.32843	5.498655	-3.59766	0.000706	0.012262	-0.74455	Phosphatase 2C family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0412140.1	1.102548	2.514643	3.568541	0.000772	0.012872	-0.74522	Zinc finger (C3HC4-type RING finger) protein family-like	elongation zone	12 h
HORVU.MOREX.r3.5HG0524060.1	1.320151	3.909294	3.55735	0.000799	0.013094	-0.74553	Remorin	elongation zone	12 h
HORVU.MOREX.r3.2HG0172400.1	-1.75025	5.128092	-3.5214	0.000892	0.013872	-0.74644	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0171810.1	-0.5188	3.837575	-3.51605	0.000906	0.013962	-0.74715	DUF1644 family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0601670.1	-0.9144	2.45038	-3.49908	0.000954	0.014386	-0.74785	Phosphatidic acid phosphatase	elongation zone	12 h
HORVU.MOREX.r3.1HG0017720.1	-0.7434	7.063635	-3.62126	0.000656	0.011718	-0.74834	Glutathione S-transferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0152140.1	-0.66342	5.200814	-3.53024	0.000868	0.013618	-0.75053	D-amino acid dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.4HG0334600.1	0.605566	2.850253	3.494527	0.000968	0.014469	-0.75257	Magnesium transporter MRS2-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0186480.1	2.160718	-0.52788	3.494388	0.000968	0.014469	-0.75289	1-aminocyclopropane-1-carboxylate synthase	elongation zone	12 h
HORVU.MOREX.r3.1HG0049840.1	-0.71647	3.999244	-3.49784	0.000958	0.0144	-0.75411	protein kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0574510.1	-1.53475	7.321758	-3.56425	0.000782	0.012985	-0.75538	#N/A	elongation zone	12 h
HORVU.MOREX.r3.4HG0375760.1	-0.77233	3.175902	-3.52006	0.000895	0.013908	-0.75578	Oxidoreductase/ transition metal ion binding protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0589860.1	0.792761	4.121931	3.546392	0.000826	0.013244	-0.75657	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0642940.1	1.860453	-1.68507	3.497425	0.000959	0.0144	-0.75664	Tryptophan decarboxylase	elongation zone	12 h
HORVU.MOREX.r3.7HG0741650.1	-0.83815	6.190632	-3.57654	0.000753	0.012678	-0.7589	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.5HG0493070.1	-0.43426	6.006758	-3.60419	0.000692	0.012162	-0.76005	Peptidylprolyl isomerase	elongation zone	12 h
HORVU.MOREX.r3.4HG0356860.1	0.938395	1.759753	3.494598	0.000968	0.014469	-0.76248	Ulp1 protease family, C-terminal catalytic domain containing protein, expressed	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.2HG0145360.1	1.040134	3.483304	3.687049	0.000535	0.010392	-0.7629	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.4HG0361420.2	-0.4902	5.485836	-3.55363	0.000808	0.01314	-0.76292	ATP dependent RNA helicase	elongation zone	12 h
HORVU.MOREX.r3.7HG0727650.1	2.627481	-1.35022	3.734055	0.000462	0.009584	-0.76329	BTB/POZ domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0253360.1	-1.0775	1.395191	-3.51498	0.000909	0.013987	-0.76599	F-box domain containing protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0335150.1	-0.30934	8.47371	-3.67639	0.000553	0.010558	-0.76616	Nuclease domain-containing protein 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0708500.1	-0.90047	2.950817	-3.48915	0.000984	0.014606	-0.76664	Chloride channel protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0466440.1	-0.39841	4.963631	-3.5667	0.000776	0.012908	-0.77124	Glucan endo-1,3-beta-glucosidase, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0403250.1	-1.08069	4.254713	-3.49054	0.00098	0.014565	-0.77392	50S ribosomal L32	elongation zone	12 h
HORVU.MOREX.r3.1HG0032930.1	0.67474	5.503727	3.624031	0.000651	0.011668	-0.77472	lipase, putative (DUF620)	elongation zone	12 h
HORVU.MOREX.r3.7HG0649240.1	1.54596	-2.99572	3.681241	0.000545	0.010463	-0.77523	protein kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0667540.1	0.627999	6.898857	3.702772	0.000509	0.010183	-0.77702	Pollen-specific protein SF3	elongation zone	12 h
HORVU.MOREX.r3.4HG0400840.1	0.906314	4.455067	3.582888	0.000739	0.012516	-0.77756	4-coumarate--CoA ligase family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0132700.1	-1.79534	1.569987	-3.50223	0.000945	0.014306	-0.77808	Phenylalanine ammonia-lyase	elongation zone	12 h
HORVU.MOREX.r3.2HG0164700.2	-0.67274	5.234489	-3.55173	0.000813	0.013153	-0.77812	Potassium transporter	elongation zone	12 h
HORVU.MOREX.r3.7HG0674480.1	-0.2996	6.371176	-3.60579	0.000688	0.01213	-0.77841	RING/U-box superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0663180.1	-1.00667	1.342669	-3.49131	0.000977	0.014552	-0.78005	Growth-regulating factor	elongation zone	12 h
HORVU.MOREX.r3.2HG0173340.1	-3.40117	1.078294	-4.13056	0.000129	0.005458	-0.78042	Pentatricopeptide repeat-containing protein, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0195110.2	-1.87546	0.674913	-3.69891	0.000515	0.010244	-0.78085	Remorin family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0470680.1	1.343119	-1.96407	3.484063	0.000999	0.014726	-0.78107	Heavy metal transport/detoxification protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0037910.1	-0.69128	4.060046	-3.49894	0.000955	0.014386	-0.7812	Starch synthase, chloroplastic/amyloplastic	elongation zone	12 h
HORVU.MOREX.r3.6HG0608390.1	0.374186	8.330662	3.688327	0.000533	0.010373	-0.78261	Nuclear matrix constituent protein 1	elongation zone	12 h
HORVU.MOREX.r3.1HG0022860.1	-0.35035	5.022173	-3.56185	0.000788	0.013028	-0.78379	Xylosyltransferase 1	elongation zone	12 h
HORVU.MOREX.r3.3HG0319430.1	0.823866	2.262365	3.482422	0.001004	0.014726	-0.78445	WD40-repeat protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0516720.1	-1.82664	6.439288	-3.49136	0.000977	0.014552	-0.78538	Glutathione-S-transferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0316640.1	-0.70542	4.162627	-3.56778	0.000774	0.012886	-0.78543	Pentatricopeptide repeat (PPR) superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0349980.1	0.615035	0.310535	3.531143	0.000866	0.013618	-0.78577	DUF241 domain protein, putative (DUF241)	elongation zone	12 h
HORVU.MOREX.r3.5HG0462220.1	0.943213	1.070356	3.545417	0.000829	0.013267	-0.78656	Calmodulin protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0355150.1	-0.6149	5.515568	-3.56842	0.000772	0.012872	-0.79279	Protein transport protein Sec61 subunit beta, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0597770.1	-0.50701	4.348024	-3.51627	0.000906	0.013962	-0.79292	F-box/LRR protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0520650.1	-0.67566	5.200623	-3.55569	0.000803	0.013128	-0.79386	Argonaute family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0240450.1	-0.75347	4.298635	-3.49168	0.000976	0.014552	-0.79422	Protein gamma response 1	elongation zone	12 h
HORVU.MOREX.r3.6HG0549520.1	0.634171	3.372434	3.516825	0.000904	0.013962	-0.80234	Beta-fructofuranosidase, insoluble protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0277200.1	-1.12157	6.184722	-3.54787	0.000822	0.01322	-0.80306	Pyruvate kinase	elongation zone	12 h
HORVU.MOREX.r3.2HG0195190.1	-0.87082	4.061362	-3.50389	0.000941	0.014244	-0.80334	Multidrug resistance protein MdtC	elongation zone	12 h
HORVU.MOREX.r3.3HG0326330.1	1.0398	0.282326	3.553807	0.000808	0.01314	-0.80341	Rho GTPase-activating protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0205760.1	-0.91344	5.328219	-3.49832	0.000957	0.0144	-0.80548	Glutamyl-tRNA(Gln) amidotransferase subunit A	elongation zone	12 h
HORVU.MOREX.r3.5HG0493080.1	0.601523	5.851163	3.56725	0.000775	0.012897	-0.80667	VWA domain containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0178480.1	0.946154	-0.05624	3.518066	0.000901	0.013961	-0.80742	RING/U-box superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0364310.1	-0.51374	4.81568	-3.51176	0.000918	0.014073	-0.80804	Protein SUPPRESSOR OF GENE SILENCING 3	elongation zone	12 h
HORVU.MOREX.r3.7HG0728870.1	-0.59884	6.913212	-3.68965	0.00053	0.01036	-0.80931	Xyloglucan endotransglucosylase/hydrolase	elongation zone	12 h
HORVU.MOREX.r3.6HG0605290.1	-0.6543	4.144726	-3.47923	0.001014	0.014816	-0.80977	Protein phosphatase 2C	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.6HG0610700.1	-0.90684	3.726004	-3.5107	0.000921	0.014087	-0.81128	Blue copper protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0714900.1	-0.72309	4.447401	-3.49205	0.000975	0.014552	-0.81828	S-acyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0234000.1	1.542139	-0.27443	3.563474	0.000784	0.012995	-0.81846	Xyloglucan endotransglucosylase/hydrolase	elongation zone	12 h
HORVU.MOREX.r3.1HG0030090.1	-1.09987	1.881613	-3.4833	0.001001	0.014726	-0.81915	Leucine-rich repeat protein kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0503950.1	-0.48232	4.442886	-3.50611	0.000934	0.014181	-0.82028	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0410830.1	1.089344	1.674186	3.544583	0.000831	0.013276	-0.82121	Transcription factor	elongation zone	12 h
HORVU.MOREX.r3.6HG0539590.1	0.983647	3.210813	3.530163	0.000868	0.013618	-0.82461	Protein disulfide-isomerase	elongation zone	12 h
HORVU.MOREX.r3.3HG0249640.1	0.623515	4.297068	3.560118	0.000792	0.013047	-0.83302	E3 ubiquitin-protein ligase	elongation zone	12 h
HORVU.MOREX.r3.5HG0432950.1	0.451544	5.320519	3.551868	0.000812	0.013153	-0.83577	L-galactose dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.1HG0086390.1	0.89146	-0.26089	3.489637	0.000982	0.014595	-0.83637	#N/A	elongation zone	12 h
HORVU.MOREX.r3.1HG0005840.1	-1.42188	1.736344	-3.59147	0.000719	0.012373	-0.83709	Embryo defective 2735	elongation zone	12 h
HORVU.MOREX.r3.5HG0510060.1	-0.65642	7.466645	-3.59092	0.000721	0.012383	-0.83862	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.6HG0604620.1	-1.34418	6.017915	-3.51445	0.000911	0.013989	-0.84237	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0486070.1	-0.64751	6.538472	-3.55259	0.000811	0.013149	-0.84375	Aminotransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0715170.1	1.530379	-0.05365	3.463691	0.001063	0.015289	-0.8438	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0514100.1	-0.62927	4.963873	-3.49799	0.000958	0.0144	-0.84535	#N/A	elongation zone	12 h
HORVU.MOREX.r3.1HG0060260.1	-0.97756	5.874721	-3.52813	0.000874	0.013663	-0.84628	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.2HG0215060.1	2.22913	-1.59998	3.574152	0.000759	0.01274	-0.84643	WAT1-related protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0568900.1	-1.11865	6.529769	-3.53831	0.000847	0.013429	-0.84667	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.2HG0105980.1	-0.67326	2.766067	-3.45831	0.00108	0.015382	-0.84694	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0550950.1	-0.48676	7.177294	-3.58609	0.000731	0.012454	-0.84931	NADP dependent sorbitol 6-phosphate dehydrogenase family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0573850.1	-0.32853	5.097663	-3.5447	0.00083	0.013276	-0.852	Protein YIF1B	elongation zone	12 h
HORVU.MOREX.r3.2HG0136010.1	-0.71292	2.505497	-3.46064	0.001072	0.015346	-0.854	DNA repair family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0524120.1	-0.3915	5.963425	-3.57496	0.000757	0.012729	-0.85445	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0189800.1	-0.68678	3.770835	-3.4838	0.001	0.014726	-0.85511	ethylene-responsive transcription factor	elongation zone	12 h
HORVU.MOREX.r3.3HG0277100.1	-0.46209	4.350493	-3.51088	0.000921	0.014087	-0.85578	Calcium-dependent lipid-binding (CaLB domain) family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0053720.1	-0.90305	1.572526	-3.46748	0.00105	0.015148	-0.85699	Protein kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0617730.1	-0.35964	7.183954	-3.63239	0.000634	0.01149	-0.85734	Galactoside 2-alpha-L-fucosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.1HG0091770.1	-1.21309	4.911247	-3.48479	0.000997	0.014726	-0.85938	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.6HG0601180.1	0.918442	3.243543	3.645766	0.000608	0.011202	-0.8614	Expansin protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0730660.1	1.50246	-2.73673	3.530432	0.000867	0.013618	-0.86439	#N/A	elongation zone	12 h
HORVU.MOREX.r3.1HG0075590.1	-0.27657	8.230864	-3.6482	0.000604	0.011167	-0.86511	Coiled-coil domain-containing protein 47	elongation zone	12 h
HORVU.MOREX.r3.4HG0335110.1	-0.9457	5.132212	-3.48246	0.001004	0.014726	-0.8654	BHLH family protein, putative, expressed	elongation zone	12 h
HORVU.MOREX.r3.5HG0462380.1	-0.63423	3.998698	-3.53134	0.000865	0.013618	-0.86576	LYR family of Fe/S cluster biogenesis protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0302090.1	-0.58639	3.520126	-3.4596	0.001076	0.015372	-0.86613	CASP-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0504700.1	-0.91605	3.74855	-3.47709	0.00102	0.014881	-0.86652	Acetyl-coenzyme A synthetase	elongation zone	12 h
HORVU.MOREX.r3.5HG0502130.1	-0.77611	6.54341	-3.52979	0.000869	0.013618	-0.86718	T-complex protein 1 subunit beta	elongation zone	12 h
HORVU.MOREX.r3.6HG0557140.1	-0.64475	3.245091	-3.4603	0.001074	0.015351	-0.86901	Myb family transcription factor-like	elongation zone	12 h
HORVU.MOREX.r3.5HG0478050.1	0.607932	5.803016	3.613842	0.000671	0.011927	-0.87005	Nucleobase ascorbate transporter	elongation zone	12 h
HORVU.MOREX.r3.7HG0737340.1	1.392017	-0.10666	3.559862	0.000793	0.013047	-0.87148	GDA1/CD39 nucleoside phosphatase family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0284100.1	0.437751	6.109021	3.593535	0.000715	0.012356	-0.87177	5'-nucleotidase SurE	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.7HG0705860.1	0.476177	7.982366	3.678827	0.000549	0.010519	-0.87219	Non-lysosomal glucosylceramidase	elongation zone	12 h
HORVU.MOREX.r3.3HG0296490.1	-0.631	6.526217	-3.56309	0.000785	0.013	-0.87223	NADH-cytochrome b5 reductase	elongation zone	12 h
HORVU.MOREX.r3.5HG0420480.1	1.979522	1.423525	3.448414	0.001113	0.015672	-0.87256	BEL1-like homeodomain protein 6	elongation zone	12 h
HORVU.MOREX.r3.4HG0331730.1	-0.30634	6.082061	-3.55804	0.000797	0.013094	-0.87951	Zinc finger, C2H2	elongation zone	12 h
HORVU.MOREX.r3.5HG0525980.1	-0.44145	8.509545	-3.64399	0.000611	0.011213	-0.88	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase comp	elongation zone	12 h
HORVU.MOREX.r3.7HG0665990.1	0.624684	6.156682	3.629205	0.00064	0.011564	-0.88211	Shikimate kinase	elongation zone	12 h
HORVU.MOREX.r3.1HG0007360.1	-0.54863	5.263881	-3.56081	0.00079	0.013047	-0.88285	Type I inositol-1,4,5-trisphosphate 5-phosphatase 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0736860.1	-2.17186	3.347913	-3.5357	0.000854	0.013502	-0.88359	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B, putative isoform 2	elongation zone	12 h
HORVU.MOREX.r3.2HG0128490.1	-0.32614	4.434925	-3.52034	0.000895	0.013907	-0.88373	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0674990.1	-0.50001	3.286295	-3.4631	0.001065	0.015297	-0.88381	Mannan endo-1,4-beta-mannosidase-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0496220.1	-1.19608	4.965587	-3.47561	0.001025	0.014916	-0.88425	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0428840.1	-0.73186	5.358224	-3.48337	0.001001	0.014726	-0.88884	BTB/POZ domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0712650.1	-0.85576	3.870701	-3.44688	0.001118	0.015713	-0.8952	DnaJ subfamily C member 2	elongation zone	12 h
HORVU.MOREX.r3.6HG0624240.1	0.865736	1.910661	3.475242	0.001026	0.014922	-0.89588	Basic helix-loop-helix transcription factor	elongation zone	12 h
HORVU.MOREX.r3.5HG0498770.1	-0.41008	6.313633	-3.55308	0.000809	0.01314	-0.89618	Hexosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.6HG0618100.1	-1.83706	2.509582	-3.48519	0.000996	0.014726	-0.89838	Protein trichome birefringence	elongation zone	12 h
HORVU.MOREX.r3.3HG0243560.1	-0.4069	5.438018	-3.51583	0.000907	0.013962	-0.89896	BES1/BZR1 homolog 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0209440.1	-0.48026	5.469564	-3.52567	0.00088	0.013745	-0.90553	Sugar transporter, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0298180.1	1.503506	-1.34466	3.435325	0.001158	0.01605	-0.90763	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0255580.1	0.489729	5.497552	3.579479	0.000746	0.012595	-0.90778	Respiratory burst oxidase, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0322660.1	-1.31269	5.027667	-3.44748	0.001116	0.015695	-0.90833	Receptor protein kinase, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0494470.1	-0.5211	3.993787	-3.45668	0.001085	0.015413	-0.90936	Transmembrane emp24 domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0655180.1	-0.53486	3.708393	-3.45054	0.001106	0.015604	-0.90981	F-box protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0003430.1	0.501143	4.894308	3.52258	0.000889	0.013844	-0.91151	TBC1 domain family member	elongation zone	12 h
HORVU.MOREX.r3.4HG0415590.1	-1.60417	-0.04239	-3.43533	0.001158	0.01605	-0.91174	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily	elongation zone	12 h
HORVU.MOREX.r3.7HG0689580.1	-0.60683	4.115082	-3.44808	0.001114	0.015677	-0.91199	Signal peptide peptidase family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0379960.1	-0.42667	5.175068	-3.50568	0.000935	0.014187	-0.91247	Exostosin family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0495790.1	-0.63472	4.487486	-3.46516	0.001058	0.015244	-0.91308	D-amino acid dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.1HG0015960.1	1.206401	-0.2749	3.432282	0.001168	0.016079	-0.91409	Protein kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0136570.1	-2.14977	1.302768	-3.54033	0.000842	0.013377	-0.91516	Cellulose synthase-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0379290.1	-0.31983	5.28798	-3.51719	0.000903	0.013962	-0.91611	COP1-interacting-like protein, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0564590.1	-0.48695	6.44927	-3.53334	0.00086	0.013572	-0.91639	O-fucosyltransferase family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0307250.1	1.74247	-2.48075	3.474127	0.00103	0.014951	-0.9164	Amino acid permease	elongation zone	12 h
HORVU.MOREX.r3.1HG0006610.1	-0.95894	8.69333	-3.58972	0.000723	0.012401	-0.91966	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.3HG0252610.1	-0.37714	7.233439	-3.56514	0.00078	0.01296	-0.92076	Protein kinase	elongation zone	12 h
HORVU.MOREX.r3.7HG0637030.1	0.971635	0.131716	3.475625	0.001025	0.014916	-0.92188	Cytochrome P450 family protein, expressed	elongation zone	12 h
HORVU.MOREX.r3.5HG0523560.1	-0.87058	6.843578	-3.55316	0.000809	0.01314	-0.92358	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.3HG0330120.1	2.289758	-3.00967	3.479617	0.001013	0.014809	-0.92632	O-methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0287840.1	-0.70993	3.05117	-3.43477	0.00116	0.016058	-0.92686	peroxisomal ABC transporter 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0099780.1	1.103458	-0.01779	3.42734	0.001186	0.016221	-0.92693	Maternal effect embryo arrest protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0356690.1	1.103072	0.745555	3.43352	0.001164	0.016068	-0.92893	Protein ZINC INDUCED FACILITATOR-LIKE 1	elongation zone	12 h

Table Sн Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0235030.1	-0.50211	3.06592	-3.43204	0.001169	0.016079	-0.93102	Dehydration-responsive element binding protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0525440.1	-0.37273	6.964938	-3.58046	0.000744	0.012578	-0.93217	Trichome birefringence-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0512230.1	1.183108	2.04829	3.425771	0.001191	0.016287	-0.93298	Protein ENHANCED DISEASE RESISTANCE 2-like	elongation zone	12 h
HORVU.MOREX.r3.4HG0358880.2	-0.52281	5.351205	-3.51931	0.000897	0.01393	-0.93563	Succinate--CoA ligase [ADP-forming] subunit beta	elongation zone	12 h
HORVU.MOREX.r3.2HG0211880.1	-0.46183	4.077958	-3.46207	0.001068	0.015301	-0.93577	Exostosin family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0095000.1	-1.58078	0.995323	-3.49102	0.000978	0.014555	-0.93582	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0111570.1	0.736155	1.289254	3.427838	0.001184	0.016219	-0.93916	Polynucleotidyl transferase, ribonuclease H-like superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0224440.1	0.867778	1.43625	3.48481	0.000997	0.014726	-0.9411	DUF4228 domain protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0477800.1	0.747897	5.596819	3.548386	0.000821	0.01322	-0.94315	Endo-1,3(4)-beta-glucanase 1	elongation zone	12 h
HORVU.MOREX.r3.5HG0510920.1	-0.38934	5.904242	-3.50607	0.000934	0.014181	-0.94597	Transcriptional adapter ADA2	elongation zone	12 h
HORVU.MOREX.r3.2HG0194850.1	0.684492	6.889643	3.594903	0.000712	0.012335	-0.94691	Cysteine/Histidine-rich C1 domain family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0726800.1	1.133392	2.279935	3.434718	0.00116	0.016058	-0.94699	3,4-dihydroxy-2-butanone 4-phosphate synthase	elongation zone	12 h
HORVU.MOREX.r3.4HG0331850.1	-0.60822	3.521487	-3.43982	0.001142	0.015898	-0.95072	Sn1-specific diacylglycerol lipase alpha	elongation zone	12 h
HORVU.MOREX.r3.7HG0751110.1	-0.61381	4.358149	-3.45778	0.001082	0.015394	-0.95118	Kinesin-like	elongation zone	12 h
HORVU.MOREX.r3.3HG0267150.1	-0.35217	5.178731	-3.49654	0.000962	0.014417	-0.95301	Calcium binding protein-like	elongation zone	12 h
HORVU.MOREX.r3.5HG0509020.1	1.013104	0.642934	3.419563	0.001214	0.016441	-0.9552	guanine nucleotide-binding protein subunit gamma	elongation zone	12 h
HORVU.MOREX.r3.3HG0314820.1	0.703931	3.291172	3.522295	0.000889	0.013845	-0.95819	26S proteasome regulatory subunit RPN2	elongation zone	12 h
HORVU.MOREX.r3.5HG0525430.1	0.745961	4.268757	3.551468	0.000813	0.013153	-0.95917	Trichome birefringence-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0091670.1	-0.56351	4.229991	-3.43262	0.001167	0.016079	-0.96454	Peroxisomal membrane PEX14-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0284170.1	-0.57584	4.134399	-3.51593	0.000907	0.013962	-0.96677	cotton fiber-like protein (DUF761)	elongation zone	12 h
HORVU.MOREX.r3.3HG0275490.1	1.707844	-2.47526	3.444522	0.001126	0.01576	-0.96898	Zinc finger CCCH domain protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0624650.1	-0.35452	8.612308	-3.63135	0.000636	0.011508	-0.96929	Transmembrane 9 superfamily member	elongation zone	12 h
HORVU.MOREX.r3.7HG0668450.1	-0.49651	5.247544	-3.48298	0.001002	0.014726	-0.97067	Alpha-mannosidase	elongation zone	12 h
HORVU.MOREX.r3.7HG0642550.1	-0.32762	6.014924	-3.51713	0.000903	0.013962	-0.97563	Peroxisomal membrane protein 11 homolog	elongation zone	12 h
HORVU.MOREX.r3.5HG0527720.1	1.082186	0.951915	3.420705	0.00121	0.016416	-0.97796	Receptor protein kinase, putative,expressed	elongation zone	12 h
HORVU.MOREX.r3.3HG0247260.1	-1.16939	0.519017	-3.47746	0.001019	0.014875	-0.97855	Leucine-rich repeat protein kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0195910.1	0.703522	2.102422	3.523828	0.000885	0.013812	-0.9787	Protease inhibitor/seed storage/lipid transfer family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0439090.1	-0.72701	2.651507	-3.40873	0.001254	0.016818	-0.97877	ERD (Early-responsive to dehydration stress) family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0727460.1	-0.83413	8.013727	-3.53864	0.000846	0.013426	-0.981	60S acidic ribosomal protein P3	elongation zone	12 h
HORVU.MOREX.r3.1HG0092730.1	0.773468	7.867854	3.624833	0.000649	0.011649	-0.986	ATP-dependent zinc metalloprotease FtsH 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0212900.1	-0.61294	6.207725	-3.48368	0.001	0.014726	-0.98864	Methylthioribose kinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0324480.1	1.356772	-1.11625	3.431356	0.001172	0.016094	-0.98963	UDP-glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0245310.1	-0.74754	4.920306	-3.47834	0.001016	0.014846	-0.99074	GDSL esterase/lipase	elongation zone	12 h
HORVU.MOREX.r3.1HG0084760.1	1.315812	-3.22969	3.541218	0.000839	0.013372	-0.99216	Myb transcription factor	elongation zone	12 h
HORVU.MOREX.r3.7HG0742070.1	-0.65421	6.57434	-3.49741	0.000959	0.0144	-0.99389	UDP-glucose 4-epimerase 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0104080.1	1.006087	-1.54865	3.401109	0.001283	0.01705	-0.99409	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0115300.2	-0.28072	7.926726	-3.57463	0.000758	0.012732	-0.99726	Superoxide dismutase [Cu-Zn]	elongation zone	12 h
HORVU.MOREX.r3.7HG0654680.1	-0.93333	5.771912	-3.43324	0.001165	0.016068	-1.00165	Starch synthase, chloroplastic/amyloplastic	elongation zone	12 h
HORVU.MOREX.r3.5HG0488050.1	1.446708	-2.9262	3.501809	0.000947	0.014313	-1.00374	Blue copper protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0676690.1	0.816004	4.543618	3.601768	0.000697	0.012162	-1.00438	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0302910.1	-0.9604	7.267731	-3.51097	0.000921	0.014087	-1.01003	Histone H2B	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0252960.1	1.299096	-1.0236	3.399728	0.001288	0.017063	-1.0106	Calmodulin-binding protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0234560.1	-1.34087	2.285408	-3.44296	0.001131	0.015774	-1.01265	Ethylene receptor 2	elongation zone	12 h
HORVU.MOREX.r3.3HG0328480.1	-1.73065	1.933392	-3.51224	0.000917	0.014073	-1.01588	Rotundifolia-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0406140.1	0.48942	5.424725	3.497041	0.00096	0.014406	-1.0164	Transmembrane protein 131	elongation zone	12 h
HORVU.MOREX.r3.4HG0402000.1	-0.63812	8.180685	-3.57848	0.000749	0.012613	-1.01895	Kinase interacting (KIP1-like) family protein, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0614500.1	-0.38563	5.054555	-3.46401	0.001062	0.015287	-1.02196	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	elongation zone	12 h
HORVU.MOREX.r3.7HG0640800.1	2.180269	0.469292	3.694259	0.000523	0.010309	-1.02229	Cell division cycle protein 123 like	elongation zone	12 h
HORVU.MOREX.r3.7HG0706860.1	-0.64394	4.054763	-3.39882	0.001292	0.017089	-1.02275	PHD finger family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0254940.1	0.868714	2.451212	3.557318	0.000799	0.013094	-1.02351	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.7HG0676000.1	-1.24175	0.270183	-3.4446	0.001126	0.01576	-1.02532	Jasmonate O-methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0115970.1	-1.05766	3.355368	-3.45353	0.001096	0.015528	-1.02592	NAD(P)H dehydrogenase (Quinone)	elongation zone	12 h
HORVU.MOREX.r3.5HG0475250.1	-0.69647	3.753494	-3.39696	0.001299	0.017131	-1.02729	Translation initiation factor IF-2	elongation zone	12 h
HORVU.MOREX.r3.5HG0421460.1	-0.68188	11.22444	-3.66956	0.000565	0.010652	-1.02788	RNA-binding protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0566940.1	0.58032	4.632192	3.463486	0.001063	0.015289	-1.02831	Sulfurtransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0652830.1	-1.91475	0.863491	-3.6596	0.000583	0.010887	-1.029	Disease resistance protein RPP13	elongation zone	12 h
HORVU.MOREX.r3.5HG0444350.1	0.824653	2.597523	3.398644	0.001292	0.017089	-1.02962	Sn1-specific diacylglycerol lipase alpha	elongation zone	12 h
HORVU.MOREX.r3.7HG0669590.1	1.389504	-0.99729	3.400606	0.001285	0.01705	-1.03221	Caleosin	elongation zone	12 h
HORVU.MOREX.r3.7HG0739030.1	0.549526	5.253412	3.508076	0.000929	0.014168	-1.03378	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0352200.1	0.687494	3.627838	3.446324	0.00112	0.015728	-1.03446	Methyltransferase-related protein, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0069030.1	1.513426	1.48038	3.388332	0.001333	0.017367	-1.0349	Calcium-transporting ATPase	elongation zone	12 h
HORVU.MOREX.r3.1HG0075230.1	-1.20937	6.583831	-3.46261	0.001066	0.015301	-1.04058	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.5HG0509970.1	1.778014	-0.93022	3.418401	0.001218	0.016477	-1.04279	Heat shock transcription factor	elongation zone	12 h
HORVU.MOREX.r3.7HG0716900.1	-0.35492	8.192568	-3.5702	0.000768	0.012843	-1.04375	Transmembrane 9 superfamily member	elongation zone	12 h
HORVU.MOREX.r3.2HG0135650.1	2.770416	-3.48765	3.605312	0.000689	0.01213	-1.04376	Laccase	elongation zone	12 h
HORVU.MOREX.r3.2HG0135210.1	0.771811	2.447492	3.558142	0.000797	0.013094	-1.04606	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	elongation zone	12 h
HORVU.MOREX.r3.3HG0323750.1	0.866479	2.450618	3.380858	0.001363	0.017603	-1.04738	bZIP transcription factor, putative (DUF630 and DUF632)	elongation zone	12 h
HORVU.MOREX.r3.2HG0134990.1	0.685889	5.499939	3.44915	0.00111	0.015648	-1.048	Myosin-related family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0382550.1	0.636612	5.636635	3.50115	0.000948	0.014332	-1.0485	Xyloglucan 6-xylosyltransferase 1	elongation zone	12 h
HORVU.MOREX.r3.1HG0087590.1	1.424365	-1.00814	3.37951	0.001369	0.01763	-1.04851	transmembrane protein, putative (DUF679 domain membrane protein 2)	elongation zone	12 h
HORVU.MOREX.r3.1HG0079920.1	0.651371	3.500385	3.467743	0.00105	0.015148	-1.04895	Disease resistance protein (NBS-LRR class) family	elongation zone	12 h
HORVU.MOREX.r3.4HG0398050.1	1.595613	-2.71986	3.437184	0.001151	0.015993	-1.05051	#N/A	elongation zone	12 h
HORVU.MOREX.r3.4HG0381880.1	-0.47828	5.392899	-3.46244	0.001067	0.015301	-1.05266	Phytochrome	elongation zone	12 h
HORVU.MOREX.r3.4HG0398910.1	-1.01886	7.14368	-3.49462	0.000967	0.014469	-1.05291	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.2HG0205050.1	2.025911	-2.49223	3.473297	0.001032	0.014978	-1.05356	Receptor-like protein kinase	elongation zone	12 h
HORVU.MOREX.r3.5HG0522130.1	-0.51327	4.373396	-3.44312	0.001131	0.015774	-1.05477	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0185850.1	-0.4627	5.208449	-3.46753	0.00105	0.015148	-1.05613	Expansin	elongation zone	12 h
HORVU.MOREX.r3.4HG0338400.1	-0.86073	8.453677	-3.53775	0.000848	0.013441	-1.05763	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.3HG0233150.1	-0.82771	5.953619	-3.45738	0.001083	0.015401	-1.06234	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.6HG0608910.1	1.218664	-1.72298	3.374192	0.001391	0.017856	-1.06241	Heavy metal transport/detoxification superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0547970.1	-0.92694	5.20494	-3.44288	0.001132	0.015774	-1.0625	#N/A	elongation zone	12 h
HORVU.MOREX.r3.4HG0403260.1	0.346316	4.85718	3.458257	0.00108	0.015382	-1.0652	Ribulose-phosphate 3-epimerase	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0069380.1	0.817388	2.129643	3.433418	0.001164	0.016068	-1.06624	Cysteine proteinase inhibitor	elongation zone	12 h
HORVU.MOREX.r3.1HG0020980.1	0.544452	7.252013	3.589018	0.000725	0.012414	-1.06749	Endo-1,31,4-beta-D-glucanase	elongation zone	12 h
HORVU.MOREX.r3.6HG0564510.1	-0.91871	4.576465	-3.381	0.001363	0.017603	-1.06769	Arabinose 5-phosphate isomerase, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0184230.1	2.393572	-3.03591	3.507479	0.00093	0.014174	-1.06813	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0223950.1	-0.66356	4.288991	-3.38873	0.001331	0.017357	-1.06813	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0132440.2	-0.45464	4.455297	-3.40713	0.00126	0.016857	-1.07039	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0513020.1	-0.33397	6.516882	-3.50869	0.000927	0.014152	-1.07144	Transmembrane protein 147	elongation zone	12 h
HORVU.MOREX.r3.7HG0709720.1	-0.46542	5.925323	-3.51831	0.0009	0.013961	-1.0729	plant/protein (Protein of unknown function, DUF538)	elongation zone	12 h
HORVU.MOREX.r3.1HG0000140.1	-0.35343	5.300482	-3.46137	0.00107	0.015323	-1.07342	Glycosyltransferase-like KOBITO 1	elongation zone	12 h
HORVU.MOREX.r3.4HG0352780.1	0.751161	1.138745	3.413052	0.001238	0.016656	-1.07666	WRKY transcription factor	elongation zone	12 h
HORVU.MOREX.r3.7HG0749070.1	1.223174	-1.82628	3.372802	0.001396	0.017896	-1.07794	nodulin MtN21 /EamA-like transporter family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0554050.1	0.891348	-1.56957	3.373736	0.001392	0.017869	-1.07815	cyclin-dependent kinase inhibitor	elongation zone	12 h
HORVU.MOREX.r3.6HG0605940.1	0.717678	3.179648	3.427365	0.001186	0.016221	-1.07968	Xyloglucan endotransglucosylase/hydrolase	elongation zone	12 h
HORVU.MOREX.r3.7HG0730800.1	-1.12616	5.096289	-3.39957	0.001289	0.017063	-1.08195	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.2HG0141980.1	-0.43246	5.307117	-3.50485	0.000938	0.014213	-1.08289	Glucan endo-1,3-beta-glucosidase 3	elongation zone	12 h
HORVU.MOREX.r3.7HG0726700.1	-0.86121	7.183777	-3.47659	0.001022	0.014893	-1.08493	Leucine-rich repeat protein kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0667630.1	1.180154	5.380802	3.500075	0.000952	0.014357	-1.08656	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.5HG0497940.1	-1.2614	4.128013	-3.3681	0.001416	0.018059	-1.08767	Homeobox leucine zipper protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0460720.1	-0.50172	6.552351	-3.47281	0.001034	0.01499	-1.08905	L-galactono-1,4-lactone dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.2HG0167570.1	-1.31702	5.317382	-3.39706	0.001299	0.017131	-1.08935	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.2HG0141140.1	1.118787	-2.85799	3.407892	0.001257	0.016849	-1.08957	DUF4228 domain protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0313040.1	-1.42151	6.108078	-3.47473	0.001028	0.014935	-1.08965	Hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyltransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0685350.1	0.602232	3.413791	3.434361	0.001161	0.016061	-1.09306	LysM receptor-like kinase protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0500680.1	-0.68109	6.785877	-3.48185	0.001006	0.01473	-1.09416	Acyl carrier protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0231000.1	0.924133	3.745714	3.481856	0.001006	0.01473	-1.09688	Gamma-glutamyltranspeptidase	elongation zone	12 h
HORVU.MOREX.r3.7HG0738680.1	0.722108	3.55287	3.445839	0.001121	0.01573	-1.09755	Vacuolar sorting receptor family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0256360.1	-0.37438	5.280798	-3.45633	0.001087	0.015419	-1.09811	BSD domain-containing protein 1	elongation zone	12 h
HORVU.MOREX.r3.1HG0077840.1	-0.46114	7.930641	-3.53727	0.00085	0.013451	-1.09969	Glucan endo-1,3-beta-glucosidase 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0665520.1	-0.53998	3.332246	-3.42527	0.001193	0.016301	-1.10037	MBOAT (Membrane bound O-acyl transferase) family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0325760.1	-0.49518	5.438001	-3.43883	0.001145	0.015935	-1.10344	Mitochondrial carrier protein-like	elongation zone	12 h
HORVU.MOREX.r3.4HG0406630.1	0.719518	4.673873	3.526775	0.000877	0.013709	-1.10434	Classical arabinogalactan protein 5	elongation zone	12 h
HORVU.MOREX.r3.7HG0647930.1	-1.39828	1.498899	-3.44308	0.001131	0.015774	-1.10637	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0613270.1	-0.44926	9.613904	-3.58334	0.000738	0.012516	-1.1064	Glutamine synthetase	elongation zone	12 h
HORVU.MOREX.r3.7HG0661490.1	-0.30853	6.094894	-3.48695	0.00099	0.014693	-1.10709	Stromal cell-derived factor 2	elongation zone	12 h
HORVU.MOREX.r3.7HG0701640.1	0.807464	2.542885	3.469902	0.001043	0.01508	-1.10717	Vesicle-associated protein 4-2	elongation zone	12 h
HORVU.MOREX.r3.5HG0519360.1	0.968408	2.680303	3.354868	0.001473	0.018499	-1.11127	Retrovirus-related Pol polyprotein from transposon TNT 1-94	elongation zone	12 h
HORVU.MOREX.r3.3HG0309820.1	-0.73799	5.758875	-3.42975	0.001177	0.016136	-1.11128	Small ubiquitin-related modifier	elongation zone	12 h
HORVU.MOREX.r3.2HG0206910.1	-1.00295	3.37302	-3.35461	0.001474	0.0185	-1.1122	Mitochondrial transcription termination factor family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0599450.1	1.723706	-2.13758	3.386836	0.001339	0.017425	-1.11388	Yellow stripe 1A transporter	elongation zone	12 h
HORVU.MOREX.r3.7HG0705490.1	-1.52851	2.356127	-3.42283	0.001202	0.016359	-1.11538	HXXXD-type acyl-transferase family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0100040.1	-2.09234	-0.29926	-3.45829	0.00108	0.015382	-1.11801	HXXXD-type acyl-transferase family protein	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.7HG0718720.1	1.046375	2.503323	3.366125	0.001424	0.018114	-1.11809	DUF1685 family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0485780.1	2.537986	-0.7336	3.371804	0.0014	0.017938	-1.11911	1-aminocyclopropane-1-carboxylate oxidase	elongation zone	12 h
HORVU.MOREX.r3.2HG0108490.1	-1.27031	3.17005	-3.35058	0.001492	0.018644	-1.12235	Xyloglucan endotransglucosylase/hydrolase	elongation zone	12 h
HORVU.MOREX.r3.5HG0476460.1	-0.75976	2.596562	-3.3543	0.001475	0.018506	-1.12369	VQ motif-containing family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0173960.1	0.667257	2.814915	3.360621	0.001448	0.018262	-1.12407	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.2HG0203500.1	-0.82561	6.139708	-3.44457	0.001126	0.01576	-1.12437	UPF0136 membrane protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0638340.1	1.233699	2.325425	3.395256	0.001306	0.017152	-1.12886	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0323600.1	0.532598	4.355593	3.450713	0.001105	0.015604	-1.13286	Phosphatidylserine decarboxylase proenzyme 2	elongation zone	12 h
HORVU.MOREX.r3.3HG0272430.1	-0.40368	5.81708	-3.45887	0.001078	0.015382	-1.13319	Pectin lyase-like superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0342640.1	-1.80842	4.773275	-3.34393	0.001522	0.018912	-1.13833	Cyclin	elongation zone	12 h
HORVU.MOREX.r3.7HG0727290.1	0.693282	3.998416	3.462295	0.001067	0.015301	-1.14211	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0651010.1	-0.93294	4.932391	-3.41349	0.001236	0.016645	-1.14292	Xyloglucan endotransglucosylase/hydrolase	elongation zone	12 h
HORVU.MOREX.r3.3HG0292080.1	-0.48101	4.723449	-3.41699	0.001223	0.016525	-1.14348	F-box family protein-like	elongation zone	12 h
HORVU.MOREX.r3.3HG0283250.1	0.617689	3.003629	3.453024	0.001097	0.015536	-1.14386	MYB transcription factor	elongation zone	12 h
HORVU.MOREX.r3.4HG0416760.1	-0.52908	4.391267	-3.40337	0.001274	0.016993	-1.14601	Non-structural protein 1	elongation zone	12 h
HORVU.MOREX.r3.4HG0416390.1	1.347277	0.67132	3.420693	0.00121	0.016416	-1.14712	Sugar transporter, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0672400.1	1.070717	3.007592	3.349056	0.001499	0.018717	-1.14892	DNA repair protein complementing XP-C cells-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0030290.1	3.260825	-1.84835	3.863468	0.000306	0.007759	-1.15015	PRA1 family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0076980.1	-0.34441	8.500486	-3.54531	0.000829	0.013267	-1.15123	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3	elongation zone	12 h
HORVU.MOREX.r3.1HG0066730.1	-0.68177	4.534097	-3.41379	0.001235	0.016641	-1.15222	Indole-3-glycerol phosphate synthase	elongation zone	12 h
HORVU.MOREX.r3.6HG0595190.1	1.519507	-2.07211	3.359425	0.001453	0.018316	-1.15482	GDSL esterase/lipase	elongation zone	12 h
HORVU.MOREX.r3.5HG0490960.1	-0.64319	3.86387	-3.36423	0.001432	0.018164	-1.15504	DNA-binding bromodomain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0438460.1	1.2713	0.165145	3.385245	0.001345	0.017473	-1.15654	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0075260.1	3.105787	0.393741	3.535071	0.000855	0.01351	-1.158	Receptor kinase 2	elongation zone	12 h
HORVU.MOREX.r3.4HG0375690.1	-1.15219	1.261321	-3.39574	0.001304	0.017152	-1.15963	DENN domain-containing protein 5B	elongation zone	12 h
HORVU.MOREX.r3.2HG0124820.1	-0.85368	3.652036	-3.34875	0.0015	0.018723	-1.16037	F-box protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0739490.1	-0.9539	7.817058	-3.48126	0.001008	0.014746	-1.16056	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.4HG0345580.1	1.914774	-3.15122	3.540894	0.00084	0.013375	-1.16065	Dirigent protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0587790.1	-1.59516	-0.11015	-3.49174	0.000976	0.014552	-1.16238	Transposon Ty3-G Gag-Pol polyprotein	elongation zone	12 h
HORVU.MOREX.r3.4HG0416220.1	-0.31577	6.683316	-3.4828	0.001003	0.014726	-1.16485	Cell number regulator 6	elongation zone	12 h
HORVU.MOREX.r3.4HG0416730.1	-0.80843	6.869699	-3.43656	0.001153	0.016012	-1.16539	Kinesin-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0362450.1	-0.9434	2.708144	-3.33292	0.001572	0.019344	-1.17196	calmodulin-binding protein (DUF1645)	elongation zone	12 h
HORVU.MOREX.r3.5HG0450100.1	-0.52611	5.024744	-3.3848	0.001347	0.017485	-1.17573	Quinolinate synthase A	elongation zone	12 h
HORVU.MOREX.r3.1HG0024230.1	-0.5737	5.422255	-3.38679	0.001339	0.017425	-1.1785	Tubulin beta chain	elongation zone	12 h
HORVU.MOREX.r3.5HG0486610.1	0.831506	3.213671	3.485919	0.000993	0.014718	-1.17957	Leucine-rich repeat receptor-like protein kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0728000.1	0.583007	5.007313	3.469666	0.001044	0.01508	-1.1833	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0504800.1	-0.81346	5.65419	-3.39331	0.001313	0.017213	-1.18409	Histone-lysine N-methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0466020.1	-0.76269	7.677987	-3.48304	0.001002	0.014726	-1.18833	Omega-3 fatty acid desaturase	elongation zone	12 h
HORVU.MOREX.r3.1HG0060270.1	-1.05896	5.417861	-3.38206	0.001358	0.017584	-1.19144	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.1HG0055730.1	-0.43234	4.544955	-3.38035	0.001365	0.017608	-1.19155	Translocase of chloroplast	elongation zone	12 h
HORVU.MOREX.r3.5HG0529130.1	-0.58652	9.571785	-3.53229	0.000863	0.013594	-1.19252	Elongation factor	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0230970.1	-0.81634	7.763065	-3.47254	0.001034	0.014991	-1.19277	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.2HG0164470.1	0.737877	3.24648	3.402184	0.001279	0.017029	-1.19281	Nudix hydrolase	elongation zone	12 h
HORVU.MOREX.r3.2HG0126440.1	1.162297	2.011284	3.366031	0.001425	0.018114	-1.19635	ATP-dependent RNA helicase-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0737470.1	1.040212	3.292476	3.578796	0.000748	0.012611	-1.19675	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.5HG0507680.1	1.287413	-1.22844	3.341747	0.001532	0.019016	-1.19914	mitogen-activated protein kinase kinase kinase 6	elongation zone	12 h
HORVU.MOREX.r3.6HG0543390.1	1.225568	0.250443	3.400451	0.001285	0.01705	-1.20079	High affinity nitrate transporter	elongation zone	12 h
HORVU.MOREX.r3.3HG0255040.1	-0.40994	4.904219	-3.38232	0.001357	0.017582	-1.20151	Mediator of RNA polymerase II transcription subunit 27	elongation zone	12 h
HORVU.MOREX.r3.1HG0004560.1	0.848348	5.305216	3.383604	0.001352	0.017536	-1.20216	ERD (Early-responsive to dehydration stress) family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0243920.1	-1.18597	3.290866	-3.31894	0.001639	0.019852	-1.20383	VQ motif-containing protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0304640.1	-0.58208	4.177695	-3.34439	0.00152	0.018909	-1.20406	Tetratricopeptide repeat-containing family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0730310.1	-0.8961	7.32045	-3.44934	0.00111	0.015648	-1.20523	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.1HG0002800.1	-1.35957	3.206208	-3.3385	0.001546	0.01915	-1.20583	Powdery mildew resistance protein Pm3	elongation zone	12 h
HORVU.MOREX.r3.3HG0316130.1	-0.7369	7.033938	-3.51456	0.00091	0.013989	-1.20603	Basic 7S globulin 2	elongation zone	12 h
HORVU.MOREX.r3.6HG0573870.1	-0.64366	4.15012	-3.3358	0.001559	0.019246	-1.20625	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.2HG0138620.1	-1.11624	3.379812	-3.32057	0.001631	0.019852	-1.20689	MBOAT (Membrane bound O-acyl transferase) family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0185600.1	1.052814	0.732582	3.422538	0.001203	0.016359	-1.20698	TRIO and F-actin-binding protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0185840.1	-0.96076	7.644996	-3.45406	0.001094	0.015514	-1.209	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0674790.1	-0.74093	5.490517	-3.37668	0.00138	0.017746	-1.20936	Microtubule associated family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0654460.1	-1.07171	6.42811	-3.40905	0.001253	0.016813	-1.20979	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.1HG0008190.1	-1.16374	-0.63382	-3.31941	0.001636	0.019852	-1.2125	Cytochrome P450	elongation zone	12 h
HORVU.MOREX.r3.3HG0266530.1	0.854064	1.443645	3.315997	0.001653	0.019898	-1.21349	carboxyl-terminal peptidase, putative (DUF239)	elongation zone	12 h
HORVU.MOREX.r3.5HG0479970.1	-0.39042	6.75595	-3.45197	0.001101	0.015569	-1.21368	Aspartyl aminopeptidase, putative, expressed	elongation zone	12 h
HORVU.MOREX.r3.2HG0165250.1	-0.40338	6.077437	-3.44323	0.00113	0.015774	-1.21642	OJ000315_02.19 protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0259960.1	-1.96866	-0.28204	-3.55981	0.000793	0.013047	-1.21715	Leucine-rich repeat protein kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0252210.1	1.172954	0.169661	3.362795	0.001439	0.018178	-1.21848	Transcription factor GLABRA 3	elongation zone	12 h
HORVU.MOREX.r3.4HG0374640.1	-0.71951	4.330972	-3.33722	0.001552	0.0192	-1.22234	DNA-binding storekeeper protein-related transcriptional regulator	elongation zone	12 h
HORVU.MOREX.r3.3HG0218330.1	-1.57496	8.028798	-3.41701	0.001223	0.016525	-1.22237	#N/A	elongation zone	12 h
HORVU.MOREX.r3.4HG0415230.1	-0.90584	2.026714	-3.30905	0.001687	0.020145	-1.22578	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0215250.1	-1.13212	6.918385	-3.43058	0.001174	0.016107	-1.22638	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.4HG0383530.1	1.090938	-0.0177	3.407607	0.001258	0.016853	-1.22725	Pathogenesis-related protein 1	elongation zone	12 h
HORVU.MOREX.r3.3HG0297140.1	-0.26881	7.212598	-3.50952	0.000925	0.014127	-1.2276	Auxin efflux carrier family protein-like	elongation zone	12 h
HORVU.MOREX.r3.2HG0196960.1	-2.61213	1.756153	-3.59214	0.000718	0.012368	-1.22847	Y' element ATP-dependent helicase YEL077C	elongation zone	12 h
HORVU.MOREX.r3.7HG0735210.1	1.656602	-3.00596	3.500743	0.00095	0.014339	-1.2313	Peptide transporter	elongation zone	12 h
HORVU.MOREX.r3.5HG0463350.1	-1.63397	5.140919	-3.32274	0.00162	0.019769	-1.23208	Cell division control 45-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0582120.1	0.477315	3.287652	3.363101	0.001437	0.018178	-1.23218	magnesium transporter NIPA (DUF803)	elongation zone	12 h
HORVU.MOREX.r3.1HG0049450.1	-0.42734	5.425708	-3.42486	0.001195	0.01631	-1.23262	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0622080.1	0.692966	1.073855	3.381616	0.00136	0.017585	-1.23291	MYB-related transcription factor	elongation zone	12 h
HORVU.MOREX.r3.2HG0157160.1	-0.83514	4.380598	-3.31791	0.001644	0.019852	-1.23441	Receptor kinase	elongation zone	12 h
HORVU.MOREX.r3.5HG0500360.1	2.916843	1.290708	3.423819	0.001198	0.01635	-1.23467	L-gulonolactone oxidase	elongation zone	12 h
HORVU.MOREX.r3.2HG0147770.1	-0.44361	5.593653	-3.40056	0.001285	0.01705	-1.23771	Growth-regulating factor	elongation zone	12 h
HORVU.MOREX.r3.4HG0339430.2	-1.84443	3.805151	-3.31663	0.00165	0.019892	-1.24232	Growth-regulating factor	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.5HG0473920.1	-0.48361	3.263199	-3.33396	0.001567	0.019305	-1.24358	OBP32pep, putative (DUF220)	elongation zone	12 h
HORVU.MOREX.r3.6HG0558330.1	-1.16252	6.152461	-3.39323	0.001314	0.017213	-1.24483	Calcium-dependent lipid-binding domain protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0493330.1	0.994298	0.977391	3.358806	0.001456	0.018338	-1.24564	UDP-glucuronate 4-epimerase 4	elongation zone	12 h
HORVU.MOREX.r3.6HG0606360.1	2.198272	-2.06608	3.317656	0.001645	0.019855	-1.24677	Peptide transporter	elongation zone	12 h
HORVU.MOREX.r3.5HG0472770.1	0.66082	4.331329	3.361641	0.001444	0.018229	-1.24744	SIN3-like 2	elongation zone	12 h
HORVU.MOREX.r3.3HG0306210.1	-0.6006	7.280706	-3.42273	0.001202	0.016359	-1.24981	RAN GTPase activating protein 2	elongation zone	12 h
HORVU.MOREX.r3.7HG0642770.1	-0.35383	5.619529	-3.39588	0.001303	0.017152	-1.24991	RNA-binding family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0530240.1	-1.14968	0.885356	-3.39153	0.00132	0.017256	-1.25161	Cytochrome P450 family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0596460.1	-0.41541	6.392262	-3.42254	0.001203	0.016359	-1.25331	Cryptochrome	elongation zone	12 h
HORVU.MOREX.r3.3HG0252240.1	-0.90173	7.225249	-3.4184	0.001218	0.016477	-1.25776	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.5HG0496930.1	0.836419	1.51856	3.297381	0.001746	0.02056	-1.25807	Inositol-tetrakisphosphate 1-kinase 4	elongation zone	12 h
HORVU.MOREX.r3.1HG0063870.1	-0.62243	6.880931	-3.42016	0.001212	0.016422	-1.25822	Kinesin-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0690090.1	0.837973	0.298554	3.353458	0.001479	0.01853	-1.25918	PLATZ transcription factor family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0343040.1	0.776077	2.501277	3.407078	0.00126	0.016857	-1.26159	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0528340.1	-0.97974	3.051746	-3.29437	0.001762	0.020637	-1.26216	F-box family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0616680.1	-1.34067	0.45557	-3.39527	0.001306	0.017152	-1.26378	F-box family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0284760.1	0.568664	6.914607	3.511768	0.000918	0.014073	-1.26665	Myosin	elongation zone	12 h
HORVU.MOREX.r3.4HG0358580.1	-1.04932	3.228773	-3.29395	0.001764	0.020639	-1.26725	Harbinger transposase-derived nuclease	elongation zone	12 h
HORVU.MOREX.r3.3HG0315000.1	-0.47241	3.461758	-3.31846	0.001641	0.019852	-1.26766	F-box protein, putative (DUF295)	elongation zone	12 h
HORVU.MOREX.r3.7HG0674320.1	-0.37467	4.709886	-3.39807	0.001295	0.017096	-1.26778	Vesicle transport protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0015750.1	1.657205	-2.91215	3.329527	0.001588	0.019467	-1.26831	transcription factor, putative (Protein of unknown function, DUF547)	elongation zone	12 h
HORVU.MOREX.r3.7HG0682120.1	-0.38256	4.669456	-3.37961	0.001368	0.01763	-1.26842	Methyltransferase-like protein 13	elongation zone	12 h
HORVU.MOREX.r3.2HG0104510.1	-0.35808	7.315942	-3.43316	0.001165	0.016068	-1.26856	FACT complex subunit SPT16	elongation zone	12 h
HORVU.MOREX.r3.5HG0471960.1	-1.20112	3.222285	-3.29323	0.001768	0.020671	-1.26927	Chromosome transmission fidelity protein 8	elongation zone	12 h
HORVU.MOREX.r3.7HG0654580.1	-1.5678	4.602405	-3.29765	0.001745	0.02056	-1.26969	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.2HG0173190.1	-1.43972	7.090069	-3.35186	0.001486	0.018584	-1.27026	ABC transporter ATP-binding protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0622030.1	-0.5847	3.435933	-3.30412	0.001712	0.020365	-1.2734	tRNA pseudouridine synthase	elongation zone	12 h
HORVU.MOREX.r3.4HG0384350.1	0.378712	5.925988	3.445886	0.001121	0.01573	-1.27347	Rab3 GTPase-activating protein catalytic subunit	elongation zone	12 h
HORVU.MOREX.r3.2HG0186980.1	1.099659	1.712815	3.301087	0.001727	0.020487	-1.27423	Vacuolar protein sorting-associated protein 53 A	elongation zone	12 h
HORVU.MOREX.r3.5HG0466890.1	-0.57769	3.242376	-3.30024	0.001732	0.020487	-1.27596	Alcohol dehydrogenase 2	elongation zone	12 h
HORVU.MOREX.r3.2HG0105680.3	-1.02681	4.721415	-3.31054	0.00168	0.020135	-1.27611	Translation initiation factor IF-2	elongation zone	12 h
HORVU.MOREX.r3.2HG0205990.1	1.897341	-2.55766	3.362788	0.001439	0.018178	-1.27657	Glutaredoxin family protein, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0654120.1	-1.19858	1.753011	-3.28907	0.00179	0.020878	-1.27662	Basic helix-loop-helix transcription factor	elongation zone	12 h
HORVU.MOREX.r3.4HG0376950.1	-2.2875	-0.73491	-3.6447	0.00061	0.011213	-1.27762	Transposon protein, putative, CACTA, En/Spm sub-class	elongation zone	12 h
HORVU.MOREX.r3.2HG0097350.1	-2.09498	5.612431	-3.30093	0.001728	0.020487	-1.28079	Agmatine coumaroyltransferase-2	elongation zone	12 h
HORVU.MOREX.r3.3HG0305800.1	0.766478	4.447	3.352212	0.001485	0.018576	-1.28158	Ribonuclease	elongation zone	12 h
HORVU.MOREX.r3.5HG0487910.1	2.001237	-2.5953	3.405349	0.001267	0.016918	-1.28226	Purine permease-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0401130.1	0.362452	6.245539	3.45112	0.001104	0.015598	-1.28242	La-related protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0536900.1	-1.47371	0.743448	-3.41094	0.001246	0.016739	-1.28312	F-box only 46	elongation zone	12 h
HORVU.MOREX.r3.3HG0276120.1	1.77701	-1.33075	3.315923	0.001653	0.019898	-1.28392	Phospholipase A1	elongation zone	12 h
HORVU.MOREX.r3.7HG0636750.1	-0.86208	7.072571	-3.42275	0.001202	0.016359	-1.28546	carbohydrate esterase, putative (DUF303)	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0310210.1	-0.53852	7.031206	-3.42051	0.00121	0.016416	-1.28954	Acyl-[acyl-carrier-protein] desaturase	elongation zone	12 h
HORVU.MOREX.r3.2HG0173680.1	-0.4292	6.209185	-3.39528	0.001306	0.017152	-1.29008	Anthranilate synthase	elongation zone	12 h
HORVU.MOREX.r3.4HG0339180.1	-1.95132	3.295927	-3.31914	0.001638	0.019852	-1.29376	F-box-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0413410.1	-0.96731	7.171548	-3.43074	0.001174	0.016107	-1.29488	Hydroxymethylglutaryl-CoA synthase	elongation zone	12 h
HORVU.MOREX.r3.6HG0557070.1	-0.49462	6.4953	-3.41184	0.001242	0.016705	-1.29519	Activator of heat shock protein ATPase	elongation zone	12 h
HORVU.MOREX.r3.7HG0676890.1	-1.4801	1.263909	-3.31805	0.001643	0.019852	-1.29612	Transmembrane protein, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0383530.3	0.947781	1.457399	3.363326	0.001436	0.018178	-1.2962	Pathogenesis-related protein 1	elongation zone	12 h
HORVU.MOREX.r3.4HG0333130.1	-1.10703	1.113277	-3.33661	0.001555	0.019223	-1.29626	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0632210.1	-0.54573	4.522362	-3.34629	0.001511	0.018826	-1.29675	Electron transfer flavoprotein beta-subunit	elongation zone	12 h
HORVU.MOREX.r3.3HG0322650.1	0.700248	3.559006	3.380429	0.001365	0.017608	-1.29827	NAD kinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0291670.1	1.294579	-0.21921	3.311651	0.001674	0.020092	-1.29841	Transmembrane protein 56	elongation zone	12 h
HORVU.MOREX.r3.7HG0745980.1	-0.40314	3.968558	-3.33287	0.001572	0.019344	-1.29978	Mutator-like transposase	elongation zone	12 h
HORVU.MOREX.r3.6HG0548820.1	-1.23534	0.468673	-3.31637	0.001651	0.019896	-1.30386	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0168790.1	-0.72427	4.208617	-3.31995	0.001634	0.019852	-1.304	Haloacid dehalogenase-like hydrolase family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0313020.1	-0.33221	5.21659	-3.37852	0.001373	0.017671	-1.30965	Alcohol dehydrogenase, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0219290.1	-0.42496	5.927719	-3.45697	0.001084	0.01541	-1.31095	WAT1-related protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0343050.1	0.494764	6.230075	3.434201	0.001162	0.016061	-1.31102	N-acetyl-gamma-glutamyl-phosphate reductase	elongation zone	12 h
HORVU.MOREX.r3.2HG0189530.1	1.269362	0.494093	3.390192	0.001326	0.017304	-1.31323	Expansin protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0629240.1	1.74505	-0.90421	3.276776	0.001856	0.021386	-1.31506	O-methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0130770.1	-0.5732	3.563473	-3.30888	0.001688	0.020145	-1.31578	maternal effect embryo arrest 60	elongation zone	12 h
HORVU.MOREX.r3.7HG0645480.1	-0.50336	4.421668	-3.32057	0.001631	0.019852	-1.31609	RNA 2'-phosphotransferase	elongation zone	12 h
HORVU.MOREX.r3.1HG0091360.1	-0.47807	6.214277	-3.39527	0.001306	0.017152	-1.31911	Delta(14)-sterol reductase	elongation zone	12 h
HORVU.MOREX.r3.1HG0094940.1	-0.42519	7.388621	-3.43129	0.001172	0.016094	-1.32142	ATP-dependent zinc metalloprotease FTSH protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0527890.1	0.319499	6.194702	3.42097	0.001209	0.016416	-1.32368	Anthranilate synthase	elongation zone	12 h
HORVU.MOREX.r3.4HG0393710.1	1.001294	2.016364	3.309986	0.001683	0.020137	-1.32778	Peptide transporter	elongation zone	12 h
HORVU.MOREX.r3.7HG0716320.1	0.530567	4.550005	3.362842	0.001438	0.018178	-1.32954	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0106430.1	-0.4843	5.367597	-3.39325	0.001313	0.017213	-1.33114	Sulfotransferase	elongation zone	12 h
HORVU.MOREX.r3.4HG0383280.1	0.706146	6.188142	3.471119	0.001039	0.015035	-1.33118	Kinesin-related protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0414200.1	-0.49057	3.59178	-3.28571	0.001807	0.021026	-1.33203	Pyridoxine/pyridoxamine 5'-phosphate oxidase	elongation zone	12 h
HORVU.MOREX.r3.3HG0231630.1	-1.46627	3.593295	-3.27945	0.001841	0.02129	-1.33246	Zinc-finger domain of monoamine-oxidase A repressor R1 protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0355390.1	-0.72352	1.970371	-3.26734	0.001908	0.021791	-1.33314	RING/U-box superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0749940.3	-0.71176	5.387912	-3.40311	0.001275	0.016993	-1.3344	Delta(24)-sterol reductase	elongation zone	12 h
HORVU.MOREX.r3.1HG0067630.1	0.396125	5.282271	3.432074	0.001169	0.016079	-1.33548	Serine/threonine-protein kinase	elongation zone	12 h
HORVU.MOREX.r3.2HG0192000.1	0.829105	0.357064	3.367043	0.00142	0.018093	-1.33609	HXXXD-type acyl-transferase family protein, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0611060.1	-0.40704	6.39405	-3.39836	0.001294	0.017092	-1.3366	Cellulose synthase, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0193000.1	-0.68266	5.418419	-3.34393	0.001522	0.018912	-1.3371	HTH-type transcriptional regulator YidZ	elongation zone	12 h
HORVU.MOREX.r3.2HG0170300.1	-0.5693	3.481684	-3.28713	0.0018	0.020962	-1.33963	Protein FAR1-RELATED SEQUENCE 11	elongation zone	12 h
HORVU.MOREX.r3.1HG0067550.1	-0.72865	6.102888	-3.37043	0.001406	0.01799	-1.34022	Adenine nucleotide alpha hydrolases-like superfamily protein, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0107450.1	-0.92971	3.576515	-3.26816	0.001903	0.021791	-1.34075	methyl-coenzyme M reductase II subunit gamma, putative (DUF3741)	elongation zone	12 h
HORVU.MOREX.r3.3HG0240670.1	-1.16159	5.35839	-3.32539	0.001608	0.019683	-1.34103	#N/A	elongation zone	12 h
HORVU.MOREX.r3.4HG0388470.1	-2.27351	0.659213	-3.57332	0.000761	0.012762	-1.34267	Rotundifolia-like protein	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.6HG0605150.1	0.904917	3.747441	3.324754	0.001611	0.019705	-1.34316	Purine permease family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0165180.1	0.488914	4.87636	3.389211	0.001329	0.017343	-1.34437	ATP-dependent Clp protease ATP-binding subunit	elongation zone	12 h
HORVU.MOREX.r3.1HG0080780.1	-0.99698	6.438004	-3.35361	0.001478	0.01853	-1.34512	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.2HG0095710.1	-0.89614	-0.29298	-3.26164	0.00194	0.022073	-1.34533	#N/A	elongation zone	12 h
HORVU.MOREX.r3.1HG0064320.1	-0.55232	6.073378	-3.37113	0.001403	0.017964	-1.34625	Argininosuccinate synthase	elongation zone	12 h
HORVU.MOREX.r3.5HG0442250.1	0.92212	3.294825	3.279356	0.001842	0.02129	-1.34701	Receptor-like protein kinase	elongation zone	12 h
HORVU.MOREX.r3.4HG0418690.1	-1.18844	0.241039	-3.30192	0.001723	0.020463	-1.34747	Invertase inhibitor	elongation zone	12 h
HORVU.MOREX.r3.5HG0502750.1	-0.90944	6.985367	-3.38583	0.001343	0.017454	-1.35277	#N/A	elongation zone	12 h
HORVU.MOREX.r3.1HG0090100.1	1.319255	1.392953	3.255854	0.001973	0.022307	-1.35728	DUF1645 family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0223980.1	-0.49591	3.988579	-3.29821	0.001742	0.020545	-1.35745	UDP-N-acetylmuramate--L-alanine ligase	elongation zone	12 h
HORVU.MOREX.r3.5HG0501170.1	0.642768	0.879425	3.364262	0.001432	0.018164	-1.35855	Eukaryotic aspartyl protease family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0303330.1	-0.81135	6.555669	-3.3658	0.001426	0.018116	-1.36036	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0500560.2	-1.00447	3.167577	-3.25635	0.00197	0.022287	-1.36147	DUF630 family protein, putative (DUF630 and DUF632)	elongation zone	12 h
HORVU.MOREX.r3.7HG0703580.1	-0.62693	4.485599	-3.31808	0.001643	0.019852	-1.36217	Glyceraldehyde-3-phosphate dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.1HG0058640.1	-1.42593	5.97699	-3.30423	0.001711	0.020365	-1.3635	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.6HG0542320.1	1.212697	2.291237	3.260863	0.001944	0.02208	-1.36527	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0201250.1	-0.56517	6.181228	-3.36851	0.001414	0.018048	-1.36673	GTP cyclohydrolase 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0137670.1	-1.08072	0.728871	-3.26402	0.001926	0.021937	-1.36828	Eukaryotic translation initiation factor-related family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0540280.1	-0.83258	5.482685	-3.29472	0.00176	0.020627	-1.3696	F-box family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0208520.1	1.906727	-2.76284	3.383407	0.001353	0.017536	-1.37136	Heavy metal transport/detoxification superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0718930.2	1.41421	-0.79034	3.330855	0.001582	0.019414	-1.37154	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.6HG0542640.1	1.180014	2.086759	3.303612	0.001715	0.020382	-1.37541	Plant/F1M20-13 protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0307400.1	1.281587	1.770343	3.25311	0.001989	0.022401	-1.37576	GRAS family transcription factor	elongation zone	12 h
HORVU.MOREX.r3.2HG0170880.1	-1.30178	3.770157	-3.24796	0.002019	0.022545	-1.37674	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.3HG0256620.1	-1.02546	6.771761	-3.33396	0.001567	0.019305	-1.37962	Expansin	elongation zone	12 h
HORVU.MOREX.r3.2HG0124550.1	1.293051	2.362034	3.248702	0.002015	0.022519	-1.3799	Protein WEAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0728060.1	0.48326	5.512337	3.360778	0.001447	0.018262	-1.3802	Aminodeoxychorismate synthase	elongation zone	12 h
HORVU.MOREX.r3.6HG0565950.1	1.393586	-1.88296	3.248825	0.002014	0.022519	-1.38387	ROP interacting CRIB motif protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0043640.1	0.423387	5.423575	3.406197	0.001264	0.016891	-1.38422	Pleckstrin-like (PH) and lipid-binding START domain protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0657400.1	-0.67192	5.076089	-3.29559	0.001756	0.020598	-1.38424	Cystathionine beta-lyase, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0597360.1	-0.5114	5.075212	-3.30686	0.001698	0.020239	-1.38437	SET domain-containing protein 9	elongation zone	12 h
HORVU.MOREX.r3.6HG0632320.1	-0.38804	5.523777	-3.35747	0.001462	0.018377	-1.3853	Leucine-rich repeat protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0472880.1	-0.50889	4.879838	-3.30997	0.001683	0.020137	-1.38766	GDP-mannose transporter, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0710180.1	-1.38509	1.647984	-3.32045	0.001631	0.019852	-1.39136	related to KPC1	elongation zone	12 h
HORVU.MOREX.r3.6HG0547030.1	1.114231	-2.48918	3.247287	0.002023	0.022545	-1.393	Harbinger transposase-derived nuclease	elongation zone	12 h
HORVU.MOREX.r3.2HG0177830.1	0.620315	4.208721	3.301504	0.001725	0.020476	-1.39498	Transporter	elongation zone	12 h
HORVU.MOREX.r3.5HG0472810.1	0.853867	2.371978	3.4104	0.001248	0.016756	-1.3967	Aquaporin	elongation zone	12 h
HORVU.MOREX.r3.5HG0495640.1	1.909416	-2.03513	3.298976	0.001738	0.020523	-1.39993	Solute carrier family 35 protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0601690.1	-0.47857	4.701066	-3.29938	0.001736	0.02051	-1.40005	YbaK/aminoacyl-tRNA synthetase-associated domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0280960.1	0.686407	1.805356	3.297401	0.001746	0.02056	-1.40291	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.1HG0051960.1	-1.17548	1.903866	-3.30921	0.001686	0.020145	-1.40514	DNA topoisomerase 2	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.4HG0353450.1	-2.11518	2.283433	-3.35811	0.001459	0.018354	-1.40716	Cell division control protein 45-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0403370.1	-0.38828	4.841977	-3.31791	0.001644	0.019852	-1.41314	O-fucosyltransferase family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0632780.1	-0.65717	1.908878	-3.23862	0.002075	0.022947	-1.41402	E3 ubiquitin-protein ligase	elongation zone	12 h
HORVU.MOREX.r3.6HG0602210.1	0.842927	4.713608	3.364083	0.001433	0.018164	-1.41481	Aquaporin	elongation zone	12 h
HORVU.MOREX.r3.2HG0105830.1	0.685766	4.383346	3.282626	0.001824	0.021158	-1.42003	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0306440.1	-1.16629	-0.68673	-3.23502	0.002097	0.023123	-1.42029	Serine/threonine-protein kinase	elongation zone	12 h
HORVU.MOREX.r3.2HG0214130.1	1.256699	3.799443	3.324615	0.001611	0.019705	-1.42096	CoA ligase	elongation zone	12 h
HORVU.MOREX.r3.7HG0742450.1	-0.64112	3.881739	-3.24892	0.002014	0.022519	-1.42205	HVA22-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0554520.1	-0.98749	5.131199	-3.25077	0.002003	0.022493	-1.42477	BRCT domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0230640.1	1.844244	-1.25694	3.234378	0.002101	0.023141	-1.42797	Thioesterase family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0631580.1	-0.57234	4.298528	-3.2714	0.001885	0.021637	-1.4283	Protein SMG8	elongation zone	12 h
HORVU.MOREX.r3.7HG0681050.1	0.429679	4.075358	3.346504	0.00151	0.018825	-1.42944	Chitinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0236500.1	0.670059	5.370928	3.331683	0.001578	0.019378	-1.42948	Pollen-specific protein SF21	elongation zone	12 h
HORVU.MOREX.r3.7HG0658270.1	-0.56183	2.885178	-3.26844	0.001902	0.021787	-1.42994	Hyp O-arabinosyltransferase-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0485410.1	2.429921	-0.44467	3.762735	0.000422	0.009111	-1.43019	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0215220.1	-0.74946	4.050855	-3.2523	0.001994	0.022429	-1.43219	Tubby-like F-box protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0543790.1	-1.06692	7.131519	-3.34657	0.00151	0.018825	-1.43324	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.3HG0219380.1	0.946576	4.367645	3.400258	0.001286	0.01705	-1.43376	Glutamate receptor ionotropic, NMDA 3A	elongation zone	12 h
HORVU.MOREX.r3.1HG0020270.1	-0.37399	5.457119	-3.31822	0.001642	0.019852	-1.43695	SAD1/UNC-84 domain protein, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0270070.1	-0.87242	2.011026	-3.22561	0.002155	0.023536	-1.43849	Polyadenylation and cleavage factor homolog 1	elongation zone	12 h
HORVU.MOREX.r3.6HG0626650.1	-0.25016	8.259289	-3.43821	0.001148	0.015954	-1.43866	26S protease regulatory subunit-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0078910.1	0.523941	4.676362	3.358439	0.001457	0.018347	-1.43946	p-loop containing nucleoside triphosphate hydrolases superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0634660.1	-0.57651	4.623502	-3.2961	0.001753	0.020579	-1.44227	Disease resistance protein (NBS-LRR class) family	elongation zone	12 h
HORVU.MOREX.r3.3HG0254850.1	-0.33702	4.808159	-3.29628	0.001752	0.020579	-1.4429	sucrose synthase 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0134220.1	-0.33399	5.083549	-3.3319	0.001577	0.019378	-1.44293	Exostosin family protein-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0573290.1	0.319681	6.719302	3.392113	0.001318	0.017237	-1.44383	Zinc finger A20 and AN1 domain stress-associated protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0141490.1	-0.66815	3.164747	-3.23447	0.0021	0.023141	-1.4443	ATP synthase gamma chain	elongation zone	12 h
HORVU.MOREX.r3.2HG0113700.1	-1.12158	4.9871	-3.29193	0.001775	0.020739	-1.4457	Rubber elongation factor family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0516490.2	-0.5225	3.181218	-3.24298	0.002049	0.022752	-1.44606	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0698910.1	-0.39278	6.327155	-3.35316	0.00148	0.018535	-1.44844	DnaJ homolog subfamily C member 2	elongation zone	12 h
HORVU.MOREX.r3.5HG0529120.1	-0.71326	7.801287	-3.36603	0.001425	0.018114	-1.45139	Elongation factor	elongation zone	12 h
HORVU.MOREX.r3.7HG0723240.1	3.038616	-0.72296	3.443958	0.001128	0.015774	-1.45358	TMV response-related protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0131280.1	0.892256	2.514635	3.241325	0.002059	0.022811	-1.4554	Homeobox-leucine zipper family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0209680.1	1.308685	0.534924	3.232343	0.002113	0.023229	-1.45773	Isopropylmalate dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.2HG0121530.1	-1.05297	2.335771	-3.22485	0.00216	0.023553	-1.45824	B3 domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0525560.1	-0.50842	4.392032	-3.2489	0.002014	0.022519	-1.46037	PHD finger alfin-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0164020.1	0.756723	1.589544	3.221437	0.002182	0.0237	-1.46098	E3 ubiquitin protein ligase drip2	elongation zone	12 h
HORVU.MOREX.r3.7HG0671470.1	-0.47825	4.81657	-3.3407	0.001536	0.019048	-1.46526	Protein trichome birefringence	elongation zone	12 h
HORVU.MOREX.r3.7HG0742470.1	-0.87696	2.928405	-3.21224	0.002241	0.024012	-1.46625	Zinc finger protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0417670.1	1.192284	0.032065	3.313765	0.001664	0.019979	-1.46809	Lipid transfer protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0364520.1	-0.38018	4.639723	-3.29997	0.001733	0.020487	-1.46935	Nuclear factor Y subunit C	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0016560.1	-1.42562	0.290348	-3.38162	0.00136	0.017585	-1.46951	Beta-carotene isomerase d27, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.2HG0208170.1	1.562628	-2.43737	3.219017	0.002197	0.023779	-1.46999	Non-specific serine/threonine protein kinase	elongation zone	12 h
HORVU.MOREX.r3.7HG0638370.1	0.729296	4.319061	3.300274	0.001732	0.020487	-1.47071	Membrane protein of ER body-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0446330.1	-0.71471	1.961051	-3.20836	0.002266	0.02416	-1.47322	SAGA-associated factor 11	elongation zone	12 h
HORVU.MOREX.r3.6HG0597790.1	0.738277	2.912708	3.254169	0.001983	0.022356	-1.47396	GRAM domain-containing protein / ABA-responsive	elongation zone	12 h
HORVU.MOREX.r3.5HG0537000.1	1.008214	-2.10915	3.213349	0.002234	0.023973	-1.47412	Oxidoreductase/transition metal ion-binding protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0267000.1	0.819897	3.929222	3.40524	0.001267	0.016918	-1.47419	Regulator of chromosome condensation (RCC1) family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0167500.2	-1.67188	4.031522	-3.20935	0.00226	0.02416	-1.47501	Repetitive proline-rich cell wall protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0383780.1	1.804277	-0.06269	3.236303	0.002089	0.023073	-1.47646	Laccase	elongation zone	12 h
HORVU.MOREX.r3.2HG0193170.1	4.478357	-0.2671	3.556571	0.000801	0.013114	-1.47762	Pollen Ole e 1 allergen/extensin	elongation zone	12 h
HORVU.MOREX.r3.7HG0727980.1	0.597201	1.541509	3.338026	0.001549	0.019165	-1.47868	ENTH/ANTH/VHS superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0702190.1	-1.63898	3.843343	-3.24151	0.002058	0.022811	-1.47899	Fertilization independent endosperm 1 protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0668850.1	-0.61305	6.214378	-3.34168	0.001532	0.019016	-1.4793	UDP-glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.4HG0333540.1	0.94212	3.467572	3.23987	0.002068	0.022883	-1.48121	Acetyltransferase, GNAT family protein, expressed	elongation zone	12 h
HORVU.MOREX.r3.6HG0615130.1	0.689772	3.141376	3.334292	0.001566	0.019305	-1.48251	TCP transcription factor	elongation zone	12 h
HORVU.MOREX.r3.3HG0316000.1	-0.73856	6.548487	-3.31122	0.001677	0.020106	-1.48394	Salicylate O-methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.1HG0072840.1	-0.36914	5.890668	-3.33543	0.001561	0.019256	-1.48413	Ectonucleoside triphosphate diphosphohydrolase 1	elongation zone	12 h
HORVU.MOREX.r3.6HG0634260.1	-0.75186	4.589475	-3.22628	0.002151	0.023517	-1.48635	TSA: Wollemia nobilis Ref_Wollemi_Transcript_29242_1275 transcribed RNA sequ	elongation zone	12 h
HORVU.MOREX.r3.5HG0509460.1	-0.94485	2.420051	-3.21613	0.002216	0.023861	-1.48646	WRKY transcription factor	elongation zone	12 h
HORVU.MOREX.r3.6HG0617860.1	-0.29822	5.538253	-3.33004	0.001586	0.019449	-1.48693	Peptidyl-prolyl cis-trans isomerase	elongation zone	12 h
HORVU.MOREX.r3.7HG0634520.1	1.163989	-2.23987	3.205429	0.002286	0.0242	-1.48743	NBS-LRR-like resistance protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0410720.1	-0.86024	2.267394	-3.20987	0.002256	0.024141	-1.48962	Alpha-2C adrenergic receptor	elongation zone	12 h
HORVU.MOREX.r3.7HG0719070.1	-0.68554	5.233224	-3.24143	0.002058	0.022811	-1.49118	SUMO-activating enzyme subunit 1A	elongation zone	12 h
HORVU.MOREX.r3.5HG0492650.1	-1.03647	7.121607	-3.31462	0.00166	0.01994	-1.49128	O-fucosyltransferase family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0721930.1	-0.55565	4.955958	-3.26019	0.001948	0.022103	-1.49469	B-cell receptor-associated protein 31-like containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0191510.1	0.841887	-0.88853	3.250404	0.002005	0.022505	-1.49482	transmembrane protein, putative (DUF247)	elongation zone	12 h
HORVU.MOREX.r3.7HG0719830.1	-1.48299	0.487996	-3.22444	0.002163	0.023553	-1.49496	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0716170.1	-1.01362	2.519767	-3.21671	0.002212	0.023852	-1.49544	F-box family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0096800.1	0.690551	4.6918	3.296775	0.00175	0.020579	-1.49861	Flavin-containing monooxygenase	elongation zone	12 h
HORVU.MOREX.r3.5HG0503200.1	-0.60979	3.671203	-3.22349	0.002169	0.023571	-1.50176	Bromodomain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0564690.1	0.41004	5.759195	3.373257	0.001394	0.017883	-1.50581	Regulator of Vps4 activity in the MVB pathway protein, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0080230.1	-1.09595	6.650954	-3.29995	0.001733	0.020487	-1.50605	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0459680.1	-0.38438	3.895086	-3.24766	0.002021	0.022545	-1.50658	RING/U-box superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0007370.1	-0.48707	3.297626	-3.21996	0.002191	0.023739	-1.50865	B3 domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0285270.1	-2.00538	0.025552	-3.33896	0.001544	0.019135	-1.51033	Guanine nucleotide exchange family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0111130.1	-0.77583	3.835075	-3.19939	0.002326	0.024453	-1.51168	Short chain dehydrogenase/reductase	elongation zone	12 h
HORVU.MOREX.r3.5HG0526200.1	-0.26585	5.485729	-3.3059	0.001703	0.020282	-1.51257	Sec14 cytosolic factor	elongation zone	12 h
HORVU.MOREX.r3.3HG0302860.1	-1.95639	4.061598	-3.19826	0.002334	0.024484	-1.51326	Pathogenesis-related thaumatin-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0734380.1	-0.47567	4.659788	-3.26683	0.001911	0.021793	-1.51346	Mechanosensitive ion channel-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0465270.1	0.741706	4.111151	3.414849	0.001231	0.01661	-1.5135	Laccase	elongation zone	12 h
HORVU.MOREX.r3.4HG0389410.1	0.751985	2.32327	3.194799	0.002357	0.024642	-1.5145	SH3 domain-containing protein 1	elongation zone	12 h

Table Sн Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.4HG0393520.1	0.74874	3.79819	3.244959	0.002037	0.022668	-1.51461	Microtubule associated protein family protein, putative, expressed	elongation zone	12 h
HORVU.MOREX.r3.6HG0539410.1	-1.74118	1.804569	-3.27822	0.001848	0.021343	-1.51748	LOW protein: UPF0503-like protein, putative (DUF740)	elongation zone	12 h
HORVU.MOREX.r3.7HG0667150.1	0.91636	-0.51034	3.230115	0.002127	0.023343	-1.51771	Rac-like GTP-binding protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0623140.1	1.922545	-2.34532	3.319168	0.001638	0.019852	-1.51824	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0660660.1	-0.48051	4.772651	-3.25383	0.001985	0.022366	-1.51857	26S protease regulatory subunit	elongation zone	12 h
HORVU.MOREX.r3.6HG0617080.1	0.507097	4.45228	3.323498	0.001617	0.019747	-1.51956	Lipid transfer protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0239940.1	-0.60537	3.204602	-3.21826	0.002202	0.023794	-1.52002	Transmembrane protein 19	elongation zone	12 h
HORVU.MOREX.r3.1HG0056570.1	0.515125	7.070581	3.48484	0.000997	0.014726	-1.52096	Expansin protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0749640.1	0.613005	4.119977	3.275536	0.001862	0.021446	-1.521	Transmembrane protein 53	elongation zone	12 h
HORVU.MOREX.r3.7HG0749080.1	1.128564	-1.66836	3.199606	0.002325	0.02445	-1.52236	G-protein coupled receptor 98	elongation zone	12 h
HORVU.MOREX.r3.4HG0354540.1	-2.4083	4.811312	-3.1987	0.002331	0.024477	-1.52409	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.6HG0614350.1	-0.52437	8.627624	-3.44254	0.001133	0.015779	-1.52455	Lipoxygenase domain-containing 1	elongation zone	12 h
HORVU.MOREX.r3.3HG0230500.1	1.226877	1.089665	3.206526	0.002278	0.024194	-1.52468	NBS-LRR disease resistance protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0355460.1	-0.39537	4.5138	-3.29611	0.001753	0.020579	-1.52575	myosin-4 protein (DUF641)	elongation zone	12 h
HORVU.MOREX.r3.7HG0641160.1	-0.37998	5.342895	-3.28213	0.001827	0.021176	-1.52711	Guanine nucleotide-binding protein subunit alpha-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0668440.1	0.581003	5.028289	3.30683	0.001698	0.020239	-1.52749	#N/A	elongation zone	12 h
HORVU.MOREX.r3.1HG0060240.1	-0.83038	2.446107	-3.18627	0.002416	0.025092	-1.53188	Thiamin pyrophosphokinase 1	elongation zone	12 h
HORVU.MOREX.r3.1HG0082750.1	-1.89983	0.305019	-3.3858	0.001343	0.017454	-1.53298	Ring finger protein, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0461400.1	-1.30105	2.587492	-3.20813	0.002268	0.02416	-1.53541	UDP-glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0644240.1	1.20748	-0.03364	3.198881	0.00233	0.024477	-1.53555	F-box protein PP2	elongation zone	12 h
HORVU.MOREX.r3.2HG0210500.1	1.219187	3.185342	3.41642	0.001225	0.016542	-1.53686	Endoglucanase	elongation zone	12 h
HORVU.MOREX.r3.7HG0747690.1	3.568482	0.558808	3.612775	0.000674	0.011946	-1.53734	Hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyltransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0647550.1	-0.50875	4.057694	-3.22015	0.00219	0.023739	-1.5409	bZIP transcription factor, putative (DUF630 and DUF632)	elongation zone	12 h
HORVU.MOREX.r3.2HG0154760.1	-0.91302	1.184214	-3.18221	0.002445	0.025246	-1.54153	cysteine-rich RLK (RECEPTOR-like protein kinase) 11	elongation zone	12 h
HORVU.MOREX.r3.4HG0379260.1	0.636392	6.080607	3.369825	0.001409	0.018011	-1.54182	Calcium binding protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0069870.1	0.680526	2.552246	3.260128	0.001949	0.022103	-1.54227	#N/A	elongation zone	12 h
HORVU.MOREX.r3.4HG0402650.1	0.825072	1.552903	3.242955	0.002049	0.022752	-1.54237	Annexin	elongation zone	12 h
HORVU.MOREX.r3.6HG0558810.1	-0.96612	5.76557	-3.2678	0.001905	0.021791	-1.54244	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.3HG0244000.1	1.683681	-2.4581	3.326078	0.001604	0.019655	-1.54308	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0450470.1	-0.55904	3.631343	-3.19713	0.002341	0.024507	-1.54499	Basic-leucine zipper (bZIP) transcription factor family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0095170.1	1.57227	5.086192	3.255443	0.001975	0.022314	-1.54503	UDP-glucose-4-epimerase	elongation zone	12 h
HORVU.MOREX.r3.4HG0386490.1	1.786727	-0.76068	3.257435	0.001964	0.022241	-1.54751	Receptor-like kinase, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0547020.1	1.15425	-2.68848	3.201668	0.002311	0.024379	-1.54896	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0195690.1	1.074979	-2.81043	3.233481	0.002106	0.023189	-1.54944	filamentous hemagglutinin transporter	elongation zone	12 h
HORVU.MOREX.r3.3HG0294840.1	-0.52459	3.760264	-3.21369	0.002231	0.023972	-1.54961	Haloacid dehalogenase (HAD) superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0525850.1	0.685206	2.978562	3.247369	0.002023	0.022545	-1.55241	Phosphatidylinositol N-acetyglucosaminlytransferase subunit P-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0628790.1	0.728557	2.686977	3.191279	0.002381	0.024831	-1.55682	Myb-like transcription factor family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0385300.1	-0.49922	9.307024	-3.40323	0.001275	0.016993	-1.55972	Elongation factor 1-alpha	elongation zone	12 h
HORVU.MOREX.r3.2HG0190710.1	-0.34368	4.642345	-3.2487	0.002015	0.022519	-1.55988	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0295640.1	1.213561	-1.27257	3.201458	0.002312	0.024382	-1.56006	Protein MIZU-KUSSEI 1	elongation zone	12 h
HORVU.MOREX.r3.3HG0303660.1	0.54769	6.126297	3.365016	0.001429	0.018147	-1.56071	Carboxypeptidase	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0003090.4	-1.69798	2.96451	-3.19774	0.002337	0.024495	-1.56196	Thionin-2.2	elongation zone	12 h
HORVU.MOREX.r3.2HG0214070.1	1.618596	-2.62397	3.231547	0.002118	0.023258	-1.56367	AT hook motif DNA-binding family protein, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0219810.1	-0.91791	3.950558	-3.17152	0.002522	0.025832	-1.564	Agenet domain containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0520260.1	-2.4668	1.284182	-3.48643	0.000992	0.014705	-1.56461	GTPase obg	elongation zone	12 h
HORVU.MOREX.r3.5HG0491380.1	-0.53889	8.151632	-3.39243	0.001317	0.017232	-1.56462	Proton pump-interactor 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0705500.1	1.096897	0.351075	3.182922	0.00244	0.025209	-1.56826	Non-lysosomal glucosylceramidase	elongation zone	12 h
HORVU.MOREX.r3.5HG0472870.1	0.639122	3.59022	3.266934	0.00191	0.021793	-1.56906	Disease resistance protein (NBS-LRR class) family	elongation zone	12 h
HORVU.MOREX.r3.2HG0199590.1	-1.26472	-1.68344	-3.20345	0.002299	0.024291	-1.56997	Organic cation transporter protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0676880.1	-0.38292	5.477475	-3.27137	0.001885	0.021637	-1.57119	BolA-like	elongation zone	12 h
HORVU.MOREX.r3.7HG0654810.1	-2.40425	-1.68567	-3.73461	0.000461	0.009584	-1.57122	actin cross-linking protein (DUF569)	elongation zone	12 h
HORVU.MOREX.r3.4HG0407470.1	0.893497	2.42529	3.315449	0.001656	0.019915	-1.57625	Serpin	elongation zone	12 h
HORVU.MOREX.r3.5HG0483880.1	-1.60123	-0.16233	-3.37584	0.001384	0.017779	-1.57664	RING/U-box superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0063020.1	1.295173	0.508236	3.276675	0.001856	0.021386	-1.5777	Resistance to phytophthora 1 protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0655100.1	0.526096	3.752132	3.277469	0.001852	0.02136	-1.57794	Peroxyureidoacrylate/ureidoacrylate amidohydrolase RutB	elongation zone	12 h
HORVU.MOREX.r3.2HG0200980.1	-0.40613	5.67298	-3.29513	0.001758	0.020614	-1.57928	Peptidyl-prolyl cis-trans isomerase	elongation zone	12 h
HORVU.MOREX.r3.3HG0304420.1	-1.07403	5.851635	-3.23855	0.002076	0.022947	-1.58016	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0616960.1	-0.61419	4.492257	-3.20033	0.00232	0.024424	-1.58047	Polyadenylate-binding protein family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0325670.1	-0.62984	3.462193	-3.17531	0.002494	0.025643	-1.58151	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0468460.1	-0.60009	6.084231	-3.27813	0.001848	0.021343	-1.5842	FCA protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0111620.1	0.757251	2.992838	3.414201	0.001234	0.016631	-1.58494	Heavy metal transport/detoxification superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0070850.1	0.89347	0.443712	3.225875	0.002154	0.023533	-1.5857	Extra-large G-like protein, putative (DUF3133)	elongation zone	12 h
HORVU.MOREX.r3.2HG0177440.1	-0.84542	5.076842	-3.23326	0.002108	0.023192	-1.58661	Ankyrin repeat	elongation zone	12 h
HORVU.MOREX.r3.6HG0633650.1	-1.17675	0.935723	-3.21759	0.002206	0.023823	-1.58701	#N/A	elongation zone	12 h
HORVU.MOREX.r3.1HG0079760.1	0.796728	0.18048	3.228958	0.002134	0.023397	-1.58789	MYB transcription factor	elongation zone	12 h
HORVU.MOREX.r3.6HG0557340.1	-0.47246	7.977821	-3.36917	0.001411	0.018035	-1.58879	Terpene cyclase/mutase family member	elongation zone	12 h
HORVU.MOREX.r3.5HG0446350.1	-0.36156	5.803999	-3.27372	0.001872	0.021548	-1.59024	RNA polymerase-associated protein RTF1-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0119800.1	1.533778	-1.32815	3.185614	0.002421	0.025127	-1.59056	GDSL esterase/lipase	elongation zone	12 h
HORVU.MOREX.r3.5HG0486330.1	-0.3159	5.745088	-3.27303	0.001876	0.021568	-1.59104	UPF0396 protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0208960.1	-0.88158	2.446722	-3.15948	0.002611	0.026441	-1.59113	Exocyst complex component EXO70B1	elongation zone	12 h
HORVU.MOREX.r3.3HG0305520.1	0.695335	1.413662	3.164047	0.002577	0.026239	-1.59254	DUF1685 family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0018730.1	-0.32082	6.708783	-3.30901	0.001687	0.020145	-1.59419	RNA-binding family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0040930.1	1.803732	-2.88506	3.317077	0.001648	0.019877	-1.59493	F-box family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0200630.1	-0.77758	9.635165	-3.39279	0.001315	0.017224	-1.59608	Adenosylhomocysteinase	elongation zone	12 h
HORVU.MOREX.r3.7HG0680960.1	1.615506	0.611498	3.158215	0.00262	0.026447	-1.59625	electron transporter, putative (Protein of unknown function, DUF547)	elongation zone	12 h
HORVU.MOREX.r3.1HG0087190.1	-0.56194	4.047935	-3.18442	0.002429	0.025148	-1.59666	Structural constituent of cell wall	elongation zone	12 h
HORVU.MOREX.r3.6HG0620240.1	-0.50722	3.057466	-3.18977	0.002392	0.024902	-1.59698	FRIGIDA interacting protein 1	elongation zone	12 h
HORVU.MOREX.r3.5HG0435800.1	-2.09664	0.267696	-3.40101	0.001283	0.01705	-1.60142	Leucine-rich repeat protein kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0437110.1	0.508929	5.656876	3.340786	0.001536	0.019048	-1.60484	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0550690.1	-1.02142	4.80697	-3.20765	0.002271	0.02416	-1.60535	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0619260.1	-0.4589	6.188825	-3.28023	0.001837	0.021272	-1.60898	Transmembrane emp24 domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0543320.1	-0.68552	3.154801	-3.16011	0.002606	0.026433	-1.60921	Mitochondrial transcription termination factor-like	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.5HG0495860.1	0.76335	4.058331	3.267239	0.001908	0.021791	-1.61031	glycosyltransferase family exostosin protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0723420.1	-0.37736	6.130958	-3.28395	0.001817	0.0211	-1.61057	Eukaryotic aspartyl protease family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0082530.1	0.468307	7.395893	3.393551	0.001312	0.017213	-1.61063	Respiratory burst oxidase	elongation zone	12 h
HORVU.MOREX.r3.4HG0358890.1	-0.57961	6.54155	-3.26739	0.001907	0.021791	-1.61183	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0285010.1	-2.01788	1.558759	-3.28799	0.001795	0.020933	-1.61464	indeterminate(ID)-domain 4	elongation zone	12 h
HORVU.MOREX.r3.3HG0308840.1	0.62646	2.063856	3.184294	0.00243	0.025148	-1.61732	Aldehyde dehydrogenase, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0593390.1	1.365032	0.157725	3.15156	0.002671	0.026814	-1.61747	Bidirectional sugar transporter SWEET	elongation zone	12 h
HORVU.MOREX.r3.6HG0558880.1	-1.29199	5.027918	-3.17399	0.002504	0.02572	-1.62659	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.7HG0747720.1	0.693604	3.70009	3.18407	0.002432	0.025148	-1.62866	Cytokinin oxidase/dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.2HG0180500.1	0.363372	5.818938	3.300639	0.00173	0.020487	-1.62868	Glutaredoxin	elongation zone	12 h
HORVU.MOREX.r3.4HG0392150.1	-1.50616	3.360314	-3.1432	0.002736	0.027326	-1.62991	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0575410.1	-2.05578	3.790358	-3.15667	0.002632	0.026526	-1.63023	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0223160.1	0.612972	5.278307	3.376808	0.00138	0.017746	-1.63584	aberrant root formation protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0400530.1	1.264247	0.815449	3.15079	0.002677	0.02686	-1.63718	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0508880.1	1.504618	-0.73312	3.141222	0.002752	0.027347	-1.639	Leucine-rich repeat protein kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0208280.1	-0.49204	7.445128	-3.32272	0.00162	0.019769	-1.63922	Sulfotransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0661470.1	0.71511	3.159382	3.171676	0.00252	0.025832	-1.63929	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0722690.1	0.509382	4.955916	3.314643	0.00166	0.01994	-1.63956	Amino acid transporter-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0342480.1	0.89056	4.010766	3.261533	0.001941	0.022073	-1.64133	Subtilisin-like protease	elongation zone	12 h
HORVU.MOREX.r3.4HG0415170.1	1.544236	-2.40064	3.138206	0.002775	0.027553	-1.64375	3'-N-debenzoyl-2'-deoxytaxol N-benzoyltransferase	elongation zone	12 h
HORVU.MOREX.r3.1HG0091820.1	-0.60967	5.321523	-3.21694	0.00221	0.023848	-1.64465	Glutamyl-tRNA (Gln) amidotransferase subunit A	elongation zone	12 h
HORVU.MOREX.r3.4HG0362350.1	-1.21447	2.471284	-3.17966	0.002463	0.025392	-1.64922	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0343260.1	1.417524	-2.7306	3.162116	0.002591	0.026328	-1.65015	NAD(P)H dehydrogenase subunit 48	elongation zone	12 h
HORVU.MOREX.r3.3HG0245320.1	-0.50118	5.238204	-3.21859	0.0022	0.02379	-1.65177	GDSL esterase/lipase	elongation zone	12 h
HORVU.MOREX.r3.1HG0092860.1	1.211127	-1.39568	3.159287	0.002612	0.026441	-1.65479	S-type anion channel	elongation zone	12 h
HORVU.MOREX.r3.4HG0335160.1	0.77858	3.629312	3.188838	0.002398	0.024957	-1.65496	Hedgehog-interacting-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0180880.1	-0.90096	1.957679	-3.13266	0.00282	0.027847	-1.65571	GH3.3	elongation zone	12 h
HORVU.MOREX.r3.6HG0605090.1	-0.3172	5.055557	-3.25154	0.001998	0.022467	-1.65637	Alpha-1,3-glucosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0120490.1	1.171234	1.876399	3.309907	0.001683	0.020137	-1.65717	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.7HG0749870.1	0.545306	4.57	3.298238	0.001742	0.020545	-1.65731	Glucuronoxylan 4-O-methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.6HG0552030.1	-0.73035	3.851578	-3.15622	0.002635	0.026547	-1.65774	Phosphatidate cytidylyltransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0124990.1	-0.63401	6.152886	-3.25819	0.00196	0.022216	-1.66018	3-oxoacyl-[acyl-carrier-protein] synthase	elongation zone	12 h
HORVU.MOREX.r3.5HG0470690.1	1.236516	-2.06961	3.133835	0.00281	0.027806	-1.6604	Heavy metal transport/detoxification protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0619760.1	-0.47856	6.476084	-3.26087	0.001944	0.02208	-1.66262	Serine--tRNA ligase	elongation zone	12 h
HORVU.MOREX.r3.5HG0428270.2	0.690779	2.536061	3.231597	0.002118	0.023258	-1.66496	Bidirectional sugar transporter SWEET	elongation zone	12 h
HORVU.MOREX.r3.2HG0116990.1	0.566387	4.613527	3.25748	0.001964	0.022241	-1.66634	Phosphatidylinositol 4-phosphate 5-kinase 4	elongation zone	12 h
HORVU.MOREX.r3.7HG0710980.1	-1.14958	1.521079	-3.19503	0.002356	0.024638	-1.667	Mitochondrial transcription termination factor-like	elongation zone	12 h
HORVU.MOREX.r3.7HG0675310.1	1.239978	1.411092	3.254688	0.00198	0.022347	-1.66749	N-lysine methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.1HG0083980.1	-0.993	4.411839	-3.13283	0.002819	0.027846	-1.66837	Thymidine kinase	elongation zone	12 h
HORVU.MOREX.r3.2HG0181510.2	0.451529	4.821103	3.272152	0.001881	0.021612	-1.66847	Beta-glucosidase	elongation zone	12 h
HORVU.MOREX.r3.6HG0547010.1	0.880449	-1.51289	3.141499	0.002749	0.027347	-1.66871	NBS-LRR-like resistance protein	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0307280.1	1.134433	-2.743	3.153533	0.002656	0.026714	-1.66925	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0493040.1	0.552633	5.221386	3.31858	0.00164	0.019852	-1.66936	Basic helix-loop-helix transcription factor	elongation zone	12 h
HORVU.MOREX.r3.6HG0621190.1	-0.60189	4.746594	-3.24419	0.002042	0.022694	-1.66938	Chaperone protein dnaJ	elongation zone	12 h
HORVU.MOREX.r3.5HG0502760.1	-0.74648	7.161462	-3.27956	0.001841	0.02129	-1.67331	Histone H4	elongation zone	12 h
HORVU.MOREX.r3.3HG0313090.1	0.737376	2.944421	3.167903	0.002548	0.026026	-1.67422	Thiamin pyrophosphokinase 1	elongation zone	12 h
HORVU.MOREX.r3.1HG0080690.1	-2.17717	4.834533	-3.12402	0.002891	0.028313	-1.67654	Endoglucanase	elongation zone	12 h
HORVU.MOREX.r3.4HG0353200.1	0.524688	2.886286	3.23998	0.002067	0.022883	-1.67738	heat-inducible transcription repressor	elongation zone	12 h
HORVU.MOREX.r3.1HG0004300.1	-1.92616	1.490539	-3.2847	0.001813	0.021077	-1.68169	Disease resistance protein (TIR-NBS-LRR class) family	elongation zone	12 h
HORVU.MOREX.r3.3HG0295440.1	-0.81047	5.026864	-3.18394	0.002433	0.025148	-1.68372	Cytochrome P450 family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0280160.1	0.422379	4.904831	3.270734	0.001889	0.021665	-1.68414	Evolutionarily conserved C-terminal region 2	elongation zone	12 h
HORVU.MOREX.r3.4HG0384780.1	3.253521	-0.01492	3.15882	0.002616	0.026447	-1.68634	Trichome birefringence-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0315410.1	0.359796	5.906295	3.283693	0.001818	0.021103	-1.6889	Vesicle-associated protein 1-2	elongation zone	12 h
HORVU.MOREX.r3.1HG0093050.1	0.81023	4.062497	3.206431	0.002279	0.024194	-1.6902	Indole-3-acetic acid-amido synthetase GH3.3	elongation zone	12 h
HORVU.MOREX.r3.4HG0385080.1	-0.57534	3.22216	-3.1476	0.002701	0.02705	-1.69117	RING/U-box superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0378960.1	-0.99437	5.668628	-3.17066	0.002528	0.025884	-1.69188	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.7HG0728630.1	-1.00506	1.895272	-3.12981	0.002843	0.028035	-1.69421	Receptor-like protein kinase	elongation zone	12 h
HORVU.MOREX.r3.6HG0616890.1	-0.94787	0.931971	-3.15765	0.002624	0.026466	-1.69565	UPF0503 protein, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.2HG0171850.1	-0.48872	5.054708	-3.17955	0.002464	0.025392	-1.69609	mediator of RNA polymerase II transcription subunit-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0655260.1	-0.96356	1.989817	-3.11677	0.002951	0.028675	-1.7011	Cortactin-binding protein 2	elongation zone	12 h
HORVU.MOREX.r3.1HG0003280.1	-2.2261	-1.64899	-3.34482	0.001518	0.018897	-1.7013	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0534420.1	0.841071	1.580423	3.242733	0.00205	0.022754	-1.70159	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0702070.1	1.293035	-1.23872	3.126692	0.002869	0.02816	-1.70193	Blue copper protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0636510.1	-0.54177	3.279937	-3.14678	0.002708	0.027079	-1.70196	PPPDE putative thiol peptidase family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0068890.1	-0.55352	3.912321	-3.13405	0.002809	0.027803	-1.70219	Hydroxyproline-rich glycoprotein family protein, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0663940.1	0.787758	0.764913	3.218496	0.0022	0.02379	-1.70261	Alpha/beta-Hydrolases superfamily protein, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0609750.1	-0.51401	4.811837	-3.21632	0.002214	0.023861	-1.70301	PRELI/MSF1-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0543750.1	-0.80048	7.794738	-3.29396	0.001764	0.020639	-1.70305	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.7HG0650530.2	1.666946	-2.50586	3.123733	0.002893	0.028323	-1.70352	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0079280.1	-0.93957	8.411999	-3.29609	0.001753	0.020579	-1.70461	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.1HG0032910.1	-0.57602	5.350159	-3.20829	0.002267	0.02416	-1.70545	Lysine-specific demethylase	elongation zone	12 h
HORVU.MOREX.r3.7HG0728190.1	-0.42379	4.089813	-3.18467	0.002428	0.025148	-1.70662	Purple acid phosphatase	elongation zone	12 h
HORVU.MOREX.r3.2HG0188200.1	0.783338	0.241735	3.161528	0.002595	0.026351	-1.70919	Calcium-dependent protein kinase	elongation zone	12 h
HORVU.MOREX.r3.2HG0181390.1	-1.49649	5.181001	-3.13312	0.002816	0.027837	-1.70957	Protein BREAST CANCER SUSCEPTIBILITY 1-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0053770.1	-1.30372	0.507378	-3.20531	0.002286	0.0242	-1.71105	Protein kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0007930.1	-0.7667	2.116239	-3.11435	0.002972	0.028819	-1.71223	calpain-type cysteine protease family	elongation zone	12 h
HORVU.MOREX.r3.3HG0237910.1	-0.99223	2.053847	-3.11722	0.002947	0.028675	-1.71339	P53/DNA damage-regulated protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0462200.1	1.559192	-0.85589	3.128152	0.002857	0.028074	-1.71353	Metacaspase	elongation zone	12 h
HORVU.MOREX.r3.7HG0719170.1	0.699368	5.542866	3.303456	0.001715	0.020382	-1.71368	O-fucosyltransferase-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0084850.1	-1.19552	4.250962	-3.11163	0.002995	0.029003	-1.71493	Histone chaperone	elongation zone	12 h
HORVU.MOREX.r3.4HG0385100.1	-0.33817	5.669475	-3.25538	0.001976	0.022314	-1.71626	Protein YIPF	elongation zone	12 h
HORVU.MOREX.r3.7HG0673330.1	1.312537	-2.01567	3.105167	0.003051	0.029335	-1.72069	Embryogenesis transmembrane protein-like	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.4HG0411270.1	-0.78687	6.581905	-3.2251	0.002159	0.023548	-1.72077	N-acetyltransferase	elongation zone	12 h
HORVU.MOREX.r3.4HG0342950.1	-0.95721	6.384536	-3.1878	0.002406	0.025019	-1.72288	50S ribosomal protein L25	elongation zone	12 h
HORVU.MOREX.r3.7HG0725440.1	0.888939	1.519211	3.108432	0.003022	0.029118	-1.7235	Pre-mRNA-splicing factor syf2	elongation zone	12 h
HORVU.MOREX.r3.5HG0472140.1	0.692391	2.018509	3.123358	0.002896	0.028327	-1.72505	Chlororespiratory reduction 3	elongation zone	12 h
HORVU.MOREX.r3.6HG0595810.1	-0.92617	1.111513	-3.1245	0.002887	0.028299	-1.7256	Pre-mRNA-processing protein 40A	elongation zone	12 h
HORVU.MOREX.r3.2HG0185570.1	0.736473	1.316705	3.182074	0.002446	0.025246	-1.72583	transcription repressor	elongation zone	12 h
HORVU.MOREX.r3.6HG0614460.1	-0.71042	3.048312	-3.10254	0.003074	0.029497	-1.72829	DNA-directed RNA polymerase subunit beta	elongation zone	12 h
HORVU.MOREX.r3.4HG0336310.1	-0.67415	6.50287	-3.22411	0.002165	0.023553	-1.72871	Zinc finger family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0033450.1	-1.60612	0.194648	-3.21289	0.002237	0.023992	-1.72938	MBOAT (membrane bound O-acyl transferase) family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0687190.1	-0.51904	3.62232	-3.12658	0.00287	0.02816	-1.73079	Glucosamine-6-phosphate deaminase	elongation zone	12 h
HORVU.MOREX.r3.4HG0387120.1	-1.01903	6.929288	-3.22547	0.002156	0.023536	-1.73232	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.5HG0430050.1	0.55481	4.495639	3.198111	0.002335	0.024484	-1.73295	Stomatal closure-related actin-binding protein 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0635700.1	-0.33382	5.807806	-3.22974	0.00213	0.023356	-1.73458	Transposon protein, putative, CACTA, En/Spm sub-class	elongation zone	12 h
HORVU.MOREX.r3.1HG0079250.1	-0.82686	7.964833	-3.26979	0.001894	0.021713	-1.73567	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.1HG0017310.1	-1.10015	6.737539	-3.18395	0.002433	0.025148	-1.74004	Auxin influx transporter	elongation zone	12 h
HORVU.MOREX.r3.7HG0726350.1	-0.58695	4.52716	-3.16431	0.002575	0.026239	-1.74107	Serine/threonine-protein kinase	elongation zone	12 h
HORVU.MOREX.r3.1HG0049520.1	-0.75271	3.446094	-3.11102	0.003	0.029025	-1.74357	Cytochrome P450 family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0117880.1	2.599524	-0.66123	3.184875	0.002426	0.025148	-1.74359	GDSL esterase/lipase	elongation zone	12 h
HORVU.MOREX.r3.7HG0671880.1	-0.74751	3.670438	-3.10093	0.003088	0.029609	-1.74522	RING/U-box protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0504160.1	-1.07219	6.884631	-3.21748	0.002207	0.023823	-1.74538	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0732330.1	-1.52362	0.94	-3.18991	0.002391	0.024902	-1.74565	Phosphosulfolactate synthase-related protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0663820.1	-0.83397	2.698491	-3.10072	0.00309	0.029613	-1.7468	Protein TIC 22, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.4HG0407980.1	-0.7173	2.024558	-3.09458	0.003144	0.02993	-1.74686	Myc-type, basic helix-loop-helix (BHLH) domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0423820.1	0.878324	2.29448	3.093612	0.003153	0.029967	-1.74717	#N/A	elongation zone	12 h
HORVU.MOREX.r3.4HG0385240.1	0.621024	6.413717	3.30879	0.001689	0.020145	-1.74819	Alpha/beta-Hydrolases superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0706310.1	0.481027	5.228141	3.208683	0.002264	0.02416	-1.74936	Alcohol dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.6HG0546180.1	-0.70925	4.078621	-3.1105	0.003005	0.029025	-1.75013	Remorin family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0181550.1	-1.01065	3.831202	-3.11047	0.003005	0.029025	-1.75035	Imidazole glycerol phosphate synthase subunit HisF	elongation zone	12 h
HORVU.MOREX.r3.3HG0275530.1	-0.75369	3.98589	-3.10973	0.003011	0.02903	-1.75262	Sodium Bile acid symporter family	elongation zone	12 h
HORVU.MOREX.r3.7HG0744790.1	-0.58148	5.538256	-3.16416	0.002576	0.026239	-1.7527	XH/XS domain-containing family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0497990.1	1.11839	3.554356	3.134921	0.002802	0.027765	-1.7527	Heat shock transcription factor	elongation zone	12 h
HORVU.MOREX.r3.6HG0602230.1	-0.50919	5.050411	-3.20099	0.002315	0.02439	-1.7542	Protein kinase	elongation zone	12 h
HORVU.MOREX.r3.5HG0516310.1	-0.97831	5.306262	-3.20802	0.002269	0.02416	-1.75433	Patatin	elongation zone	12 h
HORVU.MOREX.r3.6HG0573340.1	-0.38354	4.889095	-3.19705	0.002342	0.024507	-1.75433	Alpha/beta hydrolase family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0459660.1	-0.78159	3.348001	-3.22388	0.002166	0.023557	-1.75488	Stress responsive A/B barrel domain family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0234240.1	0.97395	0.193181	3.143618	0.002733	0.027313	-1.75535	Alpha/beta-hydrolase superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0603820.1	-0.24723	8.222526	-3.35484	0.001473	0.018499	-1.75757	3,5-epimerase/4-reductase	elongation zone	12 h
HORVU.MOREX.r3.2HG0215310.1	-1.45184	7.0907	-3.19438	0.00236	0.024647	-1.75791	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.6HG0599900.1	0.629818	3.934569	3.207628	0.002271	0.02416	-1.75813	Vesicle-associated protein 1-1	elongation zone	12 h
HORVU.MOREX.r3.5HG0487660.1	-1.05829	6.052415	-3.19225	0.002375	0.024774	-1.7591	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.4HG0378460.1	0.778869	2.042348	3.128521	0.002854	0.028071	-1.75922	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.7HG0727070.1	-0.64752	4.936044	-3.15869	0.002617	0.026447	-1.76161	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.5HG0420630.1	-0.47273	3.720927	-3.16376	0.002579	0.026247	-1.76166	Ankyrin repeat family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0635160.1	-0.39648	6.815127	-3.23568	0.002093	0.023091	-1.76229	Monocopper oxidase-like protein SKU5	elongation zone	12 h
HORVU.MOREX.r3.5HG0480540.1	-0.36845	7.034207	-3.27749	0.001852	0.02136	-1.76235	Transmembrane protein 87A	elongation zone	12 h
HORVU.MOREX.r3.6HG0604310.1	-1.12904	2.696154	-3.13368	0.002812	0.027806	-1.7628	RING finger protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0596770.1	0.737545	4.952847	3.367488	0.001419	0.018081	-1.76339	Aquaporin	elongation zone	12 h
HORVU.MOREX.r3.7HG0656030.1	0.61465	3.605835	3.21505	0.002223	0.023917	-1.7687	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.4HG0393630.1	-0.29714	9.32692	-3.36875	0.001413	0.018046	-1.77077	Transmembrane 9 superfamily member	elongation zone	12 h
HORVU.MOREX.r3.1HG0037020.1	-0.43364	3.762682	-3.12505	0.002882	0.028271	-1.77154	F-box/kelch-repeat protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0077790.1	1.008805	3.495979	3.200036	0.002322	0.024432	-1.77312	Calcium-transporting ATPase	elongation zone	12 h
HORVU.MOREX.r3.5HG0471320.1	-1.73437	0.737353	-3.22015	0.00219	0.023739	-1.77451	Amino acid transporter, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0102600.1	-0.36884	5.97563	-3.22841	0.002138	0.023409	-1.77519	Peptidylprolyl isomerase	elongation zone	12 h
HORVU.MOREX.r3.6HG0613430.1	1.684689	-1.24134	3.086207	0.00322	0.030422	-1.77808	RNA-dependent RNA polymerase	elongation zone	12 h
HORVU.MOREX.r3.5HG0477360.1	-0.68158	2.537497	-3.08278	0.003252	0.030649	-1.77819	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0190290.1	0.626476	5.33841	3.227377	0.002144	0.023455	-1.77826	SHR5-receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.2HG0157340.1	0.496722	7.39472	3.400577	0.001285	0.01705	-1.77924	Blue copper protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0549510.1	-0.67131	8.771369	-3.32104	0.001628	0.019852	-1.7821	Peptidyl-prolyl cis-trans isomerase	elongation zone	12 h
HORVU.MOREX.r3.2HG0121480.1	0.765263	1.064359	3.261259	0.001942	0.022079	-1.7826	MYB transcription factor	elongation zone	12 h
HORVU.MOREX.r3.1HG0014410.1	-0.63575	5.218845	-3.16087	0.0026	0.026389	-1.78343	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.1HG0072320.1	-0.82668	1.113845	-3.07916	0.003285	0.030825	-1.7839	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0245120.1	2.751055	-2.69428	3.205406	0.002286	0.0242	-1.78464	Cysteine protease, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0314240.1	-0.4127	5.164101	-3.20122	0.002314	0.024386	-1.78543	Potassium transporter	elongation zone	12 h
HORVU.MOREX.r3.4HG0401450.1	-0.44327	7.107053	-3.26795	0.001904	0.021791	-1.78569	Anthocyanin 5-aromatic acyltransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0155290.1	1.482062	-0.36543	3.134857	0.002802	0.027765	-1.7886	Retrotransposon protein, putative, unclassified	elongation zone	12 h
HORVU.MOREX.r3.6HG0611300.1	-0.98231	2.278681	-3.09201	0.003167	0.030076	-1.78871	AMP-dependent synthetase and ligase family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0232780.1	-0.56892	2.836303	-3.08171	0.003262	0.030701	-1.79009	R3H domain containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0525020.1	-0.80314	2.149516	-3.07988	0.003279	0.030803	-1.79105	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0499490.1	-0.28473	6.586701	-3.23663	0.002087	0.023064	-1.792	Transcription initiation factor IIB	elongation zone	12 h
HORVU.MOREX.r3.1HG0000670.1	-0.84436	2.483716	-3.07379	0.003336	0.031156	-1.79438	translocase subunit seca	elongation zone	12 h
HORVU.MOREX.r3.1HG0018390.1	-0.98561	5.772475	-3.16959	0.002536	0.025938	-1.79629	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0662220.1	-1.00768	3.864095	-3.07778	0.003298	0.030931	-1.79637	UDP-glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0240390.2	-1.25813	2.367221	-3.07555	0.003319	0.031043	-1.79889	Purine nucleoside phosphorylase DeoD-type	elongation zone	12 h
HORVU.MOREX.r3.3HG0220250.1	-0.48567	3.555795	-3.12045	0.00292	0.028505	-1.79923	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.5HG0467950.1	-0.47774	6.475334	-3.22459	0.002162	0.023553	-1.80033	Divalent metal cation transporter MntH 2	elongation zone	12 h
HORVU.MOREX.r3.7HG0680170.1	-0.4793	4.825321	-3.15763	0.002625	0.026466	-1.80043	mediator of RNA polymerase II transcription subunit	elongation zone	12 h
HORVU.MOREX.r3.5HG0512250.1	1.309951	-0.16991	3.178281	0.002473	0.025473	-1.80131	Receptor-like kinase, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0382500.1	-0.39502	5.221396	-3.1819	0.002447	0.025246	-1.80152	Seed maturation protein PM36, putative, expressed	elongation zone	12 h
HORVU.MOREX.r3.4HG0353330.1	-0.93577	5.045545	-3.11907	0.002932	0.028562	-1.80231	Protein kinase	elongation zone	12 h
HORVU.MOREX.r3.1HG0003130.1	-0.49332	5.529036	-3.21196	0.002243	0.02402	-1.80483	Regulator of chromosome condensation (RCC1) family with FYVE zinc finger doma	elongation zone	12 h
HORVU.MOREX.r3.4HG0405860.1	2.050549	1.28141	3.081837	0.00326	0.030701	-1.80521	Protein WEAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT 1	elongation zone	12 h
HORVU.MOREX.r3.6HG0629810.2	0.921281	1.891863	3.069158	0.00338	0.031411	-1.8054	Auxin-responsive protein	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.6HG0549830.1	-0.74227	2.038518	-3.06998	0.003372	0.031367	-1.80548	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0511820.1	2.279487	-3.38085	3.205578	0.002285	0.0242	-1.80714	Cyclic nucleotide-gated channel	elongation zone	12 h
HORVU.MOREX.r3.3HG0309760.1	0.81508	3.402606	3.0931	0.003158	0.029997	-1.80818	ROP-interactive CRIB motif protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0354480.1	-0.30043	6.236734	-3.22759	0.002143	0.023453	-1.81059	Aquaporin-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0200710.1	1.833556	1.897406	3.06686	0.003402	0.031531	-1.81076	Cytochrome P450 family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0120030.1	-0.72384	4.633702	-3.14283	0.002739	0.027326	-1.81082	Xylulose kinase	elongation zone	12 h
HORVU.MOREX.r3.2HG0155460.1	-0.65291	2.860269	-3.08629	0.003219	0.030422	-1.81236	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0726210.1	-0.72097	2.875567	-3.06578	0.003412	0.031613	-1.81265	Two-component response regulator	elongation zone	12 h
HORVU.MOREX.r3.5HG0511930.1	-0.8946	2.612278	-3.07011	0.003371	0.031367	-1.815	Ring finger protein, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0204340.1	-2.2925	-0.82148	-3.58767	0.000728	0.012414	-1.81523	ERD (early-responsive to dehydration stress) family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0487040.1	-0.49437	7.455763	-3.28418	0.001816	0.021097	-1.81563	Alpha/beta-Hydrolases superfamily protein, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0220360.1	-0.82439	4.616465	-3.09826	0.003111	0.029766	-1.81724	Disease resistance protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0180210.1	-1.20188	2.207614	-3.07169	0.003356	0.0313	-1.8176	methyl-coenzyme M reductase II subunit gamma, putative (DUF3741)	elongation zone	12 h
HORVU.MOREX.r3.6HG0624390.1	1.053902	1.652699	3.067491	0.003396	0.031493	-1.8194	Two-component response regulator	elongation zone	12 h
HORVU.MOREX.r3.6HG0615710.1	-0.53607	6.427382	-3.18511	0.002424	0.025148	-1.82032	Nucleobase ascorbate transporter	elongation zone	12 h
HORVU.MOREX.r3.2HG0159580.1	0.654808	4.426208	3.207669	0.002271	0.02416	-1.82202	Carboxypeptidase	elongation zone	12 h
HORVU.MOREX.r3.5HG0480600.1	1.846016	-0.20786	3.221218	0.002183	0.023703	-1.82344	Jasmonate zim-domain protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0555250.1	2.168061	0.376943	3.391173	0.001322	0.017264	-1.82347	Esterase/lipase/thioesterase-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0379530.1	-0.417	3.959492	-3.13122	0.002832	0.027935	-1.82548	O-fucosyltransferase family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0613360.1	1.369878	-0.60847	3.087913	0.003205	0.030372	-1.8275	Nucleotidylyl transferase superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0175350.1	2.260985	1.060585	3.266471	0.001913	0.021804	-1.8288	C2 and GRAM domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0303560.2	1.618222	-1.42721	3.14127	0.002751	0.027347	-1.82894	Interactor of constitutive active ROPs 2, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.7HG0749660.1	-0.65669	5.553628	-3.14278	0.002739	0.027326	-1.83583	DNA-binding protein RHL1	elongation zone	12 h
HORVU.MOREX.r3.1HG0070480.1	0.326891	6.291081	3.244411	0.00204	0.022692	-1.83611	60 kDa chaperonin	elongation zone	12 h
HORVU.MOREX.r3.2HG0122720.1	-0.98085	3.012374	-3.05461	0.003522	0.032179	-1.83805	Serine hydroxymethyltransferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0480060.1	-1.18427	0.892295	-3.06491	0.003421	0.031662	-1.83915	Protein GAMETE EXPRESSED 1	elongation zone	12 h
HORVU.MOREX.r3.4HG0399470.1	2.529684	-1.76622	3.319681	0.001635	0.019852	-1.84382	Clathrin heavy chain	elongation zone	12 h
HORVU.MOREX.r3.7HG0682460.1	-0.34739	5.61607	-3.20489	0.002289	0.024215	-1.84405	ADP-ribosylation factor, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0351070.1	0.746998	2.367322	3.146889	0.002707	0.027079	-1.84562	STRUBBELIG-receptor family 5	elongation zone	12 h
HORVU.MOREX.r3.4HG0338180.1	-0.40324	5.846029	-3.21603	0.002216	0.023861	-1.84751	Transmembrane and coiled-coil domains protein 1	elongation zone	12 h
HORVU.MOREX.r3.4HG0333550.2	0.70912	1.181427	3.072298	0.00335	0.03126	-1.84811	senescence-associated family protein, putative (DUF581)	elongation zone	12 h
HORVU.MOREX.r3.7HG0712000.1	1.730225	-3.03639	3.14822	0.002697	0.02702	-1.84844	Transposon protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0182800.1	-1.17278	3.942974	-3.06925	0.003379	0.031411	-1.85178	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.5HG0476690.1	-0.30753	5.143097	-3.17372	0.002506	0.02572	-1.85236	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0633960.1	0.881693	2.11648	3.256514	0.001969	0.022287	-1.85346	Monosaccharide-sensing protein 2	elongation zone	12 h
HORVU.MOREX.r3.1HG0078370.1	-1.78543	4.280641	-3.05097	0.003559	0.032357	-1.85361	breast cancer associated RING 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0645350.1	-0.30248	9.301069	-3.33171	0.001578	0.019378	-1.85419	1-deoxy-D-xylulose-5-phosphate synthase, Transketolase	elongation zone	12 h
HORVU.MOREX.r3.2HG0194620.1	1.879527	-2.14798	3.127957	0.002858	0.028076	-1.85449	F-box protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0081110.1	0.650019	4.269156	3.212564	0.002239	0.024002	-1.85467	Type I inositol-1,4,5-trisphosphate 5-phosphatase 1	elongation zone	12 h
HORVU.MOREX.r3.3HG0309930.1	1.053411	-0.53911	3.067551	0.003395	0.031493	-1.8558	Sucrose-phosphate synthase	elongation zone	12 h
HORVU.MOREX.r3.7HG0719410.1	-0.89347	6.134816	-3.11897	0.002933	0.028562	-1.85673	Trichome birefringence-like protein	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.5HG0456510.1	-0.44608	7.286365	-3.24905	0.002013	0.022519	-1.85958	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase comp	elongation zone	12 h
HORVU.MOREX.r3.3HG0291570.1	0.404537	6.662916	3.24719	0.002024	0.022545	-1.86159	Nuclear matrix constituent-like protein 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0130200.1	-0.42795	4.823465	-3.14154	0.002749	0.027347	-1.8622	ZCW7	elongation zone	12 h
HORVU.MOREX.r3.6HG0547550.1	-0.36026	3.546337	-3.08671	0.003216	0.030407	-1.8636	F-box family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0512320.1	-0.74987	8.205588	-3.2896	0.001787	0.020869	-1.86364	Cytochrome P450	elongation zone	12 h
HORVU.MOREX.r3.1HG0039230.1	-0.66126	5.567693	-3.12033	0.002921	0.028505	-1.86703	AT-rich interactive domain-containing protein 2	elongation zone	12 h
HORVU.MOREX.r3.3HG0286100.1	1.549848	1.587249	3.068679	0.003384	0.03144	-1.87185	CASP-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0329510.1	-0.96261	1.401423	-3.05994	0.003469	0.031904	-1.87227	Vacuolar protein sorting protein 25	elongation zone	12 h
HORVU.MOREX.r3.6HG0559000.1	-0.43074	4.951771	-3.11632	0.002955	0.028698	-1.87248	Homeobox protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0459600.1	0.639745	3.96473	3.162002	0.002592	0.026328	-1.87307	Serine/threonine-protein kinase	elongation zone	12 h
HORVU.MOREX.r3.7HG0659420.1	-2.53338	-0.00292	-3.16431	0.002575	0.026239	-1.87311	Tetratricopeptide repeat protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0708050.1	-2.63562	-1.4308	-3.45939	0.001077	0.015372	-1.87337	Cytochrome b561	elongation zone	12 h
HORVU.MOREX.r3.5HG0455080.1	-0.95704	2.618738	-3.04008	0.00367	0.03307	-1.87349	5-formyltetrahydrofolate cyclo-ligase	elongation zone	12 h
HORVU.MOREX.r3.3HG0231900.1	-0.24249	8.11606	-3.2875	0.001798	0.020951	-1.87432	Translocon-associated protein subunit beta	elongation zone	12 h
HORVU.MOREX.r3.6HG0564910.1	-1.01006	-0.11724	-3.04036	0.003667	0.033059	-1.87646	Myosin-related family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0532630.1	-1.2751	4.235353	-3.0447	0.003622	0.032772	-1.87676	Sister chromatid cohesion protein DCC1	elongation zone	12 h
HORVU.MOREX.r3.3HG0292490.1	0.834397	0.56764	3.172027	0.002518	0.025821	-1.87684	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein, putat	elongation zone	12 h
HORVU.MOREX.r3.4HG0356280.1	1.067174	0.330026	3.03784	0.003693	0.033251	-1.87684	Serine/threonine-protein kinase	elongation zone	12 h
HORVU.MOREX.r3.4HG0353950.1	2.947045	-1.81142	3.506945	0.000932	0.014175	-1.87707	ubiquitin carboxyl-terminal hydrolase	elongation zone	12 h
HORVU.MOREX.r3.2HG0182990.1	-0.65441	2.816822	-3.11347	0.002979	0.028878	-1.87831	UDP-glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0125050.1	-0.45196	4.076346	-3.10272	0.003072	0.029497	-1.87834	Protein FAR1-RELATED SEQUENCE 5	elongation zone	12 h
HORVU.MOREX.r3.3HG0298090.1	0.803517	2.186755	3.074308	0.003331	0.031125	-1.88048	Leucine-rich repeat receptor-like protein kinase	elongation zone	12 h
HORVU.MOREX.r3.2HG0152890.1	-0.65497	3.809628	-3.08598	0.003222	0.030428	-1.88136	TCP transcription factor	elongation zone	12 h
HORVU.MOREX.r3.3HG0296810.1	-0.90733	1.903174	-3.05141	0.003554	0.032357	-1.88247	60S ribosomal protein l35a	elongation zone	12 h
HORVU.MOREX.r3.1HG0057000.1	-1.22528	1.397457	-3.05856	0.003483	0.031953	-1.88341	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0149940.1	-0.47089	5.130258	-3.12939	0.002847	0.028054	-1.88478	RNA-binding family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0127020.1	0.685112	4.632959	3.193464	0.002366	0.0247	-1.88525	methyl esterase 11	elongation zone	12 h
HORVU.MOREX.r3.1HG0073030.1	-0.81021	5.962504	-3.15825	0.00262	0.026447	-1.88619	Histone H4	elongation zone	12 h
HORVU.MOREX.r3.3HG0234800.1	-0.27897	6.705697	-3.20528	0.002287	0.0242	-1.88743	Carboxymethylenebutenolidase 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0189970.1	-0.71522	2.22472	-3.03292	0.003744	0.033538	-1.88946	NBS-LRR disease resistance protein homologue	elongation zone	12 h
HORVU.MOREX.r3.7HG0656330.1	-1.49235	0.123232	-3.12871	0.002852	0.028069	-1.88976	actin cross-linking protein, putative (DUF569)	elongation zone	12 h
HORVU.MOREX.r3.2HG0217610.1	-0.30704	5.812248	-3.20198	0.002309	0.02437	-1.8903	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0399530.1	1.708693	1.156384	3.080203	0.003276	0.03079	-1.89185	Zinc finger protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0264700.1	-0.34001	4.24631	-3.11145	0.002996	0.029004	-1.89256	ELL-associated factor, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0407290.1	-1.41032	5.558259	-3.07974	0.00328	0.030803	-1.89278	Xyloglucan galactosyltransferase KATAMARI1	elongation zone	12 h
HORVU.MOREX.r3.5HG0536710.1	-0.4416	6.624729	-3.22099	0.002185	0.023706	-1.89362	NAD/NADP-dependent betaine aldehyde dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.2HG0184780.1	-0.76014	4.07506	-3.05744	0.003494	0.032008	-1.89394	Required to maintain repression 2	elongation zone	12 h
HORVU.MOREX.r3.4HG0396030.1	1.838722	0.582741	3.077569	0.0033	0.030936	-1.89638	Tubulin alpha chain	elongation zone	12 h
HORVU.MOREX.r3.2HG0170390.1	-0.31913	4.904965	-3.13926	0.002767	0.027483	-1.8984	Protein phosphatase methylesterase 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0685550.1	-0.73095	3.473275	-3.05012	0.003567	0.032388	-1.9004	S-acyltransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0745120.1	0.353556	6.029656	3.198071	0.002335	0.024484	-1.90161	Sucrose phosphate synthase	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.4HG0392690.1	0.444601	3.767902	3.134347	0.002806	0.027793	-1.90172	Acyl-CoA-binding domain protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0528570.1	0.960661	0.170023	3.094207	0.003148	0.02993	-1.90498	Protein PLANT CADMIUM RESISTANCE 2	elongation zone	12 h
HORVU.MOREX.r3.7HG0702050.1	1.015866	-0.45045	3.037414	0.003697	0.033276	-1.90601	Blue copper protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0304080.1	-0.86263	4.173396	-3.05506	0.003518	0.032152	-1.90686	Glutaredoxin-like	elongation zone	12 h
HORVU.MOREX.r3.3HG0275300.1	-0.96952	0.578299	-3.0535	0.003533	0.032266	-1.90777	Major facilitator superfamily protein, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0657010.1	0.521406	4.684137	3.206649	0.002278	0.024194	-1.90819	Vesicle-associated membrane protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0721790.1	-0.78653	2.548734	-3.02466	0.003833	0.034006	-1.90903	Pentatricopeptide repeat-containing protein, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0067930.1	0.559631	2.533288	3.080227	0.003275	0.03079	-1.91217	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.3HG0230880.1	-0.20813	7.037661	-3.24681	0.002026	0.022557	-1.91241	Steroid 5-alpha reductase	elongation zone	12 h
HORVU.MOREX.r3.3HG0316870.1	0.366972	6.819357	3.25282	0.001991	0.022408	-1.91268	RNA binding protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0226060.1	-1.26342	4.441713	-3.09588	0.003133	0.029866	-1.91294	Calcium binding family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0700930.1	-1.43826	4.508977	-3.02159	0.003866	0.034222	-1.91517	RING/U-box superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0294040.1	0.779442	3.082547	3.213537	0.002232	0.023972	-1.9154	Serine/threonine-protein kinase	elongation zone	12 h
HORVU.MOREX.r3.7HG0732610.1	-1.24274	4.827785	-3.03096	0.003765	0.03365	-1.91553	DNA polymerase alpha subunit B	elongation zone	12 h
HORVU.MOREX.r3.6HG0553290.1	-0.60792	5.490398	-3.1102	0.003007	0.029025	-1.91929	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.6HG0622120.1	0.573799	4.581543	3.251271	0.002	0.022473	-1.91954	Pathogenesis-related protein 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0123650.1	-0.39028	5.958028	-3.14166	0.002748	0.027347	-1.92009	Serine/arginine rich splicing factor, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0057860.1	0.657909	3.261596	3.235977	0.002091	0.023083	-1.92297	BTB/POZ domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0476000.1	-0.3452	5.038015	-3.16323	0.002583	0.026274	-1.92532	Molybdopterin synthase catalytic subunit	elongation zone	12 h
HORVU.MOREX.r3.1HG0074490.1	-1.22124	4.901731	-3.05192	0.003549	0.032342	-1.92568	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0725450.1	1.580461	-0.1554	3.207722	0.002271	0.02416	-1.92572	Mitochondrial carrier protein, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0587460.1	0.953828	-2.65712	3.029513	0.003781	0.0337	-1.92644	D-alanine--D-alanine ligase	elongation zone	12 h
HORVU.MOREX.r3.7HG0744970.1	-0.29501	5.768018	-3.16901	0.00254	0.025968	-1.9269	Protein OS-9	elongation zone	12 h
HORVU.MOREX.r3.2HG0154500.1	-1.03982	0.570465	-3.06325	0.003437	0.03178	-1.92699	Protein PHLOEM PROTEIN 2-LIKE A10	elongation zone	12 h
HORVU.MOREX.r3.1HG0008400.1	-0.8133	2.111607	-3.01726	0.003913	0.034492	-1.92885	F-box family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0171860.1	-0.61819	4.629161	-3.0593	0.003476	0.031939	-1.93009	mediator of RNA polymerase II transcription subunit-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0027200.1	0.811802	4.502879	3.098443	0.00311	0.029766	-1.93023	Auxin-responsive protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0523860.1	0.518181	4.167581	3.137463	0.002781	0.027598	-1.93129	Calcium-dependent protein kinase	elongation zone	12 h
HORVU.MOREX.r3.4HG0405830.1	-0.78982	2.230818	-3.01406	0.003949	0.03467	-1.93154	cold regulated protein 27	elongation zone	12 h
HORVU.MOREX.r3.3HG0328990.1	-0.41816	4.328412	-3.10572	0.003046	0.02931	-1.93252	Rab5-interacting family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0577170.1	-1.73295	1.196593	-3.16468	0.002572	0.026239	-1.93461	Argonaute family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0677860.1	-2.40034	2.903041	-3.07054	0.003367	0.031359	-1.93566	RNA polymerase II elongation factor	elongation zone	12 h
HORVU.MOREX.r3.5HG0514790.3	-0.47526	10.92396	-3.33591	0.001558	0.019246	-1.9358	Elongation factor 1-alpha	elongation zone	12 h
HORVU.MOREX.r3.4HG0417160.1	0.573336	4.344914	3.214704	0.002225	0.023928	-1.93581	Flavin-containing monooxygenase	elongation zone	12 h
HORVU.MOREX.r3.4HG0378080.1	2.881676	-1.12859	3.471349	0.001038	0.015035	-1.9363	#N/A	elongation zone	12 h
HORVU.MOREX.r3.1HG0029080.1	-0.64928	2.288361	-3.02701	0.003807	0.033836	-1.93714	60S ribosomal protein L18a-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0479210.1	-1.01622	7.833409	-3.17528	0.002494	0.025643	-1.93764	HMG-Y-related protein A	elongation zone	12 h
HORVU.MOREX.r3.2HG0150530.1	0.566041	3.135946	3.070867	0.003364	0.031344	-1.93828	E3 ubiquitin-protein ligase family	elongation zone	12 h
HORVU.MOREX.r3.3HG0301250.1	-1.17061	1.880477	-3.0167	0.003919	0.034516	-1.93842	#N/A	elongation zone	12 h
HORVU.MOREX.r3.4HG0417710.1	0.893247	0.768626	3.159737	0.002609	0.026441	-1.9395	Protease inhibitor/seed storage/lipid transfer protein family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0073320.1	-0.91593	2.923796	-3.03513	0.003721	0.033412	-1.9404	Histone H2B	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.2HG0135510.1	-0.34359	5.626394	-3.15915	0.002613	0.026441	-1.94176	Vesicle-associated 4-2-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0083110.1	-0.54962	2.265521	-3.02756	0.003801	0.033827	-1.945	UDP-D-apiose/UDP-D-xylose synthase	elongation zone	12 h
HORVU.MOREX.r3.3HG0255900.1	-0.29148	6.088112	-3.17611	0.002488	0.025607	-1.94579	SUN domain-containing protein 2	elongation zone	12 h
HORVU.MOREX.r3.6HG0632270.1	-0.43922	3.993705	-3.07726	0.003303	0.03095	-1.94886	Leucine-rich repeat family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0714120.1	-0.33138	6.206134	-3.15205	0.002667	0.026789	-1.94913	Eukaryotic translation initiation factor 3 subunit I	elongation zone	12 h
HORVU.MOREX.r3.1HG0025320.1	1.07233	0.572545	3.006327	0.004035	0.035207	-1.94964	Receptor-like kinase, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0633420.1	-0.7963	7.127371	-3.14873	0.002693	0.027002	-1.95035	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0331630.1	-0.39182	4.435596	-3.08841	0.0032	0.030344	-1.95121	Short-chain dehydrogenase/reductase family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0708820.1	-0.6856	5.143803	-3.05743	0.003494	0.032008	-1.95134	PHD finger family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0540620.1	-1.53898	4.022998	-3.00629	0.004035	0.035207	-1.95156	Malignant brain tumor repeat protein 1	elongation zone	12 h
HORVU.MOREX.r3.5HG0528910.1	0.851303	1.611089	3.094268	0.003147	0.02993	-1.952	DUF3511 domain protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0198320.1	1.558602	-0.19189	3.019617	0.003887	0.03428	-1.95255	Protein translation factor SUI1-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0298510.1	0.572642	4.425452	3.118993	0.002933	0.028562	-1.95301	1-phosphatidylinositol-3-phosphate 5-kinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0275100.1	1.283142	-2.73635	3.032277	0.003751	0.033585	-1.95377	Integrase-type DNA-binding superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0095520.1	-0.5947	4.42382	-3.10815	0.003025	0.029127	-1.95454	Histone deacetylase complex subunit SAP30	elongation zone	12 h
HORVU.MOREX.r3.5HG0483980.1	1.165309	-1.84454	3.007284	0.004024	0.035139	-1.95566	Cinnamoyl CoA reductase	elongation zone	12 h
HORVU.MOREX.r3.1HG0029730.1	0.470925	7.923005	3.280547	0.001835	0.021263	-1.95575	Malic enzyme	elongation zone	12 h
HORVU.MOREX.r3.3HG0249590.1	-0.69958	3.60705	-3.01198	0.003972	0.034843	-1.95701	Vesicle transport protein-like	elongation zone	12 h
HORVU.MOREX.r3.5HG0510210.1	-0.37319	4.966015	-3.14137	0.00275	0.027347	-1.95737	Tryptophan RNA-binding attenuator-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0647300.1	1.785206	-1.17681	3.005199	0.004048	0.03527	-1.9576	AT hook motif DNA-binding family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0189980.1	0.501743	3.503027	3.104946	0.003053	0.02934	-1.95806	PPPDE thiol peptidase family protein, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0401710.1	-1.27885	4.660057	-3.01313	0.003959	0.034745	-1.95808	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.6HG0631700.1	0.441617	8.078937	3.324292	0.001613	0.019712	-1.96123	Aquaporin	elongation zone	12 h
HORVU.MOREX.r3.2HG0190260.1	0.841578	2.916863	3.011066	0.003982	0.034902	-1.96192	SHR5-receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0229480.1	-0.38936	5.27277	-3.09645	0.003128	0.029864	-1.96504	Actin/actin-like family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0099160.1	0.984643	-0.22736	3.051875	0.003549	0.032342	-1.96606	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein, putativ	elongation zone	12 h
HORVU.MOREX.r3.5HG0526940.1	-0.36095	7.55668	-3.20302	0.002302	0.024309	-1.96613	Alpha-mannosidase	elongation zone	12 h
HORVU.MOREX.r3.6HG0623920.1	-0.20249	9.176211	-3.28919	0.001789	0.020878	-1.96622	Leucine aminopeptidase, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0008140.1	-1.05263	2.579787	-3.04228	0.003647	0.032938	-1.9678	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0130000.1	-0.35093	4.729393	-3.09766	0.003117	0.029789	-1.96871	Effector of transcription protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0732270.1	-0.565	2.663349	-3.00074	0.004099	0.035578	-1.97072	F-box protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0367380.1	-2.69387	-1.8835	-3.45291	0.001098	0.015536	-1.97145	zinc finger (ubiquitin-hydrolase) domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0180260.1	-0.69862	1.836043	-2.99652	0.004147	0.035879	-1.97155	Myb/SANT-like DNA-binding domain protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0446900.1	-0.22366	6.633774	-3.19451	0.002359	0.024647	-1.97253	Dipeptidyl peptidase	elongation zone	12 h
HORVU.MOREX.r3.7HG0751000.1	-1.25265	3.800431	-3.01423	0.003947	0.034668	-1.97319	UDP-glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0305580.1	-1.38155	7.017223	-3.07602	0.003315	0.031043	-1.98	Alcohol dehydrogenase class-3	elongation zone	12 h
HORVU.MOREX.r3.6HG0553310.1	-0.78567	4.173624	-3.00442	0.004057	0.035331	-1.98108	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0294670.1	-1.38307	-0.36802	-3.11435	0.002972	0.028819	-1.98174	demeter-like protein 3	elongation zone	12 h
HORVU.MOREX.r3.5HG0441840.1	1.318125	1.936883	3.02988	0.003777	0.03368	-1.98207	Dof zinc finger protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0197230.1	1.110772	-1.20366	3.00241	0.00408	0.035442	-1.98435	disease resistance protein (TIR-NBS-LRR class)	elongation zone	12 h
HORVU.MOREX.r3.3HG0303430.1	-0.4641	7.726619	-3.21965	0.002193	0.023748	-1.98449	TBC1 domain family member 8	elongation zone	12 h

Table Sн Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0288070.1	0.522583	0.496177	3.109651	0.003012	0.02903	-1.98525	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein, putati	elongation zone	12 h
HORVU.MOREX.r3.1HG0088990.1	-0.51988	4.115581	-3.05264	0.003542	0.032316	-1.98549	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0711850.1	-0.38883	4.991548	-3.08707	0.003212	0.03039	-1.986	RNA-binding KH domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0044470.1	0.770877	2.284476	3.035122	0.003721	0.033412	-1.98638	Cytokinin oxidase/dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.7HG0672960.1	1.534157	-2.45339	3.036797	0.003704	0.033319	-1.98698	U-box domain-containing family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0177200.1	-0.53736	3.273869	-3.05288	0.003539	0.032308	-1.98709	Cytochrome f	elongation zone	12 h
HORVU.MOREX.r3.7HG0650950.1	0.442875	4.47289	3.120185	0.002923	0.028505	-1.99007	Cysteine synthase	elongation zone	12 h
HORVU.MOREX.r3.1HG0074010.1	1.002605	1.165265	3.009735	0.003997	0.034974	-1.99413	Guanylyl cyclase	elongation zone	12 h
HORVU.MOREX.r3.3HG0221440.1	0.799814	2.700751	3.24899	0.002013	0.022519	-1.9951	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0095970.1	-1.27234	3.317154	-2.98691	0.00426	0.036533	-1.99651	NBS-LRR disease resistance protein-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0073500.1	1.886354	-2.89345	2.99601	0.004153	0.035915	-1.99676	Laccase	elongation zone	12 h
HORVU.MOREX.r3.6HG0614470.2	0.50449	0.971508	3.136743	0.002787	0.027642	-1.99818	Beta-xylosidase, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0506290.1	-0.88126	1.60619	-2.9913	0.004208	0.036196	-2.00106	Splicing factor u2af large subunit, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0072410.1	-0.26945	6.475901	-3.17261	0.002514	0.02579	-2.00136	Calcium-dependent protein kinase	elongation zone	12 h
HORVU.MOREX.r3.5HG0471520.1	0.549076	3.519872	3.080304	0.003275	0.03079	-2.00458	Ubiquitin-conjugating enzyme E2	elongation zone	12 h
HORVU.MOREX.r3.7HG0743900.1	0.510369	5.143712	3.170434	0.002529	0.025888	-2.00664	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0596240.1	-1.16534	0.960124	-3.01564	0.003931	0.034575	-2.00818	RNA-binding protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0094980.1	-0.42992	4.287159	-3.05997	0.003469	0.031904	-2.00897	Mitochondrial outer membrane porin	elongation zone	12 h
HORVU.MOREX.r3.5HG0478390.1	-0.4779	5.551367	-3.08716	0.003211	0.03039	-2.00944	PCI domain-containing protein 2	elongation zone	12 h
HORVU.MOREX.r3.5HG0495240.1	1.058	-0.87388	2.984361	0.004291	0.036763	-2.01204	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0594290.1	-1.0226	2.905971	-2.98083	0.004333	0.036957	-2.01382	histone acetyltransferase of the CBP family 12	elongation zone	12 h
HORVU.MOREX.r3.3HG0291340.1	-0.96811	3.400685	-2.98248	0.004313	0.036879	-2.01426	Deoxycytidylate deaminase-like	elongation zone	12 h
HORVU.MOREX.r3.2HG0193220.1	-0.64547	4.02011	-3.00363	0.004066	0.035366	-2.01432	Putrescine-binding periplasmic protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0196630.1	0.966007	-0.81111	3.019608	0.003887	0.03428	-2.01454	Invertase/pectin methylesterase inhibitor family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0613460.1	1.074621	2.574467	3.031068	0.003764	0.03365	-2.01474	MACPF domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0656250.1	-0.39682	7.976001	-3.21062	0.002251	0.0241	-2.0149	Proteasome subunit alpha type	elongation zone	12 h
HORVU.MOREX.r3.6HG0601160.1	0.683812	4.335499	3.28678	0.001802	0.020972	-2.01504	Expansin protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0119060.1	-0.47205	4.049026	-3.04068	0.003663	0.033043	-2.01763	zinc transporter-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0714870.1	-0.61942	5.526539	-3.12134	0.002913	0.028463	-2.01958	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.4HG0386480.1	-0.39888	8.895935	-3.24913	0.002012	0.022519	-2.01982	Calcium-transporting ATPase	elongation zone	12 h
HORVU.MOREX.r3.6HG0633510.1	0.580872	4.690627	3.158419	0.002619	0.026447	-2.0202	integral membrane metal-binding family protein (DUF2296)	elongation zone	12 h
HORVU.MOREX.r3.2HG0138540.1	0.600067	4.435354	3.266212	0.001914	0.021808	-2.02032	Blue copper protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0202220.1	0.348704	4.425224	3.057861	0.00349	0.031998	-2.02085	Protein pelota homolog	elongation zone	12 h
HORVU.MOREX.r3.1HG0079750.1	0.974438	-1.15538	2.988952	0.004236	0.036371	-2.02354	MYB transcription factor	elongation zone	12 h
HORVU.MOREX.r3.5HG0500730.1	-0.66802	4.668649	-3.03017	0.003774	0.03368	-2.02488	Mediator of RNA polymerase II transcription subunit 4	elongation zone	12 h
HORVU.MOREX.r3.5HG0479810.1	0.237483	7.043626	3.20346	0.002299	0.024291	-2.02534	Phospholipid:diacylglycerol acyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0245010.1	0.470893	4.432877	3.098402	0.00311	0.029766	-2.0271	Protein DJ-1	elongation zone	12 h
HORVU.MOREX.r3.4HG0396660.1	-1.61252	6.770443	-3.05121	0.003556	0.032357	-2.02792	Replication protein A 70 kDa DNA-binding subunit	elongation zone	12 h
HORVU.MOREX.r3.4HG0404450.1	-0.28227	5.835227	-3.11273	0.002986	0.028925	-2.03102	Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0234970.1	0.519161	0.091122	3.070163	0.00337	0.031367	-2.03224	6,7-dimethyl-8-ribityllumazine synthase	elongation zone	12 h
HORVU.MOREX.r3.5HG0429230.1	-0.49938	4.516929	-3.03577	0.003714	0.033401	-2.03238	Protein FAR1-RELATED SEQUENCE 5	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.5HG0473520.1	0.391991	6.096551	3.197493	0.002339	0.0245	-2.03286	UDP-glucose 4-epimerase family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0297940.1	-1.178	3.507795	-2.97299	0.004429	0.037408	-2.03338	Transcription initiation factor TFIID subunit 9	elongation zone	12 h
HORVU.MOREX.r3.1HG0084890.1	0.610711	1.342406	3.027806	0.003799	0.033827	-2.03734	Protein DETOXIFICATION	elongation zone	12 h
HORVU.MOREX.r3.7HG0718710.1	-0.2782	6.996212	-3.18991	0.002391	0.024902	-2.03864	Ras-related protein, expressed	elongation zone	12 h
HORVU.MOREX.r3.5HG0433490.1	-0.50341	5.319229	-3.07278	0.003345	0.031231	-2.04014	F-box/LRR protein, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0582230.1	-0.51329	3.581325	-3.01698	0.003916	0.034505	-2.04063	GDSL esterase/lipase	elongation zone	12 h
HORVU.MOREX.r3.4HG0338210.1	-0.77598	3.760864	-3.02357	0.003844	0.034053	-2.04139	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.2HG0120470.1	1.17548	3.222129	3.232344	0.002113	0.023229	-2.04479	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.3HG0225760.1	1.188559	-0.95266	3.034175	0.003731	0.033458	-2.04491	ABC transporter G family member	elongation zone	12 h
HORVU.MOREX.r3.2HG0189950.1	-0.43769	4.476014	-3.06744	0.003396	0.031493	-2.04613	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.1HG0025430.1	1.184581	0.604962	2.963721	0.004545	0.03803	-2.04629	WEB family protein (DUF827)	elongation zone	12 h
HORVU.MOREX.r3.2HG0189110.1	1.061076	0.028785	2.967114	0.004502	0.037785	-2.04849	Vesicle-associated protein 1-1	elongation zone	12 h
HORVU.MOREX.r3.3HG0281860.1	-0.59301	3.606298	-2.97797	0.004368	0.037145	-2.04947	Peptidyl-tRNA hydrolase	elongation zone	12 h
HORVU.MOREX.r3.3HG0300810.1	-0.48959	6.316915	-3.16274	0.002586	0.026299	-2.05079	Sialyltransferase-like protein 2	elongation zone	12 h
HORVU.MOREX.r3.1HG0046770.1	-0.7079	4.616852	-3.00044	0.004102	0.035593	-2.05309	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0550740.1	-0.50018	3.020677	-2.97923	0.004353	0.037092	-2.05325	F-box family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0480890.1	1.451091	-1.46482	2.961452	0.004574	0.038197	-2.05332	Dirigent protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0465810.1	2.271032	-0.29224	3.039807	0.003672	0.033081	-2.0546	Calcium-binding protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0219650.1	-0.44238	6.043804	-3.08761	0.003207	0.030372	-2.05669	RNA polymerase II-associated factor 1	elongation zone	12 h
HORVU.MOREX.r3.6HG0555810.1	-1.22175	0.610303	-3.01089	0.003984	0.034905	-2.05895	5'-AMP-activated protein kinase subunit beta-1	elongation zone	12 h
HORVU.MOREX.r3.5HG0515610.1	1.235955	-3.36667	3.023503	0.003845	0.034053	-2.05983	Collagen alpha chain	elongation zone	12 h
HORVU.MOREX.r3.2HG0181800.1	-0.7995	3.895018	-2.97983	0.004345	0.037045	-2.0604	Protodermal factor 1	elongation zone	12 h
HORVU.MOREX.r3.5HG0531850.1	-0.64019	4.723485	-3.00277	0.004076	0.035421	-2.06386	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0514490.1	-0.50507	5.559766	-3.07135	0.003359	0.031316	-2.06504	Hexosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0250870.1	-0.50008	4.187521	-3.03548	0.003718	0.033412	-2.06638	Polynucleotidyl transferase ribonuclease H-like superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0106750.1	-1.09118	0.325037	-3.00522	0.004048	0.03527	-2.06673	Alpha-1,4 glucan phosphorylase	elongation zone	12 h
HORVU.MOREX.r3.2HG0216610.1	-0.33206	6.040531	-3.14862	0.002694	0.027002	-2.06684	Protein NRT1/ PTR FAMILY 5.5	elongation zone	12 h
HORVU.MOREX.r3.5HG0536610.1	0.656104	2.755965	3.128276	0.002856	0.028074	-2.06916	Gibberellin 20 oxidase	elongation zone	12 h
HORVU.MOREX.r3.3HG0250940.1	-0.57739	3.302703	-3.00826	0.004013	0.035058	-2.07025	Polynucleotidyl transferase ribonuclease H-like superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0226150.1	1.694694	2.218815	2.995816	0.004156	0.035915	-2.07043	Protein kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0640570.1	-0.42152	6.096045	-3.09619	0.00313	0.029866	-2.07112	Plant/F18O14-17 protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0088900.1	-0.92274	2.109858	-2.96176	0.00457	0.038196	-2.07136	Orphans transcription factor	elongation zone	12 h
HORVU.MOREX.r3.3HG0278630.1	0.459883	5.03935	3.097956	0.003114	0.029778	-2.07242	Ras-related protein, expressed	elongation zone	12 h
HORVU.MOREX.r3.3HG0237870.1	-1.65932	5.343811	-2.97548	0.004398	0.037281	-2.07297	Histone-lysine N-methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.1HG0072160.1	0.705046	2.908685	2.974581	0.004409	0.037331	-2.07337	UDP-glucose pyrophosphorylase	elongation zone	12 h
HORVU.MOREX.r3.2HG0162940.1	-0.33006	6.349043	-3.11722	0.002947	0.028675	-2.07343	Chaperone protein dnaJ	elongation zone	12 h
HORVU.MOREX.r3.5HG0464630.1	0.567498	3.359325	3.141149	0.002752	0.027347	-2.07388	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.7HG0704760.1	1.212351	-2.61956	2.982818	0.004309	0.036879	-2.0744	Myb family transcription factor family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0210880.1	-1.15579	2.678515	-2.97387	0.004418	0.037371	-2.07455	#N/A	elongation zone	12 h
HORVU.MOREX.r3.4HG0349170.1	-1.02342	4.645229	-3.05091	0.003559	0.032357	-2.07542	Long-Chain Acyl-CoA Synthetase	elongation zone	12 h
HORVU.MOREX.r3.3HG0249890.1	0.769399	2.405613	3.074969	0.003325	0.03108	-2.0768	Auxin response factor	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.6HG0583730.1	-0.38431	4.393564	-3.02399	0.00384	0.034035	-2.07729	Loricrin-like	elongation zone	12 h
HORVU.MOREX.r3.7HG0653850.1	-0.6948	4.845223	-3.03346	0.003739	0.033502	-2.07815	Succinate dehydrogenase assembly factor 4, mitochondrial	elongation zone	12 h
HORVU.MOREX.r3.7HG0721800.1	-0.34807	7.386378	-3.16489	0.00257	0.026239	-2.07957	Malate dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.4HG0337870.1	0.751168	4.45297	3.094331	0.003147	0.02993	-2.08058	Homeobox-leucine zipper family protein / lipid-binding START domain-containing	elongation zone	12 h
HORVU.MOREX.r3.6HG0573150.1	0.389177	5.184389	3.06493	0.003421	0.031662	-2.08374	Copper-transporting ATPase	elongation zone	12 h
HORVU.MOREX.r3.4HG0388270.1	-0.41612	6.243595	-3.123	0.002899	0.028342	-2.08697	Ankyrin repeat family protein, putative, expressed	elongation zone	12 h
HORVU.MOREX.r3.3HG0290180.1	-1.13009	3.615358	-2.94556	0.00478	0.039249	-2.08842	Non-specific serine/threonine protein kinase	elongation zone	12 h
HORVU.MOREX.r3.2HG0176920.1	-1.23594	3.864016	-2.94683	0.004763	0.039158	-2.08871	ATP-dependent RNA helicase DeaD	elongation zone	12 h
HORVU.MOREX.r3.3HG0273790.2	0.668958	2.302445	2.95523	0.004653	0.038674	-2.08881	CTD small phosphatase-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0107300.1	1.649842	-1.31881	2.958236	0.004615	0.038477	-2.08935	HXXXD-type acyl-transferase family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0306170.1	-0.32995	5.38776	-3.08549	0.003227	0.030457	-2.09074	Selenoprotein	elongation zone	12 h
HORVU.MOREX.r3.7HG0655210.1	1.261293	-1.68992	2.985127	0.004282	0.0367	-2.0912	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.2HG0110730.1	-0.4073	4.019032	-3.00844	0.004011	0.035058	-2.0921	DNA primase	elongation zone	12 h
HORVU.MOREX.r3.2HG0161580.1	-0.50391	2.675596	-2.9567	0.004634	0.038595	-2.09308	Alpha/beta-Hydrolases superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0478610.1	0.399512	4.6112	3.102419	0.003075	0.029497	-2.09472	Malonyl-CoA decarboxylase	elongation zone	12 h
HORVU.MOREX.r3.5HG0502310.1	-0.71053	3.718859	-2.98275	0.00431	0.036879	-2.09548	NBS-LRR disease resistance protein, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0577360.1	-0.65634	5.665724	-3.21381	0.002231	0.023972	-2.09549	transmembrane protein, putative (Protein of unknown function, DUF642)	elongation zone	12 h
HORVU.MOREX.r3.1HG0005730.1	1.670036	-3.38812	3.064627	0.003424	0.031674	-2.09578	transcriptional factor B3 family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0518490.1	-0.87275	0.764022	-2.94837	0.004743	0.03909	-2.09611	C2 domain-containing protein / GRAM domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0558350.1	2.504283	-0.25422	3.095776	0.003134	0.029866	-2.09926	#N/A	elongation zone	12 h
HORVU.MOREX.r3.4HG0347760.1	0.666669	2.347769	2.96361	0.004546	0.03803	-2.09986	MYB transcription factor	elongation zone	12 h
HORVU.MOREX.r3.2HG0174650.1	0.967072	1.398683	2.940732	0.004844	0.039587	-2.10301	WPP domain-interacting protein 1	elongation zone	12 h
HORVU.MOREX.r3.3HG0281000.1	-0.85124	3.470695	-2.97455	0.00441	0.037331	-2.10337	F-box protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0432040.1	-0.63153	4.077273	-2.97714	0.004378	0.037198	-2.1042	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0209090.1	-0.60056	3.138841	-2.94935	0.00473	0.03901	-2.10474	Tetraspanin family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0250170.1	-0.58714	3.50268	-3.01135	0.003979	0.03489	-2.10484	Branched-chain amino acid aminotransferase-like	elongation zone	12 h
HORVU.MOREX.r3.2HG0123170.1	0.993826	0.673299	2.964982	0.004529	0.037933	-2.10561	Chaperone protein dnaJ	elongation zone	12 h
HORVU.MOREX.r3.2HG0126380.1	0.47792	5.874038	3.206504	0.002279	0.024194	-2.10576	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0472840.1	0.510954	2.862571	3.056943	0.003499	0.032032	-2.10612	NBS-LRR disease resistance protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0572400.1	-0.3608	3.75498	-3.01624	0.003924	0.034532	-2.10615	F-box family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0056810.1	0.417771	5.129894	3.10272	0.003072	0.029497	-2.10836	Haloacid dehalogenase-like hydrolase family protein, putative, expressed	elongation zone	12 h
HORVU.MOREX.r3.6HG0566930.1	-0.75993	4.262539	-2.96609	0.004515	0.037877	-2.10868	Biotin holocarboxylase synthetase 1-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0744890.1	1.095906	0.128022	2.940827	0.004843	0.039587	-2.10896	Methyl-coenzyme M reductase subunit beta	elongation zone	12 h
HORVU.MOREX.r3.4HG0392940.1	0.520224	5.529744	3.123413	0.002896	0.028327	-2.109	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0274100.1	-1.26865	1.731697	-3.00287	0.004074	0.035421	-2.1092	50S ribosomal protein L31	elongation zone	12 h
HORVU.MOREX.r3.3HG0280970.1	-0.41452	5.971206	-3.09662	0.003126	0.029864	-2.10954	Protein methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.6HG0624580.1	-1.1248	4.006778	-2.93989	0.004856	0.039601	-2.11073	Translation initiation factor IF-2, putative isoform 2	elongation zone	12 h
HORVU.MOREX.r3.1HG0021830.1	-0.33933	5.177385	-3.04236	0.003646	0.032938	-2.11081	SKP1-like protein 4	elongation zone	12 h
HORVU.MOREX.r3.6HG0620200.1	1.189975	-0.686	2.942733	0.004817	0.039433	-2.11136	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0091860.1	-0.32371	7.126684	-3.18645	0.002415	0.025092	-2.11234	Sugar transporter protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0407410.1	-0.94514	-0.65632	-2.93313	0.004947	0.040109	-2.11621	Glycosyltransferase	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.2HG0160760.1	0.665852	3.8459	3.045811	0.003611	0.032683	-2.11746	L-threonine 3-dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.1HG0061220.1	-1.13579	4.835261	-2.95265	0.004687	0.038809	-2.11769	DNA primase	elongation zone	12 h
HORVU.MOREX.r3.3HG0306220.1	-0.47163	4.083588	-2.99188	0.004202	0.036195	-2.11789	Transmembrane protein 62	elongation zone	12 h
HORVU.MOREX.r3.2HG0193080.1	-0.44137	3.176199	-2.97359	0.004422	0.037375	-2.11861	Protein-S-isoprenylcysteine O-methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.1HG0041250.1	-0.37019	4.039793	-2.99989	0.004109	0.035609	-2.12034	Peroxisome biogenesis protein 12	elongation zone	12 h
HORVU.MOREX.r3.1HG0059340.1	-0.28908	6.875668	-3.15506	0.002644	0.02661	-2.12046	Conserved oligomeric Golgi complex subunit 5	elongation zone	12 h
HORVU.MOREX.r3.3HG0236690.1	0.668023	1.038969	3.043804	0.003631	0.03284	-2.12458	Myb transcription factor	elongation zone	12 h
HORVU.MOREX.r3.1HG0088870.1	-0.26953	5.735596	-3.07935	0.003283	0.030822	-2.12514	ABC transporter ATP-binding protein ARB1	elongation zone	12 h
HORVU.MOREX.r3.2HG0173380.1	0.415622	4.283255	3.083436	0.003246	0.030621	-2.12539	Amino acid transporter, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0055580.1	-0.41079	5.226651	-3.0511	0.003557	0.032357	-2.12641	Kinesin-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0516470.1	-1.40758	4.720536	-2.92977	0.004993	0.040388	-2.12697	GDSL esterase/lipase	elongation zone	12 h
HORVU.MOREX.r3.5HG0444860.1	-1.36506	2.653302	-2.92727	0.005028	0.040572	-2.12748	Kinesin-related protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0298340.1	-0.73899	4.243389	-2.96005	0.004592	0.038331	-2.1291	Beta-galactosidase	elongation zone	12 h
HORVU.MOREX.r3.6HG0631050.1	-1.12145	6.885939	-3.06055	0.003463	0.031884	-2.12957	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.5HG0520670.1	-1.38496	-0.02366	-2.9785	0.004362	0.037137	-2.13022	beta glucosidase 41	elongation zone	12 h
HORVU.MOREX.r3.4HG0409880.1	1.419768	-2.34755	2.968916	0.00448	0.03765	-2.13266	Metal tolerance protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0046210.1	2.264067	-0.44242	3.03006	0.003775	0.03368	-2.13293	Receptor kinase	elongation zone	12 h
HORVU.MOREX.r3.5HG0513900.1	0.785464	-0.25185	2.928667	0.005009	0.040463	-2.13311	Leucine carboxyl methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0293570.1	-1.60574	-0.38794	-3.02074	0.003875	0.03426	-2.1348	BTB/POZ domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0128240.1	-0.38362	5.300426	-3.06193	0.00345	0.031816	-2.13532	Aldose 1-epimerase	elongation zone	12 h
HORVU.MOREX.r3.2HG0122500.2	-1.83143	-0.50803	-3.14198	0.002745	0.027347	-2.13745	GTPase obg	elongation zone	12 h
HORVU.MOREX.r3.5HG0426110.1	1.661491	-3.22479	3.027572	0.003801	0.033827	-2.13805	NBS-LRR class disease resistance protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0560140.1	1.980317	-1.9167	2.940566	0.004846	0.03959	-2.13886	Endoglucanase	elongation zone	12 h
HORVU.MOREX.r3.3HG0307950.1	-0.2717	6.122502	-3.10986	0.00301	0.02903	-2.14091	GPI transamidase component PIG-S	elongation zone	12 h
HORVU.MOREX.r3.7HG0676230.1	-0.86943	0.616952	-2.92505	0.005059	0.040741	-2.14137	Zinc finger C-x8-C-x5-C-x3-H type family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0501500.1	1.126821	3.165714	2.991273	0.004209	0.036196	-2.14205	Glucan endo-1,3-beta-glucosidase 3	elongation zone	12 h
HORVU.MOREX.r3.7HG0674600.1	1.115929	1.082795	2.949616	0.004726	0.03901	-2.1431	Aconitate hydratase	elongation zone	12 h
HORVU.MOREX.r3.2HG0110920.1	-1.88635	1.02517	-2.99268	0.004192	0.036159	-2.14538	VQ motif-containing family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0388780.1	1.83723	0.089382	3.177136	0.002481	0.025544	-2.14542	RNA polymerase sigma factor	elongation zone	12 h
HORVU.MOREX.r3.7HG0656340.1	-1.97221	-0.36508	-3.11022	0.003007	0.029025	-2.1456	Adhesion G protein-coupled receptor L3	elongation zone	12 h
HORVU.MOREX.r3.6HG0609830.1	0.661773	4.638207	3.168655	0.002543	0.025982	-2.14586	Pollen-specific arabinogalacta protein BAN102	elongation zone	12 h
HORVU.MOREX.r3.7HG0697980.1	-0.93761	0.647065	-2.93945	0.004861	0.039613	-2.15486	Fatty acid hydroxylase superfamily	elongation zone	12 h
HORVU.MOREX.r3.4HG0337500.1	-0.18104	9.290144	-3.22861	0.002137	0.023408	-2.15718	NADH-ubiquinone oxidoreductase subunit	elongation zone	12 h
HORVU.MOREX.r3.1HG0055500.1	1.013156	2.091951	3.120162	0.002923	0.028505	-2.15753	Pollen Ole e 1 allergen and extensin family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0620040.1	-1.29021	1.386644	-2.93496	0.004922	0.040007	-2.16053	Protein kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0714950.1	-0.59358	3.547437	-2.95277	0.004685	0.038809	-2.16152	Cytokinin riboside 5'-monophosphate phosphoribohydrolase	elongation zone	12 h
HORVU.MOREX.r3.2HG0122880.1	1.329168	1.048128	2.912038	0.005244	0.041806	-2.1619	Phytoene desaturase	elongation zone	12 h
HORVU.MOREX.r3.2HG0159920.1	-0.56459	3.687678	-2.9461	0.004773	0.039205	-2.16382	receptor-like kinase in flowers 1	elongation zone	12 h
HORVU.MOREX.r3.4HG0341810.1	-0.31501	7.757023	-3.14283	0.002739	0.027326	-2.16492	Cycloeucalenol cycloisomerase	elongation zone	12 h
HORVU.MOREX.r3.5HG0426480.1	-1.1734	2.819296	-2.91225	0.005241	0.041806	-2.16493	1-deoxy-D-xylulose 5-phosphate synthase 1	elongation zone	12 h
HORVU.MOREX.r3.1HG0058800.1	-0.53823	3.603853	-2.94377	0.004804	0.039373	-2.16522	Glycosyltransferase	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.7HG0667680.1	1.009409	4.54919	3.09828	0.003111	0.029766	-2.16721	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.3HG0299300.1	-1.10794	0.206257	-2.9694	0.004474	0.037622	-2.16836	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0434380.1	-0.3843	4.006199	-2.99286	0.00419	0.036157	-2.16892	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.6HG0616450.1	1.129299	0.245809	2.968129	0.004489	0.037709	-2.17079	Na(+)/H(+) exchange regulatory cofactor NHE-RF3	elongation zone	12 h
HORVU.MOREX.r3.7HG0657330.1	0.426851	6.822879	3.22414	0.002165	0.023553	-2.17354	ENTH/ANTH/VHS superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0656420.1	-1.06389	0.082394	-2.9437	0.004805	0.039373	-2.17518	SWI/SNF complex subunit SMARCC2	elongation zone	12 h
HORVU.MOREX.r3.6HG0607000.1	-1.73278	0.642043	-3.17377	0.002505	0.02572	-2.17601	Pectin acetylesterase	elongation zone	12 h
HORVU.MOREX.r3.3HG0219740.1	-0.61527	6.408651	-3.05647	0.003504	0.032039	-2.17849	50S ribosomal protein L2, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0744260.1	-2.98097	0.783361	-3.20564	0.002284	0.0242	-2.18088	NHL domain-containing protein, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0500220.1	-0.31621	6.295637	-3.09065	0.00318	0.030179	-2.18135	Protein PAT1 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0158020.1	-0.41197	4.300593	-2.97683	0.004382	0.037198	-2.18254	BTB-POZ and MATH domain protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0018430.1	-1.0677	3.282493	-2.90264	0.005381	0.042386	-2.18361	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.7HG0711270.1	0.807358	3.15201	3.186582	0.002414	0.025092	-2.18431	Xyloglucan endotransglucosylase/hydrolase	elongation zone	12 h
HORVU.MOREX.r3.2HG0190800.1	1.708104	0.966626	3.049107	0.003577	0.032459	-2.18469	F-box protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0395770.1	-0.74065	1.202249	-2.90392	0.005362	0.042352	-2.18617	Hsp70 nucleotide exchange factor fes1	elongation zone	12 h
HORVU.MOREX.r3.6HG0627090.1	0.662526	1.38286	2.91679	0.005175	0.041436	-2.18619	Alcohol dehydrogenase 3	elongation zone	12 h
HORVU.MOREX.r3.7HG0727350.1	-0.40269	10.95622	-3.24775	0.00202	0.022545	-2.18675	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0316280.1	-0.85384	4.501603	-2.94017	0.004852	0.039601	-2.18967	Transcription initiation factor TFIID subunit 9	elongation zone	12 h
HORVU.MOREX.r3.3HG0327100.1	1.167641	-3.0577	2.933764	0.004939	0.040086	-2.19108	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0512510.1	-0.60982	7.202032	-3.11074	0.003003	0.029025	-2.19166	Subtilisin-like protease	elongation zone	12 h
HORVU.MOREX.r3.6HG0546200.1	-0.55843	4.682471	-2.97816	0.004366	0.037141	-2.19229	DNA-directed RNA polymerase II subunit rpb4	elongation zone	12 h
HORVU.MOREX.r3.1HG0062630.1	0.466177	5.379794	3.034513	0.003728	0.033447	-2.19356	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0543540.1	1.35374	-0.02472	2.958892	0.004606	0.038423	-2.19473	Expansin protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0327630.1	-1.15984	4.246104	-2.90491	0.005347	0.042285	-2.1961	Cyclin family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0296990.1	0.847045	-1.49078	2.906294	0.005327	0.042206	-2.1969	LURP-one-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0605960.1	0.687148	3.198592	2.996644	0.004146	0.035879	-2.19846	Lysine-specific demethylase	elongation zone	12 h
HORVU.MOREX.r3.4HG0341080.1	-1.81	4.721757	-2.89833	0.005445	0.042719	-2.19939	interferon-activable protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0176680.1	-0.23745	6.632089	-3.0902	0.003184	0.030203	-2.20084	Serine/threonine protein phosphatase 2A regulatory subunit B	elongation zone	12 h
HORVU.MOREX.r3.6HG0618110.1	-0.70438	3.25054	-2.97672	0.004383	0.037198	-2.20279	growth-regulating factor 9	elongation zone	12 h
HORVU.MOREX.r3.1HG0070110.1	0.347249	5.55369	3.087594	0.003207	0.030372	-2.20454	Type I inositol-1,4,5-trisphosphate 5-phosphatase	elongation zone	12 h
HORVU.MOREX.r3.1HG0056990.1	0.457771	3.797448	3.019746	0.003886	0.03428	-2.20571	Camphor resistance CrcB family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0409600.1	0.487457	4.470889	3.096104	0.003131	0.029866	-2.20833	Protein kinase family protein, putative, expressed	elongation zone	12 h
HORVU.MOREX.r3.3HG0278710.1	0.660082	6.634206	3.254345	0.001982	0.022356	-2.21108	Fasciclin-like arabinogalactan protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0018110.1	0.374711	8.069235	3.20901	0.002262	0.02416	-2.2121	ABC transporter B family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0565800.1	0.770302	0.673146	2.925295	0.005055	0.040734	-2.21338	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.1HG0011820.1	0.924023	-1.28428	2.931672	0.004967	0.040223	-2.21464	Protein ABIL1	elongation zone	12 h
HORVU.MOREX.r3.3HG0293700.1	-0.66041	6.606906	-3.04098	0.00366	0.03303	-2.21532	Protein downstream neighbor of Son	elongation zone	12 h
HORVU.MOREX.r3.3HG0294100.1	-0.3761	4.223869	-3.03025	0.003773	0.03368	-2.21643	NAD(P)H dehydrogenase (Quinone)	elongation zone	12 h
HORVU.MOREX.r3.2HG0101220.2	-0.49806	2.581199	-2.92005	0.005129	0.041178	-2.21667	Formin-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0688770.1	-0.68814	3.39936	-2.91467	0.005206	0.041597	-2.2176	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0567780.1	-0.50974	3.016753	-2.92241	0.005096	0.041023	-2.2189	disease resistance protein (TIR-NBS-LRR class)	elongation zone	12 h

Table Sʜ Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.2HG0159500.1	-0.75882	5.303207	-2.96293	0.004555	0.038087	-2.21906	tRNA (Adenine-N(1)-)-methyltransferase catalytic subunit trmt61a	elongation zone	12 h
HORVU.MOREX.r3.5HG0476390.1	-0.85495	1.081391	-2.88765	0.005607	0.04358	-2.21941	Transporter-related family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0332710.1	-2.92507	-2.51339	-3.27302	0.001876	0.021568	-2.21966	DNA mismatch repair protein MutL	elongation zone	12 h
HORVU.MOREX.r3.3HG0294110.1	0.927177	-1.24039	2.885214	0.005644	0.043691	-2.22067	#N/A	elongation zone	12 h
HORVU.MOREX.r3.4HG0375440.1	-1.16763	2.464559	-2.90668	0.005322	0.042178	-2.22113	ATP-dependent Clp protease proteolytic subunit	elongation zone	12 h
HORVU.MOREX.r3.3HG0239110.1	-0.92548	4.789763	-3.05077	0.003561	0.032357	-2.22151	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.6HG0611290.1	-0.8512	7.158294	-3.02463	0.003833	0.034006	-2.22329	Acetolactate synthase	elongation zone	12 h
HORVU.MOREX.r3.6HG0550670.1	-1.81029	7.005258	-2.99238	0.004196	0.036159	-2.22545	Glycine-rich cell wall structural protein 2	elongation zone	12 h
HORVU.MOREX.r3.7HG0673710.1	1.43696	-0.09914	2.89192	0.005542	0.043254	-2.2257	Receptor-like protein kinase	elongation zone	12 h
HORVU.MOREX.r3.2HG0125780.1	-1.2602	0.405475	-2.95685	0.004632	0.038594	-2.22594	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0749100.1	0.92186	-1.03535	2.948325	0.004743	0.03909	-2.22818	arginine/serine-rich splicing factor 35	elongation zone	12 h
HORVU.MOREX.r3.3HG0319570.1	-1.15683	3.275641	-2.8859	0.005634	0.043682	-2.22826	Crossover junction endonuclease mus81	elongation zone	12 h
HORVU.MOREX.r3.3HG0280920.1	-0.62641	3.219452	-3.04127	0.003657	0.033017	-2.2287	DUF4228 domain protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0730530.1	1.009407	0.190357	2.942306	0.004823	0.039462	-2.22973	Copper transport protein family	elongation zone	12 h
HORVU.MOREX.r3.1HG0037920.1	-1.92316	0.68135	-2.98252	0.004313	0.036879	-2.23033	Protein restricted tev movement 2	elongation zone	12 h
HORVU.MOREX.r3.4HG0395120.1	-0.63162	2.404038	-2.88534	0.005643	0.043691	-2.23084	Mitochondrial carrier family	elongation zone	12 h
HORVU.MOREX.r3.3HG0234030.1	0.838639	0.965447	3.059054	0.003478	0.031944	-2.23106	Xyloglucan galactosyltransferase KATAMARI1-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0167620.1	-1.25165	2.679481	-2.89101	0.005556	0.043297	-2.2313	Plastid-lipid associated protein PAP / fibrillin family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0686830.1	-0.82458	2.110337	-2.87968	0.005731	0.044174	-2.23279	TraB family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0608800.1	-0.56853	4.150298	-2.91858	0.00515	0.041296	-2.23495	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0345260.1	1.209781	-1.43865	2.878385	0.005751	0.044248	-2.23636	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1	elongation zone	12 h
HORVU.MOREX.r3.4HG0333840.1	-0.80044	1.907765	-2.87906	0.00574	0.044183	-2.23653	Histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH5	elongation zone	12 h
HORVU.MOREX.r3.2HG0203330.1	0.432961	5.510492	3.0629	0.00344	0.031786	-2.23694	Sec14p-like phosphatidylinositol transfer family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0003150.1	-0.62639	4.554906	-2.92156	0.005108	0.041076	-2.23752	Chaperone protein DnaJ	elongation zone	12 h
HORVU.MOREX.r3.4HG0344790.1	0.453177	4.360827	2.999819	0.004109	0.035609	-2.23801	Non-specific serine/threonine protein kinase	elongation zone	12 h
HORVU.MOREX.r3.6HG0594420.1	-0.39558	3.225218	-2.91799	0.005158	0.041348	-2.24071	Transporter-related family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0514020.1	0.441112	3.72423	2.968843	0.004481	0.03765	-2.2424	GRAS transcription factor	elongation zone	12 h
HORVU.MOREX.r3.6HG0601560.1	-1.1885	0.277948	-2.92919	0.005001	0.040437	-2.24279	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0701080.1	0.875563	-1.51889	2.882938	0.00568	0.043865	-2.24322	MYB transcription factor	elongation zone	12 h
HORVU.MOREX.r3.2HG0160790.1	-0.52785	4.130952	-2.93017	0.004988	0.040374	-2.24325	Alcohol dehydrogenase 3	elongation zone	12 h
HORVU.MOREX.r3.7HG0679730.1	-1.40074	-0.42256	-2.93893	0.004868	0.039627	-2.24333	AP-1 complex subunit gamma-2	elongation zone	12 h
HORVU.MOREX.r3.3HG0296940.1	-0.77807	2.177147	-2.87404	0.00582	0.04466	-2.24494	Calcium uniporter, mitochondrial	elongation zone	12 h
HORVU.MOREX.r3.4HG0395130.1	-1.68299	-0.45189	-3.11682	0.002951	0.028675	-2.24535	Cyclin, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0345810.1	-1.26043	1.299714	-2.9212	0.005113	0.041095	-2.24656	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0140380.1	1.766269	-1.74806	2.90582	0.005334	0.042229	-2.24677	CTD small phosphatase-like protein 2, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0669750.1	0.408166	4.895319	3.081726	0.003261	0.030701	-2.24758	Sn1-specific diacylglycerol lipase alpha	elongation zone	12 h
HORVU.MOREX.r3.2HG0158180.1	0.93866	3.62095	2.953343	0.004678	0.038805	-2.24971	Proline transporter	elongation zone	12 h
HORVU.MOREX.r3.2HG0096290.1	0.608155	1.613406	2.952847	0.004684	0.038809	-2.25141	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family meml	elongation zone	12 h
HORVU.MOREX.r3.3HG0326430.1	-0.27487	5.095188	-3.02093	0.003873	0.03426	-2.25278	Diphosphomevalonate decarboxylase	elongation zone	12 h
HORVU.MOREX.r3.2HG0189010.1	0.945507	3.632309	2.952995	0.004682	0.038809	-2.2528	Glycerol-3-phosphate transporter, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0004290.1	-1.05573	6.306577	-3.00847	0.004011	0.035058	-2.25383	Chymotrypsin inhibitor	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.4HG0375550.1	-2.26771	0.494963	-3.12907	0.002849	0.028054	-2.25622	Rapid ALkalinization Factor family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0632980.1	-1.5627	5.615728	-2.91436	0.00521	0.041617	-2.25884	Replication protein A 32 kDa subunit	elongation zone	12 h
HORVU.MOREX.r3.6HG0568870.1	-0.79519	4.739053	-2.94756	0.004753	0.039139	-2.2596	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.4HG0407310.1	0.720376	3.764737	3.029891	0.003777	0.03368	-2.26017	Xyloglucan galactosyltransferase KATAMARI1-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0088530.1	0.783643	0.052643	2.872872	0.005838	0.044752	-2.26111	Cytochrome b561 domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0342680.1	0.947958	-0.60974	2.957978	0.004618	0.038489	-2.26301	Branchpoint-bridging protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0228010.1	-0.39623	4.500471	-2.96497	0.004529	0.037933	-2.26545	EKC/KEOPS complex subunit CGI121	elongation zone	12 h
HORVU.MOREX.r3.6HG0618170.1	-0.25586	6.062292	-3.03503	0.003722	0.033412	-2.26558	1-aminocyclopropane-1-carboxylate deaminase/D-cysteine desulfhydrase	elongation zone	12 h
HORVU.MOREX.r3.4HG0409670.1	1.171815	1.37934	2.970553	0.004459	0.037548	-2.26702	Respiratory burst oxidase homolog	elongation zone	12 h
HORVU.MOREX.r3.2HG0163090.1	-0.83342	7.015883	-3.01481	0.00394	0.034626	-2.26805	Heavy metal-associated protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0586570.1	-0.86434	0.923324	-2.88752	0.005609	0.04358	-2.26882	Transposon Ty3-G Gag-Pol polyprotein	elongation zone	12 h
HORVU.MOREX.r3.3HG0225640.1	-1.29815	1.458957	-2.92075	0.005119	0.041131	-2.26984	Peptidyl-tRNA hydrolase family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0543400.1	1.263887	-0.34964	2.961449	0.004574	0.038197	-2.27088	High affinity nitrate transporter	elongation zone	12 h
HORVU.MOREX.r3.5HG0491230.1	-0.92335	2.284228	-2.86224	0.00601	0.045661	-2.27102	Dihydroflavonol-4-reductase	elongation zone	12 h
HORVU.MOREX.r3.1HG0073160.1	0.42732	5.05488	3.058927	0.003479	0.031944	-2.27177	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.1HG0010920.1	0.564321	2.101242	2.972919	0.00443	0.037408	-2.27243	Protein aluminum sensitive 3	elongation zone	12 h
HORVU.MOREX.r3.6HG0619540.1	-0.35122	5.673476	-2.99152	0.004206	0.036196	-2.27257	THO complex subunit 5	elongation zone	12 h
HORVU.MOREX.r3.6HG0556240.1	0.455526	4.26639	2.987018	0.004259	0.036533	-2.27359	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0289070.1	-1.20542	2.310764	-2.90585	0.005334	0.042229	-2.27416	Protein TIC 22-like, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.2HG0098420.1	-1.14149	5.161437	-2.9029	0.005377	0.042386	-2.27687	CDT1-like protein a, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.1HG0043350.1	-0.49482	3.574077	-2.92851	0.005011	0.040464	-2.27758	Transmembrane protein, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0310460.1	-0.54787	0.959034	-2.98394	0.004296	0.036791	-2.27929	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0662830.1	-0.92379	4.730198	-2.88582	0.005635	0.043682	-2.27939	Mechanosensitive ion channel family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0495490.1	-0.42215	4.866247	-2.99107	0.004211	0.036201	-2.27964	CCR4-NOT transcription complex subunit 2	elongation zone	12 h
HORVU.MOREX.r3.5HG0446420.1	0.765283	4.215118	3.155351	0.002642	0.026601	-2.27982	GDSL esterase/lipase	elongation zone	12 h
HORVU.MOREX.r3.7HG0675770.1	-0.45552	4.417254	-3.02885	0.003788	0.033749	-2.27996	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0607590.1	0.937508	1.682477	2.867464	0.005925	0.045249	-2.28	U-box domain-containing family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0535780.1	-0.71126	6.219129	-2.99167	0.004204	0.036196	-2.28069	Transmembrane protein 70, mitochondrial	elongation zone	12 h
HORVU.MOREX.r3.2HG0212990.1	-0.66075	5.148472	-2.91159	0.00525	0.041806	-2.28074	Acyl-protein thioesterase 1	elongation zone	12 h
HORVU.MOREX.r3.6HG0552720.1	-0.41058	3.733307	-2.92037	0.005125	0.041158	-2.28244	Beta-amylase	elongation zone	12 h
HORVU.MOREX.r3.2HG0154740.1	-0.78356	1.125076	-2.85799	0.00608	0.045953	-2.28321	cysteine-rich RLK (RECEPTOR-like protein kinase) 11	elongation zone	12 h
HORVU.MOREX.r3.4HG0406380.1	-0.38527	5.163919	-2.9752	0.004402	0.037294	-2.28393	GEM-like protein 1	elongation zone	12 h
HORVU.MOREX.r3.6HG0544350.1	0.423123	5.04997	3.019794	0.003885	0.03428	-2.2846	Carboxypeptidase	elongation zone	12 h
HORVU.MOREX.r3.3HG0235320.1	1.506909	-0.14202	2.891324	0.005551	0.043292	-2.2854	Pollen Ole e 1 allergen and extensin family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0139050.1	-1.00938	3.432928	-2.86438	0.005975	0.045496	-2.28621	Protein kinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0306820.2	-1.32584	0.136032	-2.88881	0.005589	0.043492	-2.28721	ATP-dependent Clp protease ATP-binding subunit ClpX	elongation zone	12 h
HORVU.MOREX.r3.6HG0621170.1	1.754667	-0.64178	2.854987	0.00613	0.046179	-2.28721	GPI-anchored adhesin-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0437610.1	-0.82768	5.573525	-2.94937	0.00473	0.03901	-2.28908	caspase-6 protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0501270.1	-1.40767	6.400081	-2.93344	0.004943	0.04009	-2.29121	Chromatin assembly factor-1	elongation zone	12 h
HORVU.MOREX.r3.6HG0569490.1	-0.44483	6.2556	-3.00429	0.004058	0.035331	-2.29166	Rad23 UV excision repair protein family	elongation zone	12 h
HORVU.MOREX.r3.6HG0548460.1	-1.10854	4.93645	-2.91491	0.005202	0.041594	-2.29204	Histone H4	elongation zone	12 h

Table Sн Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.7HG0742370.1	1.241051	-1.39541	2.876372	0.005783	0.044393	-2.29447	Calmodulin	elongation zone	12 h
HORVU.MOREX.r3.3HG0242520.1	-0.54075	4.276799	-2.95569	0.004647	0.038656	-2.29639	Protein O-mannosyl-transferase 2	elongation zone	12 h
HORVU.MOREX.r3.2HG0126010.1	-0.35596	4.262083	-2.9474	0.004756	0.039139	-2.29656	RING/U-box superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0077960.1	0.530065	7.898538	3.129066	0.002849	0.028054	-2.29665	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0299530.1	-0.5169	3.978312	-2.92151	0.005108	0.041076	-2.29666	F-box protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0510370.1	-0.30185	4.654596	-2.97163	0.004446	0.037513	-2.29705	PHD finger protein ING	elongation zone	12 h
HORVU.MOREX.r3.2HG0199330.1	0.628715	1.351775	3.031737	0.003757	0.033621	-2.2999	Anthocyanidin reductase	elongation zone	12 h
HORVU.MOREX.r3.6HG0570230.1	0.8401	0.733369	2.84818	0.006245	0.046631	-2.30134	Aldose 1-epimerase family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0515370.1	-0.50243	3.30293	-2.91764	0.005163	0.041371	-2.30577	F-box family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0213430.1	0.76089	0.482455	2.996904	0.004143	0.035871	-2.3073	Calcium-dependent lipid-binding domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0729510.1	-0.48554	4.709018	-3.00109	0.004095	0.035557	-2.30734	WEB family protein, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.1HG0074650.2	-1.02941	0.819721	-2.84529	0.006294	0.046811	-2.30742	Solute carrier family 35 protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0240350.1	0.56487	2.152333	2.905165	0.005344	0.042285	-2.30877	Two-component response regulator	elongation zone	12 h
HORVU.MOREX.r3.2HG0132160.1	2.189127	-1.56452	3.061343	0.003456	0.031841	-2.30891	Ethylene-responsive transcription factor	elongation zone	12 h
HORVU.MOREX.r3.6HG0634070.1	-0.42937	4.157253	-2.93927	0.004864	0.039613	-2.30896	Metal tolerance-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0303380.1	0.67693	-0.86738	2.907599	0.005308	0.042087	-2.30956	Zinc finger protein CONSTANS	elongation zone	12 h
HORVU.MOREX.r3.1HG0054770.1	-0.57242	3.561935	-2.90334	0.005371	0.042365	-2.31011	#N/A	elongation zone	12 h
HORVU.MOREX.r3.4HG0335650.1	-1.33168	8.653964	-3.05852	0.003483	0.031953	-2.31164	Antimicrobial peptide MBP-1	elongation zone	12 h
HORVU.MOREX.r3.5HG0517260.1	0.540547	3.552392	2.886096	0.005631	0.043682	-2.3121	Glutamate carboxypeptidase 2	elongation zone	12 h
HORVU.MOREX.r3.5HG0504250.1	-0.73654	4.308218	-2.91379	0.005218	0.04165	-2.3131	#N/A	elongation zone	12 h
HORVU.MOREX.r3.1HG0042440.1	1.39212	-1.0109	2.855717	0.006118	0.046138	-2.31543	Long-chain-alcohol oxidase	elongation zone	12 h
HORVU.MOREX.r3.6HG0622980.1	-0.39238	4.462563	-2.93185	0.004965	0.040219	-2.31634	Protein RFT1-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0033360.1	-0.28475	4.66696	-2.97354	0.004422	0.037375	-2.31853	Cysteine synthase	elongation zone	12 h
HORVU.MOREX.r3.4HG0393260.1	-0.32201	7.041152	-3.0246	0.003833	0.034006	-2.31905	Oxidoreductase, 2OG-Fe(II) oxygenase family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0090200.1	-0.47267	5.563212	-2.9777	0.004371	0.037158	-2.31927	NBS-LRR-like resistance protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0138300.1	-0.70876	7.540969	-3.04829	0.003586	0.032498	-2.3197	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.6HG0546140.1	-0.70236	0.639454	-2.8475	0.006256	0.046701	-2.32027	F-box protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0388440.1	0.875687	4.312002	3.060968	0.003459	0.03186	-2.32134	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0470800.1	-2.18216	1.425735	-2.97882	0.004358	0.037119	-2.32311	#N/A	elongation zone	12 h
HORVU.MOREX.r3.4HG0408780.1	1.977515	0.649042	3.152131	0.002667	0.026789	-2.32533	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0054200.1	-0.33308	5.861579	-3.0037	0.004065	0.035366	-2.32606	E2 ubiquitin-conjugating-like enzyme	elongation zone	12 h
HORVU.MOREX.r3.4HG0381150.1	1.851211	-0.56149	3.105635	0.003047	0.02931	-2.32777	nuclear pore complex protein (DUF3414)	elongation zone	12 h
HORVU.MOREX.r3.2HG0165200.1	0.628891	5.318501	3.117027	0.002949	0.028675	-2.33121	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0298750.1	-0.47868	5.760333	-3.00551	0.004044	0.03527	-2.33165	magnesium transporter NIPA (DUF803)	elongation zone	12 h
HORVU.MOREX.r3.6HG0569990.1	0.274275	6.145643	3.061362	0.003455	0.031841	-2.33294	Calmodulin binding protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0120560.1	1.161665	3.65156	3.147496	0.002702	0.02705	-2.33341	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.7HG0696220.1	-0.94967	1.255372	-2.84248	0.006342	0.047069	-2.33509	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0633640.1	-0.27235	5.286476	-3.00972	0.003997	0.034974	-2.33552	Thiaminase-1	elongation zone	12 h
HORVU.MOREX.r3.4HG0340650.1	0.399662	3.253441	2.909831	0.005276	0.041943	-2.33604	Peptidyl-prolyl cis-trans isomerase	elongation zone	12 h
HORVU.MOREX.r3.3HG0249810.1	-0.39998	5.280301	-2.95375	0.004673	0.038786	-2.3367	Basic helix-loop-helix (BHLH) family transcription factor	elongation zone	12 h
HORVU.MOREX.r3.7HG0744250.1	-0.73466	5.1276	-2.91532	0.005196	0.041571	-2.33681	Indole-3-glycerol phosphate synthase-like	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.6HG0539200.1	-0.3625	5.866339	-2.98103	0.004331	0.036952	-2.33708	Translation initiation factor IF-3	elongation zone	12 h
HORVU.MOREX.r3.6HG0618180.1	1.303284	-2.40297	2.852517	0.006172	0.046337	-2.33901	Universal stress protein family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0751450.1	1.429302	0.190404	2.837129	0.006435	0.047408	-2.34023	Glycosyltransferase family 92 protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0095650.1	-1.45853	1.475239	-2.87765	0.005763	0.044304	-2.34027	Mitochondrial inner membrane protease subunit 1	elongation zone	12 h
HORVU.MOREX.r3.4HG0391260.1	0.6147	2.259948	3.034078	0.003732	0.033458	-2.34133	Clathrin heavy chain	elongation zone	12 h
HORVU.MOREX.r3.2HG0205680.1	-1.94321	1.160765	-3.04655	0.003603	0.032644	-2.34155	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0156140.1	-1.14665	0.390799	-2.86506	0.005964	0.045453	-2.34255	D-alanine--D-alanine ligase	elongation zone	12 h
HORVU.MOREX.r3.7HG0663730.1	-1.95767	2.17959	-2.85614	0.006111	0.046117	-2.34258	Galactoside 2-alpha-L-fucosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0104260.1	-0.66387	3.968231	-2.88387	0.005665	0.043799	-2.34312	Carboxypeptidase	elongation zone	12 h
HORVU.MOREX.r3.5HG0496780.1	0.436708	4.42219	2.952154	0.004693	0.038833	-2.34365	C2 domain-containing protein / GRAM domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0630650.1	-1.69052	3.863031	-2.83906	0.006401	0.047335	-2.34477	Protein DETOXIFICATION	elongation zone	12 h
HORVU.MOREX.r3.4HG0403630.1	1.562826	-3.22747	2.877447	0.005766	0.044312	-2.34488	3-ketoacyl-CoA synthase 19	elongation zone	12 h
HORVU.MOREX.r3.2HG0124660.1	0.296124	4.762294	2.9816	0.004324	0.036952	-2.34519	Dihydropteroate synthase, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0490810.1	-0.26348	7.111815	-3.06782	0.003393	0.031493	-2.34553	C2 calcium/lipid-binding and GRAM domain protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0408000.1	2.639891	-1.23574	3.124366	0.002888	0.028299	-2.34677	Cytokinin riboside 5'-monophosphate phosphoribohydrolase	elongation zone	12 h
HORVU.MOREX.r3.4HG0378710.1	-0.77229	2.281537	-2.82765	0.006602	0.048163	-2.34773	F-box/SPRY domain-containing protein 1	elongation zone	12 h
HORVU.MOREX.r3.6HG0605120.1	-0.61425	2.469228	-2.88939	0.00558	0.04344	-2.34813	RING/U-box superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0427370.1	-0.83484	1.304181	-2.85749	0.006088	0.045983	-2.34836	#N/A	elongation zone	12 h
HORVU.MOREX.r3.4HG0393890.1	-0.6528	3.825718	-2.8484	0.006241	0.046621	-2.34921	Hydroxyproline-rich glycoprotein	elongation zone	12 h
HORVU.MOREX.r3.1HG0008440.1	-0.70841	7.032439	-2.99571	0.004157	0.035915	-2.35482	Glutathione S-transferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0101250.1	0.803399	0.35887	2.844063	0.006315	0.046917	-2.35518	Protein kinase superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0656440.1	-0.45916	5.106986	-2.91871	0.005148	0.041296	-2.3562	Adenylyltransferase and sulfurtransferase MOCS3	elongation zone	12 h
HORVU.MOREX.r3.5HG0430460.1	0.489467	1.634629	2.974328	0.004413	0.037339	-2.35785	Proline-rich family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0433470.1	0.358114	8.072662	3.159287	0.002612	0.026441	-2.35919	Auxin-responsive protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0585520.2	-0.541	2.330826	-2.83341	0.0065	0.04774	-2.36016	Calmodulin binding protein-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0007670.1	0.583834	3.98467	2.921975	0.005102	0.041056	-2.36017	OCS-element binding factor 5	elongation zone	12 h
HORVU.MOREX.r3.7HG0648520.1	-1.86787	0.765033	-2.96732	0.0045	0.037778	-2.36035	Retrovirus-related Pol polyprotein from transposon TNT 1-94	elongation zone	12 h
HORVU.MOREX.r3.3HG0304230.1	2.170384	-2.34493	2.955542	0.004649	0.038656	-2.3609	Cysteine proteinase	elongation zone	12 h
HORVU.MOREX.r3.7HG0692070.1	-0.7256	3.172308	-2.83931	0.006397	0.047329	-2.36194	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0012330.1	-0.77273	6.207328	-2.94343	0.004808	0.039386	-2.36389	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0519240.1	-0.58035	3.688408	-2.85786	0.006082	0.045953	-2.36421	PHD finger-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0487640.1	-1.04074	6.108222	-2.94972	0.004725	0.03901	-2.36676	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.5HG0422490.1	-0.41388	4.367008	-2.90404	0.00536	0.042352	-2.36829	#N/A	elongation zone	12 h
HORVU.MOREX.r3.1HG0059000.1	-0.95461	2.194539	-2.82618	0.006629	0.048286	-2.37195	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.6HG0599080.1	-0.36576	8.233534	-3.08314	0.003248	0.030632	-2.37203	Hsp70-Hsp90 organizing protein 1	elongation zone	12 h
HORVU.MOREX.r3.4HG0397530.1	1.080408	3.745067	2.950686	0.004712	0.03896	-2.3731	Plant calmodulin-binding-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0209910.1	-0.41547	8.205773	-3.09559	0.003135	0.029868	-2.37503	Pyruvate kinase	elongation zone	12 h
HORVU.MOREX.r3.1HG0063000.1	-0.43826	4.145332	-2.89506	0.005494	0.042997	-2.37533	Methyl-CpG-binding domain-containing family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0725060.1	-1.52027	3.350962	-2.82993	0.006562	0.048105	-2.37705	Microtubule associated family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0670020.1	-1.49884	7.08952	-2.92998	0.00499	0.04038	-2.37845	Ribonucleoside-diphosphate reductase small chain	elongation zone	12 h
HORVU.MOREX.r3.7HG0696190.1	-0.43566	6.218033	-2.96505	0.004528	0.037933	-2.37943	Glucose-1-phosphate adenylyltransferase	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.2HG0138280.1	-0.62209	5.728929	-2.94537	0.004782	0.039253	-2.38053	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.4HG0343540.1	-1.49432	-0.26772	-2.92525	0.005056	0.040734	-2.38087	BSD domain containing protein, expressed	elongation zone	12 h
HORVU.MOREX.r3.4HG0393120.1	-1.04833	1.488884	-2.81082	0.00691	0.049645	-2.38268	Zinc finger protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0217550.1	0.388921	5.544285	3.056857	0.0035	0.032032	-2.38533	rRNA N-glycosidase	elongation zone	12 h
HORVU.MOREX.r3.6HG0608960.1	0.529995	3.939137	2.91158	0.00525	0.041806	-2.38728	Galactan beta-1,4-galactosyltransferase GALS1	elongation zone	12 h
HORVU.MOREX.r3.3HG0327710.1	-0.3268	7.225707	-3.06312	0.003438	0.03178	-2.38757	Cytochrome b5	elongation zone	12 h
HORVU.MOREX.r3.6HG0567370.2	0.79654	0.756346	2.81843	0.006769	0.048991	-2.38789	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0122140.1	-0.47674	5.407639	-2.98111	0.00433	0.036952	-2.3883	#N/A	elongation zone	12 h
HORVU.MOREX.r3.1HG0079130.1	0.362439	7.030038	3.075665	0.003318	0.031043	-2.38888	ENTH/ANTH/VHS superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0475150.1	1.030572	1.439697	2.836485	0.006446	0.047445	-2.39003	ATP-binding cassette transporter subfamily A member	elongation zone	12 h
HORVU.MOREX.r3.2HG0190300.1	0.520915	3.611092	2.950152	0.004719	0.039002	-2.39068	SHR5-receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.2HG0114840.1	-0.66714	2.755393	-2.81998	0.006741	0.048843	-2.39232	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0294310.1	0.881653	1.665951	2.811627	0.006895	0.049555	-2.39469	Breast carcinoma-amplified sequence 3-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0320350.1	1.859923	-0.52659	2.964422	0.004536	0.037976	-2.39756	Proline synthase co-transcribed bacterial	elongation zone	12 h
HORVU.MOREX.r3.6HG0623830.1	-1.88605	4.072429	-2.81313	0.006867	0.049493	-2.39788	Disease resistance protein (NBS-LRR class) family	elongation zone	12 h
HORVU.MOREX.r3.6HG0558250.1	-0.59319	4.279829	-2.89838	0.005444	0.042719	-2.40005	Disease resistance protein (NBS-LRR class) family	elongation zone	12 h
HORVU.MOREX.r3.4HG0384700.1	-0.92274	3.809991	-2.85194	0.006181	0.04639	-2.403	Protein phosphatase 2C family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0156590.1	-0.43263	6.191891	-2.96979	0.004469	0.037596	-2.40346	Protein embryo defective 1674	elongation zone	12 h
HORVU.MOREX.r3.1HG0064390.1	0.382057	5.924306	3.062444	0.003445	0.031796	-2.40454	Mitochondrial carrier family	elongation zone	12 h
HORVU.MOREX.r3.2HG0142490.1	-0.27853	6.46738	-2.98918	0.004233	0.036363	-2.40801	Protein FLX-like 1	elongation zone	12 h
HORVU.MOREX.r3.5HG0460560.1	-2.33798	-0.88929	-3.13181	0.002827	0.027901	-2.40809	Set1/Ash2 histone methyltransferase complex subunit ASH2	elongation zone	12 h
HORVU.MOREX.r3.7HG0674680.1	1.236367	-0.96251	2.827736	0.006601	0.048163	-2.40977	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.2HG0180060.1	-1.21111	1.155124	-2.86602	0.005949	0.045377	-2.41056	Receptor-kinase, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0499620.1	-0.53511	3.333821	-2.84989	0.006216	0.046499	-2.41168	Methyltransferase, FkbM family protein, expressed	elongation zone	12 h
HORVU.MOREX.r3.5HG0495580.1	-0.3148	5.893655	-2.971	0.004454	0.037542	-2.41224	Ankyrin repeat domain containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0056740.1	-0.55149	8.162243	-3.06246	0.003445	0.031796	-2.41227	Pyruvate kinase	elongation zone	12 h
HORVU.MOREX.r3.1HG0059850.1	0.524134	4.1487	2.947521	0.004754	0.039139	-2.41249	Lipase	elongation zone	12 h
HORVU.MOREX.r3.3HG0293420.1	1.061129	-1.27948	2.871752	0.005856	0.04486	-2.41536	Expansin	elongation zone	12 h
HORVU.MOREX.r3.6HG0554560.1	-1.00637	4.575431	-2.85861	0.00607	0.045938	-2.41668	BZIP transcription factor	elongation zone	12 h
HORVU.MOREX.r3.1HG0052790.1	-0.46969	6.26243	-2.98713	0.004258	0.036533	-2.41687	Nucleoid-associated protein Ccur92_18190	elongation zone	12 h
HORVU.MOREX.r3.4HG0398980.1	0.353057	5.041369	3.010092	0.003993	0.034968	-2.41886	ADP-ribosylation factor, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0401980.1	2.833202	-2.74383	2.882004	0.005694	0.043944	-2.42017	Sulfate transporter	elongation zone	12 h
HORVU.MOREX.r3.6HG0603210.1	2.042637	0.043239	3.152146	0.002666	0.026789	-2.42093	DNA-directed RNA polymerase subunit	elongation zone	12 h
HORVU.MOREX.r3.2HG0096760.1	-0.80443	4.20342	-2.82015	0.006738	0.048837	-2.42139	TOM1-like protein 2	elongation zone	12 h
HORVU.MOREX.r3.3HG0320520.1	0.680544	2.494839	2.828518	0.006587	0.048163	-2.42162	DUF241 domain protein, putative (DUF241)	elongation zone	12 h
HORVU.MOREX.r3.3HG0302340.1	-2.406	-0.09437	-3.00838	0.004012	0.035058	-2.42405	Eukaryotic aspartyl protease family protein, expressed	elongation zone	12 h
HORVU.MOREX.r3.7HG0697940.1	-1.34573	0.148475	-2.90906	0.005287	0.042	-2.4243	UvrABC system protein C	elongation zone	12 h
HORVU.MOREX.r3.5HG0467370.1	-0.7575	7.65806	-3.00004	0.004107	0.035609	-2.42757	Pleiotropic drug resistance ABC transporter	elongation zone	12 h
HORVU.MOREX.r3.6HG0628930.1	-0.49945	7.959732	-3.02025	0.00388	0.034278	-2.42951	Alcohol dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.7HG0668820.1	0.500293	4.620228	3.050435	0.003564	0.032373	-2.42981	Endoglucanase	elongation zone	12 h
HORVU.MOREX.r3.3HG0219750.1	-1.52347	-0.71619	-2.85327	0.006159	0.046276	-2.43105	Disease resistance protein (NBS-LRR class) family	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.4HG0392590.1	-0.43266	3.653452	-2.85835	0.006074	0.045944	-2.43407	Calmodulin-lysine N-methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.1HG0032230.1	-0.84171	4.670024	-2.82824	0.006592	0.048163	-2.43605	Rad3-related DNA helicase family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0243130.1	-0.68236	2.631713	-2.83875	0.006407	0.047359	-2.43625	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.5HG0514790.1	-0.40292	9.909631	-3.11551	0.002962	0.028751	-2.43635	Elongation factor 1-alpha	elongation zone	12 h
HORVU.MOREX.r3.7HG0637470.1	-0.47142	3.443051	-2.85158	0.006187	0.04639	-2.44073	NBS-LRR resistance-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0208790.1	-1.66877	3.913939	-2.86043	0.00604	0.045836	-2.44432	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.4HG0390030.1	-2.18136	0.118063	-2.82048	0.006732	0.048811	-2.44632	Nodulation-signaling pathway 2 protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0534640.1	-0.51927	8.816317	-3.04594	0.003609	0.032683	-2.44803	Elongation factor Tu	elongation zone	12 h
HORVU.MOREX.r3.3HG0259660.1	-0.58929	3.912666	-2.81681	0.006799	0.049107	-2.44876	CRS2-associated factor 1, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.3HG0276730.1	0.273047	6.945927	3.027033	0.003807	0.033836	-2.44887	Long-Chain Acyl-CoA Synthetase	elongation zone	12 h
HORVU.MOREX.r3.7HG0667660.1	0.934211	5.314359	2.990924	0.004213	0.036201	-2.44928	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.7HG0744540.1	-2.06586	-0.40765	-2.84133	0.006362	0.04718	-2.45362	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.1HG0085380.1	0.39141	4.053078	2.890854	0.005558	0.043299	-2.45436	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0397570.1	0.75818	4.104655	2.894398	0.005504	0.043043	-2.4557	Glucan endo-1,3-beta-glucosidase 3	elongation zone	12 h
HORVU.MOREX.r3.3HG0237330.1	-1.62893	0.337971	-2.85874	0.006068	0.045938	-2.45608	Protein FAR1-RELATED SEQUENCE 5	elongation zone	12 h
HORVU.MOREX.r3.7HG0687540.1	-0.29001	5.801521	-2.97074	0.004457	0.037543	-2.45788	Proteasome subunit alpha type	elongation zone	12 h
HORVU.MOREX.r3.3HG0301930.1	0.4544	4.019686	2.956413	0.004638	0.03861	-2.45813	G patch domain protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0462780.1	-0.40363	7.18947	-3.01641	0.003923	0.03453	-2.45872	Transporter, putative, expressed	elongation zone	12 h
HORVU.MOREX.r3.4HG0352540.1	-0.57039	2.652903	-2.847	0.006265	0.046718	-2.45879	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0717850.1	-0.35545	6.287604	-2.97688	0.004381	0.037198	-2.45924	Potassium efflux antiporter	elongation zone	12 h
HORVU.MOREX.r3.1HG0044290.1	0.607068	3.742696	2.811797	0.006892	0.049549	-2.45969	electron protein, putative (Protein of unknown function, DUF547)	elongation zone	12 h
HORVU.MOREX.r3.4HG0394810.1	-0.98318	5.082806	-2.80831	0.006957	0.049739	-2.45993	U-box domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0310920.1	0.629205	5.137634	2.951105	0.004707	0.03893	-2.46014	Histidine kinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0253450.1	-0.32934	5.357439	-2.94114	0.004839	0.039574	-2.46135	FHA domain containing protein, expressed	elongation zone	12 h
HORVU.MOREX.r3.3HG0293430.1	1.207805	-1.42288	2.818337	0.006771	0.048991	-2.46182	Expansin	elongation zone	12 h
HORVU.MOREX.r3.3HG0219800.1	-0.54266	3.630299	-2.80964	0.006932	0.049665	-2.46211	Dephospho-CoA kinase, putative, expressed	elongation zone	12 h
HORVU.MOREX.r3.4HG0387580.1	0.327166	4.638536	2.959243	0.004602	0.038401	-2.46241	Xylosyltransferase 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0197710.1	-1.15813	4.270225	-2.8252	0.006646	0.048379	-2.46375	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0725290.1	-0.47921	3.61352	-2.85102	0.006197	0.04639	-2.46493	YGL010w-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0008640.1	0.489631	3.733371	2.876708	0.005777	0.044368	-2.46546	7,8-dihydroneopterin aldolase	elongation zone	12 h
HORVU.MOREX.r3.7HG0736870.1	0.43898	5.259228	2.97828	0.004364	0.037141	-2.46747	Molybdenum cofactor sulfurase	elongation zone	12 h
HORVU.MOREX.r3.1HG0073520.1	-0.78185	3.742361	-2.90372	0.005365	0.042358	-2.46779	Heavy metal transport/detoxification superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0403510.1	-0.38327	4.248358	-2.89784	0.005452	0.042752	-2.46789	Protein kinase	elongation zone	12 h
HORVU.MOREX.r3.4HG0364880.1	-1.25577	-0.54939	-2.81539	0.006825	0.049261	-2.471	cysteine-rich RECEPTOR-like kinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0306030.1	-0.45642	3.28785	-2.8511	0.006195	0.04639	-2.47399	Rhomboid protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0046900.1	-0.31894	3.626727	-2.88652	0.005624	0.043667	-2.47456	1-acyl-sn-glycerol-3-phosphate acyltransferase	elongation zone	12 h
HORVU.MOREX.r3.4HG0342090.1	-0.46843	5.870045	-2.92878	0.005007	0.040463	-2.47502	Remorin	elongation zone	12 h
HORVU.MOREX.r3.7HG0730870.1	0.350572	7.493886	3.075644	0.003318	0.031043	-2.47548	Glycosyltransferases	elongation zone	12 h
HORVU.MOREX.r3.3HG0308980.1	-0.69354	4.452519	-2.82165	0.006711	0.048693	-2.47574	S-adenosyl-L-methionine-dependent methyltransferase, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0075340.1	0.776156	1.815297	2.830777	0.006547	0.04803	-2.47603	Alpha/beta-Hydrolases superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0513120.1	-0.31344	5.944244	-2.99696	0.004142	0.035871	-2.47714	Cytochrome P450 allene oxide synthase	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.2HG0167540.1	-0.22235	7.425024	-3.02086	0.003874	0.03426	-2.47785	Histidine decarboxylase	elongation zone	12 h
HORVU.MOREX.r3.6HG0615630.1	0.47469	4.54843	2.885364	0.005642	0.043691	-2.47913	Rac-like GTP-binding protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0708120.1	-1.27115	6.606021	-2.88377	0.005667	0.043799	-2.48081	High mobility group family	elongation zone	12 h
HORVU.MOREX.r3.2HG0100360.1	0.393214	4.261633	2.903572	0.005367	0.04236	-2.48468	3-oxo-5-alpha-steroid 4-dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.1HG0077170.1	-0.56227	4.830925	-2.84061	0.006374	0.047226	-2.4858	Protein EMBRYONIC FLOWER 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0171100.1	-0.44144	4.075179	-2.84696	0.006266	0.046718	-2.48621	Plectin-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0323810.1	-0.47724	6.634621	-2.93996	0.004855	0.039601	-2.48775	SWAP (Suppressor-of-White-APricot)/surp domain-containing protein / ubiquitin f	elongation zone	12 h
HORVU.MOREX.r3.4HG0387150.1	-0.87583	6.899898	-2.93963	0.004859	0.039613	-2.48913	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.7HG0739230.1	2.960629	-3.45098	3.051928	0.003549	0.032342	-2.48943	Jacalin-like lectin	elongation zone	12 h
HORVU.MOREX.r3.5HG0468940.1	-0.32013	5.005775	-2.89247	0.005533	0.043222	-2.48965	NAD(P)-binding Rossmann-fold superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0007570.1	-1.36066	-2.58012	-2.86021	0.006043	0.045842	-2.48985	Werner Syndrome-like exonuclease	elongation zone	12 h
HORVU.MOREX.r3.5HG0528890.1	-1.0161	5.084337	-2.80495	0.00702	0.049999	-2.49133	GATA transcription factor, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0165640.1	-2.49908	-0.84713	-2.99243	0.004195	0.036159	-2.49312	CsAtPR5	elongation zone	12 h
HORVU.MOREX.r3.7HG0714400.1	0.784239	2.702391	2.809847	0.006928	0.049654	-2.49407	Auxin-responsive protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0610890.1	0.467718	5.180456	2.981307	0.004328	0.036952	-2.49642	KH domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0597460.1	-1.84011	-0.69687	-2.95377	0.004672	0.038786	-2.49713	Glucose-6-phosphate isomerase	elongation zone	12 h
HORVU.MOREX.r3.2HG0135860.1	-0.386	5.818016	-2.90499	0.005346	0.042285	-2.49859	Transcription factor jumonji domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0680680.1	-0.3036	5.101819	-2.93401	0.004935	0.040075	-2.49886	3-hydroxy-3-methylglutaryl coenzyme A reductase	elongation zone	12 h
HORVU.MOREX.r3.7HG0745700.1	-0.25833	5.461365	-2.94989	0.004723	0.03901	-2.49889	Phox (PX) domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0689490.1	-0.55096	6.098735	-2.9088	0.005291	0.042014	-2.4993	Peptidyl-prolyl cis-trans isomerase	elongation zone	12 h
HORVU.MOREX.r3.5HG0436900.1	0.365132	4.896931	2.945087	0.004786	0.039269	-2.50023	Syntaxin, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0086140.1	-0.79722	4.57931	-2.81957	0.006748	0.048879	-2.50048	Oxidoreductase	elongation zone	12 h
HORVU.MOREX.r3.7HG0688300.1	-0.42671	4.553776	-2.85602	0.006113	0.046117	-2.50187	O-fucosyltransferase-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0684040.1	-0.52279	5.674326	-2.89605	0.005479	0.042914	-2.50195	Glutamate-1-semialdehyde 2,1-aminomutase	elongation zone	12 h
HORVU.MOREX.r3.3HG0265140.1	1.991628	-1.23714	2.827362	0.006608	0.048183	-2.5021	DUF3511 domain protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0401630.1	0.679082	1.754312	2.822335	0.006698	0.048636	-2.50386	Protein kinase	elongation zone	12 h
HORVU.MOREX.r3.7HG0688930.1	0.808843	-0.39064	2.817012	0.006795	0.049097	-2.50407	DUF868 family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0471790.1	-0.45592	8.627392	-3.04903	0.003578	0.032459	-2.50419	Phosphate translocator	elongation zone	12 h
HORVU.MOREX.r3.3HG0255150.1	-0.27335	5.442871	-2.93491	0.004923	0.040007	-2.50446	Sec14p-like phosphatidylinositol transfer family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0444270.1	0.445868	5.156347	3.024224	0.003837	0.034028	-2.50446	Pectin lyase-like superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0427060.1	-0.87135	5.128579	-2.83754	0.006428	0.047408	-2.50484	50S ribosomal protein L14	elongation zone	12 h
HORVU.MOREX.r3.5HG0526140.1	-0.45187	4.078722	-2.86153	0.006022	0.045715	-2.5051	NBS-LRR disease resistance protein, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0663400.1	-0.28541	6.420462	-2.97039	0.004461	0.03755	-2.50604	LysM domain-containing GPI-anchored protein 1	elongation zone	12 h
HORVU.MOREX.r3.1HG0058050.1	-0.5195	5.246818	-2.87915	0.005739	0.044183	-2.50885	8-amino-7-oxononanoate synthase	elongation zone	12 h
HORVU.MOREX.r3.7HG0636530.1	-0.39294	4.42133	-2.89149	0.005548	0.043288	-2.51003	MADS-box transcription factor 8	elongation zone	12 h
HORVU.MOREX.r3.2HG0137620.1	0.474327	3.671497	2.845662	0.006288	0.046798	-2.51036	Phototropic-responsive NPH3 family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0292680.1	0.62085	2.459133	2.908463	0.005295	0.042036	-2.51239	Replicase polyprotein 1a	elongation zone	12 h
HORVU.MOREX.r3.4HG0383340.1	-1.59328	0.295717	-2.8988	0.005438	0.042705	-2.5133	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0078040.1	0.450855	5.579406	2.994948	0.004166	0.035962	-2.51592	Absent in melanoma 1 protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0172050.1	-0.35655	8.585874	-3.0253	0.003826	0.033984	-2.51633	RNA-binding protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0664130.1	-0.36054	5.138266	-2.87097	0.005869	0.044935	-2.51765	Dipeptidyl peptidase family member 6	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0071310.1	-0.48079	4.338136	-2.80651	0.006991	0.049912	-2.52033	WEAK movement UNDER BLUE LIGHT-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0644190.1	0.564148	0.806058	2.844558	0.006307	0.046884	-2.52037	Glucan endo-1,3-beta-glucosidase, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0069110.1	-0.47836	4.126574	-2.80499	0.007019	0.049999	-2.52342	Zinc finger protein 830	elongation zone	12 h
HORVU.MOREX.r3.7HG0720720.1	-0.48704	3.515226	-2.80505	0.007018	0.049999	-2.52412	Vesicle transport protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0204960.1	-0.33121	4.354857	-2.85083	0.0062	0.046397	-2.52437	RING/U-box superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0521030.1	-0.60368	4.415413	-2.81864	0.006765	0.048986	-2.52479	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0583020.1	-0.37984	3.316584	-2.84616	0.006279	0.046769	-2.52556	Protein phosphatase 2C containing protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0554700.1	0.304527	7.324166	3.027312	0.003804	0.033836	-2.5256	Sec14p-like phosphatidylinositol transfer family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0080770.1	-0.94248	6.795288	-2.92534	0.005055	0.040734	-2.52777	Histone H4	elongation zone	12 h
HORVU.MOREX.r3.3HG0260580.1	-0.47598	4.905647	-2.84058	0.006375	0.047226	-2.52808	DUF630 family protein, putative (DUF630 and DUF632)	elongation zone	12 h
HORVU.MOREX.r3.2HG0180580.1	-1.42213	7.018787	-2.85991	0.006049	0.045842	-2.52838	Proliferating cell nuclear antigen	elongation zone	12 h
HORVU.MOREX.r3.3HG0253630.1	0.944014	3.730748	2.830293	0.006555	0.048076	-2.5286	Late embryogenesis abundant protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0703780.1	-0.54752	5.334771	-2.87017	0.005882	0.04499	-2.53103	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	elongation zone	12 h
HORVU.MOREX.r3.7HG0657370.1	-0.32765	5.109469	-2.90272	0.00538	0.042386	-2.53148	NADH-quinone oxidoreductase subunit C	elongation zone	12 h
HORVU.MOREX.r3.7HG0648600.1	-0.58197	5.915169	-2.87955	0.005733	0.044174	-2.53214	Elongation factor 4	elongation zone	12 h
HORVU.MOREX.r3.2HG0116870.1	-0.82549	6.950005	-2.91392	0.005216	0.04165	-2.53652	Condensin complex subunit 1	elongation zone	12 h
HORVU.MOREX.r3.3HG0295380.1	0.711616	1.713149	2.855187	0.006127	0.046171	-2.53917	Cytochrome P450	elongation zone	12 h
HORVU.MOREX.r3.5HG0532200.1	0.812732	4.356719	2.953918	0.00467	0.038786	-2.53936	Patatin	elongation zone	12 h
HORVU.MOREX.r3.5HG0493200.1	0.3917	8.020324	3.056629	0.003502	0.032038	-2.54429	Fasciclin-like arabinogalactan-protein-like	elongation zone	12 h
HORVU.MOREX.r3.1HG0084920.1	-0.30692	5.205134	-2.90251	0.005383	0.042386	-2.54655	ER membrane protein complex subunit 6	elongation zone	12 h
HORVU.MOREX.r3.5HG0467880.1	-0.45989	5.367745	-2.84968	0.006219	0.046509	-2.54665	DNA-directed RNA polymerase family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0278120.1	0.381498	4.5822	2.863083	0.005996	0.04559	-2.54684	CTD small phosphatase-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0706930.1	-0.49784	4.439187	-2.82686	0.006617	0.048214	-2.54753	F-box family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0019440.1	-0.39541	5.729684	-2.88795	0.005602	0.043562	-2.55203	Vegetative cell wall protein gp1	elongation zone	12 h
HORVU.MOREX.r3.5HG0537780.1	0.414884	7.666685	3.059851	0.00347	0.031904	-2.55281	COP1-interacting-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0200730.1	-0.19684	7.663906	-3.01542	0.003933	0.034581	-2.55449	Protein transport SEC13-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0569480.1	-2.5324	2.886546	-2.85984	0.00605	0.045842	-2.55623	Tubby-like F-box protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0122520.1	0.753511	0.436988	2.812281	0.006883	0.049549	-2.55627	SAUR-like auxin-responsive protein family	elongation zone	12 h
HORVU.MOREX.r3.4HG0384400.1	0.507289	4.602549	2.965347	0.004524	0.037933	-2.55742	Ethylene-overproduction protein 1	elongation zone	12 h
HORVU.MOREX.r3.5HG0439710.1	-1.97296	-0.51069	-2.97594	0.004393	0.037263	-2.55811	Zinc finger protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0296380.1	0.589903	4.241542	2.942721	0.004818	0.039433	-2.55816	Type I inositol-1,4,5-trisphosphate 5-phosphatase	elongation zone	12 h
HORVU.MOREX.r3.7HG0730350.1	-0.53824	7.382323	-2.9709	0.004455	0.037542	-2.56036	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.6HG0584860.1	-0.49169	4.293818	-2.81189	0.00689	0.049549	-2.56408	3-oxoacyl-reductase	elongation zone	12 h
HORVU.MOREX.r3.1HG0030200.1	-0.41757	4.198578	-2.87332	0.005831	0.044731	-2.56534	DUF641 family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0614110.1	0.392329	4.183035	2.947293	0.004757	0.039139	-2.56753	nucleolar GTP-binding protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0412650.1	1.761252	1.247202	2.845405	0.006292	0.046811	-2.56876	TVP38/TMEM64 family membrane protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0459320.1	-0.44249	4.812268	-2.86006	0.006046	0.045842	-2.56898	Peptidylprolyl isomerase	elongation zone	12 h
HORVU.MOREX.r3.6HG0555040.1	0.520128	3.833259	2.838256	0.006415	0.047365	-2.56959	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	elongation zone	12 h
HORVU.MOREX.r3.2HG0205550.1	-0.80192	5.79238	-2.82065	0.006729	0.048807	-2.57089	Thymidylate synthase	elongation zone	12 h
HORVU.MOREX.r3.3HG0279110.1	2.077134	-0.01382	2.81035	0.006918	0.049654	-2.5748	NAC domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0104500.1	-0.42188	4.987186	-2.84908	0.006229	0.046551	-2.57494	INO80 complex subunit C	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0003620.1	0.54509	2.573513	2.816352	0.006807	0.04915	-2.57579	Protein ZINC INDUCED FACILITATOR-LIKE 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0710170.1	-1.79832	0.072486	-2.87927	0.005737	0.044183	-2.57735	ATP-dependent DNA helicase 2 subunit KU70	elongation zone	12 h
HORVU.MOREX.r3.4HG0335830.1	0.371203	6.279353	2.946863	0.004763	0.039158	-2.57739	Importin-5	elongation zone	12 h
HORVU.MOREX.r3.2HG0173210.1	-0.89218	5.578206	-2.81364	0.006857	0.049459	-2.57903	Kinesin-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0060570.1	-0.54139	5.889922	-2.87684	0.005775	0.044368	-2.58097	Mitochondrial zinc maintenance protein 1, mitochondrial	elongation zone	12 h
HORVU.MOREX.r3.2HG0213850.1	-0.60794	5.02608	-2.85791	0.006082	0.045953	-2.58149	Eukaryotic aspartyl protease family protein, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0604810.1	-0.33432	6.104373	-2.91484	0.005203	0.041594	-2.58204	Calcium-dependent protein kinase	elongation zone	12 h
HORVU.MOREX.r3.5HG0523150.1	-0.25232	6.194464	-2.90325	0.005372	0.042365	-2.58352	Protein phosphatase 2c, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0635550.1	-1.22484	6.336423	-2.84675	0.006269	0.046728	-2.58539	Lipoxygenase domain-containing 1	elongation zone	12 h
HORVU.MOREX.r3.5HG0533660.1	-0.59365	5.124285	-2.80612	0.006998	0.049947	-2.58581	CTD small phosphatase-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0653740.1	0.459249	7.130211	2.995105	0.004164	0.035961	-2.58854	Long-Chain Acyl-CoA Synthetase	elongation zone	12 h
HORVU.MOREX.r3.5HG0519040.1	-0.34278	4.736037	-2.88155	0.005701	0.043982	-2.59029	Serine/arginine repetitive matrix protein 2, putative isoform 1	elongation zone	12 h
HORVU.MOREX.r3.1HG0059870.1	-0.37757	4.771051	-2.85118	0.006194	0.04639	-2.59032	Succinate dehydrogenase subunit 4	elongation zone	12 h
HORVU.MOREX.r3.3HG0284780.1	0.322096	5.323435	2.897345	0.00546	0.042794	-2.59155	Protein PLASTID MOVEMENT IMPAIRED 1-RELATED 1	elongation zone	12 h
HORVU.MOREX.r3.3HG0256300.1	-0.4583	7.085102	-2.91114	0.005257	0.041825	-2.59243	Glutamate--tRNA ligase	elongation zone	12 h
HORVU.MOREX.r3.4HG0381800.1	-0.26939	7.086406	-2.97125	0.004451	0.037537	-2.59265	AP-2 complex subunit mu	elongation zone	12 h
HORVU.MOREX.r3.1HG0051020.1	-0.49511	5.895904	-2.86534	0.00596	0.045444	-2.59282	Membrane protein insertase YidC	elongation zone	12 h
HORVU.MOREX.r3.7HG0651030.1	-0.27013	5.034878	-2.88256	0.005686	0.043894	-2.59384	BRISC and BRCA1-A complex member 1	elongation zone	12 h
HORVU.MOREX.r3.5HG0473900.1	0.393019	4.702091	2.883491	0.005671	0.043815	-2.59505	Galactose mutarotase-like superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0392680.1	0.79742	4.390666	2.853928	0.006148	0.046261	-2.59508	Endo-1,4-beta-xylanase	elongation zone	12 h
HORVU.MOREX.r3.4HG0406960.1	-0.32571	5.198023	-2.85902	0.006063	0.045928	-2.59785	Mitochondrial carrier protein, expressed	elongation zone	12 h
HORVU.MOREX.r3.5HG0420080.1	0.421958	3.867078	2.871716	0.005857	0.04486	-2.59871	Nodulin-like / Major Facilitator Superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0061210.1	0.324619	4.858002	2.863051	0.005997	0.04559	-2.60005	Replicase polyprotein 1a	elongation zone	12 h
HORVU.MOREX.r3.4HG0335790.2	-0.59251	4.412211	-2.95252	0.004689	0.038809	-2.60516	Lipoxygenase	elongation zone	12 h
HORVU.MOREX.r3.1HG0045040.1	-0.38017	4.222961	-2.85115	0.006194	0.04639	-2.60606	Thioredoxin	elongation zone	12 h
HORVU.MOREX.r3.2HG0210680.1	-0.27247	5.95404	-2.90403	0.00536	0.042352	-2.60679	Anamorsin homolog	elongation zone	12 h
HORVU.MOREX.r3.6HG0613230.1	-0.30685	6.009357	-2.93669	0.004899	0.039842	-2.60827	Allergen, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0249700.1	-0.55325	4.807961	-2.81461	0.006839	0.049347	-2.61371	Protein DEFECTIVE IN MERISTEM SILENCING 3	elongation zone	12 h
HORVU.MOREX.r3.4HG0358980.1	0.502063	6.464101	3.06231	0.003446	0.031796	-2.61464	Xyloglucan endotransglucosylase/hydrolase	elongation zone	12 h
HORVU.MOREX.r3.7HG0634470.1	-0.28863	7.084322	-2.95602	0.004643	0.038637	-2.61489	RING/FYVE/PHD zinc finger protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0539990.1	-0.34178	5.586062	-2.87012	0.005882	0.04499	-2.61657	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0551650.1	0.439979	2.987415	2.833713	0.006495	0.047717	-2.61942	Cyclin family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0602290.1	-0.3294	4.970789	-2.86309	0.005996	0.04559	-2.6219	Transmembrane protein-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0149120.1	-0.3032	6.262393	-2.89692	0.005466	0.042828	-2.6246	WW domain-binding protein 11	elongation zone	12 h
HORVU.MOREX.r3.2HG0205810.1	1.230134	3.581905	2.853061	0.006162	0.046285	-2.62562	Cytochrome P450 family protein, expressed	elongation zone	12 h
HORVU.MOREX.r3.3HG0310320.1	-0.68899	5.514023	-2.8669	0.005934	0.045302	-2.6275	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0493890.2	0.441228	3.23102	2.82785	0.006599	0.048163	-2.63183	Beta-ureidopropionase	elongation zone	12 h
HORVU.MOREX.r3.2HG0173600.1	0.617852	2.960526	2.919574	0.005136	0.041216	-2.63271	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0329830.1	-0.24261	5.545794	-2.88413	0.005661	0.043788	-2.63327	Pectin acetylesterase	elongation zone	12 h
HORVU.MOREX.r3.6HG0622550.1	-0.28357	5.355981	-2.8857	0.005637	0.043682	-2.63666	Cyclic nucleotide-gated channel	elongation zone	12 h
HORVU.MOREX.r3.6HG0560710.1	0.263064	7.131181	2.953284	0.004679	0.038805	-2.63737	Protein VERNALIZATION INSENSITIVE 3	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.5HG0476330.1	-0.37461	6.914052	-2.94647	0.004768	0.039181	-2.63794	Major facilitator superfamily transporter	elongation zone	12 h
HORVU.MOREX.r3.5HG0458010.1	0.274772	5.942045	2.901748	0.005394	0.042442	-2.63915	Protein kinase, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0270500.1	-0.57376	4.937967	-2.82723	0.00661	0.048184	-2.63958	Amino acid permease	elongation zone	12 h
HORVU.MOREX.r3.3HG0291710.1	-0.47247	6.615068	-2.89109	0.005554	0.043297	-2.63981	Protein PAT1-1-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0013820.1	0.522677	4.142516	2.898267	0.005446	0.042719	-2.64045	Protein IQ-DOMAIN 1	elongation zone	12 h
HORVU.MOREX.r3.4HG0412430.1	0.431772	4.229658	2.839883	0.006387	0.047281	-2.64183	Sugar transporter, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0033390.4	-1.71825	-0.46879	-2.82453	0.006658	0.048416	-2.64421	Ferrochelatase	elongation zone	12 h
HORVU.MOREX.r3.4HG0416090.1	-0.50693	3.798358	-2.80985	0.006928	0.049654	-2.64451	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0179540.1	-0.41053	4.341716	-2.84247	0.006342	0.047069	-2.64509	Ergosterol biosynthetic protein 28	elongation zone	12 h
HORVU.MOREX.r3.2HG0121570.1	-0.4111	4.65733	-2.82314	0.006684	0.048564	-2.64678	Protein LTV1	elongation zone	12 h
HORVU.MOREX.r3.6HG0624190.1	-0.33097	4.552445	-2.84299	0.006333	0.047036	-2.6504	Elongation factor 1-alpha	elongation zone	12 h
HORVU.MOREX.r3.3HG0236170.1	-0.35081	4.945465	-2.8683	0.005912	0.045179	-2.65197	Zinc finger protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0505100.1	-0.39609	5.885938	-2.90045	0.005413	0.042561	-2.65374	Cytochrome b561 and domon domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0069940.1	-0.74165	7.781675	-2.90188	0.005392	0.042442	-2.65422	60S ribosomal protein L30	elongation zone	12 h
HORVU.MOREX.r3.1HG0092880.1	0.599481	4.897051	2.825074	0.006649	0.048379	-2.65489	Calcium-dependent protein kinase	elongation zone	12 h
HORVU.MOREX.r3.6HG0612250.1	-0.38116	5.887822	-2.86294	0.005999	0.04559	-2.65733	Potassium transporter	elongation zone	12 h
HORVU.MOREX.r3.6HG0616240.1	0.741873	-0.52276	2.834332	0.006484	0.047655	-2.65988	Endoglucanase	elongation zone	12 h
HORVU.MOREX.r3.3HG0305600.1	0.407397	6.61338	2.972588	0.004434	0.037428	-2.66258	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0280530.1	0.532807	9.236452	3.048382	0.003585	0.032498	-2.66404	Glutamate synthase, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0192540.1	0.318262	6.723009	2.981399	0.004326	0.036952	-2.66625	Ubiquitin-specific protease family C19-related protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0737960.2	-0.67232	7.555618	-2.91125	0.005255	0.041825	-2.66847	Glutathione S-transferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0442460.1	0.44212	3.367563	2.917013	0.005172	0.041427	-2.66888	Protein kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0064080.1	-0.59532	7.790388	-2.9392	0.004865	0.039613	-2.66943	Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A	elongation zone	12 h
HORVU.MOREX.r3.1HG0016950.1	-0.38144	6.051221	-2.89071	0.00556	0.043299	-2.67412	O-fucosyltransferase family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0209030.1	-1.4887	0.629763	-2.81231	0.006882	0.049549	-2.67432	RING finger protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0186650.1	-0.73704	7.283329	-2.86668	0.005938	0.045312	-2.67643	Non-specific serine/threonine protein kinase	elongation zone	12 h
HORVU.MOREX.r3.1HG0052940.1	-0.40742	6.11793	-2.86198	0.006014	0.045676	-2.67732	Nuclear control of ATPase protein 2	elongation zone	12 h
HORVU.MOREX.r3.6HG0614870.1	0.713054	2.771326	2.938055	0.00488	0.039708	-2.67862	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.5HG0445020.1	-0.53028	5.533594	-2.82769	0.006602	0.048163	-2.6807	Riboflavin synthase	elongation zone	12 h
HORVU.MOREX.r3.4HG0380710.1	-0.36533	6.055872	-2.91574	0.005191	0.04154	-2.68199	Calmodulin	elongation zone	12 h
HORVU.MOREX.r3.7HG0671360.1	-0.25592	9.214028	-3.04269	0.003643	0.032929	-2.69129	Aldehyde dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.1HG0087980.1	-0.56358	7.176279	-2.87811	0.005755	0.044265	-2.69401	Ubiquitin	elongation zone	12 h
HORVU.MOREX.r3.3HG0291100.1	0.324167	8.24123	3.020343	0.003879	0.034278	-2.69582	Glutathione S-transferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0494320.1	-0.43931	7.049375	-2.89477	0.005498	0.043015	-2.69701	Nuclear transport factor 2	elongation zone	12 h
HORVU.MOREX.r3.4HG0381680.1	-0.5434	4.604183	-2.83924	0.006398	0.047329	-2.69825	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0269130.1	0.985267	4.115188	2.975572	0.004397	0.037281	-2.69994	Leucine-rich repeat protein kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0293040.1	-0.44278	5.431414	-2.81003	0.006924	0.049654	-2.70094	Purple acid phosphatase	elongation zone	12 h
HORVU.MOREX.r3.1HG0026070.2	-0.56326	8.133614	-2.91026	0.005269	0.04191	-2.7054	Ribosomal protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0083440.1	0.349658	5.222069	2.892055	0.00554	0.043254	-2.70594	Lactation elevated protein 1	elongation zone	12 h
HORVU.MOREX.r3.3HG0288080.1	-0.25833	6.241682	-2.86992	0.005886	0.044997	-2.70636	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0386800.1	0.281391	5.120324	2.870571	0.005875	0.044967	-2.70797	Ankyrin repeat family protein, putative, expressed	elongation zone	12 h

Table Sн Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.7HG0709230.1	-2.49489	0.345142	-2.8412	0.006364	0.047181	-2.71064	50S ribosomal protein L10	elongation zone	12 h
HORVU.MOREX.r3.3HG0304660.1	0.419427	3.80291	2.853427	0.006156	0.046273	-2.71194	Ceramide glucosyltransferase, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0215550.1	-0.80091	7.917138	-2.88442	0.005657	0.043769	-2.71869	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.1HG0021880.1	2.304736	0.747345	2.927569	0.005024	0.040554	-2.72121	SKP1-like protein 4	elongation zone	12 h
HORVU.MOREX.r3.4HG0378000.1	-0.27214	5.073003	-2.81804	0.006776	0.048995	-2.72127	Uroporphyrinogen decarboxylase	elongation zone	12 h
HORVU.MOREX.r3.6HG0582950.1	0.279462	6.154329	2.895439	0.005488	0.042969	-2.72272	SNARE-interacting protein KEULE	elongation zone	12 h
HORVU.MOREX.r3.2HG0144230.1	-0.32593	6.071895	-2.86814	0.005914	0.045182	-2.72551	Nucleobase ascorbate transporter	elongation zone	12 h
HORVU.MOREX.r3.4HG0383070.1	-0.54647	5.448589	-2.81338	0.006862	0.049476	-2.72603	Calmodulin-binding protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0299540.1	-0.30403	6.662261	-2.90815	0.0053	0.04204	-2.72807	Protein YIPF	elongation zone	12 h
HORVU.MOREX.r3.2HG0124470.1	-2.27754	0.969558	-2.80512	0.007017	0.049999	-2.72816	Transposon protein, putative, Mutator sub-class	elongation zone	12 h
HORVU.MOREX.r3.3HG0327200.3	-0.58346	5.932631	-2.84658	0.006272	0.046732	-2.72853	Sulfite exporter TauE/SafE family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0014430.1	-0.20412	5.638714	-2.85853	0.006071	0.045938	-2.72868	Beta 1, 3 galactosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0197760.1	0.537422	1.898016	2.899987	0.00542	0.042599	-2.73353	IQ domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0501380.1	0.344965	6.789726	2.90154	0.005397	0.04245	-2.73408	Phospholipase D	elongation zone	12 h
HORVU.MOREX.r3.4HG0337770.1	0.572173	5.839766	2.926786	0.005035	0.04061	-2.7364	Histidine kinase	elongation zone	12 h
HORVU.MOREX.r3.1HG0070430.1	0.600286	5.294003	2.885805	0.005635	0.043682	-2.73722	LURP-one-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0279750.1	0.327672	6.168153	2.899828	0.005423	0.042601	-2.73904	Auxin-responsive protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0617240.1	0.560498	4.621925	2.911764	0.005248	0.041806	-2.74077	RNA-binding protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0545460.1	0.505992	3.011798	2.853439	0.006156	0.046273	-2.74515	Transmembrane protein 97	elongation zone	12 h
HORVU.MOREX.r3.1HG0048010.1	-0.3448	5.141674	-2.81068	0.006912	0.049647	-2.75344	Membrane steroid-binding protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0359960.1	0.3106	4.67912	2.838306	0.006414	0.047365	-2.75624	Mannose-6-phosphate isomerase	elongation zone	12 h
HORVU.MOREX.r3.1HG0059120.1	-0.32844	5.049749	-2.8071	0.006979	0.04985	-2.7593	AP-3 complex subunit mu	elongation zone	12 h
HORVU.MOREX.r3.2HG0176290.1	-0.38019	6.030619	-2.80791	0.006964	0.049776	-2.762	Mitochondrial inner membrane protease ATP23	elongation zone	12 h
HORVU.MOREX.r3.5HG0491750.1	-0.31245	6.143123	-2.82846	0.006588	0.048163	-2.76221	Methyl-CpG-binding domain protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0418460.1	0.39911	1.759537	2.845938	0.006283	0.04678	-2.76356	Cysteine protease	elongation zone	12 h
HORVU.MOREX.r3.6HG0547570.1	0.394807	5.073232	2.857348	0.006091	0.045984	-2.76634	LURP-one-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0134430.1	-2.238	-1.35112	-2.84008	0.006384	0.047273	-2.7671	Peptidyl-prolyl cis-trans isomerase, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0279850.1	0.479553	3.975384	2.842154	0.006348	0.047092	-2.77077	mediator of RNA polymerase II transcription subunit	elongation zone	12 h
HORVU.MOREX.r3.4HG0409180.1	-0.27181	6.8545	-2.88802	0.005601	0.043562	-2.78211	Glutathione S-transferase	elongation zone	12 h
HORVU.MOREX.r3.1HG0076540.1	-0.35548	7.761396	-2.89369	0.005515	0.043111	-2.78422	Mitochondrial-processing peptidase subunit alpha	elongation zone	12 h
HORVU.MOREX.r3.4HG0404340.1	-0.36545	5.995886	-2.83628	0.00645	0.047454	-2.79075	Ubiquitin-fold modifier-conjugating enzyme 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0669240.1	-0.32209	6.048266	-2.82949	0.00657	0.048129	-2.79194	Microtubule-associated protein 70-2	elongation zone	12 h
HORVU.MOREX.r3.1HG0003160.1	0.5974	3.46226	2.8495	0.006222	0.046515	-2.79511	Phosphoinositide phosphatase family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0624460.1	2.059731	-1.05782	2.933604	0.004941	0.040088	-2.7989	Receptor-like protein kinase	elongation zone	12 h
HORVU.MOREX.r3.7HG0703780.2	-0.24845	6.247658	-2.85443	0.006139	0.046231	-2.79899	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	elongation zone	12 h
HORVU.MOREX.r3.7HG0634710.1	-0.22817	6.589249	-2.86294	0.005999	0.04559	-2.80191	Signal peptide peptidase-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0054110.1	0.461177	4.610299	2.825414	0.006643	0.048369	-2.80351	Phosphatidylinositol transfer protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0677770.1	0.495465	5.664941	2.911753	0.005248	0.041806	-2.80371	Alkaline alpha-galactosidase seed imbibition protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0506230.1	0.524241	5.086085	2.909257	0.005284	0.041993	-2.80584	Cysteine protease, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0055560.1	-0.42947	6.140122	-2.82833	0.00659	0.048163	-2.81073	Metallo-beta-lactamase-like	elongation zone	12 h
HORVU.MOREX.r3.4HG0345610.1	-0.24167	8.214926	-2.94029	0.00485	0.039601	-2.81225	Protein transport protein Sec24-like family	elongation zone	12 h

Table SH Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0047580.1	0.505907	5.252581	2.830803	0.006546	0.04803	-2.81453	acyl-UDP-N-acetylglucosamine O-acyltransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0733910.1	-0.38589	7.386459	-2.88672	0.005621	0.04366	-2.81867	Protein LONGIFOLIA 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0113660.1	0.353248	7.044507	2.872937	0.005837	0.044752	-2.82595	ATP-dependent zinc metalloprotease FtsH	elongation zone	12 h
HORVU.MOREX.r3.1HG0000040.1	-0.17735	6.675243	-2.865	0.005965	0.045453	-2.83816	Peroxisomal membrane protein PEX14	elongation zone	12 h
HORVU.MOREX.r3.5HG0534100.1	-0.88738	3.881038	-2.85148	0.006189	0.04639	-2.84257	Glycine rich protein 3	elongation zone	12 h
HORVU.MOREX.r3.2HG0173550.1	-0.66575	7.816522	-2.82966	0.006567	0.048124	-2.84673	Prohibitin	elongation zone	12 h
HORVU.MOREX.r3.5HG0490520.1	0.879449	1.851159	2.829068	0.006577	0.048163	-2.84962	Tonoplast dicarboxylate transporter	elongation zone	12 h
HORVU.MOREX.r3.4HG0385270.1	-0.46339	9.972412	-2.94412	0.004799	0.039359	-2.85778	Elongation factor 1-alpha	elongation zone	12 h
HORVU.MOREX.r3.4HG0391130.1	0.478829	5.666862	2.82774	0.006601	0.048163	-2.85783	E3 ubiquitin-protein ligase	elongation zone	12 h
HORVU.MOREX.r3.2HG0157170.1	0.285975	6.50561	2.864414	0.005975	0.045496	-2.86604	Dirigent protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0291160.1	0.256716	5.548618	2.834428	0.006482	0.047655	-2.86733	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0299990.1	0.507138	6.228943	2.853946	0.006148	0.046261	-2.8705	Glutathione-S-transferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0420210.1	-0.3332	6.548288	-2.80996	0.006926	0.049654	-2.8744	Plasma membrane ATPase	elongation zone	12 h
HORVU.MOREX.r3.7HG0667780.1	0.582501	5.786042	2.853699	0.006152	0.046273	-2.87689	U-box domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0522630.1	0.583768	1.481024	2.808587	0.006951	0.049719	-2.87926	Blue copper protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0122040.1	-0.26255	6.676824	-2.83654	0.006445	0.047445	-2.88237	Transmembrane emp24 domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0415030.1	-0.30111	11.24828	-3.031	0.003765	0.03365	-2.88548	Acid phosphatase 1	elongation zone	12 h
HORVU.MOREX.r3.5HG0534520.1	-2.30775	-1.49675	-2.84445	0.006308	0.046884	-2.88707	tRNA (guanine-N(7)-)-methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0300020.1	-2.1725	-1.49861	-2.80753	0.006971	0.049809	-2.89027	Apoptosis-inducing factor-like protein A	elongation zone	12 h
HORVU.MOREX.r3.2HG0206650.1	0.558893	3.016844	2.828498	0.006587	0.048163	-2.89955	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0333650.1	0.430095	5.11965	2.812934	0.00687	0.049502	-2.91434	Transmembrane protein 56	elongation zone	12 h
HORVU.MOREX.r3.6HG0605160.1	0.480223	1.355711	2.812049	0.006887	0.049549	-2.91539	glucan synthase-like 9	elongation zone	12 h
HORVU.MOREX.r3.2HG0104520.1	-0.58744	9.641823	-2.93261	0.004954	0.040151	-2.92249	Acetyl-CoA carboxylase	elongation zone	12 h
HORVU.MOREX.r3.2HG0099260.1	-0.24184	6.601234	-2.81807	0.006776	0.048995	-2.92431	HR-like lesion-inducing protein-related protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0504720.1	0.305288	6.757338	2.809005	0.006944	0.049702	-2.92804	Octicosapeptide/Phox/Bem1p domain-containing protein / tetratricopeptide repe	elongation zone	12 h
HORVU.MOREX.r3.1HG0073070.1	-0.25929	6.545638	-2.83773	0.006425	0.047405	-2.92843	Lung seven transmembrane receptor family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0132590.1	-0.25893	6.039953	-2.82164	0.006711	0.048693	-2.93448	GDP-fucose protein O-fucosyltransferase 2	elongation zone	12 h
HORVU.MOREX.r3.3HG0289910.1	-0.35414	7.237133	-2.83817	0.006417	0.047365	-2.94785	Katanin p60 ATPase-containing subunit, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0390700.1	-0.20852	6.601984	-2.80942	0.006936	0.049677	-2.95789	ERAD-associated E3 ubiquitin-protein ligase component HRD3A	elongation zone	12 h
HORVU.MOREX.r3.2HG0119650.1	0.697641	2.120735	2.85531	0.006125	0.046171	-2.96967	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.2HG0125870.1	-0.51302	9.837843	-2.88099	0.00571	0.044033	-2.9698	50S ribosomal protein L15	elongation zone	12 h
HORVU.MOREX.r3.2HG0215280.1	-0.57203	7.631962	-2.83737	0.006431	0.047408	-2.98307	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.7HG0676610.1	0.37599	6.359219	2.828539	0.006587	0.048163	-2.98615	Phospholipid-transporting ATPase	elongation zone	12 h
HORVU.MOREX.r3.7HG0750140.1	0.376532	6.437734	2.837141	0.006435	0.047408	-2.99151	NBS-LRR disease resistance protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0241720.1	-0.19348	9.227312	-2.90815	0.0053	0.04204	-2.99209	Phospholipase D	elongation zone	12 h
HORVU.MOREX.r3.5HG0517240.1	0.39148	5.444266	2.811797	0.006892	0.049549	-2.99985	myosin-binding protein (Protein of unknown function, DUF593)	elongation zone	12 h
HORVU.MOREX.r3.1HG0067500.1	0.427503	4.190069	2.808973	0.006944	0.049702	-3.01454	GDSL esterase/lipase	elongation zone	12 h
HORVU.MOREX.r3.1HG0078770.1	-0.14486	7.962974	-2.83536	0.006466	0.047556	-3.01493	#N/A	elongation zone	12 h
HORVU.MOREX.r3.4HG0386190.1	-0.28042	8.332385	-2.81792	0.006779	0.048995	-3.02673	Glutathione-S-transferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0257310.1	-0.22557	7.693219	-2.82455	0.006658	0.048416	-3.02717	Glucosidase 2 subunit beta	elongation zone	12 h
HORVU.MOREX.r3.2HG0107900.1	-0.31468	7.940345	-2.80571	0.007005	0.049984	-3.03054	Elongation factor 1-alpha	elongation zone	12 h

Table Sн Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0056580.1	0.345758	7.670039	2.837036	0.006437	0.047408	-3.03913	Expansin protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0280900.1	-0.33472	8.096043	-2.80989	0.006927	0.049654	-3.04498	ATP synthase subunit beta	elongation zone	12 h
HORVU.MOREX.r3.4HG0413800.1	0.477723	7.955857	2.934085	0.004934	0.040075	-3.04785	Rhomboid-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0254430.1	0.26856	8.132394	2.851324	0.006192	0.04639	-3.07286	Oxidoreductase	elongation zone	12 h
HORVU.MOREX.r3.1HG0024510.1	0.40608	5.713563	2.8051	0.007017	0.049999	-3.07851	Universal stress protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0105020.1	0.691857	6.347815	2.893409	0.005519	0.043127	-3.09739	Aquaporin	elongation zone	12 h
HORVU.MOREX.r3.1HG0003820.1	0.349394	7.438968	2.847067	0.006264	0.046718	-3.11774	Protein DETOXIFICATION	elongation zone	12 h
HORVU.MOREX.r3.7HG0678940.1	0.368765	6.707895	2.838395	0.006413	0.047365	-3.13689	Fasciclin-like arabinogalactan protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0197260.1	0.268839	7.526184	2.82234	0.006698	0.048636	-3.14263	WEB family protein, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.3HG0228660.1	0.337639	7.196618	2.82339	0.006679	0.048549	-3.17854	Myosin	elongation zone	12 h
HORVU.MOREX.r3.4HG0412730.1	-0.42217	10.67637	-2.8332	0.006504	0.047749	-3.2732	Purple acid phosphatase	elongation zone	12 h
HORVU.MOREX.r3.3HG0313690.1	-0.29347	9.880246	-2.80859	0.006951	0.049719	-3.34916	Glutathione S-transferase	elongation zone	12 h

Table S0 Hierarchical clustering analysis of differentially expressed genes (false discovery rate (FDR) <5%) in root cap of gravistimulated wild type roots.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.1HG0002330.1	0.1707356	-0.069731	-0.6646211	cluster 1
HORVU.MOREX.r3.1HG0008890.1	0.1645802	-0.0130841	-0.5037172	cluster 1
HORVU.MOREX.r3.1HG0014220.1	0.3493891	0.0068183	-0.8539787	cluster 1
HORVU.MOREX.r3.1HG0014560.1	0.098206	-0.0579504	-0.8326012	cluster 1
HORVU.MOREX.r3.1HG0015430.1	0.0140082	-0.1213651	-1.5951741	cluster 1
HORVU.MOREX.r3.1HG0017350.1	0.0925823	-0.0962892	-0.7454588	cluster 1
HORVU.MOREX.r3.1HG0019240.1	-0.465142	-0.6634696	-0.9857007	cluster 1
HORVU.MOREX.r3.1HG0019440.1	-0.059283	-0.0980176	-0.4338449	cluster 1
HORVU.MOREX.r3.1HG0025520.1	-0.113161	-0.2527211	-1.1252092	cluster 1
HORVU.MOREX.r3.1HG0027030.1	-0.201481	-0.2584751	-0.7571077	cluster 1
HORVU.MOREX.r3.1HG0029270.1	-0.068689	-0.1856717	-0.5638445	cluster 1
HORVU.MOREX.r3.1HG0031820.1	0.0602048	-0.289448	-0.9447196	cluster 1
HORVU.MOREX.r3.1HG0036390.1	0.0204946	-0.1146592	-0.4906721	cluster 1
HORVU.MOREX.r3.1HG0051880.1	-0.122715	-0.280313	-0.8224489	cluster 1
HORVU.MOREX.r3.1HG0051890.1	-0.135185	-0.2405748	-0.8744259	cluster 1
HORVU.MOREX.r3.1HG0053120.1	0.1660103	0.0451837	-0.7353026	cluster 1
HORVU.MOREX.r3.1HG0054960.1	-0.058411	-0.1761302	-0.7343525	cluster 1
HORVU.MOREX.r3.1HG0055320.1	0.1454075	-0.0141316	-0.3210414	cluster 1
HORVU.MOREX.r3.1HG0056360.1	0.1753546	0.0339342	-0.4873287	cluster 1
HORVU.MOREX.r3.1HG0056540.1	0.0352941	0.0874273	-0.9744306	cluster 1
HORVU.MOREX.r3.1HG0057290.1	0.0997116	-0.1008676	-0.7499372	cluster 1
HORVU.MOREX.r3.1HG0057610.1	-0.17338	-0.2743248	-0.5220569	cluster 1
HORVU.MOREX.r3.1HG0057800.1	0.2064075	-0.1769001	-1.342247	cluster 1
HORVU.MOREX.r3.1HG0058170.1	0.0526902	-0.0644834	-0.4953391	cluster 1
HORVU.MOREX.r3.1HG0059150.1	0.1383591	0.0409054	-0.7585698	cluster 1
HORVU.MOREX.r3.1HG0062030.1	0.3329477	-0.3390041	-1.455675	cluster 1
HORVU.MOREX.r3.1HG0064310.1	0.0167471	-0.0834389	-0.6617663	cluster 1
HORVU.MOREX.r3.1HG0065120.1	-0.042207	-0.1003168	-0.5499375	cluster 1
HORVU.MOREX.r3.1HG0069010.1	-0.107712	-0.3083214	-0.8324017	cluster 1
HORVU.MOREX.r3.1HG0070670.1	0.021674	-0.1568637	-0.6412713	cluster 1
HORVU.MOREX.r3.1HG0071320.1	0.0857173	0.0503672	-1.037841	cluster 1
HORVU.MOREX.r3.1HG0072100.1	0.2686935	0.0831744	-0.7749167	cluster 1
HORVU.MOREX.r3.1HG0073140.1	-0.046214	-0.2538513	-0.8635086	cluster 1
HORVU.MOREX.r3.1HG0075220.1	0.2967808	0.1601418	-1.0192773	cluster 1
HORVU.MOREX.r3.1HG0077230.1	0.1899281	-0.0093486	-0.789304	cluster 1
HORVU.MOREX.r3.1HG0077710.1	0.1542422	0.1803493	-0.7503547	cluster 1
HORVU.MOREX.r3.1HG0080260.1	-0.245798	-0.2291487	-0.5082043	cluster 1
HORVU.MOREX.r3.1HG0081120.1	-0.272373	-0.1142109	-1.4459268	cluster 1
HORVU.MOREX.r3.1HG0081860.1	0.1326211	-0.11948	-0.8788293	cluster 1
HORVU.MOREX.r3.1HG0082670.1	-0.115995	-0.3154451	-0.7413344	cluster 1
HORVU.MOREX.r3.1HG0083840.1	-0.108545	-0.0497991	-0.4975227	cluster 1
HORVU.MOREX.r3.1HG0085780.1	0.227707	0.0763213	-1.0106562	cluster 1
HORVU.MOREX.r3.1HG0089180.1	0.1740548	0.0111709	-0.6094135	cluster 1
HORVU.MOREX.r3.1HG0093750.1	-0.135597	-0.0185006	-1.0255918	cluster 1
HORVU.MOREX.r3.1HG0093880.1	0.3636581	0.1300544	-0.77277	cluster 1
HORVU.MOREX.r3.2HG0096100.1	0.0229233	-0.0662696	-0.8618271	cluster 1
HORVU.MOREX.r3.2HG0097600.1	-0.054917	-0.1509645	-0.5279722	cluster 1

Table S0 Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.2HG0099750.1	0.182292	-0.0954893	-0.5572858	cluster 1
HORVU.MOREX.r3.2HG0099980.1	-0.236216	-0.2842068	-0.7613671	cluster 1
HORVU.MOREX.r3.2HG0100060.1	0.0682534	-0.1090605	-1.0421373	cluster 1
HORVU.MOREX.r3.2HG0100270.2	0.1435812	0.0823961	-0.5912385	cluster 1
HORVU.MOREX.r3.2HG0104110.1	0.0629003	0.0021257	-0.9242198	cluster 1
HORVU.MOREX.r3.2HG0109400.1	0.1065021	-0.1021695	-1.2689128	cluster 1
HORVU.MOREX.r3.2HG0113410.1	0.1233282	-0.0049988	-0.5250859	cluster 1
HORVU.MOREX.r3.2HG0113590.1	-0.056695	-0.0157784	-0.5608697	cluster 1
HORVU.MOREX.r3.2HG0113860.1	0.1942076	-0.0043177	-1.2067332	cluster 1
HORVU.MOREX.r3.2HG0119150.1	0.0459465	0.0763396	-0.5504699	cluster 1
HORVU.MOREX.r3.2HG0119920.1	0.1578493	0.0488629	-0.671108	cluster 1
HORVU.MOREX.r3.2HG0121380.1	-0.07747	-0.2040315	-0.6364525	cluster 1
HORVU.MOREX.r3.2HG0122840.1	0.1800344	0.1011832	-0.5711731	cluster 1
HORVU.MOREX.r3.2HG0124110.1	-0.124875	-0.0871535	-0.7312259	cluster 1
HORVU.MOREX.r3.2HG0125600.1	-0.123034	-0.3901724	-1.282441	cluster 1
HORVU.MOREX.r3.2HG0127370.1	0.1575099	0.2037384	-0.6091735	cluster 1
HORVU.MOREX.r3.2HG0128270.1	0.1627538	0.1000413	-0.776112	cluster 1
HORVU.MOREX.r3.2HG0128490.1	-0.075366	-0.1253905	-0.4289783	cluster 1
HORVU.MOREX.r3.2HG0130760.1	-0.043515	-0.1034422	-0.6913018	cluster 1
HORVU.MOREX.r3.2HG0131330.1	0.1699821	0.0290188	-0.6502478	cluster 1
HORVU.MOREX.r3.2HG0133060.1	0.355961	0.0803982	-0.870611	cluster 1
HORVU.MOREX.r3.2HG0133930.1	-0.936341	-0.0392541	-2.1038791	cluster 1
HORVU.MOREX.r3.2HG0135590.1	-0.244832	-0.0869697	-0.6340419	cluster 1
HORVU.MOREX.r3.2HG0138270.1	-0.169465	-0.230731	-0.6614251	cluster 1
HORVU.MOREX.r3.2HG0147190.1	0.1119502	-0.0668936	-0.7262734	cluster 1
HORVU.MOREX.r3.2HG0154110.1	0.2194787	0.0261628	-1.033996	cluster 1
HORVU.MOREX.r3.2HG0163200.1	0.2192212	0.1676308	-0.5199979	cluster 1
HORVU.MOREX.r3.2HG0164440.1	0.2034692	0.3096843	-0.6251427	cluster 1
HORVU.MOREX.r3.2HG0165290.2	-0.095882	0.0993993	-0.7885599	cluster 1
HORVU.MOREX.r3.2HG0165780.1	0.0892943	0.1883986	-0.4339442	cluster 1
HORVU.MOREX.r3.2HG0168300.1	0.054616	-0.1043369	-1.1604944	cluster 1
HORVU.MOREX.r3.2HG0168640.1	-0.114701	-0.0881309	-0.4952482	cluster 1
HORVU.MOREX.r3.2HG0169000.1	-0.392723	-0.769097	-1.4321648	cluster 1
HORVU.MOREX.r3.2HG0169420.1	-0.027819	-0.0138016	-0.8419302	cluster 1
HORVU.MOREX.r3.2HG0172180.1	-0.121844	-0.3012642	-0.7902189	cluster 1
HORVU.MOREX.r3.2HG0173440.1	-0.014501	-0.1274453	-0.851014	cluster 1
HORVU.MOREX.r3.2HG0173750.1	0.0613164	-0.0597776	-0.5074225	cluster 1
HORVU.MOREX.r3.2HG0174560.1	-0.114083	-0.1786777	-0.5089115	cluster 1
HORVU.MOREX.r3.2HG0177780.1	0.0285171	-0.0895278	-0.4935162	cluster 1
HORVU.MOREX.r3.2HG0180040.2	0.0533812	-0.0608599	-1.1036712	cluster 1
HORVU.MOREX.r3.2HG0181020.1	0.2204522	0.0198243	-0.6008209	cluster 1
HORVU.MOREX.r3.2HG0184350.1	-0.038935	-0.0857675	-0.5818051	cluster 1
HORVU.MOREX.r3.2HG0185660.1	-0.08651	-0.1538465	-0.4095365	cluster 1
HORVU.MOREX.r3.2HG0186670.1	0.0442886	0.027498	-0.6764735	cluster 1
HORVU.MOREX.r3.2HG0187170.1	-0.018128	-0.0817307	-0.4488681	cluster 1
HORVU.MOREX.r3.2HG0187980.1	0.3392904	0.1406879	-0.5813126	cluster 1
HORVU.MOREX.r3.2HG0188070.1	0.2777649	0.1336551	-0.8322951	cluster 1

Table S0 Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.2HG0189190.1	0.2117247	0.0348889	-0.564115	cluster 1
HORVU.MOREX.r3.2HG0189340.1	-0.157698	-0.2219058	-0.9130796	cluster 1
HORVU.MOREX.r3.2HG0191970.1	0.0791868	-0.1581829	-0.8752616	cluster 1
HORVU.MOREX.r3.2HG0192860.1	0.1482787	-0.0736532	-0.5624417	cluster 1
HORVU.MOREX.r3.2HG0192920.1	0.2505769	-0.0475889	-0.8141112	cluster 1
HORVU.MOREX.r3.2HG0192960.1	0.1026076	0.1015388	-0.6391422	cluster 1
HORVU.MOREX.r3.2HG0194600.1	-0.566806	-0.5078339	-0.7637254	cluster 1
HORVU.MOREX.r3.2HG0194790.1	0.1559992	0.0290132	-0.5149481	cluster 1
HORVU.MOREX.r3.2HG0195580.1	0.2191461	0.1882456	-0.6067809	cluster 1
HORVU.MOREX.r3.2HG0197550.1	0.3083522	0.1903185	-0.8592855	cluster 1
HORVU.MOREX.r3.2HG0201420.1	-0.138068	-0.3993381	-1.0927887	cluster 1
HORVU.MOREX.r3.2HG0202110.1	0.1008244	0.0033848	-0.4397894	cluster 1
HORVU.MOREX.r3.2HG0203390.1	-0.111121	-0.4001883	-1.0824523	cluster 1
HORVU.MOREX.r3.2HG0205250.1	0.1502304	0.1656253	-0.7819281	cluster 1
HORVU.MOREX.r3.2HG0207160.1	0.2676942	0.2612654	-0.7243435	cluster 1
HORVU.MOREX.r3.2HG0211680.1	-0.070159	-0.347567	-1.0188098	cluster 1
HORVU.MOREX.r3.2HG0213480.1	0.1684082	0.1369867	-0.4820726	cluster 1
HORVU.MOREX.r3.2HG0214820.1	0.0216719	-0.3691005	-0.9907546	cluster 1
HORVU.MOREX.r3.3HG0220830.1	0.2452903	0.0003142	-1.4049309	cluster 1
HORVU.MOREX.r3.3HG0227860.1	0.0905777	-0.0332528	-0.3865948	cluster 1
HORVU.MOREX.r3.3HG0227890.1	0.0198392	-0.0569362	-1.181551	cluster 1
HORVU.MOREX.r3.3HG0228600.1	0.0683067	-0.1947412	-0.8040683	cluster 1
HORVU.MOREX.r3.3HG0231010.1	-0.030001	-0.0410105	-0.4832806	cluster 1
HORVU.MOREX.r3.3HG0231330.1	-0.065927	-0.3270764	-0.8240308	cluster 1
HORVU.MOREX.r3.3HG0231460.1	0.168657	0.1539204	-0.7719347	cluster 1
HORVU.MOREX.r3.3HG0232840.1	0.1496139	0.1093986	-0.4678902	cluster 1
HORVU.MOREX.r3.3HG0234880.1	0.1085436	0.0271935	-0.7876179	cluster 1
HORVU.MOREX.r3.3HG0234890.1	0.0597158	0.1404151	-0.7690663	cluster 1
HORVU.MOREX.r3.3HG0235800.1	0.3764253	-0.5083754	-2.3271368	cluster 1
HORVU.MOREX.r3.3HG0236350.1	-0.514395	-0.2139384	-0.8716992	cluster 1
HORVU.MOREX.r3.3HG0242790.1	0.2172794	-0.0040146	-0.4991882	cluster 1
HORVU.MOREX.r3.3HG0244080.1	0.0143144	-0.1989374	-0.9640661	cluster 1
HORVU.MOREX.r3.3HG0245010.1	-0.009652	-0.119163	-0.6249435	cluster 1
HORVU.MOREX.r3.3HG0249710.1	0.0964757	-0.1540475	-0.680477	cluster 1
HORVU.MOREX.r3.3HG0250330.1	0.0685641	-0.0833517	-0.5594949	cluster 1
HORVU.MOREX.r3.3HG0251700.1	-0.007638	-0.2978602	-0.9078617	cluster 1
HORVU.MOREX.r3.3HG0251900.1	-0.021701	-0.1306439	-0.5818368	cluster 1
HORVU.MOREX.r3.3HG0252100.1	0.0895496	-0.0647937	-0.7727761	cluster 1
HORVU.MOREX.r3.3HG0252270.1	0.1472279	-0.0650709	-0.9676407	cluster 1
HORVU.MOREX.r3.3HG0253860.1	-0.176805	-0.6068891	-1.4092203	cluster 1
HORVU.MOREX.r3.3HG0256160.1	0.1818661	0.0931427	-0.5030953	cluster 1
HORVU.MOREX.r3.3HG0256430.1	0.1617285	-0.0372638	-0.6559322	cluster 1
HORVU.MOREX.r3.3HG0256910.1	0.0327792	-0.0574169	-0.8204516	cluster 1
HORVU.MOREX.r3.3HG0266950.1	-0.129288	0.130242	-0.6905455	cluster 1
HORVU.MOREX.r3.3HG0271380.1	0.1804017	0.129765	-0.545123	cluster 1
HORVU.MOREX.r3.3HG0271550.1	0.1986398	-0.070624	-0.5219619	cluster 1
HORVU.MOREX.r3.3HG0273560.1	-0.357839	-0.5254332	-1.300763	cluster 1

Table S0 Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.3HG0273730.1	-0.164858	-0.1678612	-0.6509035	cluster 1
HORVU.MOREX.r3.3HG0275260.1	0.0111266	-0.1864652	-0.7524535	cluster 1
HORVU.MOREX.r3.3HG0275450.1	0.0212448	0.2655736	-0.9271112	cluster 1
HORVU.MOREX.r3.3HG0275500.1	-0.200904	-0.623191	-1.6564576	cluster 1
HORVU.MOREX.r3.3HG0276000.2	1.1018298	1.8100643	-0.6585563	cluster 1
HORVU.MOREX.r3.3HG0277400.1	0.3540908	0.1408818	-0.6071427	cluster 1
HORVU.MOREX.r3.3HG0281000.1	-0.005218	0.0368879	-1.1362508	cluster 1
HORVU.MOREX.r3.3HG0281780.1	-0.207269	-0.2383308	-0.6641343	cluster 1
HORVU.MOREX.r3.3HG0284890.1	0.1629977	0.2150009	-0.6938056	cluster 1
HORVU.MOREX.r3.3HG0286640.1	-0.106466	-0.2502943	-0.921725	cluster 1
HORVU.MOREX.r3.3HG0288830.1	0.0091573	-0.0170967	-0.3301356	cluster 1
HORVU.MOREX.r3.3HG0290130.1	0.0707521	-0.0632943	-0.76123	cluster 1
HORVU.MOREX.r3.3HG0290180.1	0.0603195	-0.1700186	-0.6116577	cluster 1
HORVU.MOREX.r3.3HG0291590.1	-0.088436	-0.2753589	-0.6288763	cluster 1
HORVU.MOREX.r3.3HG0291680.1	0.1814673	0.0711571	-0.9785149	cluster 1
HORVU.MOREX.r3.3HG0293070.1	0.1025929	-0.1167899	-0.6356689	cluster 1
HORVU.MOREX.r3.3HG0293570.1	-0.354902	-0.2515102	-2.9257568	cluster 1
HORVU.MOREX.r3.3HG0295550.1	0.1507494	0.0980024	-0.5186528	cluster 1
HORVU.MOREX.r3.3HG0295840.1	0.0508498	0.0271712	-0.5843366	cluster 1
HORVU.MOREX.r3.3HG0296420.1	0.0569306	-0.0195863	-0.463752	cluster 1
HORVU.MOREX.r3.3HG0299100.1	0.0169666	-0.1209807	-0.5434559	cluster 1
HORVU.MOREX.r3.3HG0300080.1	0.2541824	0.0574149	-0.7490972	cluster 1
HORVU.MOREX.r3.3HG0300580.1	0.00154	-0.2233061	-1.0561484	cluster 1
HORVU.MOREX.r3.3HG0303190.1	0.1717346	0.141804	-0.4057797	cluster 1
HORVU.MOREX.r3.3HG0303670.1	0.1681824	-0.2322876	-0.8676161	cluster 1
HORVU.MOREX.r3.3HG0305540.1	-0.098984	-0.6168426	-1.3167503	cluster 1
HORVU.MOREX.r3.3HG0306820.1	0.2426683	0.0673865	-0.5940755	cluster 1
HORVU.MOREX.r3.3HG0308250.1	0.0358422	-0.022312	-0.5375334	cluster 1
HORVU.MOREX.r3.3HG0311480.1	0.0922847	0.0494435	-0.8640716	cluster 1
HORVU.MOREX.r3.3HG0315300.1	0.0648248	-0.0581596	-0.8686528	cluster 1
HORVU.MOREX.r3.3HG0320710.1	0.0459291	-0.106247	-0.5763273	cluster 1
HORVU.MOREX.r3.3HG0323410.1	0.3461359	-0.0157362	-1.0490819	cluster 1
HORVU.MOREX.r3.3HG0328340.1	-0.080608	-0.3457436	-0.8072279	cluster 1
HORVU.MOREX.r3.3HG0329000.1	0.1757403	0.123947	-0.5454783	cluster 1
HORVU.MOREX.r3.4HG0332530.1	-0.040955	-0.1235787	-0.5665792	cluster 1
HORVU.MOREX.r3.4HG0336330.1	0.049546	0.0393657	-0.8291267	cluster 1
HORVU.MOREX.r3.4HG0338810.1	0.2379603	0.1118242	-0.5885998	cluster 1
HORVU.MOREX.r3.4HG0340420.1	0.2455155	-0.0348712	-0.4823853	cluster 1
HORVU.MOREX.r3.4HG0342860.1	-0.045176	-0.0185048	-0.835231	cluster 1
HORVU.MOREX.r3.4HG0343380.1	-0.03962	-0.1308218	-0.4306572	cluster 1
HORVU.MOREX.r3.4HG0347330.1	0.1528549	0.0584248	-0.5585683	cluster 1
HORVU.MOREX.r3.4HG0348850.1	0.2404947	0.1267945	-0.6904592	cluster 1
HORVU.MOREX.r3.4HG0352420.1	-0.031264	-0.2470611	-0.641372	cluster 1
HORVU.MOREX.r3.4HG0353950.1	-0.15119	-0.1458492	-1.6328211	cluster 1
HORVU.MOREX.r3.4HG0356780.1	0.0014687	0.0269827	-0.5457976	cluster 1
HORVU.MOREX.r3.4HG0365970.1	-0.1093	-0.0976246	-0.4987654	cluster 1
HORVU.MOREX.r3.4HG0378750.1	0.0617481	-6.277E-05	-0.5717213	cluster 1

Table S0 Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.4HG0378900.1	0.196064	0.0852259	-0.5236892	cluster 1
HORVU.MOREX.r3.4HG0381750.1	-0.117547	-0.1359577	-0.6095192	cluster 1
HORVU.MOREX.r3.4HG0381820.1	0.1308354	0.0013819	-0.6168217	cluster 1
HORVU.MOREX.r3.4HG0382640.1	0.2568095	0.2242829	-1.3880395	cluster 1
HORVU.MOREX.r3.4HG0384300.1	-0.001681	-0.0583377	-1.2011882	cluster 1
HORVU.MOREX.r3.4HG0384590.1	-0.332835	-0.3626826	-1.4357014	cluster 1
HORVU.MOREX.r3.4HG0385780.1	0.0064918	-0.1207269	-0.5374264	cluster 1
HORVU.MOREX.r3.4HG0389580.1	0.0242274	-0.0821395	-0.434092	cluster 1
HORVU.MOREX.r3.4HG0389860.1	-0.022641	-0.1038957	-0.3391206	cluster 1
HORVU.MOREX.r3.4HG0390580.1	0.0983186	0.1044467	-0.7348324	cluster 1
HORVU.MOREX.r3.4HG0391050.1	0.2521625	-0.0739531	-0.6706895	cluster 1
HORVU.MOREX.r3.4HG0391970.1	0.0045147	-0.0289776	-1.2157536	cluster 1
HORVU.MOREX.r3.4HG0392440.1	0.0293051	-0.2593695	-0.6496022	cluster 1
HORVU.MOREX.r3.4HG0393500.1	0.1140934	0.1020535	-0.8301427	cluster 1
HORVU.MOREX.r3.4HG0394470.1	-0.028764	-0.4560075	-1.1302958	cluster 1
HORVU.MOREX.r3.4HG0395120.1	-0.296843	-0.1032085	-0.650262	cluster 1
HORVU.MOREX.r3.4HG0397280.1	0.0421174	-0.0032905	-0.5443237	cluster 1
HORVU.MOREX.r3.4HG0397570.1	0.062818	-0.1718389	-0.9564125	cluster 1
HORVU.MOREX.r3.4HG0399460.1	0.1386627	-0.3977537	-2.1109442	cluster 1
HORVU.MOREX.r3.4HG0400830.1	-0.283792	-0.2380419	-2.2740873	cluster 1
HORVU.MOREX.r3.4HG0403910.1	-0.462744	-0.2304379	-1.1725856	cluster 1
HORVU.MOREX.r3.4HG0403930.1	0.2191421	-0.0297276	-1.0240076	cluster 1
HORVU.MOREX.r3.4HG0405830.1	-0.027851	-0.0722627	-0.7361311	cluster 1
HORVU.MOREX.r3.4HG0406720.1	-0.468853	-0.6609613	-1.7474568	cluster 1
HORVU.MOREX.r3.4HG0406900.1	-0.052493	-0.1494114	-0.5710678	cluster 1
HORVU.MOREX.r3.4HG0406980.1	0.2603271	0.1433092	-0.9154549	cluster 1
HORVU.MOREX.r3.4HG0407120.1	0.0538909	-0.0180769	-0.5743709	cluster 1
HORVU.MOREX.r3.4HG0411320.1	0.1112038	0.0159783	-0.4985803	cluster 1
HORVU.MOREX.r3.4HG0413890.1	0.0006388	-0.1494476	-0.424155	cluster 1
HORVU.MOREX.r3.4HG0417410.1	-0.493011	-0.3531985	-1.3495621	cluster 1
HORVU.MOREX.r3.5HG0426180.1	0.002104	-0.1640506	-0.5993603	cluster 1
HORVU.MOREX.r3.5HG0427690.1	0.1895993	0.0017769	-0.8550742	cluster 1
HORVU.MOREX.r3.5HG0436990.1	0.1520933	0.1580867	-0.637329	cluster 1
HORVU.MOREX.r3.5HG0439620.1	0.0102061	-0.1402296	-0.4894307	cluster 1
HORVU.MOREX.r3.5HG0440700.1	0.0283733	0.0290499	-0.444244	cluster 1
HORVU.MOREX.r3.5HG0445510.1	-0.048345	-0.1288695	-0.4798599	cluster 1
HORVU.MOREX.r3.5HG0446490.1	0.1124989	0.0530041	-0.8088415	cluster 1
HORVU.MOREX.r3.5HG0453430.1	-0.011561	-0.1353413	-0.849851	cluster 1
HORVU.MOREX.r3.5HG0455240.1	0.1990786	0.1165271	-0.7857424	cluster 1
HORVU.MOREX.r3.5HG0455770.1	0.2350848	0.0527657	-0.8139052	cluster 1
HORVU.MOREX.r3.5HG0455820.1	0.2251138	-0.1074046	-0.9689068	cluster 1
HORVU.MOREX.r3.5HG0456950.1	0.0185592	0.1010292	-0.4289335	cluster 1
HORVU.MOREX.r3.5HG0457960.1	0.0311898	0.0335217	-0.3381911	cluster 1
HORVU.MOREX.r3.5HG0458100.1	0.2157855	0.073006	-0.8015739	cluster 1
HORVU.MOREX.r3.5HG0460300.1	-0.170396	-0.4116975	-0.859383	cluster 1
HORVU.MOREX.r3.5HG0461790.1	0.3984617	0.1073383	-1.0271729	cluster 1
HORVU.MOREX.r3.5HG0462780.1	0.0685421	0.052287	-0.5322816	cluster 1

Table S0 Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.5HG0463370.1	0.2956809	-0.1183146	-1.1099129	cluster 1
HORVU.MOREX.r3.5HG0464600.1	0.124074	0.0020526	-0.6616022	cluster 1
HORVU.MOREX.r3.5HG0467230.2	0.0352216	-0.1302257	-0.448615	cluster 1
HORVU.MOREX.r3.5HG0468320.1	0.2729129	0.0914121	-0.8455433	cluster 1
HORVU.MOREX.r3.5HG0471410.1	0.0297267	-0.0133108	-0.4627252	cluster 1
HORVU.MOREX.r3.5HG0471560.1	0.0783714	0.0665973	-0.5959327	cluster 1
HORVU.MOREX.r3.5HG0471940.1	-0.057601	-0.1501616	-0.3613076	cluster 1
HORVU.MOREX.r3.5HG0476220.1	0.1782595	-0.0710944	-0.7292878	cluster 1
HORVU.MOREX.r3.5HG0480430.1	0.1411169	0.0038158	-0.7527898	cluster 1
HORVU.MOREX.r3.5HG0481030.1	0.2389392	0.1744726	-0.8003171	cluster 1
HORVU.MOREX.r3.5HG0481120.1	0.1169389	-0.1089151	-0.9823108	cluster 1
HORVU.MOREX.r3.5HG0481570.1	0.2363627	0.1421559	-0.8273991	cluster 1
HORVU.MOREX.r3.5HG0483810.1	0.0204578	-0.0567118	-0.4489361	cluster 1
HORVU.MOREX.r3.5HG0487890.1	0.0781162	-0.0644205	-0.8183504	cluster 1
HORVU.MOREX.r3.5HG0488620.1	0.2344706	0.0734827	-0.5842426	cluster 1
HORVU.MOREX.r3.5HG0494470.1	-0.016452	-0.0193565	-0.464456	cluster 1
HORVU.MOREX.r3.5HG0494890.1	0.0758095	-0.1661683	-0.7030441	cluster 1
HORVU.MOREX.r3.5HG0495750.1	-0.05841	-0.2452742	-1.9144681	cluster 1
HORVU.MOREX.r3.5HG0495770.1	0.1529297	0.0353129	-0.4807744	cluster 1
HORVU.MOREX.r3.5HG0496780.1	0.1548495	0.0326807	-0.5162585	cluster 1
HORVU.MOREX.r3.5HG0497170.1	0.070234	-0.0373455	-0.5609432	cluster 1
HORVU.MOREX.r3.5HG0501370.1	0.1640964	0.0254852	-0.9053354	cluster 1
HORVU.MOREX.r3.5HG0501950.1	0.0456301	-0.2756289	-1.1865335	cluster 1
HORVU.MOREX.r3.5HG0504340.1	-0.119178	-0.0650048	-0.6721698	cluster 1
HORVU.MOREX.r3.5HG0506790.1	0.1216365	-0.0420748	-0.6837788	cluster 1
HORVU.MOREX.r3.5HG0507370.1	-0.036919	0.0483272	-0.5774916	cluster 1
HORVU.MOREX.r3.5HG0509060.1	0.0658858	-0.1279841	-0.9596401	cluster 1
HORVU.MOREX.r3.5HG0510700.1	0.1073467	-0.0698439	-0.470715	cluster 1
HORVU.MOREX.r3.5HG0511040.1	0.2626462	-0.1841417	-0.9497797	cluster 1
HORVU.MOREX.r3.5HG0512430.1	0.2742379	-0.1540368	-0.8102867	cluster 1
HORVU.MOREX.r3.5HG0513000.1	-0.037123	-0.1405624	-0.4575904	cluster 1
HORVU.MOREX.r3.5HG0517300.1	0.2159498	0.0391928	-1.098873	cluster 1
HORVU.MOREX.r3.5HG0517330.1	0.101533	-0.1227283	-0.5071322	cluster 1
HORVU.MOREX.r3.5HG0517370.1	-0.162276	-0.2578441	-2.3322055	cluster 1
HORVU.MOREX.r3.5HG0519030.1	-0.084406	-0.1435039	-0.6605251	cluster 1
HORVU.MOREX.r3.5HG0519200.1	0.0015367	-0.062071	-0.8082744	cluster 1
HORVU.MOREX.r3.5HG0527770.1	0.2700764	0.1916167	-0.7964304	cluster 1
HORVU.MOREX.r3.6HG0548800.1	-0.100672	-0.3426621	-1.1749279	cluster 1
HORVU.MOREX.r3.6HG0552230.1	0.1295268	-0.2060539	-0.8487039	cluster 1
HORVU.MOREX.r3.6HG0555250.1	0.0951596	-0.1402506	-0.6986989	cluster 1
HORVU.MOREX.r3.6HG0559390.1	0.1236001	-0.1795724	-1.120197	cluster 1
HORVU.MOREX.r3.6HG0560030.1	0.1700847	-0.0490231	-0.5275027	cluster 1
HORVU.MOREX.r3.6HG0561320.1	-0.134292	-0.2913722	-1.2817497	cluster 1
HORVU.MOREX.r3.6HG0565880.1	0.067755	-0.1601905	-0.515877	cluster 1
HORVU.MOREX.r3.6HG0568690.1	0.0482127	-0.1862989	-1.0389096	cluster 1
HORVU.MOREX.r3.6HG0568720.1	0.1485002	-0.0694785	-0.8142139	cluster 1
HORVU.MOREX.r3.6HG0570660.1	-0.251501	-0.5498413	-1.3005543	cluster 1

Table S0 Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.6HG0570850.1	0.127417	0.0169309	-0.6008693	cluster 1
HORVU.MOREX.r3.6HG0577180.1	0.2508565	-0.1256526	-1.0030752	cluster 1
HORVU.MOREX.r3.6HG0591720.1	0.0498022	0.0731967	-0.4857176	cluster 1
HORVU.MOREX.r3.6HG0597880.1	0.2578119	0.1874793	-0.5704934	cluster 1
HORVU.MOREX.r3.6HG0598380.1	-0.120661	-0.4153604	-1.0412936	cluster 1
HORVU.MOREX.r3.6HG0600190.1	0.2602727	0.0129475	-0.6702258	cluster 1
HORVU.MOREX.r3.6HG0601740.1	0.1677533	0.0638366	-1.1147798	cluster 1
HORVU.MOREX.r3.6HG0603150.1	0.2919512	0.0933604	-0.7566002	cluster 1
HORVU.MOREX.r3.6HG0604990.1	-0.447725	-0.4972408	-1.3495248	cluster 1
HORVU.MOREX.r3.6HG0607470.1	0.1319364	0.1609648	-0.4571649	cluster 1
HORVU.MOREX.r3.6HG0608380.1	-0.010442	-0.059872	-0.473855	cluster 1
HORVU.MOREX.r3.6HG0609220.1	0.1201262	-0.0377395	-0.6675735	cluster 1
HORVU.MOREX.r3.6HG0611930.1	-0.577187	-0.6670841	-1.5392809	cluster 1
HORVU.MOREX.r3.6HG0614420.1	-0.004193	-0.2411698	-0.7060912	cluster 1
HORVU.MOREX.r3.6HG0615840.1	-0.491774	-0.3090927	-1.8641589	cluster 1
HORVU.MOREX.r3.6HG0617830.1	0.0998872	-0.1553865	-0.9023153	cluster 1
HORVU.MOREX.r3.6HG0622540.1	0.2053204	-0.1165191	-0.5823518	cluster 1
HORVU.MOREX.r3.6HG0623730.1	0.1644459	0.0709713	-0.9257004	cluster 1
HORVU.MOREX.r3.6HG0625490.1	-0.079074	-0.2381439	-0.5004157	cluster 1
HORVU.MOREX.r3.6HG0626000.1	-0.044269	-0.0781342	-1.0887527	cluster 1
HORVU.MOREX.r3.6HG0626330.1	0.2099912	0.1832228	-0.6671732	cluster 1
HORVU.MOREX.r3.6HG0630690.1	0.0081018	-0.1090883	-0.6131988	cluster 1
HORVU.MOREX.r3.6HG0631080.1	0.1026792	-0.1050413	-0.4997856	cluster 1
HORVU.MOREX.r3.6HG0634140.1	-0.000579	-0.1146015	-0.8232646	cluster 1
HORVU.MOREX.r3.7HG0635050.1	0.0880867	-0.0077246	-0.7648137	cluster 1
HORVU.MOREX.r3.7HG0635330.1	0.1399067	-0.632396	-1.7380487	cluster 1
HORVU.MOREX.r3.7HG0639840.1	-0.241984	-0.8490971	-1.9875216	cluster 1
HORVU.MOREX.r3.7HG0644160.1	0.346686	-0.0760785	-0.928141	cluster 1
HORVU.MOREX.r3.7HG0646880.1	0.1051319	0.0621529	-0.4806318	cluster 1
HORVU.MOREX.r3.7HG0648140.1	0.0304123	-0.2111924	-0.5829098	cluster 1
HORVU.MOREX.r3.7HG0648610.1	0.1054259	0.0656255	-0.2977385	cluster 1
HORVU.MOREX.r3.7HG0656220.1	0.0757624	0.0514909	-0.583046	cluster 1
HORVU.MOREX.r3.7HG0658130.1	0.156762	-0.0498072	-0.7854154	cluster 1
HORVU.MOREX.r3.7HG0659980.1	0.1938869	0.1546256	-0.7528913	cluster 1
HORVU.MOREX.r3.7HG0660830.1	0.0202442	-0.0344004	-0.3930426	cluster 1
HORVU.MOREX.r3.7HG0663550.1	-0.524353	-1.1082988	-2.1275594	cluster 1
HORVU.MOREX.r3.7HG0666350.1	0.1070443	-0.0164354	-0.6601946	cluster 1
HORVU.MOREX.r3.7HG0668190.1	0.005287	-0.0551883	-0.5840778	cluster 1
HORVU.MOREX.r3.7HG0668260.1	-0.305339	-0.5685239	-1.4719424	cluster 1
HORVU.MOREX.r3.7HG0669600.1	0.1709775	-0.1215489	-0.6486921	cluster 1
HORVU.MOREX.r3.7HG0670910.1	0.0779755	-0.0383785	-0.4293611	cluster 1
HORVU.MOREX.r3.7HG0671350.1	-0.027484	-0.0982013	-0.4159508	cluster 1
HORVU.MOREX.r3.7HG0671720.1	-0.176628	-0.1787856	-0.8791208	cluster 1
HORVU.MOREX.r3.7HG0675390.1	-0.051485	-0.209642	-0.8313616	cluster 1
HORVU.MOREX.r3.7HG0676620.1	-0.223148	-0.4208722	-1.4446499	cluster 1
HORVU.MOREX.r3.7HG0677380.1	0.2690831	0.2664463	-0.5500272	cluster 1
HORVU.MOREX.r3.7HG0677710.1	0.3548376	-0.2685487	-1.3310348	cluster 1

Table S0 Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.7HG0678310.1	0.1227949	0.1579376	-0.6653024	cluster 1
HORVU.MOREX.r3.7HG0678530.1	-0.011797	-0.1279937	-0.5352814	cluster 1
HORVU.MOREX.r3.7HG0682660.1	0.3288058	0.2327431	-1.9326566	cluster 1
HORVU.MOREX.r3.7HG0682960.1	0.0610082	-0.0545504	-0.7044404	cluster 1
HORVU.MOREX.r3.7HG0685620.1	0.0505644	-0.1332645	-0.3892556	cluster 1
HORVU.MOREX.r3.7HG0700200.1	0.3314231	0.1487501	-0.4546355	cluster 1
HORVU.MOREX.r3.7HG0700790.1	0.033588	-0.184451	-0.6111468	cluster 1
HORVU.MOREX.r3.7HG0702100.1	0.3679663	0.1743058	-0.8553461	cluster 1
HORVU.MOREX.r3.7HG0702990.1	0.0227395	-0.1430075	-0.5485105	cluster 1
HORVU.MOREX.r3.7HG0703000.1	0.2292592	0.0543605	-0.7113631	cluster 1
HORVU.MOREX.r3.7HG0704050.1	-0.375344	-0.514671	-0.7466578	cluster 1
HORVU.MOREX.r3.7HG0705240.1	0.2418222	-0.0298241	-0.8731412	cluster 1
HORVU.MOREX.r3.7HG0706090.1	0.0118082	-0.0816041	-0.5179133	cluster 1
HORVU.MOREX.r3.7HG0707460.1	0.154681	-0.0484387	-0.9166165	cluster 1
HORVU.MOREX.r3.7HG0708320.1	-0.242928	-0.2894651	-0.6994034	cluster 1
HORVU.MOREX.r3.7HG0708910.1	-0.005875	-0.0218331	-0.5841389	cluster 1
HORVU.MOREX.r3.7HG0709580.1	-0.623111	-0.392332	-1.1588578	cluster 1
HORVU.MOREX.r3.7HG0709700.1	0.1132441	-0.2572299	-1.0859089	cluster 1
HORVU.MOREX.r3.7HG0713100.1	0.0915034	0.0036383	-0.7228589	cluster 1
HORVU.MOREX.r3.7HG0713160.1	0.1546164	0.0117517	-0.6117935	cluster 1
HORVU.MOREX.r3.7HG0713610.1	0.0515866	0.1333606	-0.4893423	cluster 1
HORVU.MOREX.r3.7HG0714350.1	-0.127096	-0.2561708	-0.9241313	cluster 1
HORVU.MOREX.r3.7HG0719310.1	-1.1903	-0.3407218	-2.314998	cluster 1
HORVU.MOREX.r3.7HG0719840.1	-0.052685	0.0812511	-0.6876225	cluster 1
HORVU.MOREX.r3.7HG0720730.1	0.3140162	-0.109002	-1.036229	cluster 1
HORVU.MOREX.r3.7HG0720980.1	0.2862122	-0.1200729	-0.7428184	cluster 1
HORVU.MOREX.r3.7HG0721080.1	-0.187276	-0.3456837	-0.7337321	cluster 1
HORVU.MOREX.r3.7HG0721660.1	0.1128853	-0.090692	-0.7058249	cluster 1
HORVU.MOREX.r3.7HG0723280.1	0.2980273	-0.0995604	-1.8839692	cluster 1
HORVU.MOREX.r3.7HG0723770.1	-0.195223	-0.2712737	-0.5650397	cluster 1
HORVU.MOREX.r3.7HG0725210.3	0.2136778	-0.0725653	-0.6957848	cluster 1
HORVU.MOREX.r3.7HG0728500.1	0.3348645	-0.1300075	-0.9267793	cluster 1
HORVU.MOREX.r3.7HG0729010.1	0.2698452	0.0186518	-0.8651826	cluster 1
HORVU.MOREX.r3.7HG0729510.1	-0.10835	-0.3466034	-0.7606226	cluster 1
HORVU.MOREX.r3.7HG0732860.1	0.053409	-0.1874811	-0.8497754	cluster 1
HORVU.MOREX.r3.7HG0733020.1	0.1931233	-0.1032472	-0.5307724	cluster 1
HORVU.MOREX.r3.7HG0733490.1	-0.007564	-0.1972393	-0.681121	cluster 1
HORVU.MOREX.r3.7HG0735280.1	0.0500998	-0.0531069	-0.4343864	cluster 1
HORVU.MOREX.r3.7HG0736000.1	0.0433785	-0.0826895	-0.7408431	cluster 1
HORVU.MOREX.r3.7HG0743430.1	-0.030952	-0.1973464	-1.2716657	cluster 1
HORVU.MOREX.r3.7HG0748320.1	0.0360236	-0.1921464	-0.7514418	cluster 1
HORVU.MOREX.r3.7HG0749800.1	0.1722487	0.0275875	-0.7703866	cluster 1
HORVU.MOREX.r3.7HG0752830.1	0.0725296	-0.0269739	-0.4228159	cluster 1
HORVU.MOREX.r3.UnG0753160.1	0.1726371	0.1024129	-0.6114766	cluster 1
HORVU.MOREX.r3.1HG0003270.1	2.8233992	1.862729	1.634235	cluster 2
HORVU.MOREX.r3.1HG0051740.1	0.0370234	-0.6811892	-0.9873424	cluster 2
HORVU.MOREX.r3.1HG0068060.1	-0.042873	-0.2001404	-0.3550378	cluster 2

Table S0 Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.1HG0080420.1	0.2379561	-0.2697485	-0.6518095	cluster 2
HORVU.MOREX.r3.1HG0080790.1	-0.167621	-0.7173333	-1.0990947	cluster 2
HORVU.MOREX.r3.1HG0092900.1	0.5080365	-0.4951608	-1.5485724	cluster 2
HORVU.MOREX.r3.1HG0095220.1	0.136006	-0.3412548	-0.7813061	cluster 2
HORVU.MOREX.r3.2HG0110640.1	-0.086711	-0.3776334	-0.3137127	cluster 2
HORVU.MOREX.r3.2HG0117540.1	-0.124083	-0.4106064	-0.5624112	cluster 2
HORVU.MOREX.r3.2HG0119220.1	-0.052723	-0.3327517	-0.6913123	cluster 2
HORVU.MOREX.r3.2HG0120640.1	-0.274605	-1.0532317	-1.5376216	cluster 2
HORVU.MOREX.r3.2HG0121950.1	-0.236053	-0.5226593	-0.7069055	cluster 2
HORVU.MOREX.r3.2HG0125510.1	-0.286447	-1.3277697	-1.4071916	cluster 2
HORVU.MOREX.r3.2HG0140970.1	-0.086658	-0.9432994	-1.704572	cluster 2
HORVU.MOREX.r3.2HG0151920.1	-0.063584	-0.5804899	-0.8562623	cluster 2
HORVU.MOREX.r3.2HG0162620.1	0.1360319	-0.6676713	-1.5894203	cluster 2
HORVU.MOREX.r3.2HG0175220.1	0.0842263	-0.1561619	-0.4366907	cluster 2
HORVU.MOREX.r3.2HG0183730.1	0.1082802	-0.5671608	-1.2022611	cluster 2
HORVU.MOREX.r3.2HG0184620.1	-0.32692	-0.7191037	-0.7873918	cluster 2
HORVU.MOREX.r3.3HG0221140.1	0.1221567	-0.2749698	-0.7589752	cluster 2
HORVU.MOREX.r3.3HG0231430.1	0.0445826	-0.206786	-0.378026	cluster 2
HORVU.MOREX.r3.3HG0235720.1	-0.526825	-1.2098574	-1.4772443	cluster 2
HORVU.MOREX.r3.3HG0249970.1	0.0863874	-0.326294	-0.5529555	cluster 2
HORVU.MOREX.r3.3HG0257120.1	-0.052205	-0.3750885	-0.7598041	cluster 2
HORVU.MOREX.r3.3HG0295500.2	0.227079	-0.365709	-1.1006335	cluster 2
HORVU.MOREX.r3.3HG0305840.1	-0.086915	-0.6456474	-0.7956632	cluster 2
HORVU.MOREX.r3.4HG0340200.1	0.0298715	-0.335933	-0.6705089	cluster 2
HORVU.MOREX.r3.4HG0408300.1	0.0707924	-0.0811674	-0.2722344	cluster 2
HORVU.MOREX.r3.5HG0459810.1	-0.112209	-0.3342213	-0.5635667	cluster 2
HORVU.MOREX.r3.5HG0479000.1	-0.23248	-1.5089971	-1.5447502	cluster 2
HORVU.MOREX.r3.5HG0496740.1	0.1128452	-0.7820818	-1.662913	cluster 2
HORVU.MOREX.r3.5HG0500130.1	-0.068644	-1.1977382	-2.2554112	cluster 2
HORVU.MOREX.r3.5HG0516730.1	0.0303497	-0.346808	-0.8068943	cluster 2
HORVU.MOREX.r3.5HG0520850.1	-0.015761	-0.2766114	-0.5416283	cluster 2
HORVU.MOREX.r3.6HG0551620.1	0.0126099	-0.264654	-0.5492368	cluster 2
HORVU.MOREX.r3.6HG0553150.1	0.065038	-0.3376159	-0.816789	cluster 2
HORVU.MOREX.r3.6HG0557640.2	-0.110285	-0.4558812	-0.852527	cluster 2
HORVU.MOREX.r3.6HG0565830.1	0.2628817	-0.2434719	-0.705834	cluster 2
HORVU.MOREX.r3.6HG0565890.1	0.0716683	-0.3935353	-0.8171697	cluster 2
HORVU.MOREX.r3.6HG0592790.1	-0.00306	-0.1774979	-0.3776622	cluster 2
HORVU.MOREX.r3.6HG0596240.1	-0.011888	-0.5674737	-1.0823091	cluster 2
HORVU.MOREX.r3.6HG0607560.1	0.1633152	-0.2593501	-0.8087621	cluster 2
HORVU.MOREX.r3.6HG0621190.1	-0.199352	-0.9152175	-1.0412622	cluster 2
HORVU.MOREX.r3.6HG0630410.1	0.1693997	-0.6981072	-1.2062575	cluster 2
HORVU.MOREX.r3.7HG0635410.1	-0.061666	-0.6913512	-1.1357064	cluster 2
HORVU.MOREX.r3.7HG0664810.1	-0.59145	-1.1235193	-1.2315395	cluster 2
HORVU.MOREX.r3.7HG0680170.1	-0.105886	-0.3539509	-0.5322635	cluster 2
HORVU.MOREX.r3.7HG0724830.1	-0.12338	-0.4212108	-0.6871245	cluster 2
HORVU.MOREX.r3.7HG0733070.1	0.2774792	-0.1652324	-0.5134848	cluster 2
HORVU.MOREX.r3.7HG0733110.1	0.0655865	-0.4471865	-0.701074	cluster 2

Table S0 Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.7HG0740120.1	-0.045066	-0.4939793	-0.8609598	cluster 2
HORVU.MOREX.r3.1HG0024440.1	0.6240205	0.3338753	1.7616367	cluster 3
HORVU.MOREX.r3.1HG0029060.1	-0.002115	0.115194	0.3316882	cluster 3
HORVU.MOREX.r3.1HG0056810.1	-0.050522	-0.0760236	0.5789208	cluster 3
HORVU.MOREX.r3.1HG0062480.1	0.1769776	0.1754143	0.8481508	cluster 3
HORVU.MOREX.r3.1HG0072560.1	1.420637	2.1085454	1.8846069	cluster 3
HORVU.MOREX.r3.2HG0104400.1	0.1392872	-1.5799965	2.8499093	cluster 3
HORVU.MOREX.r3.2HG0116730.1	0.6039269	0.8607134	3.2531155	cluster 3
HORVU.MOREX.r3.2HG0141900.1	0.1107861	0.4220753	0.6719383	cluster 3
HORVU.MOREX.r3.2HG0141980.1	-0.086386	-0.0404557	0.6743435	cluster 3
HORVU.MOREX.r3.2HG0181380.1	0.1104037	0.2767668	0.7848569	cluster 3
HORVU.MOREX.r3.2HG0191150.1	-0.119802	0.0994863	0.987218	cluster 3
HORVU.MOREX.r3.2HG0192180.1	0.0106233	0.0702629	0.2270186	cluster 3
HORVU.MOREX.r3.2HG0198000.1	-0.05969	0.0875793	0.300141	cluster 3
HORVU.MOREX.r3.3HG0219850.1	0.4620524	1.6355633	3.5424753	cluster 3
HORVU.MOREX.r3.3HG0300110.1	0.811676	1.5112064	0.6639938	cluster 3
HORVU.MOREX.r3.3HG0309210.1	-0.08868	-0.0479044	0.4562355	cluster 3
HORVU.MOREX.r3.4HG0402190.1	1.1812933	2.5774222	1.9268757	cluster 3
HORVU.MOREX.r3.4HG0402390.1	2.9041334	4.4100052	5.2262576	cluster 3
HORVU.MOREX.r3.4HG0405330.1	1.0455541	1.7983357	1.1670497	cluster 3
HORVU.MOREX.r3.5HG0429390.1	2.0002395	3.6322175	3.1784806	cluster 3
HORVU.MOREX.r3.5HG0458770.1	0.5221025	0.6619199	0.7160158	cluster 3
HORVU.MOREX.r3.5HG0482710.1	0.226056	0.2311383	0.6233293	cluster 3
HORVU.MOREX.r3.5HG0498320.1	0.1160828	0.1697017	0.4293063	cluster 3
HORVU.MOREX.r3.5HG0504720.1	-0.10073	0.0335607	0.464637	cluster 3
HORVU.MOREX.r3.5HG0510240.1	-0.048271	1.0640468	4.8663744	cluster 3
HORVU.MOREX.r3.5HG0529140.1	-0.059179	0.0726222	0.4325476	cluster 3
HORVU.MOREX.r3.6HG0541580.1	0.0976735	0.1899155	0.2698673	cluster 3
HORVU.MOREX.r3.6HG0550260.1	0.0195363	0.1405006	0.4032082	cluster 3
HORVU.MOREX.r3.6HG0604200.1	0.7056787	-0.0247538	2.9483156	cluster 3
HORVU.MOREX.r3.6HG0627900.1	0.3557403	1.5427197	2.4470309	cluster 3
HORVU.MOREX.r3.7HG0656980.1	0.0472123	1.4907654	1.220906	cluster 3
HORVU.MOREX.r3.7HG0689920.1	0.6722508	0.54806	1.3527666	cluster 3
HORVU.MOREX.r3.7HG0705130.1	0.7312682	0.6193222	1.0084752	cluster 3
HORVU.MOREX.r3.7HG0725140.1	0.0342515	-0.2241711	0.6286018	cluster 3
HORVU.MOREX.r3.7HG0725940.1	0.1803747	0.8325886	1.0925768	cluster 3
HORVU.MOREX.r3.7HG0733550.1	0.5837047	1.680915	1.5883796	cluster 3
HORVU.MOREX.r3.7HG0739570.1	1.1470843	2.5493466	2.1625177	cluster 3
HORVU.MOREX.r3.7HG0750850.1	1.4902377	3.4536548	3.8051856	cluster 3

Table Sп Hierarchical clustering analysis of differentially expressed genes (false discovery rate (FDR) <5%) in elongation zone of gravistimulated wild type roots.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.1HG0000040.1	-0.071645	-0.124524	-0.1773485	cluster 1
HORVU.MOREX.r3.1HG0000670.1	-0.438469	-0.684321	-0.8443564	cluster 1
HORVU.MOREX.r3.1HG0001010.1	-0.377642	-0.794982	-0.8842452	cluster 1
HORVU.MOREX.r3.1HG0001460.1	-0.133788	-0.543799	-0.836291	cluster 1
HORVU.MOREX.r3.1HG0001510.1	-0.612987	-0.793475	-1.0657923	cluster 1
HORVU.MOREX.r3.1HG0002800.1	-0.331522	-0.93359	-1.3595718	cluster 1
HORVU.MOREX.r3.1HG0003090.4	-0.183698	-1.041325	-1.6979849	cluster 1
HORVU.MOREX.r3.1HG0003090.7	-0.577884	-1.191555	-1.8866381	cluster 1
HORVU.MOREX.r3.1HG0003130.1	-0.142771	-0.448507	-0.493319	cluster 1
HORVU.MOREX.r3.1HG0004290.1	-0.107222	-0.376673	-1.0557282	cluster 1
HORVU.MOREX.r3.1HG0004300.1	-0.726547	-0.889262	-1.9261646	cluster 1
HORVU.MOREX.r3.1HG0005750.1	-0.161951	-0.328139	-0.4439202	cluster 1
HORVU.MOREX.r3.1HG0006610.1	-0.127119	-0.498945	-0.9589396	cluster 1
HORVU.MOREX.r3.1HG0006650.1	-0.152638	-0.430358	-0.8783079	cluster 1
HORVU.MOREX.r3.1HG0007360.1	-0.358003	-0.434503	-0.5486322	cluster 1
HORVU.MOREX.r3.1HG0007370.1	-0.17099	-0.276913	-0.4870731	cluster 1
HORVU.MOREX.r3.1HG0008140.1	0.029832	-0.045235	-1.0526349	cluster 1
HORVU.MOREX.r3.1HG0008190.1	-0.079562	-0.49924	-1.1637413	cluster 1
HORVU.MOREX.r3.1HG0008200.1	-0.016943	-0.950898	-2.4521858	cluster 1
HORVU.MOREX.r3.1HG0008400.1	-0.002467	-0.483007	-0.8133046	cluster 1
HORVU.MOREX.r3.1HG0008440.1	0.000127	-0.155753	-0.70841	cluster 1
HORVU.MOREX.r3.1HG0010470.1	-0.129151	-0.372956	-0.5835351	cluster 1
HORVU.MOREX.r3.1HG0012170.1	-0.249119	-0.48712	-0.841958	cluster 1
HORVU.MOREX.r3.1HG0012330.1	-0.181089	-0.298638	-0.772728	cluster 1
HORVU.MOREX.r3.1HG0014410.1	-0.019009	-0.303508	-0.635752	cluster 1
HORVU.MOREX.r3.1HG0016810.1	-0.219936	-0.374805	-0.8116261	cluster 1
HORVU.MOREX.r3.1HG0016950.1	-0.149667	-0.340014	-0.3814369	cluster 1
HORVU.MOREX.r3.1HG0017310.1	-0.16519	-0.283884	-1.1001499	cluster 1
HORVU.MOREX.r3.1HG0017720.1	-0.104546	-0.614856	-0.7433992	cluster 1
HORVU.MOREX.r3.1HG0018190.2	-0.022676	-0.659745	-1.1814946	cluster 1
HORVU.MOREX.r3.1HG0018390.1	-0.125982	-0.457016	-0.9856067	cluster 1
HORVU.MOREX.r3.1HG0018730.1	-0.052508	-0.16995	-0.320822	cluster 1
HORVU.MOREX.r3.1HG0018810.1	-0.378457	-0.611311	-0.9691882	cluster 1
HORVU.MOREX.r3.1HG0019410.1	-0.225678	-0.299536	-0.9646582	cluster 1
HORVU.MOREX.r3.1HG0019440.1	-0.105029	-0.315985	-0.3954099	cluster 1
HORVU.MOREX.r3.1HG0021830.1	-0.079326	-0.203601	-0.3393333	cluster 1
HORVU.MOREX.r3.1HG0022860.1	-0.088711	-0.301696	-0.3503478	cluster 1
HORVU.MOREX.r3.1HG0023610.1	-0.273233	-0.669494	-1.3268268	cluster 1
HORVU.MOREX.r3.1HG0023620.1	-0.167881	-0.548371	-0.9138041	cluster 1
HORVU.MOREX.r3.1HG0024040.1	-0.11524	-0.359729	-0.4670541	cluster 1
HORVU.MOREX.r3.1HG0024140.1	-0.141816	-0.463273	-1.0286073	cluster 1
HORVU.MOREX.r3.1HG0024230.1	-0.062139	-0.081072	-0.5736968	cluster 1
HORVU.MOREX.r3.1HG0024280.1	-0.149099	-0.410992	-0.7193662	cluster 1
HORVU.MOREX.r3.1HG0026070.2	-0.164501	-0.190542	-0.5632605	cluster 1
HORVU.MOREX.r3.1HG0026430.1	-0.21961	-0.262259	-0.4150473	cluster 1
HORVU.MOREX.r3.1HG0028320.1	-0.169179	-0.517356	-0.6028779	cluster 1
HORVU.MOREX.r3.1HG0029080.1	-0.1787	-0.587693	-0.6492816	cluster 1

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.1HG0030090.1	-0.216979	-0.457384	-1.0998744	cluster 1
HORVU.MOREX.r3.1HG0030200.1	0.0963493	-0.098407	-0.4175741	cluster 1
HORVU.MOREX.r3.1HG0031180.1	-0.188618	-0.26601	-0.4864687	cluster 1
HORVU.MOREX.r3.1HG0032230.1	-0.058604	-0.33076	-0.8417067	cluster 1
HORVU.MOREX.r3.1HG0032910.1	-0.126575	-0.418482	-0.5760219	cluster 1
HORVU.MOREX.r3.1HG0033360.1	-0.147892	-0.192431	-0.2847466	cluster 1
HORVU.MOREX.r3.1HG0033390.4	-0.481493	-1.038087	-1.7182452	cluster 1
HORVU.MOREX.r3.1HG0036370.1	-0.107118	-0.242352	-0.390755	cluster 1
HORVU.MOREX.r3.1HG0036930.1	-0.225925	-0.407071	-1.0819263	cluster 1
HORVU.MOREX.r3.1HG0037020.1	-0.178481	-0.239307	-0.4336448	cluster 1
HORVU.MOREX.r3.1HG0038960.1	-0.273156	-0.341301	-1.0375946	cluster 1
HORVU.MOREX.r3.1HG0039230.1	-0.272132	-0.382149	-0.661259	cluster 1
HORVU.MOREX.r3.1HG0039670.1	-0.031701	-0.238142	-0.3364584	cluster 1
HORVU.MOREX.r3.1HG0042740.1	-0.098437	-0.296755	-0.4789963	cluster 1
HORVU.MOREX.r3.1HG0044530.1	-0.143886	-0.230621	-0.4752674	cluster 1
HORVU.MOREX.r3.1HG0045040.1	-0.030519	-0.202812	-0.3801681	cluster 1
HORVU.MOREX.r3.1HG0046650.1	-0.119401	-0.420107	-0.6038916	cluster 1
HORVU.MOREX.r3.1HG0046770.1	-0.217608	-0.3459	-0.7078966	cluster 1
HORVU.MOREX.r3.1HG0046900.1	-0.055034	-0.284637	-0.318943	cluster 1
HORVU.MOREX.r3.1HG0047130.1	-0.102935	-0.290613	-0.5012279	cluster 1
HORVU.MOREX.r3.1HG0048010.1	-0.11181	-0.215178	-0.3447995	cluster 1
HORVU.MOREX.r3.1HG0048030.1	-0.043702	-0.179739	-0.4603345	cluster 1
HORVU.MOREX.r3.1HG0049840.1	-0.035429	-0.460083	-0.7164691	cluster 1
HORVU.MOREX.r3.1HG0050990.1	-0.044326	-0.331078	-2.2870311	cluster 1
HORVU.MOREX.r3.1HG0051020.1	-0.186997	-0.295926	-0.4951078	cluster 1
HORVU.MOREX.r3.1HG0051740.1	-0.149533	-1.907755	-2.7104377	cluster 1
HORVU.MOREX.r3.1HG0051860.1	-0.521655	-0.64618	-0.920105	cluster 1
HORVU.MOREX.r3.1HG0052080.1	-0.097286	-0.30255	-0.4502105	cluster 1
HORVU.MOREX.r3.1HG0052120.1	-0.424983	-0.620213	-0.7628829	cluster 1
HORVU.MOREX.r3.1HG0052790.1	-0.002574	-0.24127	-0.4696911	cluster 1
HORVU.MOREX.r3.1HG0052810.1	-0.162186	-0.364431	-0.6609272	cluster 1
HORVU.MOREX.r3.1HG0053770.1	-0.214542	-0.450222	-1.3037244	cluster 1
HORVU.MOREX.r3.1HG0054200.1	0.0229659	-0.112167	-0.3330798	cluster 1
HORVU.MOREX.r3.1HG0054500.1	-0.141381	-0.502872	-0.9798408	cluster 1
HORVU.MOREX.r3.1HG0054770.1	-0.204379	-0.460411	-0.5724173	cluster 1
HORVU.MOREX.r3.1HG0055230.1	-0.112802	-0.512176	-0.8892409	cluster 1
HORVU.MOREX.r3.1HG0055380.1	-0.136801	-0.476637	-0.6613041	cluster 1
HORVU.MOREX.r3.1HG0055400.1	-0.091803	-0.233082	-0.5051363	cluster 1
HORVU.MOREX.r3.1HG0055580.1	-0.217535	-0.316879	-0.4107946	cluster 1
HORVU.MOREX.r3.1HG0055730.1	-0.181182	-0.18899	-0.4323416	cluster 1
HORVU.MOREX.r3.1HG0056280.1	-0.111364	-0.524947	-1.053041	cluster 1
HORVU.MOREX.r3.1HG0056560.1	-0.11454	-0.286266	-0.3917377	cluster 1
HORVU.MOREX.r3.1HG0056740.1	-0.200779	-0.410893	-0.551492	cluster 1
HORVU.MOREX.r3.1HG0057620.1	-0.149427	-0.357208	-0.7477856	cluster 1
HORVU.MOREX.r3.1HG0057780.1	-0.08526	-0.406475	-0.5546754	cluster 1
HORVU.MOREX.r3.1HG0057900.1	-0.305534	-0.397298	-0.6624623	cluster 1
HORVU.MOREX.r3.1HG0057990.1	-0.332	-0.607808	-0.8161959	cluster 1

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.1HG0058050.1	-0.188489	-0.272955	-0.5194952	cluster 1
HORVU.MOREX.r3.1HG0058390.1	-0.046827	-0.501733	-1.2016923	cluster 1
HORVU.MOREX.r3.1HG0058640.1	-0.146274	-0.534883	-1.4259288	cluster 1
HORVU.MOREX.r3.1HG0058800.1	-0.136702	-0.32663	-0.5382268	cluster 1
HORVU.MOREX.r3.1HG0059000.1	-0.410661	-0.673067	-0.954609	cluster 1
HORVU.MOREX.r3.1HG0059120.1	0.0082228	-0.265023	-0.3284409	cluster 1
HORVU.MOREX.r3.1HG0059350.1	-0.310436	-0.589076	-0.8252261	cluster 1
HORVU.MOREX.r3.1HG0059790.1	-0.214234	-0.530524	-0.986547	cluster 1
HORVU.MOREX.r3.1HG0060240.1	-0.39667	-0.734476	-0.8303838	cluster 1
HORVU.MOREX.r3.1HG0060260.1	-0.19775	-0.498184	-0.9775598	cluster 1
HORVU.MOREX.r3.1HG0060270.1	-0.209438	-0.627924	-1.0589566	cluster 1
HORVU.MOREX.r3.1HG0060320.1	-0.17793	-0.540094	-1.0558507	cluster 1
HORVU.MOREX.r3.1HG0060340.1	-0.04652	-0.503584	-1.4127406	cluster 1
HORVU.MOREX.r3.1HG0060570.1	-0.050198	-0.153708	-0.5413945	cluster 1
HORVU.MOREX.r3.1HG0061220.1	-0.06833	-0.411928	-1.1357942	cluster 1
HORVU.MOREX.r3.1HG0063870.1	-0.173316	-0.397724	-0.6224312	cluster 1
HORVU.MOREX.r3.1HG0064080.1	-0.161441	-0.257858	-0.5953225	cluster 1
HORVU.MOREX.r3.1HG0064220.1	-0.199911	-0.335029	-0.7590624	cluster 1
HORVU.MOREX.r3.1HG0064320.1	-0.07699	-0.180027	-0.5523171	cluster 1
HORVU.MOREX.r3.1HG0065020.1	0.0348523	-0.269963	-1.170304	cluster 1
HORVU.MOREX.r3.1HG0065370.1	-0.106742	-0.29119	-0.7791662	cluster 1
HORVU.MOREX.r3.1HG0066530.1	-0.157526	-0.392825	-1.1926228	cluster 1
HORVU.MOREX.r3.1HG0066730.1	-0.212473	-0.512146	-0.6817678	cluster 1
HORVU.MOREX.r3.1HG0067410.1	-0.095465	-0.223165	-0.4149666	cluster 1
HORVU.MOREX.r3.1HG0067550.1	-0.076405	-0.416209	-0.7286452	cluster 1
HORVU.MOREX.r3.1HG0068370.1	-0.2881	-0.85527	-1.2770371	cluster 1
HORVU.MOREX.r3.1HG0068710.1	-0.539862	-0.644922	-1.0737803	cluster 1
HORVU.MOREX.r3.1HG0068890.1	-0.214045	-0.365888	-0.5535155	cluster 1
HORVU.MOREX.r3.1HG0069290.1	-0.091143	-0.204475	-0.3333073	cluster 1
HORVU.MOREX.r3.1HG0069940.1	-0.08985	-0.200192	-0.7416549	cluster 1
HORVU.MOREX.r3.1HG0071310.1	0.2367884	-0.156589	-0.4807924	cluster 1
HORVU.MOREX.r3.1HG0072110.1	-0.130093	-0.303295	-0.8139992	cluster 1
HORVU.MOREX.r3.1HG0072320.1	-0.562477	-0.568571	-0.8266783	cluster 1
HORVU.MOREX.r3.1HG0072410.1	-0.076207	-0.23978	-0.2694548	cluster 1
HORVU.MOREX.r3.1HG0072520.1	-0.290377	-0.694298	-1.0645262	cluster 1
HORVU.MOREX.r3.1HG0072530.1	-0.341481	-0.655417	-1.1449186	cluster 1
HORVU.MOREX.r3.1HG0072540.1	-0.3341	-0.569029	-1.2075381	cluster 1
HORVU.MOREX.r3.1HG0073030.1	-0.084773	-0.477778	-0.810206	cluster 1
HORVU.MOREX.r3.1HG0073050.1	-0.488801	-0.547014	-1.4627183	cluster 1
HORVU.MOREX.r3.1HG0073070.1	-0.055412	-0.182142	-0.2592944	cluster 1
HORVU.MOREX.r3.1HG0073170.1	-0.075394	-0.612165	-0.8972417	cluster 1
HORVU.MOREX.r3.1HG0073320.1	-0.406974	-0.606669	-0.9159297	cluster 1
HORVU.MOREX.r3.1HG0073330.1	-0.116256	-0.410177	-0.4614661	cluster 1
HORVU.MOREX.r3.1HG0074260.1	-0.150953	-0.29947	-0.4001584	cluster 1
HORVU.MOREX.r3.1HG0074490.1	-0.103373	-0.514311	-1.2212446	cluster 1
HORVU.MOREX.r3.1HG0074500.1	-0.215708	-0.554579	-1.0786443	cluster 1
HORVU.MOREX.r3.1HG0074600.1	-0.014879	-0.376475	-1.2244556	cluster 1

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.1HG0075230.1	-0.181992	-0.560358	-1.2093664	cluster 1
HORVU.MOREX.r3.1HG0075590.1	-0.097289	-0.219511	-0.2765667	cluster 1
HORVU.MOREX.r3.1HG0076060.1	-0.175558	-0.363665	-0.4204095	cluster 1
HORVU.MOREX.r3.1HG0076540.1	-0.072142	-0.220057	-0.3554766	cluster 1
HORVU.MOREX.r3.1HG0076980.1	-0.078762	-0.270896	-0.3444065	cluster 1
HORVU.MOREX.r3.1HG0077170.1	0.1600867	-0.137227	-0.5622657	cluster 1
HORVU.MOREX.r3.1HG0077840.1	-0.016089	-0.286722	-0.4611398	cluster 1
HORVU.MOREX.r3.1HG0077880.1	-0.177941	-0.31771	-1.0754309	cluster 1
HORVU.MOREX.r3.1HG0077950.1	-0.074884	-0.310284	-0.3894016	cluster 1
HORVU.MOREX.r3.1HG0078370.1	-0.214938	-0.412978	-1.7854262	cluster 1
HORVU.MOREX.r3.1HG0078750.1	-0.22172	-0.501184	-0.5644803	cluster 1
HORVU.MOREX.r3.1HG0078770.1	-0.030589	-0.121128	-0.1448566	cluster 1
HORVU.MOREX.r3.1HG0079250.1	-0.118705	-0.33521	-0.8268634	cluster 1
HORVU.MOREX.r3.1HG0079280.1	-0.162388	-0.439595	-0.9395741	cluster 1
HORVU.MOREX.r3.1HG0079800.1	-0.202182	-0.501695	-0.7085236	cluster 1
HORVU.MOREX.r3.1HG0079870.1	-0.369286	-0.820073	-1.1327439	cluster 1
HORVU.MOREX.r3.1HG0080230.1	-0.124723	-0.440592	-1.0959477	cluster 1
HORVU.MOREX.r3.1HG0080370.1	-0.149332	-0.316705	-0.4841854	cluster 1
HORVU.MOREX.r3.1HG0080690.1	-0.834104	-0.890462	-2.1771715	cluster 1
HORVU.MOREX.r3.1HG0080760.1	-0.250615	-0.580502	-1.0702099	cluster 1
HORVU.MOREX.r3.1HG0080770.1	-0.12037	-0.439135	-0.9424823	cluster 1
HORVU.MOREX.r3.1HG0080780.1	-0.137393	-0.53814	-0.9969792	cluster 1
HORVU.MOREX.r3.1HG0081220.1	-0.15209	-0.417209	-0.6739663	cluster 1
HORVU.MOREX.r3.1HG0082630.1	-0.10244	-0.36116	-0.470862	cluster 1
HORVU.MOREX.r3.1HG0082770.1	-0.088956	-0.286728	-0.3556985	cluster 1
HORVU.MOREX.r3.1HG0083110.1	0.015112	-0.235565	-0.5496173	cluster 1
HORVU.MOREX.r3.1HG0084540.1	-0.142345	-0.38105	-0.5155577	cluster 1
HORVU.MOREX.r3.1HG0084850.1	-0.259554	-0.711168	-1.195516	cluster 1
HORVU.MOREX.r3.1HG0084920.1	0.023018	-0.198592	-0.3069225	cluster 1
HORVU.MOREX.r3.1HG0085140.1	-0.147025	-0.343182	-0.5442868	cluster 1
HORVU.MOREX.r3.1HG0085420.1	-0.110057	-0.423937	-0.7578857	cluster 1
HORVU.MOREX.r3.1HG0085700.1	-0.345336	-0.468882	-0.9633685	cluster 1
HORVU.MOREX.r3.1HG0086010.1	-0.100527	-0.179081	-0.6194021	cluster 1
HORVU.MOREX.r3.1HG0086140.1	-0.30656	-0.455471	-0.7972206	cluster 1
HORVU.MOREX.r3.1HG0087150.1	-0.212304	-0.595539	-0.8760306	cluster 1
HORVU.MOREX.r3.1HG0087190.1	-0.257724	-0.395481	-0.5619376	cluster 1
HORVU.MOREX.r3.1HG0087980.1	-0.06494	-0.212942	-0.5635841	cluster 1
HORVU.MOREX.r3.1HG0088870.1	-0.084584	-0.170154	-0.2695324	cluster 1
HORVU.MOREX.r3.1HG0088900.1	-0.286546	-0.525796	-0.9227434	cluster 1
HORVU.MOREX.r3.1HG0088990.1	-0.123571	-0.366833	-0.5198763	cluster 1
HORVU.MOREX.r3.1HG0089130.1	-0.157362	-0.353039	-0.4242991	cluster 1
HORVU.MOREX.r3.1HG0089220.1	-0.266468	-0.849343	-1.0779379	cluster 1
HORVU.MOREX.r3.1HG0089750.1	-0.130187	-0.411166	-1.1368502	cluster 1
HORVU.MOREX.r3.1HG0090760.1	-0.404317	-0.416619	-0.6036512	cluster 1
HORVU.MOREX.r3.1HG0091330.1	0.0901205	-0.342249	-0.9788283	cluster 1
HORVU.MOREX.r3.1HG0091360.1	-0.122726	-0.33111	-0.4780708	cluster 1
HORVU.MOREX.r3.1HG0091670.1	-0.217443	-0.476509	-0.5635125	cluster 1

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.1HG0091770.1	-0.049803	-0.549965	-1.2130895	cluster 1
HORVU.MOREX.r3.1HG0091820.1	-0.049758	-0.425615	-0.6096677	cluster 1
HORVU.MOREX.r3.1HG0091860.1	-0.106875	-0.255762	-0.3237083	cluster 1
HORVU.MOREX.r3.1HG0091870.1	-0.07343	-0.346194	-0.6111268	cluster 1
HORVU.MOREX.r3.1HG0092810.1	-0.048961	-0.519802	-1.1548745	cluster 1
HORVU.MOREX.r3.1HG0093750.1	-0.335496	-0.593977	-0.9393611	cluster 1
HORVU.MOREX.r3.1HG0094940.1	-0.103662	-0.266	-0.4251903	cluster 1
HORVU.MOREX.r3.1HG0095210.1	-0.069131	-0.226301	-0.348763	cluster 1
HORVU.MOREX.r3.1HG0095440.1	-0.154967	-0.256627	-0.3432853	cluster 1
HORVU.MOREX.r3.2HG0095520.1	-0.089357	-0.359405	-0.5946982	cluster 1
HORVU.MOREX.r3.2HG0095650.1	0.2344835	-0.038861	-1.4585334	cluster 1
HORVU.MOREX.r3.2HG0095710.1	-0.165009	-0.367995	-0.8961363	cluster 1
HORVU.MOREX.r3.2HG0095970.1	0.0305742	-0.75694	-1.272342	cluster 1
HORVU.MOREX.r3.2HG0096600.1	-0.159346	-0.412181	-0.5964173	cluster 1
HORVU.MOREX.r3.2HG0096760.1	-0.027579	-0.221576	-0.8044271	cluster 1
HORVU.MOREX.r3.2HG0097360.1	-0.196544	-0.338193	-0.8257672	cluster 1
HORVU.MOREX.r3.2HG0097360.3	-0.270235	-0.612642	-1.1548022	cluster 1
HORVU.MOREX.r3.2HG0097390.1	-0.241772	-0.678806	-0.9076011	cluster 1
HORVU.MOREX.r3.2HG0097950.1	-0.210855	-0.560446	-0.870493	cluster 1
HORVU.MOREX.r3.2HG0098420.1	-0.13539	-0.330129	-1.1414945	cluster 1
HORVU.MOREX.r3.2HG0099260.1	-0.052397	-0.160273	-0.2418427	cluster 1
HORVU.MOREX.r3.2HG0099740.1	-0.136727	-0.304046	-0.3932536	cluster 1
HORVU.MOREX.r3.2HG0100040.1	-0.167265	-0.45725	-2.0923434	cluster 1
HORVU.MOREX.r3.2HG0104260.1	-0.190136	-0.461552	-0.6638723	cluster 1
HORVU.MOREX.r3.2HG0104480.1	-0.176111	-0.466432	-0.7913353	cluster 1
HORVU.MOREX.r3.2HG0104500.1	-0.079758	-0.258261	-0.4218833	cluster 1
HORVU.MOREX.r3.2HG0104510.1	-0.135732	-0.187992	-0.3580829	cluster 1
HORVU.MOREX.r3.2HG0105680.3	-0.326239	-0.486491	-1.0268083	cluster 1
HORVU.MOREX.r3.2HG0105980.1	-0.396491	-0.435585	-0.6732587	cluster 1
HORVU.MOREX.r3.2HG0106430.1	-0.001113	-0.20332	-0.4842964	cluster 1
HORVU.MOREX.r3.2HG0106750.1	-0.188562	-0.806451	-1.0911822	cluster 1
HORVU.MOREX.r3.2HG0107450.1	0.0259002	-0.417632	-0.9297142	cluster 1
HORVU.MOREX.r3.2HG0107470.1	-0.18259	-0.354834	-0.6522059	cluster 1
HORVU.MOREX.r3.2HG0107740.1	-0.142411	-0.353075	-0.5643446	cluster 1
HORVU.MOREX.r3.2HG0107820.1	-0.227116	-0.524651	-0.6777043	cluster 1
HORVU.MOREX.r3.2HG0107900.1	-0.107317	-0.242271	-0.3146779	cluster 1
HORVU.MOREX.r3.2HG0110060.1	-0.177789	-0.262715	-0.5774648	cluster 1
HORVU.MOREX.r3.2HG0110130.1	-0.130025	-0.569712	-1.0201166	cluster 1
HORVU.MOREX.r3.2HG0110580.1	-0.251766	-0.363459	-0.5595737	cluster 1
HORVU.MOREX.r3.2HG0110730.1	-0.108897	-0.367931	-0.4073033	cluster 1
HORVU.MOREX.r3.2HG0110840.1	-0.137	-0.392845	-0.6225663	cluster 1
HORVU.MOREX.r3.2HG0110920.1	0.0093348	-0.169307	-1.8863476	cluster 1
HORVU.MOREX.r3.2HG0111130.1	0.248764	-0.257083	-0.7758288	cluster 1
HORVU.MOREX.r3.2HG0113700.1	0.0212599	-0.227534	-1.1215831	cluster 1
HORVU.MOREX.r3.2HG0114840.1	-0.228084	-0.269203	-0.6671363	cluster 1
HORVU.MOREX.r3.2HG0115300.2	-0.083328	-0.152473	-0.2807162	cluster 1
HORVU.MOREX.r3.2HG0115480.1	-0.286427	-0.519993	-0.6926657	cluster 1

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.2HG0115780.1	0.1134533	-0.51977	-1.1816623	cluster 1
HORVU.MOREX.r3.2HG0115930.1	-0.214079	-0.50204	-0.6523408	cluster 1
HORVU.MOREX.r3.2HG0115970.1	0.0611034	-0.476529	-1.0576632	cluster 1
HORVU.MOREX.r3.2HG0116540.1	-0.070387	-0.39954	-0.5996536	cluster 1
HORVU.MOREX.r3.2HG0116870.1	-0.189529	-0.50958	-0.8254902	cluster 1
HORVU.MOREX.r3.2HG0118580.1	-0.14647	-0.713252	-1.0614147	cluster 1
HORVU.MOREX.r3.2HG0119060.1	-0.219285	-0.371699	-0.4720529	cluster 1
HORVU.MOREX.r3.2HG0119220.1	-0.211415	-0.463912	-0.5456335	cluster 1
HORVU.MOREX.r3.2HG0120030.1	-0.124486	-0.636145	-0.7238389	cluster 1
HORVU.MOREX.r3.2HG0121830.1	-0.153995	-0.246546	-0.3361858	cluster 1
HORVU.MOREX.r3.2HG0122040.1	-0.09104	-0.22291	-0.2625496	cluster 1
HORVU.MOREX.r3.2HG0122140.1	-0.180866	-0.40154	-0.4767424	cluster 1
HORVU.MOREX.r3.2HG0123650.1	-0.04694	-0.182486	-0.3902826	cluster 1
HORVU.MOREX.r3.2HG0124130.1	-0.165196	-0.426497	-0.7236887	cluster 1
HORVU.MOREX.r3.2HG0124820.1	-0.185655	-0.418642	-0.8536779	cluster 1
HORVU.MOREX.r3.2HG0124990.1	-0.206806	-0.368187	-0.6340075	cluster 1
HORVU.MOREX.r3.2HG0125050.1	-0.185359	-0.329336	-0.4519597	cluster 1
HORVU.MOREX.r3.2HG0125780.1	-0.110717	-0.671355	-1.2601952	cluster 1
HORVU.MOREX.r3.2HG0125870.1	-0.064663	-0.194271	-0.5130197	cluster 1
HORVU.MOREX.r3.2HG0126010.1	-0.075528	-0.211478	-0.3559582	cluster 1
HORVU.MOREX.r3.2HG0127530.1	-0.352958	-0.897155	-1.488231	cluster 1
HORVU.MOREX.r3.2HG0128230.1	0.025941	-0.342984	-0.9415368	cluster 1
HORVU.MOREX.r3.2HG0128840.1	-0.052212	-0.280712	-0.5947437	cluster 1
HORVU.MOREX.r3.2HG0128890.1	-0.203016	-0.367148	-0.683621	cluster 1
HORVU.MOREX.r3.2HG0129200.1	-0.083783	-0.139018	-0.5883573	cluster 1
HORVU.MOREX.r3.2HG0130000.1	-0.037357	-0.228341	-0.3509321	cluster 1
HORVU.MOREX.r3.2HG0130180.1	-0.104604	-0.237342	-0.3030084	cluster 1
HORVU.MOREX.r3.2HG0130200.1	-0.172676	-0.389335	-0.4279482	cluster 1
HORVU.MOREX.r3.2HG0130770.1	0.0153705	-0.243458	-0.5732018	cluster 1
HORVU.MOREX.r3.2HG0132440.2	-0.127483	-0.138168	-0.4546447	cluster 1
HORVU.MOREX.r3.2HG0132700.1	-0.152424	-0.579105	-1.795339	cluster 1
HORVU.MOREX.r3.2HG0134220.1	-0.054179	-0.284603	-0.3339927	cluster 1
HORVU.MOREX.r3.2HG0134430.1	-0.529686	-1.333204	-2.2379963	cluster 1
HORVU.MOREX.r3.2HG0134700.1	-0.092173	-0.502229	-0.7719558	cluster 1
HORVU.MOREX.r3.2HG0136570.1	-0.306474	-0.455575	-2.1497726	cluster 1
HORVU.MOREX.r3.2HG0136670.1	-0.088922	-0.986027	-1.9058988	cluster 1
HORVU.MOREX.r3.2HG0137670.1	-0.401046	-0.980536	-1.0807166	cluster 1
HORVU.MOREX.r3.2HG0138280.1	-0.037415	-0.155592	-0.6220855	cluster 1
HORVU.MOREX.r3.2HG0138300.1	-0.055584	-0.352456	-0.7087585	cluster 1
HORVU.MOREX.r3.2HG0138620.1	-0.404916	-0.546314	-1.116241	cluster 1
HORVU.MOREX.r3.2HG0139050.1	0.0930897	-0.406323	-1.0093808	cluster 1
HORVU.MOREX.r3.2HG0139370.1	0.0264594	-0.36251	-0.7941697	cluster 1
HORVU.MOREX.r3.2HG0139910.1	-0.047241	-0.497112	-1.0090869	cluster 1
HORVU.MOREX.r3.2HG0141490.1	-0.263341	-0.484516	-0.6681454	cluster 1
HORVU.MOREX.r3.2HG0146580.1	-0.156103	-0.36425	-0.5505038	cluster 1
HORVU.MOREX.r3.2HG0147770.1	-0.163058	-0.281204	-0.4436069	cluster 1
HORVU.MOREX.r3.2HG0149120.1	-0.153745	-0.188882	-0.3032045	cluster 1

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.2HG0149940.1	-0.196568	-0.409185	-0.4708896	cluster 1
HORVU.MOREX.r3.2HG0150450.1	-0.188254	-0.476474	-0.6592005	cluster 1
HORVU.MOREX.r3.2HG0151910.1	-0.196639	-0.697255	-1.0244033	cluster 1
HORVU.MOREX.r3.2HG0151920.1	-0.14807	-0.560621	-0.937555	cluster 1
HORVU.MOREX.r3.2HG0152140.1	-0.09649	-0.268293	-0.6634219	cluster 1
HORVU.MOREX.r3.2HG0152370.1	-0.071849	-0.420731	-0.6082781	cluster 1
HORVU.MOREX.r3.2HG0154740.1	-0.512702	-0.679296	-0.7835556	cluster 1
HORVU.MOREX.r3.2HG0154760.1	-0.133005	-0.598735	-0.9130175	cluster 1
HORVU.MOREX.r3.2HG0155450.1	-0.15577	-0.565461	-0.8543335	cluster 1
HORVU.MOREX.r3.2HG0155460.1	-0.172534	-0.451907	-0.6529114	cluster 1
HORVU.MOREX.r3.2HG0155810.1	-0.270665	-0.661728	-0.9430821	cluster 1
HORVU.MOREX.r3.2HG0156590.1	-0.053559	-0.241695	-0.4326334	cluster 1
HORVU.MOREX.r3.2HG0157160.1	-0.307624	-0.314861	-0.835145	cluster 1
HORVU.MOREX.r3.2HG0157290.1	-0.260212	-0.678873	-1.0739248	cluster 1
HORVU.MOREX.r3.2HG0158020.1	-0.219433	-0.330355	-0.411972	cluster 1
HORVU.MOREX.r3.2HG0158620.1	-0.01903	-0.274628	-0.4212415	cluster 1
HORVU.MOREX.r3.2HG0159500.1	-0.174523	-0.439394	-0.7588238	cluster 1
HORVU.MOREX.r3.2HG0159540.1	-0.613017	-0.82915	-1.0129392	cluster 1
HORVU.MOREX.r3.2HG0159920.1	-0.213478	-0.385033	-0.5645933	cluster 1
HORVU.MOREX.r3.2HG0160550.1	-0.274036	-0.794337	-2.716791	cluster 1
HORVU.MOREX.r3.2HG0160560.1	-0.530672	-1.321614	-1.4680875	cluster 1
HORVU.MOREX.r3.2HG0160700.1	2.0996491	2.049175	1.32696119	cluster 1
HORVU.MOREX.r3.2HG0160790.1	-0.02349	-0.09619	-0.5278546	cluster 1
HORVU.MOREX.r3.2HG0161020.1	-0.171999	-0.34568	-0.8661492	cluster 1
HORVU.MOREX.r3.2HG0161670.1	-0.133304	-0.333342	-0.5223391	cluster 1
HORVU.MOREX.r3.2HG0162940.1	-0.168547	-0.21352	-0.3300561	cluster 1
HORVU.MOREX.r3.2HG0163090.1	0.1544503	-0.235319	-0.8334186	cluster 1
HORVU.MOREX.r3.2HG0164650.1	-0.052745	-0.199233	-0.4735161	cluster 1
HORVU.MOREX.r3.2HG0164700.2	-0.130199	-0.361979	-0.6727413	cluster 1
HORVU.MOREX.r3.2HG0165250.1	-0.180908	-0.342351	-0.4033817	cluster 1
HORVU.MOREX.r3.2HG0165840.1	-0.127416	-0.559245	-0.7276125	cluster 1
HORVU.MOREX.r3.2HG0167500.2	0.0473956	-0.184061	-1.671877	cluster 1
HORVU.MOREX.r3.2HG0167570.1	-0.091062	-0.569095	-1.3170208	cluster 1
HORVU.MOREX.r3.2HG0167620.1	-0.186775	-0.242001	-1.2516465	cluster 1
HORVU.MOREX.r3.2HG0168010.1	-0.190579	-0.340969	-0.5559603	cluster 1
HORVU.MOREX.r3.2HG0168090.1	-0.148237	-0.339162	-0.479939	cluster 1
HORVU.MOREX.r3.2HG0168270.1	-0.168038	-0.535135	-0.6121322	cluster 1
HORVU.MOREX.r3.2HG0168730.1	-0.156901	-0.280808	-0.5281516	cluster 1
HORVU.MOREX.r3.2HG0168790.1	-0.218259	-0.455337	-0.7242725	cluster 1
HORVU.MOREX.r3.2HG0169700.1	-0.171016	-0.425236	-0.7408696	cluster 1
HORVU.MOREX.r3.2HG0169720.1	-0.069796	-0.136412	-0.4961491	cluster 1
HORVU.MOREX.r3.2HG0170300.1	-0.229741	-0.425032	-0.5693042	cluster 1
HORVU.MOREX.r3.2HG0170390.1	0.0210103	-0.194068	-0.3191257	cluster 1
HORVU.MOREX.r3.2HG0170560.1	-0.169778	-0.244654	-1.2182252	cluster 1
HORVU.MOREX.r3.2HG0170880.1	-0.140018	-0.456729	-1.3017766	cluster 1
HORVU.MOREX.r3.2HG0171550.1	-0.104165	-0.64018	-0.8125073	cluster 1
HORVU.MOREX.r3.2HG0171860.1	-0.172697	-0.260442	-0.618192	cluster 1

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.2HG0172050.1	-0.073516	-0.095321	-0.3565514	cluster 1
HORVU.MOREX.r3.2HG0172400.1	0.0232819	-0.885943	-1.7502537	cluster 1
HORVU.MOREX.r3.2HG0172730.1	-0.16599	-0.433281	-0.532916	cluster 1
HORVU.MOREX.r3.2HG0172790.1	-0.111495	-0.465494	-0.8142454	cluster 1
HORVU.MOREX.r3.2HG0173190.1	-0.248269	-0.456951	-1.4397215	cluster 1
HORVU.MOREX.r3.2HG0173210.1	-0.211964	-0.43618	-0.8921819	cluster 1
HORVU.MOREX.r3.2HG0173340.1	-0.672694	-1.024944	-3.4011705	cluster 1
HORVU.MOREX.r3.2HG0173550.1	-0.12745	-0.142497	-0.6657476	cluster 1
HORVU.MOREX.r3.2HG0173680.1	-0.065129	-0.212515	-0.4291996	cluster 1
HORVU.MOREX.r3.2HG0174820.1	-0.026387	-0.315706	-0.4958504	cluster 1
HORVU.MOREX.r3.2HG0175320.1	-0.278855	-0.341635	-0.8507718	cluster 1
HORVU.MOREX.r3.2HG0176290.1	-0.132214	-0.213024	-0.3801937	cluster 1
HORVU.MOREX.r3.2HG0176680.1	-0.046792	-0.118489	-0.2374491	cluster 1
HORVU.MOREX.r3.2HG0176920.1	-0.262881	-0.359843	-1.2359358	cluster 1
HORVU.MOREX.r3.2HG0177200.1	0.027253	-0.431642	-0.5373577	cluster 1
HORVU.MOREX.r3.2HG0177440.1	-0.278161	-0.547659	-0.8454242	cluster 1
HORVU.MOREX.r3.2HG0178160.1	-0.184445	-0.569243	-0.6504268	cluster 1
HORVU.MOREX.r3.2HG0179410.1	-0.115718	-0.364064	-0.569688	cluster 1
HORVU.MOREX.r3.2HG0179540.1	-0.124311	-0.150309	-0.4105338	cluster 1
HORVU.MOREX.r3.2HG0180060.1	-0.137065	-0.664672	-1.211109	cluster 1
HORVU.MOREX.r3.2HG0180090.1	-0.041684	-0.385505	-0.596626	cluster 1
HORVU.MOREX.r3.2HG0180210.1	-0.109261	-0.643828	-1.2018793	cluster 1
HORVU.MOREX.r3.2HG0180260.1	-0.405119	-0.522241	-0.698624	cluster 1
HORVU.MOREX.r3.2HG0180580.1	-0.110076	-0.40217	-1.4221313	cluster 1
HORVU.MOREX.r3.2HG0180880.1	-0.193847	-0.624619	-0.9009626	cluster 1
HORVU.MOREX.r3.2HG0181390.1	-0.216082	-0.524876	-1.4964878	cluster 1
HORVU.MOREX.r3.2HG0181660.1	-0.160828	-0.406047	-0.8346062	cluster 1
HORVU.MOREX.r3.2HG0181800.1	-0.349773	-0.599705	-0.7995019	cluster 1
HORVU.MOREX.r3.2HG0182020.2	-0.540107	-0.692229	-1.3458377	cluster 1
HORVU.MOREX.r3.2HG0182280.1	-0.236545	-0.506593	-0.7276101	cluster 1
HORVU.MOREX.r3.2HG0182800.1	-0.314825	-0.69223	-1.1727827	cluster 1
HORVU.MOREX.r3.2HG0183740.1	-0.160999	-0.625029	-1.2185225	cluster 1
HORVU.MOREX.r3.2HG0183780.1	-0.141197	-0.437104	-0.5578557	cluster 1
HORVU.MOREX.r3.2HG0184620.1	-0.542433	-1.007238	-1.0762834	cluster 1
HORVU.MOREX.r3.2HG0184780.1	-0.190778	-0.443959	-0.7601437	cluster 1
HORVU.MOREX.r3.2HG0185840.1	-0.150161	-0.435802	-0.9607608	cluster 1
HORVU.MOREX.r3.2HG0185850.1	-0.047482	-0.281538	-0.4626977	cluster 1
HORVU.MOREX.r3.2HG0186650.1	-0.173337	-0.225558	-0.7370369	cluster 1
HORVU.MOREX.r3.2HG0186680.1	-0.220169	-0.500706	-0.6940226	cluster 1
HORVU.MOREX.r3.2HG0187440.1	-0.113755	-0.357394	-0.5374455	cluster 1
HORVU.MOREX.r3.2HG0187640.1	-0.344579	-0.492267	-0.7954147	cluster 1
HORVU.MOREX.r3.2HG0188300.1	-0.143614	-0.425722	-0.6026267	cluster 1
HORVU.MOREX.r3.2HG0189800.1	-0.27634	-0.509165	-0.6867791	cluster 1
HORVU.MOREX.r3.2HG0189940.1	-0.13915	-0.532157	-1.3204146	cluster 1
HORVU.MOREX.r3.2HG0189950.1	-0.047778	-0.166634	-0.4376899	cluster 1
HORVU.MOREX.r3.2HG0190220.1	-0.184515	-0.591466	-0.998013	cluster 1
HORVU.MOREX.r3.2HG0190230.1	-0.251482	-0.587172	-1.4737691	cluster 1

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.2HG0190470.1	-0.186053	-0.466043	-0.5873399	cluster 1
HORVU.MOREX.r3.2HG0190680.1	-0.165902	-0.254017	-0.4810851	cluster 1
HORVU.MOREX.r3.2HG0190710.1	-0.103241	-0.251953	-0.343677	cluster 1
HORVU.MOREX.r3.2HG0192900.1	-0.14576	-0.608535	-1.3209815	cluster 1
HORVU.MOREX.r3.2HG0193080.1	-0.115497	-0.213986	-0.4413659	cluster 1
HORVU.MOREX.r3.2HG0193220.1	-0.21748	-0.279497	-0.6454699	cluster 1
HORVU.MOREX.r3.2HG0193930.1	-0.118934	-0.462256	-0.6992255	cluster 1
HORVU.MOREX.r3.2HG0194450.1	-0.065113	-0.18727	-0.381859	cluster 1
HORVU.MOREX.r3.2HG0194840.1	-0.156688	-1.263726	-1.8597546	cluster 1
HORVU.MOREX.r3.2HG0195110.2	-0.379744	-0.677136	-1.8754575	cluster 1
HORVU.MOREX.r3.2HG0195190.1	-0.128876	-0.328486	-0.8708187	cluster 1
HORVU.MOREX.r3.2HG0197560.1	-0.265836	-0.500201	-0.7677648	cluster 1
HORVU.MOREX.r3.2HG0197680.1	-0.143467	-0.163153	-0.3968303	cluster 1
HORVU.MOREX.r3.2HG0197710.1	-0.242123	-0.711377	-1.1581298	cluster 1
HORVU.MOREX.r3.2HG0199520.1	-0.231423	-1.19727	-1.6691928	cluster 1
HORVU.MOREX.r3.2HG0199560.1	-0.10429	-0.706589	-1.8280722	cluster 1
HORVU.MOREX.r3.2HG0199590.1	-0.570944	-1.056623	-1.2647195	cluster 1
HORVU.MOREX.r3.2HG0199600.1	-0.493	-1.489763	-2.217265	cluster 1
HORVU.MOREX.r3.2HG0200630.1	-0.109808	-0.355475	-0.7775816	cluster 1
HORVU.MOREX.r3.2HG0200640.1	-0.16703	-0.256722	-0.5216467	cluster 1
HORVU.MOREX.r3.2HG0200980.1	-0.045959	-0.171844	-0.4061348	cluster 1
HORVU.MOREX.r3.2HG0203500.1	-0.123255	-0.239296	-0.8256111	cluster 1
HORVU.MOREX.r3.2HG0204920.1	-0.162813	-0.572041	-1.3845879	cluster 1
HORVU.MOREX.r3.2HG0204940.1	-0.160487	-0.496076	-0.6690274	cluster 1
HORVU.MOREX.r3.2HG0204960.1	-0.182984	-0.28201	-0.3312112	cluster 1
HORVU.MOREX.r3.2HG0205200.1	-0.211409	-0.457111	-0.7688419	cluster 1
HORVU.MOREX.r3.2HG0205550.1	-0.201367	-0.426763	-0.8019225	cluster 1
HORVU.MOREX.r3.2HG0205750.1	-0.195928	-0.456015	-0.6426124	cluster 1
HORVU.MOREX.r3.2HG0206910.1	-0.196755	-0.517186	-1.0029526	cluster 1
HORVU.MOREX.r3.2HG0208790.1	-0.349134	-1.197783	-1.6687659	cluster 1
HORVU.MOREX.r3.2HG0209300.1	-0.092672	-0.631859	-1.1824651	cluster 1
HORVU.MOREX.r3.2HG0209440.1	-0.115503	-0.221954	-0.4802608	cluster 1
HORVU.MOREX.r3.2HG0209910.1	0.0546079	-0.296826	-0.4154749	cluster 1
HORVU.MOREX.r3.2HG0210420.1	-0.154001	-0.360597	-0.5717427	cluster 1
HORVU.MOREX.r3.2HG0210880.1	0.1371645	0.0302801	-1.1557906	cluster 1
HORVU.MOREX.r3.2HG0212570.1	-0.193354	-0.405159	-0.5208923	cluster 1
HORVU.MOREX.r3.2HG0212900.1	-0.060892	-0.240509	-0.6129391	cluster 1
HORVU.MOREX.r3.2HG0213250.1	-0.15275	-0.538482	-0.7092201	cluster 1
HORVU.MOREX.r3.2HG0213850.1	-0.011557	-0.135704	-0.6079445	cluster 1
HORVU.MOREX.r3.2HG0214090.1	-0.194082	-0.541106	-1.0790097	cluster 1
HORVU.MOREX.r3.2HG0215220.1	0.3156464	-0.337822	-0.7494649	cluster 1
HORVU.MOREX.r3.2HG0215250.1	0.1623403	-0.523518	-1.1321166	cluster 1
HORVU.MOREX.r3.2HG0215280.1	-0.031021	-0.358731	-0.5720262	cluster 1
HORVU.MOREX.r3.2HG0215310.1	0.1124949	-0.300838	-1.4518362	cluster 1
HORVU.MOREX.r3.2HG0215550.1	0.1403848	-0.018232	-0.8009071	cluster 1
HORVU.MOREX.r3.2HG0216610.1	-0.122363	-0.279792	-0.3320576	cluster 1
HORVU.MOREX.r3.2HG0217610.1	-0.040075	-0.21691	-0.3070362	cluster 1

Table Sπ Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.2HG0218010.1	-0.14466	-0.383605	-0.4903498	cluster 1
HORVU.MOREX.r3.3HG0218100.1	-0.125372	-0.330788	-0.3622098	cluster 1
HORVU.MOREX.r3.3HG0218330.1	0.0072857	-0.56199	-1.5749569	cluster 1
HORVU.MOREX.r3.3HG0219290.1	-0.267742	-0.279616	-0.4249593	cluster 1
HORVU.MOREX.r3.3HG0219650.1	-0.070838	-0.15453	-0.4423778	cluster 1
HORVU.MOREX.r3.3HG0219740.1	-0.172104	-0.317892	-0.6152745	cluster 1
HORVU.MOREX.r3.3HG0219800.1	-0.029697	-0.262911	-0.542665	cluster 1
HORVU.MOREX.r3.3HG0219810.1	-0.37275	-0.442903	-0.9179098	cluster 1
HORVU.MOREX.r3.3HG0220250.1	-0.221401	-0.34977	-0.4856685	cluster 1
HORVU.MOREX.r3.3HG0220360.1	-0.126673	-0.496967	-0.8243858	cluster 1
HORVU.MOREX.r3.3HG0221460.1	-0.090241	-0.098305	-0.5980666	cluster 1
HORVU.MOREX.r3.3HG0223950.1	0.0829855	-0.268924	-0.6635622	cluster 1
HORVU.MOREX.r3.3HG0223980.1	-0.22551	-0.349647	-0.4959089	cluster 1
HORVU.MOREX.r3.3HG0224680.1	-0.072198	-0.281699	-0.4108601	cluster 1
HORVU.MOREX.r3.3HG0225610.1	-0.288524	-0.328496	-0.8636404	cluster 1
HORVU.MOREX.r3.3HG0226060.1	-0.229348	-0.5027	-1.2634158	cluster 1
HORVU.MOREX.r3.3HG0229480.1	-0.093827	-0.159974	-0.3893624	cluster 1
HORVU.MOREX.r3.3HG0230190.1	-0.236364	-0.356318	-1.1796632	cluster 1
HORVU.MOREX.r3.3HG0230970.1	-0.109852	-0.438205	-0.8163375	cluster 1
HORVU.MOREX.r3.3HG0231050.1	-0.131468	-0.479898	-0.8809321	cluster 1
HORVU.MOREX.r3.3HG0231630.1	-0.13687	-0.730602	-1.466273	cluster 1
HORVU.MOREX.r3.3HG0231780.1	-0.119593	-0.437619	-1.0611853	cluster 1
HORVU.MOREX.r3.3HG0231900.1	-0.055668	-0.187305	-0.2424899	cluster 1
HORVU.MOREX.r3.3HG0232780.1	0.0663294	-0.434466	-0.5689191	cluster 1
HORVU.MOREX.r3.3HG0233150.1	-0.096706	-0.277548	-0.8277078	cluster 1
HORVU.MOREX.r3.3HG0234560.1	-0.134236	-1.078676	-1.3408735	cluster 1
HORVU.MOREX.r3.3HG0234800.1	-0.124679	-0.221639	-0.2789724	cluster 1
HORVU.MOREX.r3.3HG0236170.1	-0.055837	-0.20051	-0.3508077	cluster 1
HORVU.MOREX.r3.3HG0237870.1	-0.103412	-0.576425	-1.6593224	cluster 1
HORVU.MOREX.r3.3HG0237910.1	-0.354448	-0.708414	-0.9922342	cluster 1
HORVU.MOREX.r3.3HG0238180.1	-0.245973	-0.494704	-0.5746101	cluster 1
HORVU.MOREX.r3.3HG0239110.1	-0.354672	-0.652166	-0.9254847	cluster 1
HORVU.MOREX.r3.3HG0240390.2	-0.662318	-0.76606	-1.2581255	cluster 1
HORVU.MOREX.r3.3HG0240450.1	-0.158411	-0.40163	-0.7534721	cluster 1
HORVU.MOREX.r3.3HG0240640.1	-0.139937	-0.693355	-1.4793637	cluster 1
HORVU.MOREX.r3.3HG0240670.1	-0.177471	-0.451187	-1.1615878	cluster 1
HORVU.MOREX.r3.3HG0240710.1	-0.253345	-0.801872	-1.4033411	cluster 1
HORVU.MOREX.r3.3HG0241000.1	-0.23877	-1.145729	-1.7322621	cluster 1
HORVU.MOREX.r3.3HG0241630.1	-0.220412	-0.504613	-0.6515102	cluster 1
HORVU.MOREX.r3.3HG0241720.1	-0.03839	-0.157978	-0.1934811	cluster 1
HORVU.MOREX.r3.3HG0242030.1	-0.059841	-0.154442	-1.6653751	cluster 1
HORVU.MOREX.r3.3HG0242520.1	-0.098191	-0.399811	-0.5407455	cluster 1
HORVU.MOREX.r3.3HG0242870.1	-0.116097	-0.292479	-0.3235167	cluster 1
HORVU.MOREX.r3.3HG0244690.1	-0.080686	-0.489595	-0.8390583	cluster 1
HORVU.MOREX.r3.3HG0245310.1	0.0273886	-0.405969	-0.7475374	cluster 1
HORVU.MOREX.r3.3HG0246370.1	-0.25615	-0.432403	-0.6589591	cluster 1
HORVU.MOREX.r3.3HG0246560.1	-0.189221	-0.513876	-0.7699912	cluster 1

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.3HG0247250.1	-0.141916	-0.283166	-1.3240752	cluster 1
HORVU.MOREX.r3.3HG0247260.1	-0.36892	-0.888752	-1.1693937	cluster 1
HORVU.MOREX.r3.3HG0248280.1	-0.139838	-0.216864	-0.3936771	cluster 1
HORVU.MOREX.r3.3HG0249590.1	-0.375729	-0.430333	-0.6995825	cluster 1
HORVU.MOREX.r3.3HG0249700.1	-0.133678	-0.457757	-0.5532478	cluster 1
HORVU.MOREX.r3.3HG0249810.1	-0.129046	-0.145227	-0.3999752	cluster 1
HORVU.MOREX.r3.3HG0250170.1	0.0153043	-0.131782	-0.5871409	cluster 1
HORVU.MOREX.r3.3HG0250630.1	-0.254622	-0.537133	-0.6985942	cluster 1
HORVU.MOREX.r3.3HG0251830.1	-0.356283	-0.391232	-1.1215397	cluster 1
HORVU.MOREX.r3.3HG0251950.1	-0.242722	-0.458711	-0.6915756	cluster 1
HORVU.MOREX.r3.3HG0252240.1	-0.131064	-0.396222	-0.9017322	cluster 1
HORVU.MOREX.r3.3HG0252610.1	-0.160318	-0.337298	-0.3771383	cluster 1
HORVU.MOREX.r3.3HG0253360.1	-0.475094	-0.541572	-1.0775016	cluster 1
HORVU.MOREX.r3.3HG0253440.1	-0.032487	-0.363593	-0.8320019	cluster 1
HORVU.MOREX.r3.3HG0254850.1	-0.015903	-0.166361	-0.3370218	cluster 1
HORVU.MOREX.r3.3HG0255040.1	-0.225901	-0.373302	-0.4099441	cluster 1
HORVU.MOREX.r3.3HG0255150.1	-0.146222	-0.226422	-0.2733467	cluster 1
HORVU.MOREX.r3.3HG0255220.1	-0.241422	-0.543248	-0.998544	cluster 1
HORVU.MOREX.r3.3HG0255900.1	-0.134357	-0.201523	-0.2914825	cluster 1
HORVU.MOREX.r3.3HG0256300.1	-0.108122	-0.265612	-0.4583029	cluster 1
HORVU.MOREX.r3.3HG0256360.1	-0.087076	-0.280291	-0.374385	cluster 1
HORVU.MOREX.r3.3HG0256380.1	-0.140095	-0.328872	-0.8566649	cluster 1
HORVU.MOREX.r3.3HG0256580.1	-0.136381	-0.254027	-0.4907328	cluster 1
HORVU.MOREX.r3.3HG0256620.1	-0.118856	-0.728438	-1.0254593	cluster 1
HORVU.MOREX.r3.3HG0257130.1	-0.283517	-0.506689	-0.7760597	cluster 1
HORVU.MOREX.r3.3HG0259660.1	-0.191272	-0.441023	-0.5892941	cluster 1
HORVU.MOREX.r3.3HG0259960.1	0.0744353	-1.297706	-1.9686553	cluster 1
HORVU.MOREX.r3.3HG0260580.1	-0.051405	-0.162657	-0.4759776	cluster 1
HORVU.MOREX.r3.3HG0261980.1	-0.034974	-0.271694	-0.5902238	cluster 1
HORVU.MOREX.r3.3HG0262210.1	-0.168114	-0.280944	-0.328426	cluster 1
HORVU.MOREX.r3.3HG0266960.1	-0.131143	-0.289426	-0.6094999	cluster 1
HORVU.MOREX.r3.3HG0267150.1	-0.082957	-0.288586	-0.352175	cluster 1
HORVU.MOREX.r3.3HG0270070.1	-0.194179	-0.415184	-0.8724205	cluster 1
HORVU.MOREX.r3.3HG0270400.1	-0.301809	-0.518499	-0.8898794	cluster 1
HORVU.MOREX.r3.3HG0270500.1	-0.220232	-0.482652	-0.5737567	cluster 1
HORVU.MOREX.r3.3HG0270910.1	-0.072651	-0.253474	-0.2953239	cluster 1
HORVU.MOREX.r3.3HG0272160.2	-0.274508	-0.465267	-0.7060044	cluster 1
HORVU.MOREX.r3.3HG0272430.1	-0.056853	-0.165352	-0.4036842	cluster 1
HORVU.MOREX.r3.3HG0275530.1	-0.113086	-0.307145	-0.7536933	cluster 1
HORVU.MOREX.r3.3HG0277100.1	-0.127665	-0.419388	-0.4620881	cluster 1
HORVU.MOREX.r3.3HG0277200.1	-0.272808	-0.680377	-1.1215708	cluster 1
HORVU.MOREX.r3.3HG0279760.1	-0.503867	-0.552255	-0.7878619	cluster 1
HORVU.MOREX.r3.3HG0280310.1	-0.212239	-0.495671	-0.6812373	cluster 1
HORVU.MOREX.r3.3HG0280900.1	-0.036837	-0.190958	-0.3347234	cluster 1
HORVU.MOREX.r3.3HG0281000.1	-0.094973	-0.223989	-0.8512444	cluster 1
HORVU.MOREX.r3.3HG0282170.1	-0.577209	-0.948347	-1.825963	cluster 1
HORVU.MOREX.r3.3HG0283990.1	-0.117159	-0.316105	-0.525227	cluster 1

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.3HG0284170.1	-0.144863	-0.489183	-0.5758377	cluster 1
HORVU.MOREX.r3.3HG0285010.1	-0.765206	-0.943498	-2.0178816	cluster 1
HORVU.MOREX.r3.3HG0285270.1	-0.335414	-0.824703	-2.0053754	cluster 1
HORVU.MOREX.r3.3HG0285570.1	-0.162313	-0.601252	-0.7285259	cluster 1
HORVU.MOREX.r3.3HG0286160.1	-0.292278	-0.811066	-1.7481436	cluster 1
HORVU.MOREX.r3.3HG0287070.1	-0.133152	-0.838915	-1.2917272	cluster 1
HORVU.MOREX.r3.3HG0287800.1	0.1339816	-0.221696	-0.6885903	cluster 1
HORVU.MOREX.r3.3HG0287840.1	-0.199367	-0.611982	-0.7099253	cluster 1
HORVU.MOREX.r3.3HG0288240.1	-0.205668	-0.310078	-0.6990169	cluster 1
HORVU.MOREX.r3.3HG0288420.1	0.0100033	-0.169455	-0.9249703	cluster 1
HORVU.MOREX.r3.3HG0288700.1	-0.274665	-0.590487	-0.6701073	cluster 1
HORVU.MOREX.r3.3HG0288940.1	-0.263878	-0.481211	-0.7157122	cluster 1
HORVU.MOREX.r3.3HG0289910.1	-0.055999	-0.221969	-0.3541359	cluster 1
HORVU.MOREX.r3.3HG0289970.1	-0.162318	-0.28301	-0.6045168	cluster 1
HORVU.MOREX.r3.3HG0290180.1	-0.256618	-0.498685	-1.1300931	cluster 1
HORVU.MOREX.r3.3HG0290510.1	-0.049319	-0.510759	-0.8913259	cluster 1
HORVU.MOREX.r3.3HG0291490.1	-0.197087	-0.44142	-0.9611394	cluster 1
HORVU.MOREX.r3.3HG0291710.1	-0.237267	-0.420506	-0.4724722	cluster 1
HORVU.MOREX.r3.3HG0293040.1	-0.189637	-0.239068	-0.4427811	cluster 1
HORVU.MOREX.r3.3HG0293700.1	-0.213003	-0.433337	-0.6604125	cluster 1
HORVU.MOREX.r3.3HG0294100.1	-0.166916	-0.340918	-0.3761033	cluster 1
HORVU.MOREX.r3.3HG0294840.1	-0.045392	-0.18564	-0.5245908	cluster 1
HORVU.MOREX.r3.3HG0295020.1	-0.084589	-0.31783	-0.56766	cluster 1
HORVU.MOREX.r3.3HG0295330.1	-0.140062	-0.405564	-0.6056142	cluster 1
HORVU.MOREX.r3.3HG0295440.1	-0.175854	-0.374836	-0.8104747	cluster 1
HORVU.MOREX.r3.3HG0295450.1	-0.087159	-0.537072	-0.8221331	cluster 1
HORVU.MOREX.r3.3HG0296490.1	-0.012781	-0.103117	-0.6310038	cluster 1
HORVU.MOREX.r3.3HG0296810.1	-0.330369	-0.442928	-0.9073306	cluster 1
HORVU.MOREX.r3.3HG0296940.1	-0.404681	-0.438639	-0.7780682	cluster 1
HORVU.MOREX.r3.3HG0297140.1	-0.128292	-0.188447	-0.26881	cluster 1
HORVU.MOREX.r3.3HG0297180.1	-0.591426	-0.843079	-1.7608999	cluster 1
HORVU.MOREX.r3.3HG0297940.1	-0.06286	-0.960919	-1.1779962	cluster 1
HORVU.MOREX.r3.3HG0298340.1	-0.286744	-0.396123	-0.738991	cluster 1
HORVU.MOREX.r3.3HG0298390.1	-0.293623	-0.523294	-1.155846	cluster 1
HORVU.MOREX.r3.3HG0298750.1	-0.033868	-0.320112	-0.4786808	cluster 1
HORVU.MOREX.r3.3HG0299010.1	-0.382724	-0.539569	-1.071483	cluster 1
HORVU.MOREX.r3.3HG0299200.1	-0.150773	-0.358807	-0.6619428	cluster 1
HORVU.MOREX.r3.3HG0299280.1	-0.129571	-0.361193	-0.7325662	cluster 1
HORVU.MOREX.r3.3HG0299300.1	0.1040784	-0.793205	-1.1079439	cluster 1
HORVU.MOREX.r3.3HG0299530.1	0.1216835	-0.313153	-0.5168956	cluster 1
HORVU.MOREX.r3.3HG0299540.1	-0.09918	-0.221253	-0.3040279	cluster 1
HORVU.MOREX.r3.3HG0299820.1	-0.243889	-0.577134	-1.061206	cluster 1
HORVU.MOREX.r3.3HG0300020.1	0.2560973	-0.681768	-2.172499	cluster 1
HORVU.MOREX.r3.3HG0301250.1	-0.268101	-0.864757	-1.1706077	cluster 1
HORVU.MOREX.r3.3HG0301750.1	-0.10808	-0.456495	-0.6238556	cluster 1
HORVU.MOREX.r3.3HG0302090.1	-0.06493	-0.137075	-0.586395	cluster 1
HORVU.MOREX.r3.3HG0302140.1	-0.152563	-0.312717	-0.4769035	cluster 1

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.3HG0302860.1	0.8047109	-0.100145	-1.9563874	cluster 1
HORVU.MOREX.r3.3HG0302910.1	-0.114349	-0.383689	-0.9603979	cluster 1
HORVU.MOREX.r3.3HG0303330.1	-0.121177	-0.291992	-0.8113502	cluster 1
HORVU.MOREX.r3.3HG0303430.1	-0.133288	-0.372844	-0.4640951	cluster 1
HORVU.MOREX.r3.3HG0303970.1	-0.074889	-0.395173	-0.6779429	cluster 1
HORVU.MOREX.r3.3HG0304080.1	-0.019526	-0.474277	-0.8626337	cluster 1
HORVU.MOREX.r3.3HG0304420.1	-0.136011	-0.379394	-1.0740291	cluster 1
HORVU.MOREX.r3.3HG0304640.1	-0.039855	-0.349929	-0.5820753	cluster 1
HORVU.MOREX.r3.3HG0304710.1	-0.117879	-0.287969	-0.346661	cluster 1
HORVU.MOREX.r3.3HG0305150.1	-0.230037	-0.69222	-0.9446847	cluster 1
HORVU.MOREX.r3.3HG0305270.1	-0.217125	-0.295205	-0.627447	cluster 1
HORVU.MOREX.r3.3HG0305500.1	0.1561274	-0.222634	-1.3145458	cluster 1
HORVU.MOREX.r3.3HG0305580.1	0.1242108	-0.387167	-1.3815488	cluster 1
HORVU.MOREX.r3.3HG0306030.1	-0.105565	-0.261625	-0.4564221	cluster 1
HORVU.MOREX.r3.3HG0306170.1	-0.055892	-0.145347	-0.32995	cluster 1
HORVU.MOREX.r3.3HG0306210.1	-0.131027	-0.215962	-0.6006012	cluster 1
HORVU.MOREX.r3.3HG0306220.1	-0.088388	-0.408085	-0.471634	cluster 1
HORVU.MOREX.r3.3HG0306420.1	-0.327989	-0.398514	-1.0430224	cluster 1
HORVU.MOREX.r3.3HG0306440.1	-0.16585	-0.812018	-1.166288	cluster 1
HORVU.MOREX.r3.3HG0306820.2	-0.349779	-0.866324	-1.3258413	cluster 1
HORVU.MOREX.r3.3HG0307120.1	-0.153053	-0.361715	-0.6358684	cluster 1
HORVU.MOREX.r3.3HG0308420.1	0.0914717	-0.604517	-0.8279024	cluster 1
HORVU.MOREX.r3.3HG0308820.1	-0.115504	-0.276578	-0.3613674	cluster 1
HORVU.MOREX.r3.3HG0309410.1	-0.517402	-0.972681	-1.3512535	cluster 1
HORVU.MOREX.r3.3HG0309460.1	-0.074743	-0.284965	-0.3338557	cluster 1
HORVU.MOREX.r3.3HG0309820.1	-0.019137	-0.227125	-0.7379945	cluster 1
HORVU.MOREX.r3.3HG0310210.1	-0.148528	-0.278551	-0.5385161	cluster 1
HORVU.MOREX.r3.3HG0310320.1	-0.055874	-0.306726	-0.6889858	cluster 1
HORVU.MOREX.r3.3HG0310540.1	-0.127021	-0.498619	-0.5852403	cluster 1
HORVU.MOREX.r3.3HG0313040.1	-0.295317	-0.636241	-1.4215096	cluster 1
HORVU.MOREX.r3.3HG0313490.1	-0.129221	-0.440114	-0.9070372	cluster 1
HORVU.MOREX.r3.3HG0313690.1	-0.071126	-0.12746	-0.2934731	cluster 1
HORVU.MOREX.r3.3HG0314270.1	-0.124534	-0.534095	-0.7887598	cluster 1
HORVU.MOREX.r3.3HG0315000.1	-0.137706	-0.258206	-0.4724098	cluster 1
HORVU.MOREX.r3.3HG0316000.1	-0.127668	-0.60661	-0.7385573	cluster 1
HORVU.MOREX.r3.3HG0316110.1	-0.245983	-0.534869	-1.0504752	cluster 1
HORVU.MOREX.r3.3HG0316280.1	-0.184719	-0.374697	-0.8538376	cluster 1
HORVU.MOREX.r3.3HG0316640.1	-0.372364	-0.640982	-0.7054226	cluster 1
HORVU.MOREX.r3.3HG0318400.1	-0.013993	-0.202029	-0.9627932	cluster 1
HORVU.MOREX.r3.3HG0319760.1	-0.169943	-0.291739	-0.4562695	cluster 1
HORVU.MOREX.r3.3HG0319960.1	-0.125226	-0.453155	-0.9454177	cluster 1
HORVU.MOREX.r3.3HG0320040.1	-0.492825	-0.740241	-1.4702151	cluster 1
HORVU.MOREX.r3.3HG0320840.1	-0.114514	-0.246791	-0.4363357	cluster 1
HORVU.MOREX.r3.3HG0322660.1	-0.009946	-0.227472	-1.3126946	cluster 1
HORVU.MOREX.r3.3HG0323530.1	-0.060302	-0.21161	-0.7659833	cluster 1
HORVU.MOREX.r3.3HG0325760.1	-0.162663	-0.304926	-0.495179	cluster 1
HORVU.MOREX.r3.3HG0327170.1	-0.141397	-0.423876	-0.5524671	cluster 1

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.3HG0327200.3	-0.314218	-0.474313	-0.5834595	cluster 1
HORVU.MOREX.r3.3HG0327630.1	-0.28005	-0.360357	-1.1598417	cluster 1
HORVU.MOREX.r3.3HG0327710.1	-0.08448	-0.238175	-0.3268001	cluster 1
HORVU.MOREX.r3.3HG0327810.1	-0.160024	-0.485271	-0.6033858	cluster 1
HORVU.MOREX.r3.3HG0328340.1	-0.353535	-0.527215	-1.6131196	cluster 1
HORVU.MOREX.r3.3HG0328480.1	-0.536475	-1.031843	-1.7306506	cluster 1
HORVU.MOREX.r3.3HG0328990.1	-0.018362	-0.297842	-0.4181607	cluster 1
HORVU.MOREX.r3.3HG0329830.1	-0.078209	-0.157845	-0.2426092	cluster 1
HORVU.MOREX.r3.3HG0330980.1	-0.123833	-0.381879	-0.4385183	cluster 1
HORVU.MOREX.r3.3HG0331030.1	-0.228502	-0.424614	-0.4774815	cluster 1
HORVU.MOREX.r3.4HG0331850.1	-0.13993	-0.402414	-0.6082197	cluster 1
HORVU.MOREX.r3.4HG0333130.1	-0.565435	-0.879041	-1.1070301	cluster 1
HORVU.MOREX.r3.4HG0333840.1	-0.150543	-0.423726	-0.8004422	cluster 1
HORVU.MOREX.r3.4HG0335110.1	-0.327801	-0.607782	-0.9457045	cluster 1
HORVU.MOREX.r3.4HG0335150.1	-0.089601	-0.227157	-0.3093424	cluster 1
HORVU.MOREX.r3.4HG0335650.1	-0.29059	-0.70595	-1.3316759	cluster 1
HORVU.MOREX.r3.4HG0335690.1	-0.055254	-0.419542	-0.6433416	cluster 1
HORVU.MOREX.r3.4HG0335790.2	-0.218619	-0.237669	-0.5925053	cluster 1
HORVU.MOREX.r3.4HG0336310.1	-0.164011	-0.371162	-0.6741489	cluster 1
HORVU.MOREX.r3.4HG0337120.1	-0.035982	-0.212683	-0.6505132	cluster 1
HORVU.MOREX.r3.4HG0337500.1	-0.036754	-0.133957	-0.1810437	cluster 1
HORVU.MOREX.r3.4HG0338180.1	-0.076914	-0.245034	-0.4032402	cluster 1
HORVU.MOREX.r3.4HG0338210.1	-0.067749	-0.360667	-0.7759765	cluster 1
HORVU.MOREX.r3.4HG0338400.1	-0.141062	-0.366588	-0.8607311	cluster 1
HORVU.MOREX.r3.4HG0339180.1	-0.252025	-1.173939	-1.9513218	cluster 1
HORVU.MOREX.r3.4HG0339430.2	-0.451211	-0.836488	-1.8444257	cluster 1
HORVU.MOREX.r3.4HG0339750.1	-0.13566	-0.186062	-0.6116615	cluster 1
HORVU.MOREX.r3.4HG0340200.1	-0.181384	-0.626989	-1.0051655	cluster 1
HORVU.MOREX.r3.4HG0340920.1	-0.082401	-0.169444	-0.4379429	cluster 1
HORVU.MOREX.r3.4HG0341080.1	-0.273763	-0.67648	-1.8100013	cluster 1
HORVU.MOREX.r3.4HG0341810.1	-0.136861	-0.257877	-0.3150077	cluster 1
HORVU.MOREX.r3.4HG0342090.1	-0.113438	-0.150665	-0.4684307	cluster 1
HORVU.MOREX.r3.4HG0342160.1	-0.253861	-0.363561	-0.4802373	cluster 1
HORVU.MOREX.r3.4HG0342640.1	-0.194333	-0.528217	-1.808421	cluster 1
HORVU.MOREX.r3.4HG0342850.1	-0.085012	-0.304409	-0.4053954	cluster 1
HORVU.MOREX.r3.4HG0342950.1	-0.293596	-0.336706	-0.957211	cluster 1
HORVU.MOREX.r3.4HG0344990.1	-0.215404	-0.766952	-1.2309492	cluster 1
HORVU.MOREX.r3.4HG0346720.1	-0.172152	-0.411621	-0.6839953	cluster 1
HORVU.MOREX.r3.4HG0349170.1	-0.336471	-0.500202	-1.0234216	cluster 1
HORVU.MOREX.r3.4HG0349530.1	-0.238848	-0.396966	-0.4404921	cluster 1
HORVU.MOREX.r3.4HG0350800.1	0.4696285	-0.584577	-2.5380005	cluster 1
HORVU.MOREX.r3.4HG0353330.1	-0.284836	-0.503407	-0.9357699	cluster 1
HORVU.MOREX.r3.4HG0353450.1	-0.439724	-0.73863	-2.115183	cluster 1
HORVU.MOREX.r3.4HG0354480.1	-0.046077	-0.113958	-0.3004255	cluster 1
HORVU.MOREX.r3.4HG0354540.1	-0.11519	-0.349752	-2.4083044	cluster 1
HORVU.MOREX.r3.4HG0354970.1	-0.087296	-0.277413	-0.6802499	cluster 1
HORVU.MOREX.r3.4HG0355150.1	-0.14746	-0.313481	-0.6148953	cluster 1

Table SΠ Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.4HG0357230.1	0.0257401	-0.445226	-1.2268151	cluster 1
HORVU.MOREX.r3.4HG0358310.1	-0.231043	-0.352879	-0.7157995	cluster 1
HORVU.MOREX.r3.4HG0358580.1	-0.066706	-0.374257	-1.0493184	cluster 1
HORVU.MOREX.r3.4HG0358880.2	-0.146453	-0.300945	-0.522805	cluster 1
HORVU.MOREX.r3.4HG0358890.1	-0.173941	-0.256255	-0.5796136	cluster 1
HORVU.MOREX.r3.4HG0361420.2	-0.069486	-0.369699	-0.4902013	cluster 1
HORVU.MOREX.r3.4HG0361680.1	-0.42961	-0.87521	-1.2830612	cluster 1
HORVU.MOREX.r3.4HG0362450.1	-0.460453	-0.48639	-0.9434047	cluster 1
HORVU.MOREX.r3.4HG0364310.1	-0.108025	-0.30134	-0.5137443	cluster 1
HORVU.MOREX.r3.4HG0364520.1	-0.104446	-0.194497	-0.380177	cluster 1
HORVU.MOREX.r3.4HG0367380.1	-0.67793	-1.321525	-2.6938687	cluster 1
HORVU.MOREX.r3.4HG0369880.1	-0.195898	-1.070415	-1.5680736	cluster 1
HORVU.MOREX.r3.4HG0372280.1	-0.32752	-0.724046	-1.6445618	cluster 1
HORVU.MOREX.r3.4HG0374640.1	-0.152825	-0.420288	-0.7195119	cluster 1
HORVU.MOREX.r3.4HG0375550.1	-0.675131	-1.346595	-2.2677136	cluster 1
HORVU.MOREX.r3.4HG0375690.1	-0.065895	-0.37703	-1.1521943	cluster 1
HORVU.MOREX.r3.4HG0375760.1	-0.084617	-0.229821	-0.7723314	cluster 1
HORVU.MOREX.r3.4HG0376950.1	-0.521269	-1.510157	-2.2875001	cluster 1
HORVU.MOREX.r3.4HG0377020.1	-0.13919	-0.294229	-0.3552233	cluster 1
HORVU.MOREX.r3.4HG0377070.1	-0.184358	-0.464871	-0.5346444	cluster 1
HORVU.MOREX.r3.4HG0378580.1	-0.240317	-0.539403	-0.6870235	cluster 1
HORVU.MOREX.r3.4HG0378710.1	-0.169922	-0.482442	-0.7722851	cluster 1
HORVU.MOREX.r3.4HG0378960.1	-0.266631	-0.545358	-0.9943749	cluster 1
HORVU.MOREX.r3.4HG0379960.1	-0.018742	-0.151219	-0.4266713	cluster 1
HORVU.MOREX.r3.4HG0380710.1	-0.071625	-0.25288	-0.3653337	cluster 1
HORVU.MOREX.r3.4HG0381310.1	-0.078991	-0.712993	-1.0288265	cluster 1
HORVU.MOREX.r3.4HG0381680.1	-0.133526	-0.28718	-0.5433962	cluster 1
HORVU.MOREX.r3.4HG0381880.1	-0.116201	-0.415551	-0.4782793	cluster 1
HORVU.MOREX.r3.4HG0382500.1	-0.141508	-0.324907	-0.3950199	cluster 1
HORVU.MOREX.r3.4HG0382760.1	-0.291802	-0.472674	-0.9330541	cluster 1
HORVU.MOREX.r3.4HG0383070.1	-0.206758	-0.486628	-0.5464747	cluster 1
HORVU.MOREX.r3.4HG0383870.1	-0.199645	-0.46203	-0.7961873	cluster 1
HORVU.MOREX.r3.4HG0384110.1	-0.078175	-0.309068	-0.3775722	cluster 1
HORVU.MOREX.r3.4HG0384700.1	-0.478101	-0.549769	-0.9227407	cluster 1
HORVU.MOREX.r3.4HG0385080.1	-0.106665	-0.162032	-0.5753367	cluster 1
HORVU.MOREX.r3.4HG0385100.1	-0.098855	-0.25588	-0.3381732	cluster 1
HORVU.MOREX.r3.4HG0385270.1	-0.100593	-0.26726	-0.4633914	cluster 1
HORVU.MOREX.r3.4HG0385300.1	-0.122212	-0.290636	-0.4992224	cluster 1
HORVU.MOREX.r3.4HG0385780.1	-0.035605	-0.278428	-0.5608728	cluster 1
HORVU.MOREX.r3.4HG0385880.1	-0.249969	-0.595731	-0.932234	cluster 1
HORVU.MOREX.r3.4HG0386000.2	-0.316867	-0.323233	-0.5177861	cluster 1
HORVU.MOREX.r3.4HG0386190.1	-0.04106	-0.109	-0.2804241	cluster 1
HORVU.MOREX.r3.4HG0386480.1	-0.162104	-0.324584	-0.3988844	cluster 1
HORVU.MOREX.r3.4HG0386830.1	0.0939924	-0.46654	-1.0408594	cluster 1
HORVU.MOREX.r3.4HG0387120.1	-0.180567	-0.49297	-1.0190293	cluster 1
HORVU.MOREX.r3.4HG0387150.1	-0.045952	-0.392939	-0.875827	cluster 1
HORVU.MOREX.r3.4HG0388270.1	-0.205618	-0.373403	-0.4161157	cluster 1

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.4HG0390030.1	-0.658142	-0.810853	-2.1813579	cluster 1
HORVU.MOREX.r3.4HG0391330.1	-0.108701	-0.4174	-0.534566	cluster 1
HORVU.MOREX.r3.4HG0392150.1	0.0690786	-0.421996	-1.5061598	cluster 1
HORVU.MOREX.r3.4HG0392160.1	-0.139579	-0.611611	-1.2616238	cluster 1
HORVU.MOREX.r3.4HG0393120.1	-0.348134	-0.371416	-1.0483317	cluster 1
HORVU.MOREX.r3.4HG0393260.1	-0.063712	-0.095408	-0.3220089	cluster 1
HORVU.MOREX.r3.4HG0393630.1	-0.094206	-0.251055	-0.2971404	cluster 1
HORVU.MOREX.r3.4HG0393890.1	0.0591768	-0.468575	-0.6528003	cluster 1
HORVU.MOREX.r3.4HG0394690.1	-0.143459	-0.167882	-0.3297057	cluster 1
HORVU.MOREX.r3.4HG0394810.1	-0.279647	-0.453144	-0.9831815	cluster 1
HORVU.MOREX.r3.4HG0394980.1	-0.307281	-0.403415	-0.8316173	cluster 1
HORVU.MOREX.r3.4HG0395120.1	-0.069213	-0.123892	-0.631625	cluster 1
HORVU.MOREX.r3.4HG0395220.1	-0.112752	-0.464357	-0.6522316	cluster 1
HORVU.MOREX.r3.4HG0396220.1	-0.100954	-0.308114	-0.3849942	cluster 1
HORVU.MOREX.r3.4HG0396660.1	-0.057927	-0.451731	-1.6125181	cluster 1
HORVU.MOREX.r3.4HG0396710.1	-0.17085	-0.584794	-1.1570608	cluster 1
HORVU.MOREX.r3.4HG0398420.1	-0.246197	-0.423128	-0.5509643	cluster 1
HORVU.MOREX.r3.4HG0398900.1	-0.206199	-0.617502	-1.0400882	cluster 1
HORVU.MOREX.r3.4HG0398910.1	-0.204757	-0.52852	-1.0188622	cluster 1
HORVU.MOREX.r3.4HG0400800.1	0.0106904	-0.229913	-0.426318	cluster 1
HORVU.MOREX.r3.4HG0400990.1	-0.237998	-0.526986	-0.7805544	cluster 1
HORVU.MOREX.r3.4HG0401450.1	-0.278717	-0.394576	-0.4432732	cluster 1
HORVU.MOREX.r3.4HG0401710.1	-0.168331	-0.544497	-1.2788517	cluster 1
HORVU.MOREX.r3.4HG0401720.1	-0.188296	-0.565064	-1.1285892	cluster 1
HORVU.MOREX.r3.4HG0402030.1	-0.233811	-0.488545	-0.5885886	cluster 1
HORVU.MOREX.r3.4HG0402600.2	-0.282409	-0.31583	-1.2258447	cluster 1
HORVU.MOREX.r3.4HG0403070.1	-0.144869	-0.438474	-0.6719997	cluster 1
HORVU.MOREX.r3.4HG0403250.1	-0.297497	-0.661895	-1.080686	cluster 1
HORVU.MOREX.r3.4HG0404340.1	-0.06588	-0.269008	-0.3654471	cluster 1
HORVU.MOREX.r3.4HG0404450.1	-0.035418	-0.047512	-0.2822729	cluster 1
HORVU.MOREX.r3.4HG0404750.1	-0.207453	-0.803663	-2.0069474	cluster 1
HORVU.MOREX.r3.4HG0406380.1	-0.024941	-0.201893	-0.3852673	cluster 1
HORVU.MOREX.r3.4HG0406960.1	-0.161863	-0.225985	-0.3257137	cluster 1
HORVU.MOREX.r3.4HG0407290.1	0.0115131	-0.428804	-1.4103224	cluster 1
HORVU.MOREX.r3.4HG0407410.1	-0.182641	-0.297975	-0.9451391	cluster 1
HORVU.MOREX.r3.4HG0407980.1	-0.016514	-0.148909	-0.7172955	cluster 1
HORVU.MOREX.r3.4HG0410720.1	-0.278606	-0.437323	-0.8602379	cluster 1
HORVU.MOREX.r3.4HG0411270.1	-0.068719	-0.302788	-0.7868665	cluster 1
HORVU.MOREX.r3.4HG0411960.1	-0.132768	-0.383825	-0.9173044	cluster 1
HORVU.MOREX.r3.4HG0412030.1	-0.281051	-0.529297	-0.6222541	cluster 1
HORVU.MOREX.r3.4HG0413410.1	-0.250306	-0.462422	-0.9673097	cluster 1
HORVU.MOREX.r3.4HG0414200.1	-0.271174	-0.380106	-0.4905726	cluster 1
HORVU.MOREX.r3.4HG0415030.1	-0.064407	-0.158585	-0.3011072	cluster 1
HORVU.MOREX.r3.4HG0415230.1	-0.28607	-0.668266	-0.905844	cluster 1
HORVU.MOREX.r3.4HG0415420.1	-0.160822	-0.713833	-0.9823515	cluster 1
HORVU.MOREX.r3.4HG0415590.1	-0.783516	-1.435547	-1.6041733	cluster 1
HORVU.MOREX.r3.4HG0415600.1	-0.017555	-0.740146	-1.6847485	cluster 1

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.4HG0415720.1	-0.053527	-0.432013	-0.7108292	cluster 1
HORVU.MOREX.r3.4HG0416070.1	0.2637421	-0.505991	-2.1461068	cluster 1
HORVU.MOREX.r3.4HG0416220.1	-0.103926	-0.224476	-0.3157687	cluster 1
HORVU.MOREX.r3.4HG0416730.1	-0.125933	-0.512197	-0.8084348	cluster 1
HORVU.MOREX.r3.4HG0417410.1	-0.574144	-0.849607	-1.6895623	cluster 1
HORVU.MOREX.r3.4HG0418530.1	-0.501548	-0.635461	-1.4742094	cluster 1
HORVU.MOREX.r3.4HG0418640.1	-0.145755	-0.152818	-0.6914223	cluster 1
HORVU.MOREX.r3.4HG0418690.1	-0.154026	-0.403809	-1.1884371	cluster 1
HORVU.MOREX.r3.5HG0420150.1	-0.08752	-0.262195	-0.4410016	cluster 1
HORVU.MOREX.r3.5HG0420210.1	-0.024909	-0.213441	-0.3332005	cluster 1
HORVU.MOREX.r3.5HG0421460.1	-0.082273	-0.165365	-0.6818786	cluster 1
HORVU.MOREX.r3.5HG0422490.1	-0.04789	-0.07745	-0.4138775	cluster 1
HORVU.MOREX.r3.5HG0425680.1	-0.214913	-0.338977	-0.4555909	cluster 1
HORVU.MOREX.r3.5HG0426060.1	-0.227911	-0.457938	-0.6257845	cluster 1
HORVU.MOREX.r3.5HG0426480.1	-0.233434	-0.287119	-1.1734032	cluster 1
HORVU.MOREX.r3.5HG0427060.1	-0.258452	-0.332426	-0.8713509	cluster 1
HORVU.MOREX.r3.5HG0427370.1	-0.144446	-0.428781	-0.8348413	cluster 1
HORVU.MOREX.r3.5HG0428840.1	-0.133444	-0.36841	-0.7318554	cluster 1
HORVU.MOREX.r3.5HG0429230.1	-0.165596	-0.349302	-0.49938	cluster 1
HORVU.MOREX.r3.5HG0429930.1	-0.32797	-0.512412	-1.0588528	cluster 1
HORVU.MOREX.r3.5HG0432040.1	-0.155799	-0.559888	-0.6315268	cluster 1
HORVU.MOREX.r3.5HG0432640.1	-0.108819	-0.295572	-0.3894179	cluster 1
HORVU.MOREX.r3.5HG0433490.1	-0.208955	-0.266373	-0.5034093	cluster 1
HORVU.MOREX.r3.5HG0433570.1	-0.169745	-0.222535	-0.580701	cluster 1
HORVU.MOREX.r3.5HG0435800.1	-0.454926	-0.95736	-2.0966367	cluster 1
HORVU.MOREX.r3.5HG0437610.1	-0.002842	-0.178124	-0.8276831	cluster 1
HORVU.MOREX.r3.5HG0438160.1	-0.17195	-0.256853	-0.5415301	cluster 1
HORVU.MOREX.r3.5HG0438750.1	0.1583185	-0.493062	-0.7283115	cluster 1
HORVU.MOREX.r3.5HG0444060.1	-0.302357	-0.885659	-1.0841803	cluster 1
HORVU.MOREX.r3.5HG0444860.1	-0.163494	-0.706663	-1.3650608	cluster 1
HORVU.MOREX.r3.5HG0445020.1	-0.123422	-0.358476	-0.5302803	cluster 1
HORVU.MOREX.r3.5HG0446210.1	-0.199827	-0.464107	-1.069582	cluster 1
HORVU.MOREX.r3.5HG0446330.1	-0.138583	-0.513316	-0.7147087	cluster 1
HORVU.MOREX.r3.5HG0446350.1	-0.080374	-0.25548	-0.3615626	cluster 1
HORVU.MOREX.r3.5HG0447720.1	-0.162886	-0.362749	-0.6370921	cluster 1
HORVU.MOREX.r3.5HG0450100.1	-0.104976	-0.296985	-0.5261148	cluster 1
HORVU.MOREX.r3.5HG0450470.1	-0.054589	-0.220525	-0.5590352	cluster 1
HORVU.MOREX.r3.5HG0454860.1	-0.187892	-0.338099	-0.4102621	cluster 1
HORVU.MOREX.r3.5HG0456510.1	-0.069159	-0.343121	-0.4460837	cluster 1
HORVU.MOREX.r3.5HG0459270.1	-0.173339	-0.479544	-0.8485506	cluster 1
HORVU.MOREX.r3.5HG0459660.1	-0.07731	-0.354216	-0.7815851	cluster 1
HORVU.MOREX.r3.5HG0459680.1	-0.096768	-0.183233	-0.3843765	cluster 1
HORVU.MOREX.r3.5HG0460720.1	-0.076616	-0.281629	-0.5017231	cluster 1
HORVU.MOREX.r3.5HG0461170.1	-0.112985	-0.327771	-0.6830765	cluster 1
HORVU.MOREX.r3.5HG0461400.1	-0.038045	-0.537371	-1.3010497	cluster 1
HORVU.MOREX.r3.5HG0461830.1	-0.0853	-0.238625	-1.4149577	cluster 1
HORVU.MOREX.r3.5HG0462380.1	-0.288473	-0.377294	-0.6342317	cluster 1

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.5HG0462780.1	-0.17759	-0.349005	-0.4036322	cluster 1
HORVU.MOREX.r3.5HG0463350.1	-0.145433	-0.734358	-1.6339683	cluster 1
HORVU.MOREX.r3.5HG0463760.1	-0.105654	-0.49392	-0.747709	cluster 1
HORVU.MOREX.r3.5HG0465260.1	-0.376562	-0.632548	-0.7770126	cluster 1
HORVU.MOREX.r3.5HG0465520.1	-0.370998	-0.475167	-1.8639912	cluster 1
HORVU.MOREX.r3.5HG0466010.1	-0.122164	-0.225025	-0.6696366	cluster 1
HORVU.MOREX.r3.5HG0466190.1	-0.191196	-0.255447	-0.7094792	cluster 1
HORVU.MOREX.r3.5HG0466890.1	-0.021693	-0.466145	-0.5776881	cluster 1
HORVU.MOREX.r3.5HG0467370.1	-0.203793	-0.481914	-0.7575021	cluster 1
HORVU.MOREX.r3.5HG0467880.1	-0.003148	-0.172388	-0.4598904	cluster 1
HORVU.MOREX.r3.5HG0467950.1	-0.31389	-0.419203	-0.4777401	cluster 1
HORVU.MOREX.r3.5HG0468460.1	-0.127443	-0.361307	-0.6000874	cluster 1
HORVU.MOREX.r3.5HG0468940.1	-0.129469	-0.144926	-0.3201336	cluster 1
HORVU.MOREX.r3.5HG0470030.1	-0.158427	-0.404541	-0.4953998	cluster 1
HORVU.MOREX.r3.5HG0470170.1	-0.19311	-0.526318	-0.592036	cluster 1
HORVU.MOREX.r3.5HG0470800.1	0.7275915	-0.374609	-2.1821604	cluster 1
HORVU.MOREX.r3.5HG0471790.1	-0.110304	-0.331141	-0.4559165	cluster 1
HORVU.MOREX.r3.5HG0471960.1	-0.004208	-0.429914	-1.2011233	cluster 1
HORVU.MOREX.r3.5HG0472880.1	-0.172909	-0.281933	-0.5088918	cluster 1
HORVU.MOREX.r3.5HG0473920.1	-0.375461	-0.461909	-0.4836124	cluster 1
HORVU.MOREX.r3.5HG0475250.1	-0.085014	-0.261249	-0.6964655	cluster 1
HORVU.MOREX.r3.5HG0476000.1	-0.110004	-0.266129	-0.3452014	cluster 1
HORVU.MOREX.r3.5HG0476330.1	-0.048948	-0.331058	-0.3746148	cluster 1
HORVU.MOREX.r3.5HG0476380.1	-0.137002	-0.347556	-0.6614743	cluster 1
HORVU.MOREX.r3.5HG0476460.1	0.1319611	-0.182961	-0.7597641	cluster 1
HORVU.MOREX.r3.5HG0477040.1	-0.158882	-0.408917	-0.6574259	cluster 1
HORVU.MOREX.r3.5HG0477180.1	-0.175929	-0.389786	-0.5789351	cluster 1
HORVU.MOREX.r3.5HG0477360.1	-0.039631	-0.499111	-0.6815793	cluster 1
HORVU.MOREX.r3.5HG0478390.1	-0.118401	-0.269869	-0.4779025	cluster 1
HORVU.MOREX.r3.5HG0478450.1	-0.192386	-0.388657	-0.417434	cluster 1
HORVU.MOREX.r3.5HG0479210.1	-0.188358	-0.52051	-1.0162223	cluster 1
HORVU.MOREX.r3.5HG0479970.1	-0.120583	-0.254801	-0.3904151	cluster 1
HORVU.MOREX.r3.5HG0480540.1	-0.041509	-0.232904	-0.3684535	cluster 1
HORVU.MOREX.r3.5HG0481440.1	-0.181333	-0.21774	-0.4766231	cluster 1
HORVU.MOREX.r3.5HG0482360.1	0.0745564	-0.46641	-0.7843659	cluster 1
HORVU.MOREX.r3.5HG0482590.1	-0.132298	-0.559607	-0.9263454	cluster 1
HORVU.MOREX.r3.5HG0485220.1	-0.199026	-0.507254	-0.6075654	cluster 1
HORVU.MOREX.r3.5HG0485800.1	-0.18989	-0.417902	-0.5032049	cluster 1
HORVU.MOREX.r3.5HG0485860.1	-0.257651	-0.48557	-0.6617041	cluster 1
HORVU.MOREX.r3.5HG0486070.1	-0.144918	-0.271329	-0.6475072	cluster 1
HORVU.MOREX.r3.5HG0486330.1	-0.048573	-0.135892	-0.3159013	cluster 1
HORVU.MOREX.r3.5HG0487040.1	0.0566432	-0.267227	-0.4943747	cluster 1
HORVU.MOREX.r3.5HG0487640.1	-0.093607	-0.641279	-1.0407351	cluster 1
HORVU.MOREX.r3.5HG0487660.1	-0.217624	-0.633378	-1.0582883	cluster 1
HORVU.MOREX.r3.5HG0489130.1	-0.110733	-0.543887	-1.382232	cluster 1
HORVU.MOREX.r3.5HG0490720.1	-1.79272	-2.350369	-3.9447452	cluster 1
HORVU.MOREX.r3.5HG0490810.1	-0.05943	-0.197519	-0.2634756	cluster 1

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.5HG0490830.1	-0.085344	-0.146106	-0.4166418	cluster 1
HORVU.MOREX.r3.5HG0491380.1	-0.110673	-0.478207	-0.5388866	cluster 1
HORVU.MOREX.r3.5HG0491750.1	-0.092746	-0.230883	-0.3124519	cluster 1
HORVU.MOREX.r3.5HG0492650.1	-0.022488	-0.27686	-1.0364724	cluster 1
HORVU.MOREX.r3.5HG0493070.1	-0.122015	-0.35629	-0.4342602	cluster 1
HORVU.MOREX.r3.5HG0493850.1	-0.088564	-0.256549	-0.5279151	cluster 1
HORVU.MOREX.r3.5HG0494320.1	-0.056222	-0.100717	-0.4393089	cluster 1
HORVU.MOREX.r3.5HG0494470.1	0.0229095	-0.116089	-0.521104	cluster 1
HORVU.MOREX.r3.5HG0495580.1	-0.079477	-0.164793	-0.3147977	cluster 1
HORVU.MOREX.r3.5HG0495790.1	-0.160887	-0.419527	-0.6347201	cluster 1
HORVU.MOREX.r3.5HG0495840.1	0.0035152	-0.287856	-0.3910271	cluster 1
HORVU.MOREX.r3.5HG0496220.1	-0.156064	-0.454739	-1.1960839	cluster 1
HORVU.MOREX.r3.5HG0497360.1	0.0601987	-0.140292	-0.5607761	cluster 1
HORVU.MOREX.r3.5HG0497940.1	-0.485998	-0.791284	-1.2613961	cluster 1
HORVU.MOREX.r3.5HG0498150.1	-0.159561	-0.646318	-1.2856173	cluster 1
HORVU.MOREX.r3.5HG0498770.1	-0.109113	-0.340288	-0.4100756	cluster 1
HORVU.MOREX.r3.5HG0499000.1	2.3647132	2.1218982	1.50728133	cluster 1
HORVU.MOREX.r3.5HG0499490.1	-0.108544	-0.144045	-0.2847346	cluster 1
HORVU.MOREX.r3.5HG0499620.1	-0.101615	-0.383001	-0.5351115	cluster 1
HORVU.MOREX.r3.5HG0500220.1	-0.158601	-0.282739	-0.3162118	cluster 1
HORVU.MOREX.r3.5HG0500560.2	-0.22635	-0.882928	-1.0044721	cluster 1
HORVU.MOREX.r3.5HG0500680.1	-0.150547	-0.390053	-0.6810883	cluster 1
HORVU.MOREX.r3.5HG0500730.1	-0.085445	-0.376971	-0.6680202	cluster 1
HORVU.MOREX.r3.5HG0501120.1	-0.129259	-0.26871	-0.3221837	cluster 1
HORVU.MOREX.r3.5HG0501200.1	-0.225379	-0.490892	-0.5402406	cluster 1
HORVU.MOREX.r3.5HG0501270.1	-0.137922	-0.52833	-1.4076696	cluster 1
HORVU.MOREX.r3.5HG0501980.1	-0.183212	-0.353262	-0.4485465	cluster 1
HORVU.MOREX.r3.5HG0502130.1	-0.147955	-0.391233	-0.7761111	cluster 1
HORVU.MOREX.r3.5HG0502310.1	-0.196656	-0.635931	-0.710535	cluster 1
HORVU.MOREX.r3.5HG0502750.1	-0.096127	-0.372251	-0.9094411	cluster 1
HORVU.MOREX.r3.5HG0502760.1	-0.073732	-0.303695	-0.7464793	cluster 1
HORVU.MOREX.r3.5HG0503950.1	-0.133301	-0.365726	-0.4823158	cluster 1
HORVU.MOREX.r3.5HG0504160.1	-0.105746	-0.314844	-1.0721874	cluster 1
HORVU.MOREX.r3.5HG0504250.1	-0.160806	-0.363591	-0.7365398	cluster 1
HORVU.MOREX.r3.5HG0504670.1	-0.456707	-0.632888	-1.3021566	cluster 1
HORVU.MOREX.r3.5HG0504710.1	-0.114832	-0.211946	-0.3962978	cluster 1
HORVU.MOREX.r3.5HG0504800.1	-0.035177	-0.484558	-0.8134552	cluster 1
HORVU.MOREX.r3.5HG0505100.1	-0.138924	-0.330778	-0.3960939	cluster 1
HORVU.MOREX.r3.5HG0508190.1	-0.186162	-0.390828	-0.7119832	cluster 1
HORVU.MOREX.r3.5HG0510060.1	-0.075469	-0.256016	-0.6564189	cluster 1
HORVU.MOREX.r3.5HG0510590.4	-0.243129	-0.756586	-1.47342	cluster 1
HORVU.MOREX.r3.5HG0510920.1	-0.127388	-0.308239	-0.389345	cluster 1
HORVU.MOREX.r3.5HG0510940.1	-0.213918	-0.568567	-1.4615132	cluster 1
HORVU.MOREX.r3.5HG0511860.1	-0.148252	-0.435656	-0.9293757	cluster 1
HORVU.MOREX.r3.5HG0511930.1	0.2269265	-0.67185	-0.8945959	cluster 1
HORVU.MOREX.r3.5HG0512320.1	-0.305306	-0.546114	-0.7498745	cluster 1
HORVU.MOREX.r3.5HG0512510.1	-0.065184	-0.157201	-0.6098173	cluster 1

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.5HG0513020.1	-0.093005	-0.267105	-0.3339665	cluster 1
HORVU.MOREX.r3.5HG0513120.1	-0.046063	-0.087371	-0.3134437	cluster 1
HORVU.MOREX.r3.5HG0513440.1	-0.058705	-0.314961	-0.4091539	cluster 1
HORVU.MOREX.r3.5HG0514100.1	-0.060005	-0.287394	-0.6292722	cluster 1
HORVU.MOREX.r3.5HG0514110.1	-0.103543	-0.3816	-0.6477007	cluster 1
HORVU.MOREX.r3.5HG0514490.1	-0.135669	-0.310424	-0.505075	cluster 1
HORVU.MOREX.r3.5HG0514790.1	-0.093666	-0.242443	-0.4029237	cluster 1
HORVU.MOREX.r3.5HG0514790.3	-0.117309	-0.296945	-0.4752577	cluster 1
HORVU.MOREX.r3.5HG0514950.1	-0.004511	-0.196927	-0.5784034	cluster 1
HORVU.MOREX.r3.5HG0515370.1	-0.147268	-0.364991	-0.502435	cluster 1
HORVU.MOREX.r3.5HG0516310.1	-0.144465	-0.345284	-0.978312	cluster 1
HORVU.MOREX.r3.5HG0516470.1	-0.389694	-0.863386	-1.4075846	cluster 1
HORVU.MOREX.r3.5HG0516490.2	-0.067545	-0.173028	-0.5224994	cluster 1
HORVU.MOREX.r3.5HG0516720.1	-0.099159	-0.577595	-1.8266352	cluster 1
HORVU.MOREX.r3.5HG0517640.1	-0.334622	-0.684101	-0.9409454	cluster 1
HORVU.MOREX.r3.5HG0518490.1	-0.270225	-0.558026	-0.8727459	cluster 1
HORVU.MOREX.r3.5HG0519240.1	-0.250013	-0.536071	-0.580351	cluster 1
HORVU.MOREX.r3.5HG0519810.1	-0.082753	-0.391947	-0.5518064	cluster 1
HORVU.MOREX.r3.5HG0520260.1	-0.783208	-0.855478	-2.4668028	cluster 1
HORVU.MOREX.r3.5HG0520670.1	-0.796169	-1.034934	-1.3849627	cluster 1
HORVU.MOREX.r3.5HG0521030.1	-0.043173	-0.386634	-0.6036831	cluster 1
HORVU.MOREX.r3.5HG0522060.1	-0.164633	-0.433521	-0.803681	cluster 1
HORVU.MOREX.r3.5HG0523150.1	0.0351798	-0.138438	-0.2523233	cluster 1
HORVU.MOREX.r3.5HG0523560.1	-0.170678	-0.490673	-0.8705797	cluster 1
HORVU.MOREX.r3.5HG0524010.1	-0.550485	-0.70662	-1.3107967	cluster 1
HORVU.MOREX.r3.5HG0524800.1	-0.262463	-1.372057	-1.6252392	cluster 1
HORVU.MOREX.r3.5HG0525020.1	-0.122096	-0.244444	-0.8031354	cluster 1
HORVU.MOREX.r3.5HG0525440.1	-0.07228	-0.247331	-0.3727253	cluster 1
HORVU.MOREX.r3.5HG0525560.1	0.0536787	-0.219266	-0.5084243	cluster 1
HORVU.MOREX.r3.5HG0525980.1	-0.083957	-0.287406	-0.4414487	cluster 1
HORVU.MOREX.r3.5HG0526250.1	-0.090948	-0.205844	-0.3253673	cluster 1
HORVU.MOREX.r3.5HG0526940.1	-0.133589	-0.278363	-0.3609518	cluster 1
HORVU.MOREX.r3.5HG0527650.1	-0.20443	-0.486414	-0.6945739	cluster 1
HORVU.MOREX.r3.5HG0527670.1	-0.046059	-0.61131	-1.9486555	cluster 1
HORVU.MOREX.r3.5HG0528340.1	-0.308398	-0.659851	-0.9797436	cluster 1
HORVU.MOREX.r3.5HG0528520.1	-0.182602	-0.378013	-0.5191138	cluster 1
HORVU.MOREX.r3.5HG0528890.1	-0.119078	-0.275562	-1.0161001	cluster 1
HORVU.MOREX.r3.5HG0529120.1	-0.06845	-0.364191	-0.7132555	cluster 1
HORVU.MOREX.r3.5HG0529130.1	-0.176822	-0.293857	-0.5865178	cluster 1
HORVU.MOREX.r3.5HG0529500.1	-0.112009	-0.318854	-0.3493907	cluster 1
HORVU.MOREX.r3.5HG0530750.1	-0.121243	-0.341036	-0.4972007	cluster 1
HORVU.MOREX.r3.5HG0531850.1	-0.100767	-0.366563	-0.6401909	cluster 1
HORVU.MOREX.r3.5HG0532150.1	2.5233464	2.4596495	2.12318072	cluster 1
HORVU.MOREX.r3.5HG0532630.1	-0.217936	-0.480784	-1.2750969	cluster 1
HORVU.MOREX.r3.5HG0532960.1	-0.212279	-0.407444	-0.5507634	cluster 1
HORVU.MOREX.r3.5HG0533630.1	-0.067051	-0.725516	-1.444453	cluster 1
HORVU.MOREX.r3.5HG0533660.1	-0.082845	-0.246383	-0.593649	cluster 1

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.5HG0534340.1	-0.104357	-0.563631	-1.0525089	cluster 1
HORVU.MOREX.r3.5HG0534520.1	-1.050897	-1.098633	-2.3077461	cluster 1
HORVU.MOREX.r3.5HG0534640.1	-0.089248	-0.196648	-0.5192665	cluster 1
HORVU.MOREX.r3.5HG0536490.1	-0.341643	-0.644494	-1.5120693	cluster 1
HORVU.MOREX.r3.5HG0536710.1	-0.108267	-0.251241	-0.4415964	cluster 1
HORVU.MOREX.r3.5HG0536900.1	-0.388373	-0.497828	-1.4737137	cluster 1
HORVU.MOREX.r3.6HG0539200.1	-0.159588	-0.178725	-0.3625018	cluster 1
HORVU.MOREX.r3.6HG0539460.1	-0.067962	-0.229186	-0.3163651	cluster 1
HORVU.MOREX.r3.6HG0539990.1	0.0096768	-0.163307	-0.3417815	cluster 1
HORVU.MOREX.r3.6HG0540280.1	-0.139952	-0.387102	-0.8325777	cluster 1
HORVU.MOREX.r3.6HG0540620.1	-0.209532	-0.711663	-1.5389765	cluster 1
HORVU.MOREX.r3.6HG0541250.1	-0.040144	-0.209566	-0.2505157	cluster 1
HORVU.MOREX.r3.6HG0541940.1	-0.124719	-0.45334	-0.5346758	cluster 1
HORVU.MOREX.r3.6HG0542970.1	-0.081606	-0.481892	-1.0953234	cluster 1
HORVU.MOREX.r3.6HG0543250.1	-0.160758	-0.516459	-0.7937058	cluster 1
HORVU.MOREX.r3.6HG0543320.1	-0.075517	-0.601413	-0.6855234	cluster 1
HORVU.MOREX.r3.6HG0543400.1	1.7121169	1.3278864	1.26388651	cluster 1
HORVU.MOREX.r3.6HG0543720.1	0.012743	-0.459471	-0.9085489	cluster 1
HORVU.MOREX.r3.6HG0543730.1	-0.183019	-0.57209	-0.8529852	cluster 1
HORVU.MOREX.r3.6HG0543740.1	-0.206847	-0.547469	-0.9817973	cluster 1
HORVU.MOREX.r3.6HG0543750.1	-0.178295	-0.475736	-0.8004844	cluster 1
HORVU.MOREX.r3.6HG0543770.1	-0.191993	-0.537121	-0.9086951	cluster 1
HORVU.MOREX.r3.6HG0543780.1	-0.223047	-0.625823	-0.9423179	cluster 1
HORVU.MOREX.r3.6HG0543790.1	-0.136678	-0.433918	-1.0669179	cluster 1
HORVU.MOREX.r3.6HG0543800.1	-0.253389	-0.577924	-0.9281217	cluster 1
HORVU.MOREX.r3.6HG0545620.1	-0.18558	-0.379591	-0.5578175	cluster 1
HORVU.MOREX.r3.6HG0545630.1	-0.042163	-0.383086	-1.4940692	cluster 1
HORVU.MOREX.r3.6HG0545970.1	-0.120034	-0.360244	-0.4801082	cluster 1
HORVU.MOREX.r3.6HG0546180.1	-0.141295	-0.541487	-0.7092508	cluster 1
HORVU.MOREX.r3.6HG0546200.1	-1.75E-05	-0.291992	-0.558433	cluster 1
HORVU.MOREX.r3.6HG0547550.1	0.0503365	-0.264659	-0.3602582	cluster 1
HORVU.MOREX.r3.6HG0547970.1	-0.241155	-0.71596	-0.9269406	cluster 1
HORVU.MOREX.r3.6HG0548460.1	-0.07358	-0.491766	-1.1085409	cluster 1
HORVU.MOREX.r3.6HG0548670.1	-0.193966	-0.658034	-1.1623691	cluster 1
HORVU.MOREX.r3.6HG0548820.1	-0.658338	-1.080766	-1.2353357	cluster 1
HORVU.MOREX.r3.6HG0549510.1	-0.106393	-0.212633	-0.6713129	cluster 1
HORVU.MOREX.r3.6HG0549830.1	0.0703942	-0.295495	-0.7422728	cluster 1
HORVU.MOREX.r3.6HG0550670.1	-0.060651	-0.756972	-1.8102906	cluster 1
HORVU.MOREX.r3.6HG0550690.1	-0.050241	-0.533345	-1.0214195	cluster 1
HORVU.MOREX.r3.6HG0550700.1	-0.496152	-0.648986	-2.2968634	cluster 1
HORVU.MOREX.r3.6HG0550740.1	0.037321	-0.417627	-0.5001768	cluster 1
HORVU.MOREX.r3.6HG0550950.1	-0.095569	-0.232834	-0.486758	cluster 1
HORVU.MOREX.r3.6HG0551740.1	-0.053592	-0.394004	-0.7025778	cluster 1
HORVU.MOREX.r3.6HG0552030.1	-0.191493	-0.32119	-0.7303511	cluster 1
HORVU.MOREX.r3.6HG0552720.1	-0.167026	-0.358805	-0.4105796	cluster 1
HORVU.MOREX.r3.6HG0552800.1	-0.215235	-0.622583	-1.1339797	cluster 1
HORVU.MOREX.r3.6HG0552860.1	-0.305328	-0.591965	-1.3249857	cluster 1

Table Sn Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.6HG0553290.1	-0.083877	-0.305043	-0.6079216	cluster 1
HORVU.MOREX.r3.6HG0554520.1	-0.199605	-0.331028	-0.9874885	cluster 1
HORVU.MOREX.r3.6HG0554560.1	0.1963069	-0.038654	-1.0063706	cluster 1
HORVU.MOREX.r3.6HG0554790.1	-0.096292	-0.233471	-0.3005031	cluster 1
HORVU.MOREX.r3.6HG0555500.1	-0.175097	-0.461786	-0.618865	cluster 1
HORVU.MOREX.r3.6HG0555700.1	-0.196569	-0.369213	-0.5635567	cluster 1
HORVU.MOREX.r3.6HG0557140.1	-0.045645	-0.343177	-0.6447453	cluster 1
HORVU.MOREX.r3.6HG0557340.1	-0.153551	-0.382255	-0.4724565	cluster 1
HORVU.MOREX.r3.6HG0558330.1	0.028089	-0.409693	-1.1625206	cluster 1
HORVU.MOREX.r3.6HG0558800.1	-0.152338	-0.350004	-0.6439828	cluster 1
HORVU.MOREX.r3.6HG0558810.1	-0.229006	-0.541518	-0.9661162	cluster 1
HORVU.MOREX.r3.6HG0558840.1	-0.085703	-0.262509	-0.291443	cluster 1
HORVU.MOREX.r3.6HG0558880.1	-0.114661	-0.373337	-1.2919911	cluster 1
HORVU.MOREX.r3.6HG0559000.1	-0.268953	-0.393251	-0.4307431	cluster 1
HORVU.MOREX.r3.6HG0560290.1	0.4472467	-0.113597	-2.4548625	cluster 1
HORVU.MOREX.r3.6HG0564510.1	0.0114972	-0.190698	-0.9187131	cluster 1
HORVU.MOREX.r3.6HG0564590.1	-0.056744	-0.331409	-0.4869545	cluster 1
HORVU.MOREX.r3.6HG0567330.1	-0.12387	-0.448646	-1.2531021	cluster 1
HORVU.MOREX.r3.6HG0568870.1	-0.045602	-0.465213	-0.7951865	cluster 1
HORVU.MOREX.r3.6HG0568880.1	-0.138397	-0.584181	-1.2644704	cluster 1
HORVU.MOREX.r3.6HG0568900.1	-0.195344	-0.578485	-1.1186505	cluster 1
HORVU.MOREX.r3.6HG0569490.1	-0.152879	-0.280017	-0.4448282	cluster 1
HORVU.MOREX.r3.6HG0570960.1	-0.198814	-0.605972	-1.1964963	cluster 1
HORVU.MOREX.r3.6HG0572960.1	-0.448195	-1.037814	-1.5756738	cluster 1
HORVU.MOREX.r3.6HG0573340.1	-0.177053	-0.32049	-0.3835374	cluster 1
HORVU.MOREX.r3.6HG0573850.1	-0.135246	-0.202562	-0.3285277	cluster 1
HORVU.MOREX.r3.6HG0573870.1	-0.015555	-0.181699	-0.6436575	cluster 1
HORVU.MOREX.r3.6HG0574510.1	0.3521514	-0.237465	-1.5347521	cluster 1
HORVU.MOREX.r3.6HG0575410.1	-0.432236	-0.868028	-2.0557757	cluster 1
HORVU.MOREX.r3.6HG0575690.1	-0.119582	-0.625271	-0.8532731	cluster 1
HORVU.MOREX.r3.6HG0576550.1	-0.195785	-0.545986	-0.7001287	cluster 1
HORVU.MOREX.r3.6HG0577170.1	-0.174211	-0.932948	-1.7329456	cluster 1
HORVU.MOREX.r3.6HG0581010.1	-0.270151	-0.447324	-0.7952286	cluster 1
HORVU.MOREX.r3.6HG0581020.1	-0.084033	-0.329945	-0.3831694	cluster 1
HORVU.MOREX.r3.6HG0582230.1	0.0804078	-0.168859	-0.5132912	cluster 1
HORVU.MOREX.r3.6HG0583020.1	-0.110065	-0.240644	-0.3798351	cluster 1
HORVU.MOREX.r3.6HG0584860.1	0.0155137	-0.305834	-0.4916906	cluster 1
HORVU.MOREX.r3.6HG0585520.2	-0.187737	-0.376382	-0.5409994	cluster 1
HORVU.MOREX.r3.6HG0586290.1	-0.445832	-0.580732	-0.8778517	cluster 1
HORVU.MOREX.r3.6HG0586850.1	-0.274042	-0.844347	-1.267564	cluster 1
HORVU.MOREX.r3.6HG0587140.1	-0.201252	-0.413123	-0.7067387	cluster 1
HORVU.MOREX.r3.6HG0587790.1	-0.652999	-0.998668	-1.5951561	cluster 1
HORVU.MOREX.r3.6HG0588350.1	-0.273513	-0.499329	-0.7133528	cluster 1
HORVU.MOREX.r3.6HG0590430.1	-0.172371	-0.302229	-0.4119242	cluster 1
HORVU.MOREX.r3.6HG0593200.1	-0.216678	-0.871244	-1.0180012	cluster 1
HORVU.MOREX.r3.6HG0594420.1	0.0266503	-0.0987	-0.3955817	cluster 1
HORVU.MOREX.r3.6HG0595810.1	-0.27463	-0.33438	-0.9261727	cluster 1

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.6HG0595860.1	-0.048797	-0.30248	-0.4568244	cluster 1
HORVU.MOREX.r3.6HG0596460.1	-0.127101	-0.208021	-0.4154092	cluster 1
HORVU.MOREX.r3.6HG0597320.1	-0.148617	-0.287288	-0.3111842	cluster 1
HORVU.MOREX.r3.6HG0597360.1	-0.103421	-0.228069	-0.5113958	cluster 1
HORVU.MOREX.r3.6HG0597590.1	-0.162113	-0.407571	-0.5068844	cluster 1
HORVU.MOREX.r3.6HG0597620.1	-0.092541	-0.381399	-0.4709729	cluster 1
HORVU.MOREX.r3.6HG0597770.1	-0.169845	-0.460768	-0.5070072	cluster 1
HORVU.MOREX.r3.6HG0600500.1	-0.196866	-0.518997	-0.8637638	cluster 1
HORVU.MOREX.r3.6HG0601560.1	-0.863825	-1.01753	-1.1885003	cluster 1
HORVU.MOREX.r3.6HG0601690.1	-0.185185	-0.326747	-0.4785737	cluster 1
HORVU.MOREX.r3.6HG0602290.1	-0.12907	-0.217141	-0.3294031	cluster 1
HORVU.MOREX.r3.6HG0603410.1	-0.109436	-0.462683	-0.7603923	cluster 1
HORVU.MOREX.r3.6HG0603530.1	0.0002071	-0.595904	-1.0911653	cluster 1
HORVU.MOREX.r3.6HG0603820.1	-0.074595	-0.162005	-0.247231	cluster 1
HORVU.MOREX.r3.6HG0604200.1	-0.003365	-1.00506	-1.3983131	cluster 1
HORVU.MOREX.r3.6HG0604620.1	-0.15296	-0.557243	-1.3441761	cluster 1
HORVU.MOREX.r3.6HG0604810.1	-0.064523	-0.298405	-0.3343238	cluster 1
HORVU.MOREX.r3.6HG0604860.1	-0.627473	-0.819276	-1.0953738	cluster 1
HORVU.MOREX.r3.6HG0605290.1	-0.387361	-0.473305	-0.6542963	cluster 1
HORVU.MOREX.r3.6HG0607000.1	-0.505787	-0.9256	-1.7327798	cluster 1
HORVU.MOREX.r3.6HG0607360.1	-0.135846	-0.555846	-0.7976135	cluster 1
HORVU.MOREX.r3.6HG0608780.1	-0.217584	-0.416974	-0.6072037	cluster 1
HORVU.MOREX.r3.6HG0608800.1	-0.127509	-0.309221	-0.5685331	cluster 1
HORVU.MOREX.r3.6HG0609100.1	-0.46752	-0.593136	-1.1145585	cluster 1
HORVU.MOREX.r3.6HG0609520.1	-0.131174	-0.468917	-0.8377816	cluster 1
HORVU.MOREX.r3.6HG0609560.1	-0.368463	-0.639049	-1.1261645	cluster 1
HORVU.MOREX.r3.6HG0609720.1	-0.180461	-0.704473	-0.8075552	cluster 1
HORVU.MOREX.r3.6HG0609750.1	-0.037484	-0.161733	-0.5140055	cluster 1
HORVU.MOREX.r3.6HG0610700.1	-0.012566	-0.607274	-0.906836	cluster 1
HORVU.MOREX.r3.6HG0611060.1	-0.113073	-0.315331	-0.4070372	cluster 1
HORVU.MOREX.r3.6HG0611290.1	-0.157683	-0.226004	-0.8512012	cluster 1
HORVU.MOREX.r3.6HG0611300.1	0.0457688	-0.263475	-0.9823054	cluster 1
HORVU.MOREX.r3.6HG0612070.1	-0.152228	-0.434324	-0.525986	cluster 1
HORVU.MOREX.r3.6HG0612180.1	0.0134935	-0.479933	-0.8275732	cluster 1
HORVU.MOREX.r3.6HG0612250.1	-0.045218	-0.131449	-0.3811627	cluster 1
HORVU.MOREX.r3.6HG0613270.1	-0.039291	-0.209214	-0.4492613	cluster 1
HORVU.MOREX.r3.6HG0614350.1	-0.062384	-0.239571	-0.5243657	cluster 1
HORVU.MOREX.r3.6HG0614460.1	-0.21881	-0.333585	-0.7104182	cluster 1
HORVU.MOREX.r3.6HG0614500.1	-0.095265	-0.200484	-0.3856272	cluster 1
HORVU.MOREX.r3.6HG0615710.1	-0.047347	-0.167197	-0.5360668	cluster 1
HORVU.MOREX.r3.6HG0616480.1	-0.141398	-0.255995	-0.6056354	cluster 1
HORVU.MOREX.r3.6HG0616680.1	-0.181669	-0.311575	-1.340675	cluster 1
HORVU.MOREX.r3.6HG0616710.1	-0.195746	-0.650215	-0.9854517	cluster 1
HORVU.MOREX.r3.6HG0616790.1	-0.203734	-0.365348	-0.5905028	cluster 1
HORVU.MOREX.r3.6HG0616960.1	-0.134653	-0.199891	-0.6141932	cluster 1
HORVU.MOREX.r3.6HG0617860.1	-0.144798	-0.186554	-0.2982219	cluster 1
HORVU.MOREX.r3.6HG0618100.1	-0.050866	-0.45235	-1.8370623	cluster 1

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.6HG0618110.1	-0.053755	-0.344908	-0.7043801	cluster 1
HORVU.MOREX.r3.6HG0618170.1	0.0039983	-0.17359	-0.2558558	cluster 1
HORVU.MOREX.r3.6HG0618630.1	-0.045632	-0.366512	-0.6031653	cluster 1
HORVU.MOREX.r3.6HG0619260.1	-0.062207	-0.297993	-0.4589042	cluster 1
HORVU.MOREX.r3.6HG0619540.1	0.0365632	-0.146762	-0.351223	cluster 1
HORVU.MOREX.r3.6HG0619760.1	-0.191497	-0.43564	-0.4785616	cluster 1
HORVU.MOREX.r3.6HG0620040.1	-0.569807	-1.12627	-1.2902095	cluster 1
HORVU.MOREX.r3.6HG0620240.1	-0.25637	-0.402508	-0.5072228	cluster 1
HORVU.MOREX.r3.6HG0620650.1	-0.215603	-0.26121	-0.5769564	cluster 1
HORVU.MOREX.r3.6HG0621690.1	-0.084347	-0.435478	-0.7427506	cluster 1
HORVU.MOREX.r3.6HG0622030.1	-0.185696	-0.487685	-0.5847006	cluster 1
HORVU.MOREX.r3.6HG0622300.1	-0.104044	-0.450725	-0.7942567	cluster 1
HORVU.MOREX.r3.6HG0623140.1	2.8931926	2.3679238	1.92254547	cluster 1
HORVU.MOREX.r3.6HG0623830.1	0.1543554	-0.035479	-1.8860509	cluster 1
HORVU.MOREX.r3.6HG0623920.1	-0.030793	-0.091294	-0.2024879	cluster 1
HORVU.MOREX.r3.6HG0624190.1	-0.128871	-0.295866	-0.3309713	cluster 1
HORVU.MOREX.r3.6HG0624580.1	-0.017266	-0.297154	-1.1248018	cluster 1
HORVU.MOREX.r3.6HG0624630.1	-0.092227	-0.307584	-0.4434398	cluster 1
HORVU.MOREX.r3.6HG0624650.1	-0.082536	-0.205596	-0.3545164	cluster 1
HORVU.MOREX.r3.6HG0627570.1	-0.136437	-0.539164	-0.7442745	cluster 1
HORVU.MOREX.r3.6HG0627920.1	-0.118676	-0.285747	-0.3309031	cluster 1
HORVU.MOREX.r3.6HG0628930.1	-0.110921	-0.209581	-0.4994471	cluster 1
HORVU.MOREX.r3.6HG0629220.1	-0.2681	-0.542515	-0.7523083	cluster 1
HORVU.MOREX.r3.6HG0631050.1	-0.020991	-0.183303	-1.1214454	cluster 1
HORVU.MOREX.r3.6HG0631580.1	-0.16739	-0.361011	-0.5723441	cluster 1
HORVU.MOREX.r3.6HG0631760.1	-0.170698	-0.324464	-0.5334179	cluster 1
HORVU.MOREX.r3.6HG0632210.1	0.0810498	-0.101504	-0.5457316	cluster 1
HORVU.MOREX.r3.6HG0632780.1	-0.302065	-0.38065	-0.6571739	cluster 1
HORVU.MOREX.r3.6HG0632980.1	-0.173918	-0.578965	-1.562704	cluster 1
HORVU.MOREX.r3.6HG0633160.1	-0.422387	-0.456114	-0.7772551	cluster 1
HORVU.MOREX.r3.6HG0633420.1	-0.202335	-0.302528	-0.7963007	cluster 1
HORVU.MOREX.r3.6HG0633640.1	-0.102613	-0.174541	-0.2723529	cluster 1
HORVU.MOREX.r3.6HG0634070.1	-0.110411	-0.348775	-0.4293681	cluster 1
HORVU.MOREX.r3.6HG0634260.1	-0.006188	-0.39369	-0.7518639	cluster 1
HORVU.MOREX.r3.7HG0634660.1	-0.22261	-0.431385	-0.5765137	cluster 1
HORVU.MOREX.r3.7HG0634710.1	-0.119864	-0.203271	-0.2281727	cluster 1
HORVU.MOREX.r3.7HG0635320.1	-0.160727	-0.393076	-0.5982559	cluster 1
HORVU.MOREX.r3.7HG0635550.1	-0.229231	-0.302084	-1.2248388	cluster 1
HORVU.MOREX.r3.7HG0635700.1	-0.087885	-0.219946	-0.3338246	cluster 1
HORVU.MOREX.r3.7HG0636510.1	-0.260127	-0.406094	-0.5417717	cluster 1
HORVU.MOREX.r3.7HG0636530.1	-0.094616	-0.222455	-0.3929379	cluster 1
HORVU.MOREX.r3.7HG0636660.1	-0.047626	-0.185569	-0.4099518	cluster 1
HORVU.MOREX.r3.7HG0636750.1	-0.0737	-0.400214	-0.8620779	cluster 1
HORVU.MOREX.r3.7HG0637470.1	-0.113137	-0.363452	-0.4714156	cluster 1
HORVU.MOREX.r3.7HG0637760.1	-0.221907	-0.42383	-0.632365	cluster 1
HORVU.MOREX.r3.7HG0638340.1	1.3564459	1.291694	1.23369918	cluster 1
HORVU.MOREX.r3.7HG0638850.1	-0.140797	-0.424577	-0.5714483	cluster 1

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.7HG0640570.1	-0.039458	-0.201169	-0.4215153	cluster 1
HORVU.MOREX.r3.7HG0641160.1	-0.168173	-0.213976	-0.3799753	cluster 1
HORVU.MOREX.r3.7HG0642550.1	-0.086905	-0.24661	-0.3276198	cluster 1
HORVU.MOREX.r3.7HG0642770.1	-0.045991	-0.270793	-0.3538325	cluster 1
HORVU.MOREX.r3.7HG0643230.1	-0.166227	-0.517072	-0.7595003	cluster 1
HORVU.MOREX.r3.7HG0645350.1	-0.000586	-0.142832	-0.3024828	cluster 1
HORVU.MOREX.r3.7HG0645480.1	-0.233966	-0.319076	-0.5033557	cluster 1
HORVU.MOREX.r3.7HG0647520.1	-0.113709	-0.401838	-0.7704195	cluster 1
HORVU.MOREX.r3.7HG0647550.1	-0.143077	-0.462468	-0.5087458	cluster 1
HORVU.MOREX.r3.7HG0647930.1	-0.307559	-1.095103	-1.3982835	cluster 1
HORVU.MOREX.r3.7HG0648520.1	-0.509666	-0.534049	-1.8678721	cluster 1
HORVU.MOREX.r3.7HG0648600.1	-0.14247	-0.313815	-0.5819736	cluster 1
HORVU.MOREX.r3.7HG0650210.1	-0.066146	-0.34155	-0.4127646	cluster 1
HORVU.MOREX.r3.7HG0650250.1	-0.194615	-0.513916	-0.6299226	cluster 1
HORVU.MOREX.r3.7HG0650970.1	-0.180302	-0.588829	-1.176132	cluster 1
HORVU.MOREX.r3.7HG0650980.1	-0.231316	-0.58227	-0.9585001	cluster 1
HORVU.MOREX.r3.7HG0651010.1	-0.31858	-0.855394	-0.9329356	cluster 1
HORVU.MOREX.r3.7HG0651030.1	-0.095301	-0.188984	-0.2701294	cluster 1
HORVU.MOREX.r3.7HG0651110.1	-0.230318	-0.35594	-0.4334242	cluster 1
HORVU.MOREX.r3.7HG0652830.1	-0.500769	-1.088361	-1.9147495	cluster 1
HORVU.MOREX.r3.7HG0653850.1	-0.206184	-0.42687	-0.6948013	cluster 1
HORVU.MOREX.r3.7HG0654120.1	-0.561266	-0.88787	-1.1985793	cluster 1
HORVU.MOREX.r3.7HG0654410.1	-0.167674	-0.462908	-0.8840223	cluster 1
HORVU.MOREX.r3.7HG0654460.1	-0.135353	-0.501507	-1.0717078	cluster 1
HORVU.MOREX.r3.7HG0654480.1	-0.230905	-0.820741	-1.0693943	cluster 1
HORVU.MOREX.r3.7HG0654510.1	-0.327359	-0.697149	-1.3495929	cluster 1
HORVU.MOREX.r3.7HG0654580.1	-0.197862	-0.512079	-1.5678007	cluster 1
HORVU.MOREX.r3.7HG0654680.1	-0.053544	-0.240875	-0.9333271	cluster 1
HORVU.MOREX.r3.7HG0655180.1	-0.133992	-0.287163	-0.5348613	cluster 1
HORVU.MOREX.r3.7HG0655210.1	1.8347523	1.7303599	1.26129321	cluster 1
HORVU.MOREX.r3.7HG0656250.1	-0.073877	-0.220912	-0.3968207	cluster 1
HORVU.MOREX.r3.7HG0656340.1	-0.274754	-0.984231	-1.9722095	cluster 1
HORVU.MOREX.r3.7HG0656430.1	-0.076029	-0.215066	-0.371474	cluster 1
HORVU.MOREX.r3.7HG0656750.1	-0.117691	-0.419695	-0.7872498	cluster 1
HORVU.MOREX.r3.7HG0657370.1	-0.126133	-0.227293	-0.3276496	cluster 1
HORVU.MOREX.r3.7HG0657400.1	-0.174464	-0.286906	-0.6719245	cluster 1
HORVU.MOREX.r3.7HG0659420.1	-0.110464	-0.608047	-2.5333763	cluster 1
HORVU.MOREX.r3.7HG0660310.1	-0.193217	-0.239191	-0.6410892	cluster 1
HORVU.MOREX.r3.7HG0660660.1	-0.135902	-0.223746	-0.480509	cluster 1
HORVU.MOREX.r3.7HG0660760.1	-0.199956	-0.632249	-1.1535636	cluster 1
HORVU.MOREX.r3.7HG0661060.1	-0.065558	-0.29189	-0.4474257	cluster 1
HORVU.MOREX.r3.7HG0661480.1	-0.125365	-0.295651	-0.3558575	cluster 1
HORVU.MOREX.r3.7HG0661890.1	-0.138678	-0.411495	-0.5739824	cluster 1
HORVU.MOREX.r3.7HG0662160.1	-0.236196	-0.244414	-0.586524	cluster 1
HORVU.MOREX.r3.7HG0662210.1	-0.091926	-0.254713	-0.5790927	cluster 1
HORVU.MOREX.r3.7HG0662220.1	-0.108194	-0.687347	-1.0076766	cluster 1
HORVU.MOREX.r3.7HG0662650.1	-0.182877	-0.712817	-1.0096494	cluster 1

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.7HG0662830.1	-0.106215	-0.123595	-0.9237938	cluster 1
HORVU.MOREX.r3.7HG0663150.1	0.0678366	-0.156122	-0.3919222	cluster 1
HORVU.MOREX.r3.7HG0663180.1	-0.181334	-0.695322	-1.0066708	cluster 1
HORVU.MOREX.r3.7HG0663400.1	-0.024533	-0.114788	-0.2854097	cluster 1
HORVU.MOREX.r3.7HG0663730.1	0.0127606	-0.482258	-1.9576747	cluster 1
HORVU.MOREX.r3.7HG0664130.1	-0.128656	-0.209484	-0.3605416	cluster 1
HORVU.MOREX.r3.7HG0665400.1	-0.202368	-0.303001	-0.7806399	cluster 1
HORVU.MOREX.r3.7HG0665520.1	-0.053235	-0.331659	-0.5399756	cluster 1
HORVU.MOREX.r3.7HG0666340.1	-0.083134	-0.440476	-0.6611363	cluster 1
HORVU.MOREX.r3.7HG0667280.1	-0.174941	-0.431613	-0.5394402	cluster 1
HORVU.MOREX.r3.7HG0668850.1	-0.123102	-0.377072	-0.6130462	cluster 1
HORVU.MOREX.r3.7HG0669240.1	-0.171567	-0.296455	-0.3220881	cluster 1
HORVU.MOREX.r3.7HG0670020.1	-0.03904	-0.525027	-1.4988357	cluster 1
HORVU.MOREX.r3.7HG0671880.1	-0.11702	-0.415995	-0.7475091	cluster 1
HORVU.MOREX.r3.7HG0673610.1	-0.131863	-0.251661	-0.5587134	cluster 1
HORVU.MOREX.r3.7HG0674440.1	-0.044694	-0.453809	-0.5554254	cluster 1
HORVU.MOREX.r3.7HG0674480.1	-0.086969	-0.217718	-0.2995958	cluster 1
HORVU.MOREX.r3.7HG0674750.1	-0.158349	-0.26186	-0.4465006	cluster 1
HORVU.MOREX.r3.7HG0674790.1	-0.024804	-0.179051	-0.7409316	cluster 1
HORVU.MOREX.r3.7HG0676000.1	-0.135898	-0.74651	-1.2417459	cluster 1
HORVU.MOREX.r3.7HG0676230.1	-0.081152	-0.494662	-0.8694304	cluster 1
HORVU.MOREX.r3.7HG0676350.1	-0.090925	-0.324776	-0.6021678	cluster 1
HORVU.MOREX.r3.7HG0676570.1	-0.105052	-0.670906	-0.754483	cluster 1
HORVU.MOREX.r3.7HG0676890.1	-0.298882	-0.57958	-1.4801034	cluster 1
HORVU.MOREX.r3.7HG0677230.1	-0.19451	-0.846785	-1.4829404	cluster 1
HORVU.MOREX.r3.7HG0677510.1	-0.137647	-0.432649	-0.59865	cluster 1
HORVU.MOREX.r3.7HG0677580.1	-0.076853	-0.581738	-1.499187	cluster 1
HORVU.MOREX.r3.7HG0677860.1	-0.655353	-0.931231	-2.4003369	cluster 1
HORVU.MOREX.r3.7HG0677940.1	-0.156659	-0.289668	-0.3575406	cluster 1
HORVU.MOREX.r3.7HG0679350.1	-0.124085	-0.508575	-0.8090444	cluster 1
HORVU.MOREX.r3.7HG0679730.1	-0.655764	-0.845431	-1.4007413	cluster 1
HORVU.MOREX.r3.7HG0679760.1	-0.112621	-0.472933	-0.5682749	cluster 1
HORVU.MOREX.r3.7HG0680170.1	-0.19124	-0.35253	-0.4792956	cluster 1
HORVU.MOREX.r3.7HG0680680.1	-0.184219	-0.276535	-0.3036024	cluster 1
HORVU.MOREX.r3.7HG0682120.1	-0.13942	-0.243464	-0.3825648	cluster 1
HORVU.MOREX.r3.7HG0684040.1	-0.106939	-0.252789	-0.5227941	cluster 1
HORVU.MOREX.r3.7HG0685550.1	-0.100185	-0.279594	-0.7309508	cluster 1
HORVU.MOREX.r3.7HG0686000.1	-0.202797	-0.478567	-0.6570539	cluster 1
HORVU.MOREX.r3.7HG0686830.1	-0.121564	-0.492091	-0.8245815	cluster 1
HORVU.MOREX.r3.7HG0687050.1	-0.119937	-0.335545	-0.4636151	cluster 1
HORVU.MOREX.r3.7HG0687080.1	-0.229433	-0.401607	-0.5547604	cluster 1
HORVU.MOREX.r3.7HG0687190.1	-0.170013	-0.18717	-0.5190393	cluster 1
HORVU.MOREX.r3.7HG0687630.1	-0.169298	-0.537407	-0.7622627	cluster 1
HORVU.MOREX.r3.7HG0688300.1	-0.014668	-0.244412	-0.4267074	cluster 1
HORVU.MOREX.r3.7HG0689490.1	-0.146435	-0.253472	-0.5509563	cluster 1
HORVU.MOREX.r3.7HG0695500.1	-0.108798	-0.358754	-0.446606	cluster 1
HORVU.MOREX.r3.7HG0696190.1	-0.065495	-0.141331	-0.4356585	cluster 1

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.7HG0696220.1	-0.121042	-0.153208	-0.9496701	cluster 1
HORVU.MOREX.r3.7HG0698910.1	-0.069497	-0.30609	-0.3927772	cluster 1
HORVU.MOREX.r3.7HG0700930.1	-0.054687	-0.342451	-1.4382572	cluster 1
HORVU.MOREX.r3.7HG0703580.1	-0.154695	-0.340258	-0.6269324	cluster 1
HORVU.MOREX.r3.7HG0703780.1	-0.163881	-0.275805	-0.5475225	cluster 1
HORVU.MOREX.r3.7HG0703780.2	-0.093231	-0.187604	-0.2484471	cluster 1
HORVU.MOREX.r3.7HG0705490.1	-0.338225	-0.532682	-1.528505	cluster 1
HORVU.MOREX.r3.7HG0705700.1	-0.178573	-0.368019	-0.6988959	cluster 1
HORVU.MOREX.r3.7HG0706140.1	-0.160804	-0.357811	-0.5611145	cluster 1
HORVU.MOREX.r3.7HG0706330.1	-0.169117	-0.280805	-0.5281658	cluster 1
HORVU.MOREX.r3.7HG0706860.1	-0.288051	-0.359972	-0.6439385	cluster 1
HORVU.MOREX.r3.7HG0706930.1	0.009728	-0.355013	-0.4978365	cluster 1
HORVU.MOREX.r3.7HG0708120.1	-0.008908	-0.315109	-1.271149	cluster 1
HORVU.MOREX.r3.7HG0708320.1	-0.285227	-0.526197	-0.6768737	cluster 1
HORVU.MOREX.r3.7HG0708500.1	-0.049101	-0.349748	-0.9004663	cluster 1
HORVU.MOREX.r3.7HG0708820.1	-0.056712	-0.207484	-0.6855952	cluster 1
HORVU.MOREX.r3.7HG0709110.1	-0.202043	-0.618362	-1.5696279	cluster 1
HORVU.MOREX.r3.7HG0709230.1	-0.616893	-0.85014	-2.4948944	cluster 1
HORVU.MOREX.r3.7HG0709860.1	-0.100549	-0.279522	-0.6928871	cluster 1
HORVU.MOREX.r3.7HG0710980.1	0.0007696	-0.329803	-1.1495816	cluster 1
HORVU.MOREX.r3.7HG0711850.1	-0.181235	-0.337918	-0.388833	cluster 1
HORVU.MOREX.r3.7HG0712650.1	-0.270573	-0.518248	-0.8557637	cluster 1
HORVU.MOREX.r3.7HG0712850.1	-0.078997	-0.333915	-0.512629	cluster 1
HORVU.MOREX.r3.7HG0714120.1	-0.102133	-0.268439	-0.3313837	cluster 1
HORVU.MOREX.r3.7HG0714510.1	-0.317924	-0.442413	-1.1559138	cluster 1
HORVU.MOREX.r3.7HG0714870.1	-0.082615	-0.506534	-0.6194152	cluster 1
HORVU.MOREX.r3.7HG0714910.1	-0.115071	-0.375343	-0.7035154	cluster 1
HORVU.MOREX.r3.7HG0714930.1	-0.151498	-0.284934	-0.3979646	cluster 1
HORVU.MOREX.r3.7HG0714950.1	-0.1894	-0.42833	-0.5935839	cluster 1
HORVU.MOREX.r3.7HG0715570.1	-0.197607	-0.487681	-0.6433136	cluster 1
HORVU.MOREX.r3.7HG0716170.1	-0.116099	-0.78014	-1.0136248	cluster 1
HORVU.MOREX.r3.7HG0716900.1	-0.096514	-0.271943	-0.3549208	cluster 1
HORVU.MOREX.r3.7HG0718710.1	-0.090745	-0.235178	-0.2781975	cluster 1
HORVU.MOREX.r3.7HG0719070.1	-0.130119	-0.137319	-0.6855384	cluster 1
HORVU.MOREX.r3.7HG0719410.1	-0.173565	-0.244727	-0.8934651	cluster 1
HORVU.MOREX.r3.7HG0719720.1	-0.123505	-0.398525	-0.7186812	cluster 1
HORVU.MOREX.r3.7HG0720130.1	-0.161254	-0.407649	-0.591589	cluster 1
HORVU.MOREX.r3.7HG0720670.1	-0.057808	-0.359034	-0.8829704	cluster 1
HORVU.MOREX.r3.7HG0720790.1	-0.586399	-0.876625	-1.1746271	cluster 1
HORVU.MOREX.r3.7HG0721760.1	-0.121892	-0.283438	-0.3845036	cluster 1
HORVU.MOREX.r3.7HG0721790.1	-0.303067	-0.688737	-0.7865252	cluster 1
HORVU.MOREX.r3.7HG0721800.1	-0.077775	-0.287488	-0.3480656	cluster 1
HORVU.MOREX.r3.7HG0721930.1	-0.247642	-0.313167	-0.5556501	cluster 1
HORVU.MOREX.r3.7HG0723420.1	-0.124151	-0.196288	-0.3773619	cluster 1
HORVU.MOREX.r3.7HG0725060.1	-0.48511	-0.629375	-1.5202651	cluster 1
HORVU.MOREX.r3.7HG0726210.1	-0.277083	-0.480339	-0.7209696	cluster 1
HORVU.MOREX.r3.7HG0726350.1	0.0035137	-0.34395	-0.5869455	cluster 1

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.7HG0726700.1	-0.097543	-0.370089	-0.8612115	cluster 1
HORVU.MOREX.r3.7HG0726790.1	-0.149551	-0.301441	-0.4855129	cluster 1
HORVU.MOREX.r3.7HG0727070.1	-0.136339	-0.411342	-0.6475236	cluster 1
HORVU.MOREX.r3.7HG0727350.1	-0.140516	-0.369975	-0.4026862	cluster 1
HORVU.MOREX.r3.7HG0727460.1	-0.149635	-0.279721	-0.8341254	cluster 1
HORVU.MOREX.r3.7HG0728190.1	-0.137765	-0.334828	-0.4237947	cluster 1
HORVU.MOREX.r3.7HG0728220.1	-0.209479	-0.323363	-0.5219552	cluster 1
HORVU.MOREX.r3.7HG0728630.1	0.0848225	-0.653313	-1.0050638	cluster 1
HORVU.MOREX.r3.7HG0728910.1	-0.105664	-0.152004	-0.8345446	cluster 1
HORVU.MOREX.r3.7HG0730070.1	-0.113278	-0.625955	-1.3355518	cluster 1
HORVU.MOREX.r3.7HG0730310.1	-0.142713	-0.508358	-0.8960971	cluster 1
HORVU.MOREX.r3.7HG0730350.1	-0.14344	-0.346178	-0.5382438	cluster 1
HORVU.MOREX.r3.7HG0730800.1	-0.26359	-0.63261	-1.1261643	cluster 1
HORVU.MOREX.r3.7HG0730820.1	-0.189394	-0.617362	-0.9696442	cluster 1
HORVU.MOREX.r3.7HG0730840.1	-0.343589	-0.636674	-1.0896918	cluster 1
HORVU.MOREX.r3.7HG0731490.1	-0.3258	-0.452923	-0.5993975	cluster 1
HORVU.MOREX.r3.7HG0732270.1	0.0796105	-0.151539	-0.5649961	cluster 1
HORVU.MOREX.r3.7HG0732290.1	-0.03798	-0.862297	-1.7091001	cluster 1
HORVU.MOREX.r3.7HG0732330.1	-0.870155	-1.042089	-1.5236155	cluster 1
HORVU.MOREX.r3.7HG0732610.1	-0.19077	-0.627832	-1.2427384	cluster 1
HORVU.MOREX.r3.7HG0733910.1	-0.112638	-0.28049	-0.3858919	cluster 1
HORVU.MOREX.r3.7HG0734670.1	-0.115313	-0.440215	-0.560796	cluster 1
HORVU.MOREX.r3.7HG0735840.1	-0.564004	-1.04726	-1.2687473	cluster 1
HORVU.MOREX.r3.7HG0736960.1	-0.209552	-0.806234	-1.1528079	cluster 1
HORVU.MOREX.r3.7HG0737440.1	-0.186253	-0.813779	-1.1761342	cluster 1
HORVU.MOREX.r3.7HG0737870.1	-0.013682	-0.605608	-1.71847	cluster 1
HORVU.MOREX.r3.7HG0739380.1	-0.140426	-0.47347	-0.9423897	cluster 1
HORVU.MOREX.r3.7HG0739400.1	-0.324056	-0.716058	-1.2105552	cluster 1
HORVU.MOREX.r3.7HG0739460.1	-0.1767	-0.512547	-1.0485936	cluster 1
HORVU.MOREX.r3.7HG0739480.1	-0.201196	-0.48366	-0.8839477	cluster 1
HORVU.MOREX.r3.7HG0739490.1	-0.208689	-0.461091	-0.9538976	cluster 1
HORVU.MOREX.r3.7HG0739640.1	-0.223411	-0.576685	-0.9622662	cluster 1
HORVU.MOREX.r3.7HG0739910.1	-0.054828	-0.479194	-0.678719	cluster 1
HORVU.MOREX.r3.7HG0741080.1	-0.672432	-0.796848	-0.8366293	cluster 1
HORVU.MOREX.r3.7HG0741640.1	-0.325964	-0.756658	-0.9646278	cluster 1
HORVU.MOREX.r3.7HG0741650.1	-0.125074	-0.569975	-0.8381484	cluster 1
HORVU.MOREX.r3.7HG0742070.1	-0.178064	-0.394719	-0.6542131	cluster 1
HORVU.MOREX.r3.7HG0742450.1	-0.104021	-0.329626	-0.641118	cluster 1
HORVU.MOREX.r3.7HG0742470.1	-0.36422	-0.439455	-0.8769606	cluster 1
HORVU.MOREX.r3.7HG0744250.1	-0.243621	-0.430026	-0.7346591	cluster 1
HORVU.MOREX.r3.7HG0744260.1	-0.607973	-1.32412	-2.9809703	cluster 1
HORVU.MOREX.r3.7HG0744540.1	0.1405138	-0.192473	-2.0658572	cluster 1
HORVU.MOREX.r3.7HG0744790.1	0.0128261	-0.265496	-0.581483	cluster 1
HORVU.MOREX.r3.7HG0744970.1	-0.070899	-0.256537	-0.2950067	cluster 1
HORVU.MOREX.r3.7HG0745980.1	-0.081069	-0.342585	-0.4031379	cluster 1
HORVU.MOREX.r3.7HG0746230.1	-0.070312	-0.374381	-0.6037365	cluster 1
HORVU.MOREX.r3.7HG0746770.1	-0.227242	-0.498766	-0.6970324	cluster 1

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.7HG0749150.1	0.1075723	-0.097489	-2.0555127	cluster 1
HORVU.MOREX.r3.7HG0749170.1	-0.343989	-0.626683	-1.3516979	cluster 1
HORVU.MOREX.r3.7HG0749660.1	-0.033838	-0.180697	-0.6566934	cluster 1
HORVU.MOREX.r3.7HG0749940.3	-0.173912	-0.586304	-0.7117558	cluster 1
HORVU.MOREX.r3.7HG0751000.1	-0.037894	-0.469851	-1.2526513	cluster 1
HORVU.MOREX.r3.7HG0751110.1	-0.190387	-0.510756	-0.6138129	cluster 1
HORVU.MOREX.r3.7HG0751290.1	-0.660763	-0.908229	-1.0176798	cluster 1
HORVU.MOREX.r3.1HG0002570.1	0.816034	1.3298146	1.61969582	cluster 2
HORVU.MOREX.r3.1HG0002960.1	0.8480958	1.1891287	1.30211439	cluster 2
HORVU.MOREX.r3.1HG0003160.1	0.2815356	0.461246	0.59740027	cluster 2
HORVU.MOREX.r3.1HG0003430.1	0.1910299	0.4586132	0.50114337	cluster 2
HORVU.MOREX.r3.1HG0004560.1	-0.022642	0.8777935	0.84834751	cluster 2
HORVU.MOREX.r3.1HG0006400.1	0.1146551	0.7031986	0.82396251	cluster 2
HORVU.MOREX.r3.1HG0006660.1	0.4186282	0.9539727	0.94286013	cluster 2
HORVU.MOREX.r3.1HG0007670.1	-0.169503	0.3231918	0.58383366	cluster 2
HORVU.MOREX.r3.1HG0010920.1	0.401162	0.5468505	0.56432129	cluster 2
HORVU.MOREX.r3.1HG0011820.1	0.4297878	0.9730911	0.92402335	cluster 2
HORVU.MOREX.r3.1HG0013820.1	0.1688292	0.3662798	0.52267715	cluster 2
HORVU.MOREX.r3.1HG0014680.1	0.8092587	1.3972174	1.37838415	cluster 2
HORVU.MOREX.r3.1HG0015750.1	0.6461444	1.7678989	1.65720455	cluster 2
HORVU.MOREX.r3.1HG0015960.1	0.2752366	1.2472685	1.20640107	cluster 2
HORVU.MOREX.r3.1HG0018110.1	0.1850191	0.2824626	0.37471105	cluster 2
HORVU.MOREX.r3.1HG0018590.1	0.377141	0.6107542	0.84173356	cluster 2
HORVU.MOREX.r3.1HG0021880.1	0.7647028	2.4449034	2.30473582	cluster 2
HORVU.MOREX.r3.1HG0023200.1	0.3561223	1.268951	1.27112406	cluster 2
HORVU.MOREX.r3.1HG0024900.1	0.0310827	0.1763802	0.34858337	cluster 2
HORVU.MOREX.r3.1HG0025430.1	0.3553935	1.2727393	1.1845806	cluster 2
HORVU.MOREX.r3.1HG0026010.1	0.3545835	0.4935198	0.64887578	cluster 2
HORVU.MOREX.r3.1HG0026080.1	0.3773057	0.6697716	0.64487517	cluster 2
HORVU.MOREX.r3.1HG0026830.1	0.3568673	0.5057221	0.62992631	cluster 2
HORVU.MOREX.r3.1HG0029730.1	0.2412764	0.3823849	0.47092527	cluster 2
HORVU.MOREX.r3.1HG0032930.1	0.122655	0.670299	0.67473973	cluster 2
HORVU.MOREX.r3.1HG0035400.1	0.1905985	0.5406722	0.66107006	cluster 2
HORVU.MOREX.r3.1HG0038800.1	0.1954959	0.6345157	0.70049348	cluster 2
HORVU.MOREX.r3.1HG0040930.1	0.8895017	1.7882863	1.80373232	cluster 2
HORVU.MOREX.r3.1HG0041280.1	0.4552104	0.8644407	0.98091236	cluster 2
HORVU.MOREX.r3.1HG0044470.1	0.2535506	0.7005231	0.77087652	cluster 2
HORVU.MOREX.r3.1HG0046180.1	0.2889429	0.4092173	0.49234211	cluster 2
HORVU.MOREX.r3.1HG0047100.1	0.4002883	1.1687198	1.15087066	cluster 2
HORVU.MOREX.r3.1HG0047580.1	0.161516	0.3993397	0.50590673	cluster 2
HORVU.MOREX.r3.1HG0050440.1	1.1427038	1.6308828	1.80523882	cluster 2
HORVU.MOREX.r3.1HG0050700.1	0.68656	1.4703829	1.41346892	cluster 2
HORVU.MOREX.r3.1HG0050920.1	0.4405744	0.8341891	1.04312538	cluster 2
HORVU.MOREX.r3.1HG0051920.1	0.3662728	0.9571774	0.93966354	cluster 2
HORVU.MOREX.r3.1HG0053450.1	0.4461442	0.8577287	0.92566908	cluster 2
HORVU.MOREX.r3.1HG0054010.1	0.3164991	0.5716175	0.63374806	cluster 2
HORVU.MOREX.r3.1HG0054070.1	0.6250529	0.9386297	1.20247035	cluster 2

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.1HG0054110.1	0.2333108	0.3679888	0.46117724	cluster 2
HORVU.MOREX.r3.1HG0054510.1	0.7755924	1.0213169	1.11389941	cluster 2
HORVU.MOREX.r3.1HG0055240.1	2.1640636	2.2385391	2.28817889	cluster 2
HORVU.MOREX.r3.1HG0056240.1	0.3077347	0.6718929	0.74188459	cluster 2
HORVU.MOREX.r3.1HG0056570.1	0.2650334	0.4121611	0.51512523	cluster 2
HORVU.MOREX.r3.1HG0056580.1	0.1856858	0.2706326	0.34575771	cluster 2
HORVU.MOREX.r3.1HG0056810.1	0.1974665	0.3538185	0.41777063	cluster 2
HORVU.MOREX.r3.1HG0056990.1	-0.126232	0.1188655	0.45777116	cluster 2
HORVU.MOREX.r3.1HG0057860.1	0.2926234	0.6115088	0.65790933	cluster 2
HORVU.MOREX.r3.1HG0061210.1	0.1557527	0.2821924	0.32461919	cluster 2
HORVU.MOREX.r3.1HG0061390.1	0.1600274	0.5309879	0.7218625	cluster 2
HORVU.MOREX.r3.1HG0061660.1	0.5192854	0.8859364	0.98617271	cluster 2
HORVU.MOREX.r3.1HG0061710.1	0.1552148	0.4241786	0.50222289	cluster 2
HORVU.MOREX.r3.1HG0062110.1	0.8732405	1.3550929	1.35788268	cluster 2
HORVU.MOREX.r3.1HG0062980.1	0.4314587	0.7410038	1.03359978	cluster 2
HORVU.MOREX.r3.1HG0063430.1	0.1334172	0.3139	0.39567343	cluster 2
HORVU.MOREX.r3.1HG0064740.1	0.1060772	0.5370709	0.75737343	cluster 2
HORVU.MOREX.r3.1HG0065520.1	0.0545143	0.3096202	0.52584262	cluster 2
HORVU.MOREX.r3.1HG0065860.1	0.4890558	0.8488967	1.05962715	cluster 2
HORVU.MOREX.r3.1HG0066610.1	0.7729362	1.1409509	1.12183008	cluster 2
HORVU.MOREX.r3.1HG0067500.1	0.0757265	0.2535178	0.42750343	cluster 2
HORVU.MOREX.r3.1HG0067630.1	0.1278233	0.3343533	0.39612494	cluster 2
HORVU.MOREX.r3.1HG0067930.1	0.1286308	0.3808856	0.55963106	cluster 2
HORVU.MOREX.r3.1HG0067980.1	1.1432184	1.4805668	1.56074787	cluster 2
HORVU.MOREX.r3.1HG0068010.1	1.1317354	1.6387976	1.61049372	cluster 2
HORVU.MOREX.r3.1HG0069380.1	0.2306783	0.824246	0.81738825	cluster 2
HORVU.MOREX.r3.1HG0070110.1	0.144219	0.2750925	0.34724864	cluster 2
HORVU.MOREX.r3.1HG0070340.1	1.0667337	1.5971119	1.5663168	cluster 2
HORVU.MOREX.r3.1HG0070430.1	-0.038802	0.2344276	0.60028624	cluster 2
HORVU.MOREX.r3.1HG0070850.1	0.4133316	0.8047114	0.89347048	cluster 2
HORVU.MOREX.r3.1HG0072160.1	0.2770799	0.6884414	0.70504596	cluster 2
HORVU.MOREX.r3.1HG0072510.1	0.5431199	1.0432019	1.25919789	cluster 2
HORVU.MOREX.r3.1HG0072680.1	0.328617	0.746658	0.9050929	cluster 2
HORVU.MOREX.r3.1HG0073010.1	0.4497443	0.8382302	0.95892818	cluster 2
HORVU.MOREX.r3.1HG0073160.1	0.1885816	0.4061384	0.42731956	cluster 2
HORVU.MOREX.r3.1HG0073390.1	0.9925304	1.6807759	1.86620372	cluster 2
HORVU.MOREX.r3.1HG0073500.1	0.489418	1.6829513	1.88635403	cluster 2
HORVU.MOREX.r3.1HG0073550.1	1.4658151	2.0831008	2.09899008	cluster 2
HORVU.MOREX.r3.1HG0074010.1	0.4620102	0.9071867	1.0026054	cluster 2
HORVU.MOREX.r3.1HG0075320.1	0.7816868	1.1791158	1.34370577	cluster 2
HORVU.MOREX.r3.1HG0075440.1	0.4944808	0.716354	0.8320652	cluster 2
HORVU.MOREX.r3.1HG0076120.1	0.3149319	0.5684553	0.68528036	cluster 2
HORVU.MOREX.r3.1HG0077790.1	0.3056013	0.893749	1.00880469	cluster 2
HORVU.MOREX.r3.1HG0078040.1	0.1764706	0.3862847	0.45085531	cluster 2
HORVU.MOREX.r3.1HG0078910.1	0.1789599	0.3371299	0.52394093	cluster 2
HORVU.MOREX.r3.1HG0078970.1	1.0924665	1.6063089	1.99171783	cluster 2
HORVU.MOREX.r3.1HG0079020.1	1.0870269	2.1099641	2.03949696	cluster 2

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.1HG0079750.1	0.4190078	1.0094094	0.9744382	cluster 2
HORVU.MOREX.r3.1HG0079760.1	0.4314093	0.6363233	0.79672809	cluster 2
HORVU.MOREX.r3.1HG0079920.1	0.3361798	0.6173308	0.6513715	cluster 2
HORVU.MOREX.r3.1HG0081110.1	0.0059002	0.3542383	0.65001886	cluster 2
HORVU.MOREX.r3.1HG0082530.1	0.1196339	0.2679148	0.46830668	cluster 2
HORVU.MOREX.r3.1HG0083440.1	-0.030056	0.1969053	0.34965751	cluster 2
HORVU.MOREX.r3.1HG0084970.1	0.8014998	1.2288608	1.27796679	cluster 2
HORVU.MOREX.r3.1HG0085380.1	0.1572528	0.3175546	0.3914105	cluster 2
HORVU.MOREX.r3.1HG0086090.1	0.3035259	0.6194064	1.04015992	cluster 2
HORVU.MOREX.r3.1HG0086390.1	0.2549845	0.7967687	0.89146002	cluster 2
HORVU.MOREX.r3.1HG0087590.1	0.8094329	1.456679	1.42436505	cluster 2
HORVU.MOREX.r3.1HG0087620.1	0.6565543	1.0056498	1.05313113	cluster 2
HORVU.MOREX.r3.1HG0090100.1	0.7165692	1.2540656	1.31925538	cluster 2
HORVU.MOREX.r3.1HG0091240.1	0.192182	0.4585977	0.56887539	cluster 2
HORVU.MOREX.r3.1HG0092010.1	0.4914559	0.7236539	0.81422792	cluster 2
HORVU.MOREX.r3.1HG0092730.1	0.236626	0.6166629	0.77346805	cluster 2
HORVU.MOREX.r3.1HG0095170.1	0.8601542	1.5836265	1.57227006	cluster 2
HORVU.MOREX.r3.2HG0096290.1	0.1697319	0.4266028	0.60815498	cluster 2
HORVU.MOREX.r3.2HG0099780.1	0.4150032	0.724752	1.10345775	cluster 2
HORVU.MOREX.r3.2HG0099900.1	0.2870693	0.5805348	0.57411585	cluster 2
HORVU.MOREX.r3.2HG0100900.2	0.7694444	1.466048	1.59847627	cluster 2
HORVU.MOREX.r3.2HG0102670.1	1.8547983	2.2314588	2.3913667	cluster 2
HORVU.MOREX.r3.2HG0104080.1	0.5863758	0.8885191	1.00608694	cluster 2
HORVU.MOREX.r3.2HG0105020.1	0.3320269	0.5026094	0.69185748	cluster 2
HORVU.MOREX.r3.2HG0106260.1	1.5296484	2.1383183	2.5738544	cluster 2
HORVU.MOREX.r3.2HG0107300.1	0.8474797	1.4586036	1.64984172	cluster 2
HORVU.MOREX.r3.2HG0109340.1	0.4941929	1.1236998	1.2043941	cluster 2
HORVU.MOREX.r3.2HG0111620.1	0.3389687	0.6832929	0.75725143	cluster 2
HORVU.MOREX.r3.2HG0112030.1	0.1177364	0.3804763	0.51672242	cluster 2
HORVU.MOREX.r3.2HG0112670.1	1.124314	1.793326	1.8373569	cluster 2
HORVU.MOREX.r3.2HG0113880.1	0.2605632	0.4587301	0.62138027	cluster 2
HORVU.MOREX.r3.2HG0113990.1	1.652593	2.2789359	2.25069031	cluster 2
HORVU.MOREX.r3.2HG0116990.1	0.2554949	0.5555379	0.56638687	cluster 2
HORVU.MOREX.r3.2HG0117880.1	1.9599887	2.6174308	2.59952396	cluster 2
HORVU.MOREX.r3.2HG0119650.1	0.2576946	0.457482	0.69764091	cluster 2
HORVU.MOREX.r3.2HG0119800.1	1.0987614	1.4900502	1.53377838	cluster 2
HORVU.MOREX.r3.2HG0120320.1	0.377562	0.5789971	0.82476645	cluster 2
HORVU.MOREX.r3.2HG0120650.1	0.7099929	1.0125719	1.15429085	cluster 2
HORVU.MOREX.r3.2HG0121200.1	0.5073511	0.743407	0.90263914	cluster 2
HORVU.MOREX.r3.2HG0121480.1	0.3044656	0.687162	0.76526272	cluster 2
HORVU.MOREX.r3.2HG0122510.1	0.3761735	0.5250866	0.70689603	cluster 2
HORVU.MOREX.r3.2HG0122520.1	0.1152367	0.5835001	0.75351087	cluster 2
HORVU.MOREX.r3.2HG0123170.1	0.3764052	0.656127	0.9938262	cluster 2
HORVU.MOREX.r3.2HG0124660.1	-0.014887	0.1596953	0.29612374	cluster 2
HORVU.MOREX.r3.2HG0127020.1	0.1809534	0.5127101	0.68511203	cluster 2
HORVU.MOREX.r3.2HG0129450.1	0.4115037	0.9624815	0.95965053	cluster 2
HORVU.MOREX.r3.2HG0132160.1	0.5832001	2.3261431	2.18912656	cluster 2

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.2HG0134990.1	0.4536518	0.6062987	0.68588902	cluster 2
HORVU.MOREX.r3.2HG0135210.1	0.3780272	0.6727723	0.77181105	cluster 2
HORVU.MOREX.r3.2HG0138540.1	0.3085631	0.5798993	0.6000674	cluster 2
HORVU.MOREX.r3.2HG0140170.1	0.2706125	0.7297222	0.74070197	cluster 2
HORVU.MOREX.r3.2HG0140380.1	1.5615412	1.675108	1.76626899	cluster 2
HORVU.MOREX.r3.2HG0141140.1	0.9139418	1.060458	1.11878653	cluster 2
HORVU.MOREX.r3.2HG0145360.1	0.5039365	0.9907402	1.04013448	cluster 2
HORVU.MOREX.r3.2HG0150530.1	0.1210945	0.4404153	0.56604141	cluster 2
HORVU.MOREX.r3.2HG0155750.1	0.9979915	1.8172943	2.01468789	cluster 2
HORVU.MOREX.r3.2HG0156610.1	1.1955286	1.9668569	1.99590465	cluster 2
HORVU.MOREX.r3.2HG0157170.1	0.0892596	0.2925576	0.28597544	cluster 2
HORVU.MOREX.r3.2HG0157340.1	0.2365324	0.415833	0.49672226	cluster 2
HORVU.MOREX.r3.2HG0158180.1	0.5049772	0.9209716	0.93866018	cluster 2
HORVU.MOREX.r3.2HG0164160.2	0.8756918	1.4548757	1.55391465	cluster 2
HORVU.MOREX.r3.2HG0165180.1	0.162007	0.3244045	0.48891405	cluster 2
HORVU.MOREX.r3.2HG0165920.1	0.7383041	1.0390414	1.32369249	cluster 2
HORVU.MOREX.r3.2HG0168070.1	0.8585737	1.3022418	1.54383282	cluster 2
HORVU.MOREX.r3.2HG0168330.1	0.1734171	0.4352607	0.5097686	cluster 2
HORVU.MOREX.r3.2HG0173600.1	0.2766916	0.5268451	0.61785162	cluster 2
HORVU.MOREX.r3.2HG0173960.1	0.4870302	0.6833282	0.66725743	cluster 2
HORVU.MOREX.r3.2HG0174650.1	0.8497415	0.9243346	0.96707212	cluster 2
HORVU.MOREX.r3.2HG0174750.1	0.299016	1.205453	1.19501899	cluster 2
HORVU.MOREX.r3.2HG0175380.1	0.9053362	1.6285147	1.65633196	cluster 2
HORVU.MOREX.r3.2HG0178050.1	0.3553613	0.6719366	0.76918271	cluster 2
HORVU.MOREX.r3.2HG0179560.1	0.5620998	1.2650234	1.19788231	cluster 2
HORVU.MOREX.r3.2HG0180500.1	0.1028389	0.2320499	0.36337228	cluster 2
HORVU.MOREX.r3.2HG0181510.2	0.0948066	0.3408424	0.45152873	cluster 2
HORVU.MOREX.r3.2HG0181680.1	0.9902678	1.8076092	2.00934686	cluster 2
HORVU.MOREX.r3.2HG0182210.2	0.3718404	0.6267738	0.86392819	cluster 2
HORVU.MOREX.r3.2HG0182400.1	0.2782616	0.7873183	0.9242027	cluster 2
HORVU.MOREX.r3.2HG0184180.1	0.449513	0.8846691	1.13761939	cluster 2
HORVU.MOREX.r3.2HG0184230.1	0.3538529	2.484088	2.39357162	cluster 2
HORVU.MOREX.r3.2HG0185370.1	2.0892432	2.6125066	2.71949862	cluster 2
HORVU.MOREX.r3.2HG0185570.1	0.1081284	0.5133423	0.73647328	cluster 2
HORVU.MOREX.r3.2HG0188200.1	0.5634929	0.6913168	0.78333772	cluster 2
HORVU.MOREX.r3.2HG0189980.1	0.0695638	0.3528309	0.50174275	cluster 2
HORVU.MOREX.r3.2HG0190290.1	0.4486419	0.6013912	0.62647603	cluster 2
HORVU.MOREX.r3.2HG0192000.1	0.4654997	0.7865423	0.82910508	cluster 2
HORVU.MOREX.r3.2HG0192270.1	1.6090773	2.3650346	2.55024845	cluster 2
HORVU.MOREX.r3.2HG0192400.1	0.3662454	0.6147984	0.7856642	cluster 2
HORVU.MOREX.r3.2HG0192540.1	0.1144642	0.2114541	0.31826157	cluster 2
HORVU.MOREX.r3.2HG0195910.1	0.3344327	0.56002	0.70352231	cluster 2
HORVU.MOREX.r3.2HG0197760.1	0.2338253	0.386019	0.53742174	cluster 2
HORVU.MOREX.r3.2HG0198870.1	0.9372408	1.1802771	1.17767397	cluster 2
HORVU.MOREX.r3.2HG0200710.1	0.7596757	1.5594746	1.8335563	cluster 2
HORVU.MOREX.r3.2HG0202220.1	0.1173856	0.2586358	0.34870383	cluster 2
HORVU.MOREX.r3.2HG0203330.1	0.2694214	0.3680154	0.43296135	cluster 2

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.2HG0205050.1	0.7536856	1.4715989	2.02591118	cluster 2
HORVU.MOREX.r3.2HG0205810.1	0.3280324	1.2016192	1.23013379	cluster 2
HORVU.MOREX.r3.2HG0206470.1	0.2694722	0.4030391	0.55066039	cluster 2
HORVU.MOREX.r3.2HG0206650.1	0.2620155	0.4397694	0.55889322	cluster 2
HORVU.MOREX.r3.2HG0207130.1	0.4068899	1.4490313	1.53422862	cluster 2
HORVU.MOREX.r3.2HG0207720.1	0.5067106	0.9111347	1.14572552	cluster 2
HORVU.MOREX.r3.2HG0207860.1	1.2944609	1.4486193	1.58711801	cluster 2
HORVU.MOREX.r3.2HG0208170.1	0.2352241	1.3862978	1.56262846	cluster 2
HORVU.MOREX.r3.2HG0209810.1	0.0662381	0.2299367	0.43206324	cluster 2
HORVU.MOREX.r3.2HG0210610.1	0.3736037	0.9086098	0.92546459	cluster 2
HORVU.MOREX.r3.2HG0217550.1	0.2170308	0.2891089	0.38892147	cluster 2
HORVU.MOREX.r3.3HG0218800.1	1.3408989	2.0365772	1.97108408	cluster 2
HORVU.MOREX.r3.3HG0219410.1	0.3314618	0.7538848	0.81639832	cluster 2
HORVU.MOREX.r3.3HG0221180.1	0.6790219	1.1981478	1.20578344	cluster 2
HORVU.MOREX.r3.3HG0221240.1	0.4260681	0.626593	0.78135254	cluster 2
HORVU.MOREX.r3.3HG0221440.1	0.3967657	0.8068423	0.79981404	cluster 2
HORVU.MOREX.r3.3HG0223160.1	0.260881	0.5494062	0.61297236	cluster 2
HORVU.MOREX.r3.3HG0224440.1	0.2521341	0.8101636	0.86777827	cluster 2
HORVU.MOREX.r3.3HG0225760.1	0.3849776	1.178426	1.18855926	cluster 2
HORVU.MOREX.r3.3HG0230090.1	0.3232532	0.5851915	0.94060617	cluster 2
HORVU.MOREX.r3.3HG0230500.1	0.8450312	1.0647175	1.22687651	cluster 2
HORVU.MOREX.r3.3HG0230870.1	0.961177	1.6638412	1.70204986	cluster 2
HORVU.MOREX.r3.3HG0231000.1	0.3280071	0.9797396	0.92413278	cluster 2
HORVU.MOREX.r3.3HG0231240.1	0.5431899	0.810961	1.05285024	cluster 2
HORVU.MOREX.r3.3HG0233990.1	0.8122961	1.2915571	1.24043971	cluster 2
HORVU.MOREX.r3.3HG0234240.1	0.3978413	0.9288043	0.97395022	cluster 2
HORVU.MOREX.r3.3HG0236500.1	0.2220856	0.6874581	0.67005911	cluster 2
HORVU.MOREX.r3.3HG0236690.1	0.4484496	0.6348102	0.66802296	cluster 2
HORVU.MOREX.r3.3HG0237990.1	0.522957	0.8426499	0.88595667	cluster 2
HORVU.MOREX.r3.3HG0242150.1	1.5930177	2.8160289	3.27182942	cluster 2
HORVU.MOREX.r3.3HG0245010.1	0.1656037	0.3584781	0.47089257	cluster 2
HORVU.MOREX.r3.3HG0246030.1	0.2451723	0.6744941	1.08833755	cluster 2
HORVU.MOREX.r3.3HG0246500.1	0.3732535	0.7684238	0.86297927	cluster 2
HORVU.MOREX.r3.3HG0246670.1	1.2505966	1.6748638	1.75670347	cluster 2
HORVU.MOREX.r3.3HG0248440.1	0.1967806	0.4395193	0.69610435	cluster 2
HORVU.MOREX.r3.3HG0249400.1	0.5126295	0.8759675	1.21276614	cluster 2
HORVU.MOREX.r3.3HG0249640.1	0.2657831	0.5988288	0.62351463	cluster 2
HORVU.MOREX.r3.3HG0249890.1	0.1908097	0.6359167	0.76939864	cluster 2
HORVU.MOREX.r3.3HG0252170.1	0.8956447	1.6729829	1.65645577	cluster 2
HORVU.MOREX.r3.3HG0252210.1	0.6918987	0.9490763	1.17295354	cluster 2
HORVU.MOREX.r3.3HG0252250.1	0.6987571	1.3986258	1.60335922	cluster 2
HORVU.MOREX.r3.3HG0252380.1	0.1710449	0.899178	1.02187193	cluster 2
HORVU.MOREX.r3.3HG0254430.1	-0.025285	0.2238274	0.2685602	cluster 2
HORVU.MOREX.r3.3HG0254930.1	1.8775805	2.620343	2.68949759	cluster 2
HORVU.MOREX.r3.3HG0254940.1	0.4143863	0.860821	0.86871366	cluster 2
HORVU.MOREX.r3.3HG0254950.1	0.7777211	1.4584539	1.40223712	cluster 2
HORVU.MOREX.r3.3HG0255020.1	0.4974885	0.9494325	0.98417562	cluster 2

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.3HG0255580.1	0.1565359	0.3025266	0.48972851	cluster 2
HORVU.MOREX.r3.3HG0255700.1	0.6050989	0.9367771	0.94903354	cluster 2
HORVU.MOREX.r3.3HG0257840.1	0.7573933	1.3827047	1.38972203	cluster 2
HORVU.MOREX.r3.3HG0264650.1	0.737846	1.8000893	1.69217634	cluster 2
HORVU.MOREX.r3.3HG0266530.1	0.276387	0.6074802	0.85406364	cluster 2
HORVU.MOREX.r3.3HG0267000.1	0.2663401	0.504754	0.81989737	cluster 2
HORVU.MOREX.r3.3HG0271380.1	0.2859479	0.4741105	0.60762866	cluster 2
HORVU.MOREX.r3.3HG0273790.2	0.1458978	0.6251988	0.668958	cluster 2
HORVU.MOREX.r3.3HG0275060.1	0.6942171	1.3793674	1.55736662	cluster 2
HORVU.MOREX.r3.3HG0275100.1	0.2138621	1.2206472	1.28314239	cluster 2
HORVU.MOREX.r3.3HG0275770.1	0.2103829	0.5128552	0.72826346	cluster 2
HORVU.MOREX.r3.3HG0276130.1	0.5630525	1.0544702	1.09624594	cluster 2
HORVU.MOREX.r3.3HG0276160.2	0.8450076	1.2238195	1.55791778	cluster 2
HORVU.MOREX.r3.3HG0276730.1	0.1223194	0.2069207	0.27304692	cluster 2
HORVU.MOREX.r3.3HG0278120.1	0.2083986	0.3600599	0.38149806	cluster 2
HORVU.MOREX.r3.3HG0278170.1	0.9548513	1.7076948	1.70670555	cluster 2
HORVU.MOREX.r3.3HG0278710.1	0.296406	0.4826987	0.66008226	cluster 2
HORVU.MOREX.r3.3HG0279750.1	0.207975	0.3143969	0.32767197	cluster 2
HORVU.MOREX.r3.3HG0279850.1	-0.059459	0.3299392	0.47955293	cluster 2
HORVU.MOREX.r3.3HG0280060.1	0.6899142	1.8979377	2.09462376	cluster 2
HORVU.MOREX.r3.3HG0280160.1	0.0395933	0.2655924	0.42237899	cluster 2
HORVU.MOREX.r3.3HG0280960.1	0.2730958	0.7139438	0.68640652	cluster 2
HORVU.MOREX.r3.3HG0283250.1	0.1756096	0.439437	0.6176891	cluster 2
HORVU.MOREX.r3.3HG0283740.1	0.1571979	0.3460681	0.54575535	cluster 2
HORVU.MOREX.r3.3HG0284100.1	0.1955155	0.3840195	0.43775086	cluster 2
HORVU.MOREX.r3.3HG0284780.1	0.0401797	0.3559578	0.3220962	cluster 2
HORVU.MOREX.r3.3HG0285780.1	0.3742395	0.8296677	1.03195173	cluster 2
HORVU.MOREX.r3.3HG0285840.1	0.4650272	0.7566451	0.98992789	cluster 2
HORVU.MOREX.r3.3HG0287000.1	0.4184393	0.7786466	1.00541978	cluster 2
HORVU.MOREX.r3.3HG0287690.1	0.3638968	0.9060343	0.93261865	cluster 2
HORVU.MOREX.r3.3HG0288070.1	0.1652256	0.5652533	0.52258319	cluster 2
HORVU.MOREX.r3.3HG0288710.1	0.9306129	1.4825416	1.44900912	cluster 2
HORVU.MOREX.r3.3HG0288710.2	1.1291964	1.6664555	1.7527596	cluster 2
HORVU.MOREX.r3.3HG0288960.1	0.5413086	1.0478369	1.24567004	cluster 2
HORVU.MOREX.r3.3HG0291030.1	0.3112427	0.6142111	0.84448301	cluster 2
HORVU.MOREX.r3.3HG0291040.1	0.0753592	0.7613512	0.78598658	cluster 2
HORVU.MOREX.r3.3HG0291100.1	0.1292693	0.3142801	0.3241665	cluster 2
HORVU.MOREX.r3.3HG0291160.1	0.1120419	0.2082623	0.25671613	cluster 2
HORVU.MOREX.r3.3HG0293130.1	0.7673112	1.0615266	1.08817398	cluster 2
HORVU.MOREX.r3.3HG0293310.1	0.8866974	1.9219134	1.8702952	cluster 2
HORVU.MOREX.r3.3HG0293320.1	1.0305108	1.3440974	1.50808586	cluster 2
HORVU.MOREX.r3.3HG0293490.1	0.8345457	1.0987903	1.08783324	cluster 2
HORVU.MOREX.r3.3HG0293760.1	0.6830217	1.3727751	1.45386285	cluster 2
HORVU.MOREX.r3.3HG0294040.1	0.404668	0.6441345	0.77944156	cluster 2
HORVU.MOREX.r3.3HG0294110.1	0.4317541	0.6554953	0.9271765	cluster 2
HORVU.MOREX.r3.3HG0294310.1	0.6319281	0.7702235	0.88165333	cluster 2
HORVU.MOREX.r3.3HG0294950.1	0.5721569	1.1659046	1.23153616	cluster 2

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.3HG0294970.2	0.2580354	0.531544	0.85279494	cluster 2
HORVU.MOREX.r3.3HG0295380.1	0.244323	0.7373603	0.71161573	cluster 2
HORVU.MOREX.r3.3HG0296380.1	0.2139823	0.4967027	0.58990296	cluster 2
HORVU.MOREX.r3.3HG0296990.1	-0.028178	0.9248453	0.84704542	cluster 2
HORVU.MOREX.r3.3HG0298090.1	-0.054641	0.6582396	0.80351652	cluster 2
HORVU.MOREX.r3.3HG0298540.1	0.3203182	0.5833246	0.6584545	cluster 2
HORVU.MOREX.r3.3HG0301930.1	0.2016251	0.3889631	0.45439954	cluster 2
HORVU.MOREX.r3.3HG0303210.1	0.5020722	1.0455784	1.17174944	cluster 2
HORVU.MOREX.r3.3HG0303380.1	0.1781205	0.6848632	0.67693005	cluster 2
HORVU.MOREX.r3.3HG0303410.1	0.3390692	0.7666368	0.78439139	cluster 2
HORVU.MOREX.r3.3HG0303560.2	0.5327535	1.2702987	1.61822217	cluster 2
HORVU.MOREX.r3.3HG0303660.1	0.1834872	0.3823286	0.54769047	cluster 2
HORVU.MOREX.r3.3HG0304370.1	0.1834196	0.3751105	0.60819535	cluster 2
HORVU.MOREX.r3.3HG0304490.1	0.8293216	1.0838474	1.31250048	cluster 2
HORVU.MOREX.r3.3HG0305520.1	0.104132	0.5599306	0.69533456	cluster 2
HORVU.MOREX.r3.3HG0305800.1	0.4568399	0.724486	0.76647775	cluster 2
HORVU.MOREX.r3.3HG0306840.1	0.0239969	0.4021271	0.55810977	cluster 2
HORVU.MOREX.r3.3HG0307280.1	0.7045634	0.9952811	1.1344328	cluster 2
HORVU.MOREX.r3.3HG0307400.1	0.7801407	1.2549735	1.28158699	cluster 2
HORVU.MOREX.r3.3HG0308350.1	0.5269863	0.9100809	1.03734012	cluster 2
HORVU.MOREX.r3.3HG0308840.1	0.1481768	0.3742646	0.6264595	cluster 2
HORVU.MOREX.r3.3HG0309930.1	0.4885017	0.975444	1.05341105	cluster 2
HORVU.MOREX.r3.3HG0310920.1	0.2619564	0.5265518	0.62920463	cluster 2
HORVU.MOREX.r3.3HG0312430.1	0.8334222	2.0270515	1.90003817	cluster 2
HORVU.MOREX.r3.3HG0313900.1	1.5263673	1.7945304	1.87306177	cluster 2
HORVU.MOREX.r3.3HG0314070.1	0.4156637	1.3869242	1.44404811	cluster 2
HORVU.MOREX.r3.3HG0314820.1	0.3095286	0.5594509	0.70393134	cluster 2
HORVU.MOREX.r3.3HG0315410.1	0.1108427	0.2769116	0.35979591	cluster 2
HORVU.MOREX.r3.3HG0318700.1	0.1403915	0.3221063	0.50887756	cluster 2
HORVU.MOREX.r3.3HG0319900.1	1.0318526	1.5263922	1.5319189	cluster 2
HORVU.MOREX.r3.3HG0323600.1	0.1933303	0.4262943	0.53259787	cluster 2
HORVU.MOREX.r3.3HG0326330.1	0.3923725	0.9899287	1.03980027	cluster 2
HORVU.MOREX.r3.3HG0327100.1	0.1043931	0.9616848	1.16764068	cluster 2
HORVU.MOREX.r3.3HG0329040.1	1.5667103	2.4205926	2.62444447	cluster 2
HORVU.MOREX.r3.3HG0329870.1	1.3405947	1.8628077	2.00959851	cluster 2
HORVU.MOREX.r3.3HG0330120.1	0.9415784	1.5871535	2.2897583	cluster 2
HORVU.MOREX.r3.4HG0333450.1	0.4112081	0.6776574	0.76167709	cluster 2
HORVU.MOREX.r3.4HG0333650.1	0.0390368	0.3753369	0.43009465	cluster 2
HORVU.MOREX.r3.4HG0334360.1	0.4920948	1.0129823	1.10859449	cluster 2
HORVU.MOREX.r3.4HG0334600.1	0.2362238	0.4697044	0.60556625	cluster 2
HORVU.MOREX.r3.4HG0335160.1	0.575435	0.8010621	0.77857999	cluster 2
HORVU.MOREX.r3.4HG0335830.1	0.1900917	0.2945307	0.3712031	cluster 2
HORVU.MOREX.r3.4HG0337040.1	0.4629059	0.7655924	0.99127762	cluster 2
HORVU.MOREX.r3.4HG0337770.1	0.0355463	0.463949	0.57217308	cluster 2
HORVU.MOREX.r3.4HG0337870.1	0.1402813	0.8222738	0.75116839	cluster 2
HORVU.MOREX.r3.4HG0338070.1	0.5763057	0.9751026	1.07352575	cluster 2
HORVU.MOREX.r3.4HG0339890.1	0.9900853	1.6938507	1.68582548	cluster 2

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.4HG0340910.2	1.5464803	2.3316632	2.52756548	cluster 2
HORVU.MOREX.r3.4HG0341050.1	0.6468136	1.3654148	1.50733577	cluster 2
HORVU.MOREX.r3.4HG0341800.1	0.3931678	0.6513793	0.83585319	cluster 2
HORVU.MOREX.r3.4HG0342080.1	0.2705359	0.6939733	0.7656478	cluster 2
HORVU.MOREX.r3.4HG0342660.1	0.6725532	1.2454115	1.266999	cluster 2
HORVU.MOREX.r3.4HG0343040.1	0.1746996	0.5204223	0.7760771	cluster 2
HORVU.MOREX.r3.4HG0343050.1	0.2833578	0.4298264	0.49476416	cluster 2
HORVU.MOREX.r3.4HG0343260.1	0.5825461	1.1123837	1.41752398	cluster 2
HORVU.MOREX.r3.4HG0344370.1	0.8558216	1.6664461	1.8305369	cluster 2
HORVU.MOREX.r3.4HG0344790.1	0.2268993	0.4391813	0.45317672	cluster 2
HORVU.MOREX.r3.4HG0345260.1	1.0256867	1.1938476	1.20978148	cluster 2
HORVU.MOREX.r3.4HG0345990.1	-0.064489	0.3767458	0.51143182	cluster 2
HORVU.MOREX.r3.4HG0346830.1	1.1709522	1.9494157	2.07744307	cluster 2
HORVU.MOREX.r3.4HG0347760.1	0.1447569	0.4451303	0.66666929	cluster 2
HORVU.MOREX.r3.4HG0348380.1	0.5362334	0.8289037	0.91855597	cluster 2
HORVU.MOREX.r3.4HG0349080.1	0.2161735	0.4842153	0.72832219	cluster 2
HORVU.MOREX.r3.4HG0351070.1	0.0673531	0.3588632	0.74699814	cluster 2
HORVU.MOREX.r3.4HG0352200.1	0.45411	0.6246446	0.68749416	cluster 2
HORVU.MOREX.r3.4HG0352780.1	0.2452678	0.5738966	0.75116078	cluster 2
HORVU.MOREX.r3.4HG0353390.1	0.2763529	0.8060027	0.84907564	cluster 2
HORVU.MOREX.r3.4HG0354010.1	1.6504168	2.1037581	2.2176036	cluster 2
HORVU.MOREX.r3.4HG0354980.1	0.477069	0.6872052	0.97622784	cluster 2
HORVU.MOREX.r3.4HG0356280.1	0.4156574	0.955948	1.0671736	cluster 2
HORVU.MOREX.r3.4HG0356690.1	0.496617	0.8638757	1.10307239	cluster 2
HORVU.MOREX.r3.4HG0356860.1	0.4296005	0.9932794	0.93839516	cluster 2
HORVU.MOREX.r3.4HG0359960.1	0.0481177	0.2615211	0.3106003	cluster 2
HORVU.MOREX.r3.4HG0364050.1	0.3615742	0.7555068	0.76165059	cluster 2
HORVU.MOREX.r3.4HG0378080.1	1.3501296	2.8965001	2.88167628	cluster 2
HORVU.MOREX.r3.4HG0379260.1	0.3001805	0.5027635	0.63639233	cluster 2
HORVU.MOREX.r3.4HG0379400.1	0.4957518	0.8120354	1.06799756	cluster 2
HORVU.MOREX.r3.4HG0379660.1	0.6626674	1.4889937	1.43081562	cluster 2
HORVU.MOREX.r3.4HG0380540.1	0.4686172	0.7116699	0.8090097	cluster 2
HORVU.MOREX.r3.4HG0381790.1	0.4115763	1.1527833	1.08853007	cluster 2
HORVU.MOREX.r3.4HG0381990.1	0.3432611	0.924176	1.46516005	cluster 2
HORVU.MOREX.r3.4HG0382550.1	0.2568968	0.6590222	0.63661169	cluster 2
HORVU.MOREX.r3.4HG0382610.1	0.6480635	1.3044924	1.24352216	cluster 2
HORVU.MOREX.r3.4HG0383280.1	0.1986514	0.4795672	0.70614599	cluster 2
HORVU.MOREX.r3.4HG0383530.3	0.3284265	0.7387163	0.94778101	cluster 2
HORVU.MOREX.r3.4HG0383670.1	0.5060547	1.153631	1.29406186	cluster 2
HORVU.MOREX.r3.4HG0383780.1	0.799171	1.8433864	1.80427655	cluster 2
HORVU.MOREX.r3.4HG0384390.1	0.8730756	1.1942553	1.39596124	cluster 2
HORVU.MOREX.r3.4HG0384400.1	0.2391783	0.4010898	0.50728861	cluster 2
HORVU.MOREX.r3.4HG0384780.1	1.8829206	3.1804654	3.25352083	cluster 2
HORVU.MOREX.r3.4HG0386800.1	0.0156825	0.2490754	0.28139142	cluster 2
HORVU.MOREX.r3.4HG0387580.1	0.0049719	0.2238315	0.32716647	cluster 2
HORVU.MOREX.r3.4HG0388310.1	0.3021673	0.4118418	0.42517248	cluster 2
HORVU.MOREX.r3.4HG0388440.1	0.3905342	0.8014992	0.87568721	cluster 2

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.4HG0389200.1	0.4199592	0.7002946	0.81906453	cluster 2
HORVU.MOREX.r3.4HG0391130.1	0.2318906	0.4926743	0.47882861	cluster 2
HORVU.MOREX.r3.4HG0391260.1	0.2829957	0.4690374	0.61470029	cluster 2
HORVU.MOREX.r3.4HG0392230.1	0.6502808	1.0714124	1.38221333	cluster 2
HORVU.MOREX.r3.4HG0392680.1	0.3636547	0.5668818	0.79741976	cluster 2
HORVU.MOREX.r3.4HG0392940.1	0.2260992	0.4908348	0.52022384	cluster 2
HORVU.MOREX.r3.4HG0393520.1	0.272282	0.7815714	0.74873951	cluster 2
HORVU.MOREX.r3.4HG0393710.1	0.2070321	0.8328329	1.00129397	cluster 2
HORVU.MOREX.r3.4HG0393870.1	0.8422932	1.5099747	1.68495442	cluster 2
HORVU.MOREX.r3.4HG0394870.1	0.2343377	0.8269788	1.10620424	cluster 2
HORVU.MOREX.r3.4HG0395940.1	0.9225598	1.4318554	1.45687047	cluster 2
HORVU.MOREX.r3.4HG0396030.1	0.9705374	1.9385054	1.83872192	cluster 2
HORVU.MOREX.r3.4HG0397010.1	0.9666427	1.5883306	1.92837147	cluster 2
HORVU.MOREX.r3.4HG0397530.1	0.3634674	0.8982456	1.0804083	cluster 2
HORVU.MOREX.r3.4HG0398050.1	0.7947834	1.416871	1.59561309	cluster 2
HORVU.MOREX.r3.4HG0398090.1	0.2618222	0.6719989	0.81460377	cluster 2
HORVU.MOREX.r3.4HG0398550.1	0.4094856	0.9569696	1.04927534	cluster 2
HORVU.MOREX.r3.4HG0399470.1	0.8254288	2.2371615	2.52968369	cluster 2
HORVU.MOREX.r3.4HG0399530.1	1.2854404	1.7500597	1.70869347	cluster 2
HORVU.MOREX.r3.4HG0400040.1	0.3088012	0.4532839	0.60372683	cluster 2
HORVU.MOREX.r3.4HG0400840.1	0.4045477	0.7406587	0.90631406	cluster 2
HORVU.MOREX.r3.4HG0400920.1	0.7049011	1.2452702	1.31393698	cluster 2
HORVU.MOREX.r3.4HG0401630.1	0.4531026	0.6001547	0.67908155	cluster 2
HORVU.MOREX.r3.4HG0401980.1	1.4130215	2.7376907	2.83320209	cluster 2
HORVU.MOREX.r3.4HG0402650.1	0.3316932	0.762461	0.82507227	cluster 2
HORVU.MOREX.r3.4HG0402730.1	1.0848712	1.9165727	1.83720141	cluster 2
HORVU.MOREX.r3.4HG0404740.1	0.181578	0.4822729	0.80757972	cluster 2
HORVU.MOREX.r3.4HG0405400.1	0.9809624	1.8846201	1.84235306	cluster 2
HORVU.MOREX.r3.4HG0405780.1	0.2309227	0.4082526	0.63931514	cluster 2
HORVU.MOREX.r3.4HG0405920.1	0.6550032	1.5808902	1.53146869	cluster 2
HORVU.MOREX.r3.4HG0406060.1	0.8964474	2.2873495	2.60646335	cluster 2
HORVU.MOREX.r3.4HG0406140.1	0.0768009	0.4622742	0.48942009	cluster 2
HORVU.MOREX.r3.4HG0406600.1	0.5288912	0.7448671	0.88836529	cluster 2
HORVU.MOREX.r3.4HG0406630.1	0.2646697	0.5942882	0.71951802	cluster 2
HORVU.MOREX.r3.4HG0407470.1	0.4171851	0.8652511	0.89349686	cluster 2
HORVU.MOREX.r3.4HG0407990.1	0.2373114	0.6788043	0.87073362	cluster 2
HORVU.MOREX.r3.4HG0408000.1	1.1643976	1.8015354	2.63989086	cluster 2
HORVU.MOREX.r3.4HG0408780.1	-0.943287	2.0851534	1.97751546	cluster 2
HORVU.MOREX.r3.4HG0409670.1	0.8149989	1.0992152	1.17181536	cluster 2
HORVU.MOREX.r3.4HG0410090.1	0.3287014	0.4503451	0.5981346	cluster 2
HORVU.MOREX.r3.4HG0412090.1	0.7596638	1.8386347	1.81770888	cluster 2
HORVU.MOREX.r3.4HG0412430.1	-0.022167	0.4239312	0.43177193	cluster 2
HORVU.MOREX.r3.4HG0412790.1	0.532284	0.6579071	0.73362573	cluster 2
HORVU.MOREX.r3.4HG0413800.1	0.1734431	0.3904929	0.47772268	cluster 2
HORVU.MOREX.r3.4HG0415170.1	0.2963256	1.1164611	1.54423623	cluster 2
HORVU.MOREX.r3.4HG0416390.1	0.9077139	1.2040081	1.34727728	cluster 2
HORVU.MOREX.r3.4HG0417010.1	1.1506263	1.9261093	1.94717723	cluster 2

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.4HG0417160.1	0.2855021	0.5117306	0.5733361	cluster 2
HORVU.MOREX.r3.4HG0417320.1	0.8115794	1.409745	1.5882952	cluster 2
HORVU.MOREX.r3.4HG0417670.1	0.8401505	1.218021	1.19228366	cluster 2
HORVU.MOREX.r3.4HG0418460.1	0.2791984	0.3610209	0.39910965	cluster 2
HORVU.MOREX.r3.5HG0419590.1	0.1288701	0.4173495	0.51122227	cluster 2
HORVU.MOREX.r3.5HG0420080.1	0.1730085	0.3711592	0.42195773	cluster 2
HORVU.MOREX.r3.5HG0420830.1	0.3019412	1.1288759	1.28831804	cluster 2
HORVU.MOREX.r3.5HG0420970.1	0.3232078	0.6296639	0.89150456	cluster 2
HORVU.MOREX.r3.5HG0420980.1	0.3949095	0.5844236	0.79194101	cluster 2
HORVU.MOREX.r3.5HG0422080.1	0.2802278	0.4229508	0.4267247	cluster 2
HORVU.MOREX.r3.5HG0425250.1	0.7698766	1.2337542	1.55042174	cluster 2
HORVU.MOREX.r3.5HG0428270.2	0.0671169	0.4139552	0.69077879	cluster 2
HORVU.MOREX.r3.5HG0430940.1	0.4923077	0.9284412	1.09685903	cluster 2
HORVU.MOREX.r3.5HG0432950.1	0.1672651	0.4212326	0.45154427	cluster 2
HORVU.MOREX.r3.5HG0433470.1	0.2047951	0.2934084	0.35811409	cluster 2
HORVU.MOREX.r3.5HG0437110.1	0.1078287	0.2902869	0.50892863	cluster 2
HORVU.MOREX.r3.5HG0442460.1	0.1475444	0.3101127	0.44211993	cluster 2
HORVU.MOREX.r3.5HG0444350.1	0.2384017	0.7529188	0.8246533	cluster 2
HORVU.MOREX.r3.5HG0446420.1	0.399862	0.6221633	0.76528343	cluster 2
HORVU.MOREX.r3.5HG0449620.1	0.3227242	0.6800839	0.72840761	cluster 2
HORVU.MOREX.r3.5HG0454230.1	0.3450621	0.7756468	0.75101708	cluster 2
HORVU.MOREX.r3.5HG0457310.1	0.3793025	1.1601469	1.1265514	cluster 2
HORVU.MOREX.r3.5HG0458010.1	0.1073535	0.182246	0.27477234	cluster 2
HORVU.MOREX.r3.5HG0461280.1	0.3619618	0.5180967	0.5913279	cluster 2
HORVU.MOREX.r3.5HG0461950.1	-0.007288	0.8501847	0.80316713	cluster 2
HORVU.MOREX.r3.5HG0462220.1	0.368836	0.7981703	0.94321337	cluster 2
HORVU.MOREX.r3.5HG0463550.1	0.4243225	0.8470079	1.04395853	cluster 2
HORVU.MOREX.r3.5HG0464440.1	0.8676465	1.0462781	1.03930402	cluster 2
HORVU.MOREX.r3.5HG0465270.1	0.3607954	0.6702523	0.74170566	cluster 2
HORVU.MOREX.r3.5HG0465400.1	0.5373646	1.1918769	1.21332619	cluster 2
HORVU.MOREX.r3.5HG0465690.1	0.2593417	0.5542937	0.82829633	cluster 2
HORVU.MOREX.r3.5HG0469120.1	1.2168502	1.5890204	1.73777658	cluster 2
HORVU.MOREX.r3.5HG0471520.1	0.2693765	0.3952702	0.54907622	cluster 2
HORVU.MOREX.r3.5HG0472810.1	0.4125309	0.8835838	0.85386721	cluster 2
HORVU.MOREX.r3.5HG0472840.1	0.0019756	0.2382994	0.5109538	cluster 2
HORVU.MOREX.r3.5HG0472870.1	0.193304	0.527352	0.63912229	cluster 2
HORVU.MOREX.r3.5HG0473520.1	0.1275543	0.2431925	0.39199122	cluster 2
HORVU.MOREX.r3.5HG0477220.1	0.7841996	1.0146353	1.05301851	cluster 2
HORVU.MOREX.r3.5HG0477800.1	0.4977347	0.6934595	0.74789724	cluster 2
HORVU.MOREX.r3.5HG0478050.1	0.2641038	0.45175	0.60793165	cluster 2
HORVU.MOREX.r3.5HG0479500.1	1.2590247	1.4855937	1.60256641	cluster 2
HORVU.MOREX.r3.5HG0479810.1	0.0426092	0.1361107	0.23748287	cluster 2
HORVU.MOREX.r3.5HG0480600.1	-0.152634	1.3959017	1.84601562	cluster 2
HORVU.MOREX.r3.5HG0482670.1	0.8283812	1.3690747	1.54939215	cluster 2
HORVU.MOREX.r3.5HG0484180.1	0.301845	0.4084648	0.44929194	cluster 2
HORVU.MOREX.r3.5HG0484660.1	0.6494517	1.4891231	1.49141657	cluster 2
HORVU.MOREX.r3.5HG0485610.1	0.8402966	1.1851522	1.35797644	cluster 2

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.5HG0486610.1	0.3195001	0.728249	0.83150623	cluster 2
HORVU.MOREX.r3.5HG0486750.1	0.2180509	0.7341424	0.87387666	cluster 2
HORVU.MOREX.r3.5HG0490520.1	0.1978655	0.6820398	0.87944905	cluster 2
HORVU.MOREX.r3.5HG0490610.1	0.8011162	1.8063093	1.71784466	cluster 2
HORVU.MOREX.r3.5HG0490800.1	0.9275562	1.2475257	1.64621621	cluster 2
HORVU.MOREX.r3.5HG0493040.1	0.2080434	0.5060233	0.55263335	cluster 2
HORVU.MOREX.r3.5HG0494040.1	0.2203348	1.6371662	1.85311292	cluster 2
HORVU.MOREX.r3.5HG0495240.1	0.4517982	0.773699	1.05799994	cluster 2
HORVU.MOREX.r3.5HG0495730.1	0.5876246	0.9852875	1.15328876	cluster 2
HORVU.MOREX.r3.5HG0495860.1	0.5515498	0.7776646	0.76335005	cluster 2
HORVU.MOREX.r3.5HG0496780.1	0.173293	0.2889691	0.43670843	cluster 2
HORVU.MOREX.r3.5HG0496930.1	0.2323162	0.6896972	0.83641896	cluster 2
HORVU.MOREX.r3.5HG0497490.1	0.8369841	1.3476139	1.76946037	cluster 2
HORVU.MOREX.r3.5HG0497900.1	0.5995338	0.9889431	0.99618653	cluster 2
HORVU.MOREX.r3.5HG0501170.1	0.3852307	0.5130394	0.64276813	cluster 2
HORVU.MOREX.r3.5HG0501380.1	0.0844627	0.2130409	0.34496489	cluster 2
HORVU.MOREX.r3.5HG0504720.1	0.1014129	0.3259423	0.30528838	cluster 2
HORVU.MOREX.r3.5HG0508870.1	0.2668091	0.5499848	0.75040954	cluster 2
HORVU.MOREX.r3.5HG0509020.1	0.2692762	0.7428903	1.01310401	cluster 2
HORVU.MOREX.r3.5HG0511090.1	0.3390588	0.5528819	0.69682833	cluster 2
HORVU.MOREX.r3.5HG0511450.1	0.3371689	0.4258705	0.43400053	cluster 2
HORVU.MOREX.r3.5HG0513740.1	0.6270661	1.1857086	1.59899486	cluster 2
HORVU.MOREX.r3.5HG0513780.1	0.1784336	0.6028146	0.64852256	cluster 2
HORVU.MOREX.r3.5HG0513900.1	0.5238724	0.6676236	0.78546448	cluster 2
HORVU.MOREX.r3.5HG0513980.1	0.7987007	1.2576441	1.34151688	cluster 2
HORVU.MOREX.r3.5HG0517190.1	0.3748177	0.612034	0.70295419	cluster 2
HORVU.MOREX.r3.5HG0517240.1	0.1112988	0.2599837	0.39148009	cluster 2
HORVU.MOREX.r3.5HG0517260.1	0.2473357	0.4833552	0.54054673	cluster 2
HORVU.MOREX.r3.5HG0517490.1	0.2353696	0.4646789	0.764187	cluster 2
HORVU.MOREX.r3.5HG0519360.1	0.4833657	0.6959955	0.96840789	cluster 2
HORVU.MOREX.r3.5HG0521630.1	0.0963929	0.513868	0.66457976	cluster 2
HORVU.MOREX.r3.5HG0523860.1	0.1661731	0.3948824	0.5181811	cluster 2
HORVU.MOREX.r3.5HG0524060.1	0.7913655	1.2930894	1.32015096	cluster 2
HORVU.MOREX.r3.5HG0525430.1	0.3646986	0.7086655	0.74596087	cluster 2
HORVU.MOREX.r3.5HG0525850.1	0.2909068	0.5240224	0.68520648	cluster 2
HORVU.MOREX.r3.5HG0527460.1	0.9758297	1.4137042	1.40692609	cluster 2
HORVU.MOREX.r3.5HG0527720.1	0.7336271	0.9795008	1.0821862	cluster 2
HORVU.MOREX.r3.5HG0528280.1	0.2352558	0.4249636	0.51270501	cluster 2
HORVU.MOREX.r3.5HG0528310.1	0.5307114	0.5710331	0.60443093	cluster 2
HORVU.MOREX.r3.5HG0531070.1	2.5625885	3.4057006	3.68460448	cluster 2
HORVU.MOREX.r3.5HG0532200.1	0.541597	0.6596337	0.81273203	cluster 2
HORVU.MOREX.r3.5HG0532560.1	1.4614443	1.8418639	1.89784638	cluster 2
HORVU.MOREX.r3.5HG0533760.1	0.8064972	1.2863139	1.36594148	cluster 2
HORVU.MOREX.r3.5HG0534420.1	0.343871	0.784436	0.84107089	cluster 2
HORVU.MOREX.r3.5HG0535180.1	1.1571559	1.6750447	1.72444736	cluster 2
HORVU.MOREX.r3.5HG0536200.1	0.8263819	1.101929	1.076437	cluster 2
HORVU.MOREX.r3.5HG0536610.1	0.1008134	0.6016052	0.65610442	cluster 2

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.5HG0537150.1	0.7193756	1.4313003	1.70040162	cluster 2
HORVU.MOREX.r3.5HG0537360.1	1.4914172	2.099833	2.28994247	cluster 2
HORVU.MOREX.r3.6HG0539590.1	0.5752701	0.7797706	0.98364708	cluster 2
HORVU.MOREX.r3.6HG0542030.1	0.6563637	1.0902273	1.30863958	cluster 2
HORVU.MOREX.r3.6HG0542040.1	0.520591	0.9251602	1.32881351	cluster 2
HORVU.MOREX.r3.6HG0542050.1	0.8135932	1.2932291	1.55494779	cluster 2
HORVU.MOREX.r3.6HG0542320.1	0.3619709	1.2739338	1.21269683	cluster 2
HORVU.MOREX.r3.6HG0544350.1	0.1825648	0.3996631	0.42312297	cluster 2
HORVU.MOREX.r3.6HG0546160.1	0.4494889	0.7885519	1.07728293	cluster 2
HORVU.MOREX.r3.6HG0547010.1	0.4113203	0.6171305	0.88044854	cluster 2
HORVU.MOREX.r3.6HG0547020.1	0.3323692	0.905998	1.15425002	cluster 2
HORVU.MOREX.r3.6HG0547030.1	0.4545781	0.7414847	1.11423101	cluster 2
HORVU.MOREX.r3.6HG0547570.1	0.0745734	0.2591938	0.3948071	cluster 2
HORVU.MOREX.r3.6HG0547660.1	1.4830317	2.2438891	2.39181162	cluster 2
HORVU.MOREX.r3.6HG0549810.1	0.1829943	0.3580765	0.52235269	cluster 2
HORVU.MOREX.r3.6HG0550600.1	0.8517285	1.3576493	1.56083185	cluster 2
HORVU.MOREX.r3.6HG0551650.1	0.2633161	0.4528928	0.43997862	cluster 2
HORVU.MOREX.r3.6HG0554050.1	0.5180914	0.8651744	0.89134845	cluster 2
HORVU.MOREX.r3.6HG0554700.1	0.0898452	0.2560453	0.30452703	cluster 2
HORVU.MOREX.r3.6HG0554840.1	0.2615541	0.6312156	0.87777144	cluster 2
HORVU.MOREX.r3.6HG0555040.1	0.287924	0.5201071	0.52012828	cluster 2
HORVU.MOREX.r3.6HG0555250.1	0.3416737	1.7096039	2.16806086	cluster 2
HORVU.MOREX.r3.6HG0556240.1	0.2417086	0.3349085	0.45552598	cluster 2
HORVU.MOREX.r3.6HG0557920.1	0.4135744	0.9231393	1.06960137	cluster 2
HORVU.MOREX.r3.6HG0559990.1	0.464411	0.8158961	0.94593506	cluster 2
HORVU.MOREX.r3.6HG0560710.1	0.1098479	0.2120663	0.26306374	cluster 2
HORVU.MOREX.r3.6HG0560930.1	0.3078785	0.4763428	0.64037642	cluster 2
HORVU.MOREX.r3.6HG0565950.1	0.8249902	1.1625846	1.3935857	cluster 2
HORVU.MOREX.r3.6HG0566940.1	0.3821272	0.5756211	0.58031974	cluster 2
HORVU.MOREX.r3.6HG0567150.1	0.5391259	1.0741839	1.15932802	cluster 2
HORVU.MOREX.r3.6HG0567370.2	0.3978744	0.7186024	0.79653984	cluster 2
HORVU.MOREX.r3.6HG0568910.1	0.3789607	0.5723245	0.82335041	cluster 2
HORVU.MOREX.r3.6HG0570430.1	-0.06227	0.224238	0.37468298	cluster 2
HORVU.MOREX.r3.6HG0573150.1	0.1594812	0.2897869	0.3891766	cluster 2
HORVU.MOREX.r3.6HG0573290.1	0.1302786	0.3153781	0.31968137	cluster 2
HORVU.MOREX.r3.6HG0573920.1	0.766951	1.4144927	1.47543076	cluster 2
HORVU.MOREX.r3.6HG0574950.1	0.2496861	0.4242427	0.65298771	cluster 2
HORVU.MOREX.r3.6HG0582120.1	0.20045	0.4747158	0.47731547	cluster 2
HORVU.MOREX.r3.6HG0582480.1	0.3956409	0.7421302	0.92358983	cluster 2
HORVU.MOREX.r3.6HG0585240.1	0.5852624	1.0308635	1.03198216	cluster 2
HORVU.MOREX.r3.6HG0588520.1	0.4279784	0.9427609	0.97156598	cluster 2
HORVU.MOREX.r3.6HG0589860.1	0.424529	0.7956522	0.79276116	cluster 2
HORVU.MOREX.r3.6HG0593050.1	0.3094143	0.588504	0.91078424	cluster 2
HORVU.MOREX.r3.6HG0593390.1	1.0727411	1.2641774	1.36503238	cluster 2
HORVU.MOREX.r3.6HG0596770.1	0.3412317	0.6308943	0.73754549	cluster 2
HORVU.MOREX.r3.6HG0597400.2	0.4998391	0.90667	1.31877775	cluster 2
HORVU.MOREX.r3.6HG0599900.1	0.2909016	0.5333152	0.62981831	cluster 2

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.6HG0601160.1	0.3158278	0.5490306	0.68381175	cluster 2
HORVU.MOREX.r3.6HG0601180.1	0.488909	0.7011847	0.91844231	cluster 2
HORVU.MOREX.r3.6HG0601260.1	0.511754	1.0425773	1.10705238	cluster 2
HORVU.MOREX.r3.6HG0601680.1	0.415202	0.6723902	0.8621493	cluster 2
HORVU.MOREX.r3.6HG0601830.1	1.0243086	1.6885951	1.74978443	cluster 2
HORVU.MOREX.r3.6HG0602210.1	0.5105762	0.6931835	0.84292741	cluster 2
HORVU.MOREX.r3.6HG0603210.1	0.7727444	1.4604009	2.04263675	cluster 2
HORVU.MOREX.r3.6HG0605150.1	0.3535078	0.6842286	0.90491722	cluster 2
HORVU.MOREX.r3.6HG0605160.1	0.1637581	0.3544376	0.48022311	cluster 2
HORVU.MOREX.r3.6HG0605940.1	0.3250967	0.6384968	0.71767755	cluster 2
HORVU.MOREX.r3.6HG0605960.1	0.277122	0.5627489	0.68714776	cluster 2
HORVU.MOREX.r3.6HG0606140.1	-0.141648	1.0420557	2.00505825	cluster 2
HORVU.MOREX.r3.6HG0606360.1	1.031606	2.0810804	2.19827158	cluster 2
HORVU.MOREX.r3.6HG0607960.1	0.1238032	0.3404552	0.53025735	cluster 2
HORVU.MOREX.r3.6HG0608910.1	0.762652	1.0527539	1.21866412	cluster 2
HORVU.MOREX.r3.6HG0610500.1	0.5111657	0.9589503	1.09267208	cluster 2
HORVU.MOREX.r3.6HG0610890.1	0.1242264	0.3310396	0.4677181	cluster 2
HORVU.MOREX.r3.6HG0614110.1	0.1992911	0.3322784	0.39232921	cluster 2
HORVU.MOREX.r3.6HG0614840.1	0.0167346	0.3206517	0.56924838	cluster 2
HORVU.MOREX.r3.6HG0614870.1	0.3853101	0.670507	0.71305407	cluster 2
HORVU.MOREX.r3.6HG0615130.1	0.2970304	0.663016	0.68977244	cluster 2
HORVU.MOREX.r3.6HG0615630.1	0.1912273	0.4608209	0.47468987	cluster 2
HORVU.MOREX.r3.6HG0616130.1	0.19623	0.4546644	0.58864528	cluster 2
HORVU.MOREX.r3.6HG0616300.1	0.1392149	0.3896496	0.5502242	cluster 2
HORVU.MOREX.r3.6HG0617080.1	0.1546483	0.3857756	0.5070965	cluster 2
HORVU.MOREX.r3.6HG0619500.1	0.6282363	1.4464878	1.49013116	cluster 2
HORVU.MOREX.r3.6HG0620520.1	0.3558299	0.7667271	0.9000793	cluster 2
HORVU.MOREX.r3.6HG0620630.1	0.4602424	0.9172385	1.01213706	cluster 2
HORVU.MOREX.r3.6HG0620720.1	0.6013842	0.9252779	0.95546276	cluster 2
HORVU.MOREX.r3.6HG0622080.1	0.3824593	0.6294396	0.69296603	cluster 2
HORVU.MOREX.r3.6HG0622120.1	0.2692973	0.4714377	0.57379924	cluster 2
HORVU.MOREX.r3.6HG0622250.1	0.9393621	1.4391752	1.38710931	cluster 2
HORVU.MOREX.r3.6HG0624240.1	0.4357281	0.7386809	0.86573578	cluster 2
HORVU.MOREX.r3.6HG0624460.1	0.0187827	1.2833566	2.05973085	cluster 2
HORVU.MOREX.r3.6HG0625570.1	0.3311309	0.5716644	0.65982525	cluster 2
HORVU.MOREX.r3.6HG0626070.1	0.2709765	0.4237318	0.56957533	cluster 2
HORVU.MOREX.r3.6HG0628790.1	0.2688086	0.4943078	0.72855732	cluster 2
HORVU.MOREX.r3.6HG0629240.1	1.3152298	1.4994885	1.74505029	cluster 2
HORVU.MOREX.r3.6HG0631600.1	0.5506977	1.1166081	1.12470387	cluster 2
HORVU.MOREX.r3.6HG0631700.1	0.1635609	0.3671579	0.44161692	cluster 2
HORVU.MOREX.r3.6HG0631710.1	0.6147842	1.0170948	1.05782311	cluster 2
HORVU.MOREX.r3.6HG0632020.2	0.8245057	1.1398974	1.44812562	cluster 2
HORVU.MOREX.r3.6HG0633510.1	0.2162093	0.3727915	0.58087212	cluster 2
HORVU.MOREX.r3.7HG0636370.1	-0.154745	0.6267003	1.41091824	cluster 2
HORVU.MOREX.r3.7HG0636630.1	0.5256918	1.0699841	1.23352911	cluster 2
HORVU.MOREX.r3.7HG0638370.1	0.323149	0.605877	0.72929621	cluster 2
HORVU.MOREX.r3.7HG0639360.1	0.3404557	0.6165901	0.74913007	cluster 2

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.7HG0640800.1	1.1123416	1.6968407	2.1802692	cluster 2
HORVU.MOREX.r3.7HG0641030.1	0.6312965	1.4336324	1.34905455	cluster 2
HORVU.MOREX.r3.7HG0641750.1	2.1002884	2.8860427	2.97912163	cluster 2
HORVU.MOREX.r3.7HG0642940.1	0.2559375	1.9017177	1.86045285	cluster 2
HORVU.MOREX.r3.7HG0644190.1	0.2202766	0.4281783	0.56414754	cluster 2
HORVU.MOREX.r3.7HG0648620.1	0.9283434	1.3347288	1.42138496	cluster 2
HORVU.MOREX.r3.7HG0649950.1	0.2948762	0.6041181	0.64772697	cluster 2
HORVU.MOREX.r3.7HG0650300.1	0.2487571	0.4879088	0.67397048	cluster 2
HORVU.MOREX.r3.7HG0650530.2	1.2490283	1.6020453	1.66694647	cluster 2
HORVU.MOREX.r3.7HG0650950.1	0.0013464	0.2622808	0.44287508	cluster 2
HORVU.MOREX.r3.7HG0653380.1	0.9012942	1.3602381	1.43901056	cluster 2
HORVU.MOREX.r3.7HG0655100.1	0.2582812	0.4796561	0.52609551	cluster 2
HORVU.MOREX.r3.7HG0656030.1	0.1608324	0.4685297	0.61465027	cluster 2
HORVU.MOREX.r3.7HG0657010.1	0.2492701	0.4034795	0.52140551	cluster 2
HORVU.MOREX.r3.7HG0657330.1	0.1585255	0.2883706	0.42685057	cluster 2
HORVU.MOREX.r3.7HG0659040.1	0.2778608	0.8372696	0.96093387	cluster 2
HORVU.MOREX.r3.7HG0661470.1	0.3378853	0.649975	0.71511032	cluster 2
HORVU.MOREX.r3.7HG0661830.1	1.1463543	2.311953	2.19335103	cluster 2
HORVU.MOREX.r3.7HG0664720.1	0.6858335	1.1720211	1.14764425	cluster 2
HORVU.MOREX.r3.7HG0665990.1	0.1996344	0.5791237	0.62468426	cluster 2
HORVU.MOREX.r3.7HG0667540.1	0.2050488	0.4309773	0.62799912	cluster 2
HORVU.MOREX.r3.7HG0667610.1	1.1030737	1.5331211	1.52933442	cluster 2
HORVU.MOREX.r3.7HG0667620.1	0.893003	1.390352	1.51892579	cluster 2
HORVU.MOREX.r3.7HG0667630.1	0.7991252	1.0749149	1.18015378	cluster 2
HORVU.MOREX.r3.7HG0667660.1	0.4127201	0.6768874	0.93421058	cluster 2
HORVU.MOREX.r3.7HG0667680.1	0.4618684	0.7090718	1.00940936	cluster 2
HORVU.MOREX.r3.7HG0667780.1	0.1856161	0.5576689	0.58250129	cluster 2
HORVU.MOREX.r3.7HG0668440.1	0.5007339	0.5590214	0.58100318	cluster 2
HORVU.MOREX.r3.7HG0669590.1	0.4147112	1.4633242	1.38950404	cluster 2
HORVU.MOREX.r3.7HG0670690.1	0.4063011	0.6171257	0.62126112	cluster 2
HORVU.MOREX.r3.7HG0672960.1	0.7646285	1.1752983	1.53415731	cluster 2
HORVU.MOREX.r3.7HG0673710.1	0.5399536	1.2426141	1.43695975	cluster 2
HORVU.MOREX.r3.7HG0674600.1	0.3618624	0.6940338	1.11592901	cluster 2
HORVU.MOREX.r3.7HG0674720.1	1.2608873	2.2130867	2.11722617	cluster 2
HORVU.MOREX.r3.7HG0676690.1	0.4287134	0.8020907	0.81600374	cluster 2
HORVU.MOREX.r3.7HG0677770.1	0.1595816	0.51013	0.49546538	cluster 2
HORVU.MOREX.r3.7HG0679050.1	0.2594055	0.5656885	0.7228548	cluster 2
HORVU.MOREX.r3.7HG0679060.1	-0.009673	0.3316562	0.79732488	cluster 2
HORVU.MOREX.r3.7HG0681050.1	0.1644495	0.2917135	0.4296793	cluster 2
HORVU.MOREX.r3.7HG0683940.1	0.5078305	0.7645397	0.89184404	cluster 2
HORVU.MOREX.r3.7HG0684180.1	0.288567	0.6461458	0.61388343	cluster 2
HORVU.MOREX.r3.7HG0684880.1	0.3850775	0.7208246	0.79923951	cluster 2
HORVU.MOREX.r3.7HG0685360.1	0.2818553	0.4289727	0.60499427	cluster 2
HORVU.MOREX.r3.7HG0685920.1	0.1563281	0.4299148	0.5382098	cluster 2
HORVU.MOREX.r3.7HG0685970.1	0.2689053	0.4909085	0.76916821	cluster 2
HORVU.MOREX.r3.7HG0688930.1	0.3464928	0.8284437	0.80884317	cluster 2
HORVU.MOREX.r3.7HG0690090.1	0.293307	0.7387097	0.8379731	cluster 2

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.7HG0699010.1	0.5478962	1.3781398	2.21993619	cluster 2
HORVU.MOREX.r3.7HG0699020.1	0.9413463	1.4926843	1.85111967	cluster 2
HORVU.MOREX.r3.7HG0702070.1	0.1648653	0.8832185	1.29303519	cluster 2
HORVU.MOREX.r3.7HG0704450.1	0.2471358	0.5251608	0.6036671	cluster 2
HORVU.MOREX.r3.7HG0705500.1	-0.353763	1.0926535	1.09689662	cluster 2
HORVU.MOREX.r3.7HG0705860.1	0.0512008	0.3069656	0.47617723	cluster 2
HORVU.MOREX.r3.7HG0706310.1	0.3041754	0.4370852	0.48102721	cluster 2
HORVU.MOREX.r3.7HG0707160.1	1.0650226	1.6882276	1.66223207	cluster 2
HORVU.MOREX.r3.7HG0707220.1	0.1437703	0.6143529	0.62104562	cluster 2
HORVU.MOREX.r3.7HG0707700.1	0.4027753	1.2813403	1.299693	cluster 2
HORVU.MOREX.r3.7HG0709270.1	0.6162508	0.8876136	1.01067133	cluster 2
HORVU.MOREX.r3.7HG0711270.1	0.3761801	0.7568498	0.80735751	cluster 2
HORVU.MOREX.r3.7HG0711890.1	0.4657853	1.0349723	1.31182187	cluster 2
HORVU.MOREX.r3.7HG0715170.1	1.3493185	1.5050292	1.53037937	cluster 2
HORVU.MOREX.r3.7HG0717610.1	0.2193268	0.5897254	0.7718575	cluster 2
HORVU.MOREX.r3.7HG0718170.1	0.4822731	0.8101556	1.02239264	cluster 2
HORVU.MOREX.r3.7HG0718190.1	0.3629962	0.6908468	0.87321273	cluster 2
HORVU.MOREX.r3.7HG0718200.1	0.2861182	0.6426695	0.85426654	cluster 2
HORVU.MOREX.r3.7HG0718540.1	0.1767034	0.6245295	0.78858041	cluster 2
HORVU.MOREX.r3.7HG0718720.1	0.3023671	0.9275159	1.04637524	cluster 2
HORVU.MOREX.r3.7HG0718830.1	0.5322107	0.7212304	0.84611557	cluster 2
HORVU.MOREX.r3.7HG0718930.2	0.876005	1.3337527	1.41420998	cluster 2
HORVU.MOREX.r3.7HG0719170.1	0.1369497	0.5489585	0.6993676	cluster 2
HORVU.MOREX.r3.7HG0720100.1	0.26822	0.7850186	0.76892662	cluster 2
HORVU.MOREX.r3.7HG0721690.1	0.5945101	1.2770139	1.25755181	cluster 2
HORVU.MOREX.r3.7HG0722360.1	0.8556942	1.6579914	1.63620645	cluster 2
HORVU.MOREX.r3.7HG0722690.1	0.1149204	0.3309091	0.50938211	cluster 2
HORVU.MOREX.r3.7HG0723730.1	0.3540922	0.6391943	0.90352887	cluster 2
HORVU.MOREX.r3.7HG0724060.1	0.6458837	1.4720508	1.59710113	cluster 2
HORVU.MOREX.r3.7HG0724140.1	0.5940254	1.0527349	1.0710578	cluster 2
HORVU.MOREX.r3.7HG0725450.1	0.2488084	1.1230295	1.58046086	cluster 2
HORVU.MOREX.r3.7HG0726770.1	0.6632144	0.9362614	1.19564074	cluster 2
HORVU.MOREX.r3.7HG0726800.1	0.5385227	0.9064497	1.13339153	cluster 2
HORVU.MOREX.r3.7HG0727290.1	0.2858006	0.5017598	0.69328248	cluster 2
HORVU.MOREX.r3.7HG0727750.1	0.4565523	1.2713684	1.32364467	cluster 2
HORVU.MOREX.r3.7HG0727980.1	0.1937819	0.3807121	0.59720063	cluster 2
HORVU.MOREX.r3.7HG0728060.1	0.1216479	0.4787506	0.48325967	cluster 2
HORVU.MOREX.r3.7HG0730510.1	0.8509991	1.3663026	1.49259686	cluster 2
HORVU.MOREX.r3.7HG0731950.1	0.2889116	0.6582949	0.78541346	cluster 2
HORVU.MOREX.r3.7HG0736150.1	0.6526935	1.2176069	1.32390434	cluster 2
HORVU.MOREX.r3.7HG0736870.1	0.0994965	0.251	0.43898021	cluster 2
HORVU.MOREX.r3.7HG0737470.1	0.657427	1.0278927	1.04021175	cluster 2
HORVU.MOREX.r3.7HG0737890.1	0.4605395	1.0125301	1.13516466	cluster 2
HORVU.MOREX.r3.7HG0738680.1	0.4751268	0.700665	0.72210838	cluster 2
HORVU.MOREX.r3.7HG0738770.1	0.6228843	0.9265767	1.21144757	cluster 2
HORVU.MOREX.r3.7HG0739030.1	0.1261805	0.4185308	0.54952571	cluster 2
HORVU.MOREX.r3.7HG0739120.1	0.6367749	1.0566231	1.10893669	cluster 2

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.7HG0742080.1	0.8008977	1.3684256	1.57602568	cluster 2
HORVU.MOREX.r3.7HG0743900.1	0.0221244	0.2491488	0.51036886	cluster 2
HORVU.MOREX.r3.7HG0744890.1	0.7665333	1.0109883	1.09590618	cluster 2
HORVU.MOREX.r3.7HG0747690.1	3.0485897	3.5558559	3.5684823	cluster 2
HORVU.MOREX.r3.7HG0747940.1	0.2078592	0.444076	0.45911291	cluster 2
HORVU.MOREX.r3.7HG0748070.1	0.8146708	1.352132	1.31915482	cluster 2
HORVU.MOREX.r3.7HG0749070.1	0.3711935	0.9861429	1.22317384	cluster 2
HORVU.MOREX.r3.7HG0749080.1	0.0282132	1.0131946	1.12856448	cluster 2
HORVU.MOREX.r3.7HG0749090.1	0.2502276	1.0832272	1.18146177	cluster 2
HORVU.MOREX.r3.7HG0749100.1	0.2043081	0.8330815	0.92186048	cluster 2
HORVU.MOREX.r3.7HG0749640.1	0.0602674	0.4354517	0.61300476	cluster 2
HORVU.MOREX.r3.7HG0749870.1	0.2883228	0.4127493	0.54530599	cluster 2
HORVU.MOREX.r3.7HG0750140.1	0.1655989	0.3765363	0.37653161	cluster 2
HORVU.MOREX.r3.7HG0750170.1	0.8117068	1.2800809	1.56679351	cluster 2
HORVU.MOREX.r3.7HG0751300.1	0.6516701	1.4318477	1.47771629	cluster 2
HORVU.MOREX.r3.7HG0751340.1	0.5787381	1.0448161	1.0172609	cluster 2
HORVU.MOREX.r3.7HG0752370.1	0.2443724	0.6179565	0.76548163	cluster 2
HORVU.MOREX.r3.1HG0002630.1	0.1711594	1.9896814	0.46660601	cluster 3
HORVU.MOREX.r3.1HG0003620.1	0.3138326	0.5928033	0.5450898	cluster 3
HORVU.MOREX.r3.1HG0005700.1	1.0631149	2.2824019	1.94990724	cluster 3
HORVU.MOREX.r3.1HG0005730.1	0.7849748	2.1219919	1.67003551	cluster 3
HORVU.MOREX.r3.1HG0010340.1	1.5592583	2.4536826	2.20032447	cluster 3
HORVU.MOREX.r3.1HG0012340.1	0.6722211	1.3412727	1.25333711	cluster 3
HORVU.MOREX.r3.1HG0017280.1	0.8374164	1.7056726	1.59651037	cluster 3
HORVU.MOREX.r3.1HG0017770.1	0.4544104	0.7517881	0.63944908	cluster 3
HORVU.MOREX.r3.1HG0024510.1	0.2267448	0.4286452	0.40608049	cluster 3
HORVU.MOREX.r3.1HG0025320.1	0.613492	1.2169377	1.07232972	cluster 3
HORVU.MOREX.r3.1HG0027200.1	0.7464108	1.1617697	0.81180175	cluster 3
HORVU.MOREX.r3.1HG0042290.1	0.0574144	0.4066945	0.34009793	cluster 3
HORVU.MOREX.r3.1HG0044290.1	0.2085412	0.8069825	0.60706767	cluster 3
HORVU.MOREX.r3.1HG0044800.1	1.2830162	2.1568566	1.80537799	cluster 3
HORVU.MOREX.r3.1HG0046210.1	1.7563681	2.432764	2.2640672	cluster 3
HORVU.MOREX.r3.1HG0047570.1	0.1905652	0.7051528	0.5919737	cluster 3
HORVU.MOREX.r3.1HG0050220.1	0.9252035	1.467589	1.40353289	cluster 3
HORVU.MOREX.r3.1HG0053060.1	0.6190743	1.0949658	1.04145333	cluster 3
HORVU.MOREX.r3.1HG0054170.1	0.9433977	1.926734	1.56146538	cluster 3
HORVU.MOREX.r3.1HG0054180.1	0.8191721	1.7437234	1.53861711	cluster 3
HORVU.MOREX.r3.1HG0054190.1	1.21786	2.2431323	1.88452959	cluster 3
HORVU.MOREX.r3.1HG0055500.1	0.6284683	1.2057958	1.01315561	cluster 3
HORVU.MOREX.r3.1HG0056620.1	1.0613668	1.936995	1.82998389	cluster 3
HORVU.MOREX.r3.1HG0062630.1	0.2563032	0.5211878	0.46617722	cluster 3
HORVU.MOREX.r3.1HG0066800.1	0.7309063	1.4529727	1.17637157	cluster 3
HORVU.MOREX.r3.1HG0069030.1	1.2248662	1.6209528	1.51342566	cluster 3
HORVU.MOREX.r3.1HG0069410.1	0.6270373	1.1136511	0.92525564	cluster 3
HORVU.MOREX.r3.1HG0071420.1	0.659344	0.9175095	0.71187787	cluster 3
HORVU.MOREX.r3.1HG0073430.1	0.1941013	0.4226951	0.33224878	cluster 3
HORVU.MOREX.r3.1HG0075260.1	2.5500555	3.5917174	3.10578727	cluster 3

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.1HG0075340.1	0.3320698	0.9745518	0.77615585	cluster 3
HORVU.MOREX.r3.1HG0075730.1	0.635621	1.1428067	1.0477762	cluster 3
HORVU.MOREX.r3.1HG0077960.1	0.2938817	0.7137327	0.5300652	cluster 3
HORVU.MOREX.r3.1HG0080180.1	1.9535087	2.3634378	2.19937724	cluster 3
HORVU.MOREX.r3.1HG0081950.1	2.2709035	3.02783	2.57640243	cluster 3
HORVU.MOREX.r3.1HG0086370.1	1.1999165	2.4399783	2.10522523	cluster 3
HORVU.MOREX.r3.1HG0088530.1	0.3068814	0.9592564	0.78364279	cluster 3
HORVU.MOREX.r3.1HG0092200.1	0.3910832	1.3644708	0.56997417	cluster 3
HORVU.MOREX.r3.1HG0092860.1	0.3222543	1.3788585	1.2111266	cluster 3
HORVU.MOREX.r3.1HG0093050.1	0.5405552	1.0930189	0.81022969	cluster 3
HORVU.MOREX.r3.1HG0094110.1	1.911838	2.6213036	2.00917259	cluster 3
HORVU.MOREX.r3.2HG0096230.1	0.5403085	1.3345003	0.81438353	cluster 3
HORVU.MOREX.r3.2HG0096520.1	0.3392425	1.5790662	1.4271017	cluster 3
HORVU.MOREX.r3.2HG0096800.1	0.380927	0.7518304	0.69055058	cluster 3
HORVU.MOREX.r3.2HG0105830.1	0.3618823	0.7921987	0.68576609	cluster 3
HORVU.MOREX.r3.2HG0112190.1	1.0595431	1.7810511	1.55388523	cluster 3
HORVU.MOREX.r3.2HG0112690.1	1.1115037	1.3132885	1.26073711	cluster 3
HORVU.MOREX.r3.2HG0113720.1	0.7358426	1.3766037	1.16483125	cluster 3
HORVU.MOREX.r3.2HG0117830.1	1.0322649	1.8281935	1.39659553	cluster 3
HORVU.MOREX.r3.2HG0118220.1	0.6849396	1.2005412	1.08306497	cluster 3
HORVU.MOREX.r3.2HG0119080.1	0.2754023	0.8202671	0.60203402	cluster 3
HORVU.MOREX.r3.2HG0120470.1	0.6878973	1.3167354	1.17548026	cluster 3
HORVU.MOREX.r3.2HG0120490.1	0.6908535	1.3151249	1.17123373	cluster 3
HORVU.MOREX.r3.2HG0120560.1	0.7204918	1.3190281	1.161665	cluster 3
HORVU.MOREX.r3.2HG0121410.1	0.5299154	0.9256832	0.701258	cluster 3
HORVU.MOREX.r3.2HG0121630.1	0.3627151	0.7387854	0.55379348	cluster 3
HORVU.MOREX.r3.2HG0121670.1	0.4341492	0.7372941	0.50348341	cluster 3
HORVU.MOREX.r3.2HG0122880.1	0.5541906	1.4521582	1.32916844	cluster 3
HORVU.MOREX.r3.2HG0124550.1	1.0530838	1.3884352	1.29305111	cluster 3
HORVU.MOREX.r3.2HG0124850.1	1.1344358	1.7515246	1.65931916	cluster 3
HORVU.MOREX.r3.2HG0127260.1	0.8566943	1.4226129	1.31323357	cluster 3
HORVU.MOREX.r3.2HG0139810.1	0.6391969	1.0241819	0.92747759	cluster 3
HORVU.MOREX.r3.2HG0144760.1	0.4923039	1.2240785	1.10775071	cluster 3
HORVU.MOREX.r3.2HG0157410.1	0.8008322	1.2827141	1.21201271	cluster 3
HORVU.MOREX.r3.2HG0157450.1	0.6323934	1.0853997	1.02574131	cluster 3
HORVU.MOREX.r3.2HG0160690.1	0.4966044	1.0381931	0.82364778	cluster 3
HORVU.MOREX.r3.2HG0164020.1	0.6279206	1.1690404	0.75672277	cluster 3
HORVU.MOREX.r3.2HG0164470.1	0.5899381	0.8859545	0.73787661	cluster 3
HORVU.MOREX.r3.2HG0170230.1	0.4756654	0.6205134	0.57442443	cluster 3
HORVU.MOREX.r3.2HG0171780.1	1.0559533	1.5694528	1.16564535	cluster 3
HORVU.MOREX.r3.2HG0177790.1	1.1244072	2.1076834	1.60997698	cluster 3
HORVU.MOREX.r3.2HG0178480.1	0.5904511	1.1582042	0.94615385	cluster 3
HORVU.MOREX.r3.2HG0179320.1	0.2457168	0.7990075	0.58470685	cluster 3
HORVU.MOREX.r3.2HG0179790.1	0.5119616	1.0905045	0.72312472	cluster 3
HORVU.MOREX.r3.2HG0180010.1	0.8964688	1.6113559	1.37511721	cluster 3
HORVU.MOREX.r3.2HG0182650.1	0.4272274	2.0442696	1.12709483	cluster 3
HORVU.MOREX.r3.2HG0185600.1	0.714457	1.2198044	1.05281393	cluster 3

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.2HG0186480.1	1.1047789	2.389649	2.16071754	cluster 3
HORVU.MOREX.r3.2HG0186750.1	0.5331418	2.9190879	0.8443993	cluster 3
HORVU.MOREX.r3.2HG0187450.1	0.7612022	1.5025257	1.35973473	cluster 3
HORVU.MOREX.r3.2HG0189010.1	0.5339469	1.0113907	0.94550697	cluster 3
HORVU.MOREX.r3.2HG0189530.1	0.8482455	1.5025059	1.26936228	cluster 3
HORVU.MOREX.r3.2HG0189670.1	0.9204562	1.5866451	1.51279104	cluster 3
HORVU.MOREX.r3.2HG0190300.1	0.4676555	0.5979554	0.52091469	cluster 3
HORVU.MOREX.r3.2HG0192100.1	1.070724	1.8982312	1.68325945	cluster 3
HORVU.MOREX.r3.2HG0192410.1	0.890758	1.9465455	1.68137018	cluster 3
HORVU.MOREX.r3.2HG0193170.1	3.6640461	5.2023163	4.47835727	cluster 3
HORVU.MOREX.r3.2HG0193490.1	0.7376333	1.4119295	0.96590353	cluster 3
HORVU.MOREX.r3.2HG0194620.1	0.980254	2.0662313	1.87952744	cluster 3
HORVU.MOREX.r3.2HG0195690.1	0.7582451	1.6692054	1.07497895	cluster 3
HORVU.MOREX.r3.2HG0196520.1	0.2885222	0.736155	0.63318261	cluster 3
HORVU.MOREX.r3.2HG0196800.1	0.8724415	2.308663	2.02439845	cluster 3
HORVU.MOREX.r3.2HG0197110.1	0.2337897	0.3555761	0.26597198	cluster 3
HORVU.MOREX.r3.2HG0197230.1	0.721065	1.2399644	1.11077221	cluster 3
HORVU.MOREX.r3.2HG0197540.1	0.2789629	1.2485438	0.84213138	cluster 3
HORVU.MOREX.r3.2HG0198320.1	0.9876411	1.7139737	1.55860221	cluster 3
HORVU.MOREX.r3.2HG0199160.1	0.2774651	0.5976138	0.53367882	cluster 3
HORVU.MOREX.r3.2HG0202250.1	1.0529513	1.3503838	1.2943979	cluster 3
HORVU.MOREX.r3.2HG0203070.1	0.4929699	1.0286154	0.87215367	cluster 3
HORVU.MOREX.r3.2HG0205420.1	0.4736651	0.8810024	0.8222821	cluster 3
HORVU.MOREX.r3.2HG0205990.1	1.6154246	2.2776938	1.89734079	cluster 3
HORVU.MOREX.r3.2HG0208520.1	1.2428445	2.3492031	1.90672709	cluster 3
HORVU.MOREX.r3.2HG0209680.1	0.3782002	1.5149124	1.30868509	cluster 3
HORVU.MOREX.r3.2HG0210500.1	0.7432536	1.4401568	1.21918749	cluster 3
HORVU.MOREX.r3.2HG0210510.1	0.6554861	1.0386631	0.96490302	cluster 3
HORVU.MOREX.r3.2HG0212860.1	1.12497	1.8819863	1.76056432	cluster 3
HORVU.MOREX.r3.2HG0214070.1	1.0739833	2.2200397	1.61859641	cluster 3
HORVU.MOREX.r3.2HG0214130.1	0.9015364	1.4784312	1.25669869	cluster 3
HORVU.MOREX.r3.2HG0217090.1	1.3578365	2.2543033	1.86592829	cluster 3
HORVU.MOREX.r3.3HG0219380.1	0.6293154	1.0460411	0.94657638	cluster 3
HORVU.MOREX.r3.3HG0225880.1	0.3562515	0.9080649	0.61147233	cluster 3
HORVU.MOREX.r3.3HG0228940.1	0.8885458	1.1608421	1.11924368	cluster 3
HORVU.MOREX.r3.3HG0230640.1	1.2626452	2.1498645	1.84424381	cluster 3
HORVU.MOREX.r3.3HG0234000.1	1.1717256	1.9594596	1.54213879	cluster 3
HORVU.MOREX.r3.3HG0234010.1	1.0424388	1.626236	1.46465529	cluster 3
HORVU.MOREX.r3.3HG0234030.1	0.3967579	0.9326129	0.83863909	cluster 3
HORVU.MOREX.r3.3HG0234970.1	0.2472746	0.6808934	0.51916076	cluster 3
HORVU.MOREX.r3.3HG0235320.1	0.8330944	2.090663	1.5069093	cluster 3
HORVU.MOREX.r3.3HG0235350.1	1.2096463	2.5296998	2.00644621	cluster 3
HORVU.MOREX.r3.3HG0239900.1	0.5999186	1.3665604	0.7924196	cluster 3
HORVU.MOREX.r3.3HG0239980.1	0.2951308	1.0442109	0.86909149	cluster 3
HORVU.MOREX.r3.3HG0240350.1	0.3704946	0.6667146	0.56487049	cluster 3
HORVU.MOREX.r3.3HG0242770.1	0.22128	0.6537208	0.45196031	cluster 3
HORVU.MOREX.r3.3HG0244000.1	1.062452	2.0120722	1.68368127	cluster 3

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.3HG0244040.1	0.4836287	1.2285902	0.893857	cluster 3
HORVU.MOREX.r3.3HG0245120.1	2.3474942	3.008632	2.75105463	cluster 3
HORVU.MOREX.r3.3HG0245250.1	2.6149236	4.0011948	3.23905423	cluster 3
HORVU.MOREX.r3.3HG0246300.1	0.1292844	0.4852659	0.34127403	cluster 3
HORVU.MOREX.r3.3HG0250060.1	1.0479656	2.5488608	1.99188759	cluster 3
HORVU.MOREX.r3.3HG0252960.1	1.1087823	1.5277099	1.29909636	cluster 3
HORVU.MOREX.r3.3HG0253860.1	1.2048684	2.2359774	1.40856828	cluster 3
HORVU.MOREX.r3.3HG0258240.1	0.4599494	1.3517616	0.93703102	cluster 3
HORVU.MOREX.r3.3HG0264640.1	-0.09276	1.4500437	0.83294059	cluster 3
HORVU.MOREX.r3.3HG0265140.1	1.5471385	2.4299566	1.99162846	cluster 3
HORVU.MOREX.r3.3HG0269130.1	0.6192941	1.2298994	0.98526732	cluster 3
HORVU.MOREX.r3.3HG0275090.1	1.7547882	2.2925491	1.9218451	cluster 3
HORVU.MOREX.r3.3HG0275490.1	1.0334564	1.9055257	1.70784416	cluster 3
HORVU.MOREX.r3.3HG0276120.1	0.8867794	1.93491	1.77700969	cluster 3
HORVU.MOREX.r3.3HG0278630.1	0.2406564	0.5193078	0.45988332	cluster 3
HORVU.MOREX.r3.3HG0279100.1	0.9252075	1.1891752	1.01137387	cluster 3
HORVU.MOREX.r3.3HG0285150.1	0.5458466	0.8589187	0.81773433	cluster 3
HORVU.MOREX.r3.3HG0285440.1	0.9720005	1.7141319	1.49152921	cluster 3
HORVU.MOREX.r3.3HG0286100.1	1.3374496	2.0602449	1.54984812	cluster 3
HORVU.MOREX.r3.3HG0290300.1	1.1074348	2.9956127	1.73496857	cluster 3
HORVU.MOREX.r3.3HG0292490.1	0.4252445	0.897386	0.83439692	cluster 3
HORVU.MOREX.r3.3HG0292680.1	0.3480327	0.6873488	0.62085004	cluster 3
HORVU.MOREX.r3.3HG0294390.1	0.2485188	0.7169626	0.30449036	cluster 3
HORVU.MOREX.r3.3HG0294960.1	0.8456551	1.7854641	1.55170444	cluster 3
HORVU.MOREX.r3.3HG0295640.1	0.5578424	1.319709	1.21356137	cluster 3
HORVU.MOREX.r3.3HG0296120.1	0.6779504	1.531733	1.11603476	cluster 3
HORVU.MOREX.r3.3HG0298080.1	0.4345492	1.2062768	1.08617308	cluster 3
HORVU.MOREX.r3.3HG0298180.1	0.8187417	1.7149992	1.50350633	cluster 3
HORVU.MOREX.r3.3HG0298510.1	0.329936	0.7106195	0.5726424	cluster 3
HORVU.MOREX.r3.3HG0298790.1	0.5148781	0.8288828	0.63477045	cluster 3
HORVU.MOREX.r3.3HG0302230.1	0.3024303	0.6112375	0.43190034	cluster 3
HORVU.MOREX.r3.3HG0303240.1	0.9116472	1.2660741	1.11420955	cluster 3
HORVU.MOREX.r3.3HG0305440.1	0.8643178	1.5666716	0.97526344	cluster 3
HORVU.MOREX.r3.3HG0307240.1	2.6195977	3.0473965	2.70112743	cluster 3
HORVU.MOREX.r3.3HG0307250.1	1.5947862	2.116851	1.7424705	cluster 3
HORVU.MOREX.r3.3HG0309760.1	0.540732	1.1335568	0.81508027	cluster 3
HORVU.MOREX.r3.3HG0309780.1	2.2034485	3.0540032	2.84011543	cluster 3
HORVU.MOREX.r3.3HG0310110.1	1.6053668	1.9320626	1.75034226	cluster 3
HORVU.MOREX.r3.3HG0310390.1	-0.224291	1.633224	0.66658981	cluster 3
HORVU.MOREX.r3.3HG0313090.1	0.495117	0.8080619	0.73737565	cluster 3
HORVU.MOREX.r3.3HG0313320.1	0.383243	1.5017975	1.33907217	cluster 3
HORVU.MOREX.r3.3HG0317780.1	0.836648	1.3484772	1.21671848	cluster 3
HORVU.MOREX.r3.3HG0318590.1	1.9662537	2.8236098	2.63609669	cluster 3
HORVU.MOREX.r3.3HG0319430.1	0.5926847	0.9180671	0.82386622	cluster 3
HORVU.MOREX.r3.3HG0321700.1	0.4348523	0.8269235	0.68354288	cluster 3
HORVU.MOREX.r3.3HG0322650.1	0.494499	0.8209263	0.70024765	cluster 3
HORVU.MOREX.r3.3HG0323750.1	0.7604213	0.9168295	0.86647867	cluster 3

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.3HG0325250.1	2.8303653	3.8272581	3.37321448	cluster 3
HORVU.MOREX.r3.3HG0328430.1	0.5000046	1.7154025	0.87623675	cluster 3
HORVU.MOREX.r3.3HG0329950.1	1.0426997	2.0173073	1.63146116	cluster 3
HORVU.MOREX.r3.3HG0330200.1	0.7872128	1.317891	1.23348626	cluster 3
HORVU.MOREX.r3.3HG0330220.1	0.3105887	1.170575	1.03358316	cluster 3
HORVU.MOREX.r3.4HG0331440.1	1.1050685	1.5029967	1.22483615	cluster 3
HORVU.MOREX.r3.4HG0335170.1	0.6011743	1.3636845	1.25029495	cluster 3
HORVU.MOREX.r3.4HG0337950.1	1.6835407	2.5528601	2.27156529	cluster 3
HORVU.MOREX.r3.4HG0340030.1	0.6666234	1.9054957	1.39495362	cluster 3
HORVU.MOREX.r3.4HG0342480.1	0.7205496	0.9991801	0.89056024	cluster 3
HORVU.MOREX.r3.4HG0342680.1	0.6153629	1.2654457	0.94795787	cluster 3
HORVU.MOREX.r3.4HG0344550.1	0.8312747	1.6923254	1.06466948	cluster 3
HORVU.MOREX.r3.4HG0345580.1	1.4882406	2.4305487	1.91477372	cluster 3
HORVU.MOREX.r3.4HG0348800.1	0.3939965	1.2995825	1.13020082	cluster 3
HORVU.MOREX.r3.4HG0351290.1	0.3928932	1.0509139	0.47622544	cluster 3
HORVU.MOREX.r3.4HG0351750.1	1.470455	2.3362083	2.02113489	cluster 3
HORVU.MOREX.r3.4HG0353120.1	0.1511889	1.4223427	1.1709541	cluster 3
HORVU.MOREX.r3.4HG0355210.1	0.916253	2.0940685	1.60108941	cluster 3
HORVU.MOREX.r3.4HG0381150.1	0.7934923	2.0748825	1.85121144	cluster 3
HORVU.MOREX.r3.4HG0382620.1	0.2655961	0.6455969	0.48102118	cluster 3
HORVU.MOREX.r3.4HG0383530.1	0.6392348	1.160899	1.09093805	cluster 3
HORVU.MOREX.r3.4HG0384620.1	0.3592195	1.0461923	0.92359023	cluster 3
HORVU.MOREX.r3.4HG0386490.1	1.1026408	2.0003374	1.7867265	cluster 3
HORVU.MOREX.r3.4HG0389250.1	0.5581347	1.3098591	0.87133647	cluster 3
HORVU.MOREX.r3.4HG0390770.1	0.7110921	1.1278313	1.0822598	cluster 3
HORVU.MOREX.r3.4HG0394330.1	0.7667639	1.2983732	1.22561783	cluster 3
HORVU.MOREX.r3.4HG0394460.1	0.2243026	1.5822182	1.08193766	cluster 3
HORVU.MOREX.r3.4HG0395540.1	1.7548703	2.0826682	1.8518538	cluster 3
HORVU.MOREX.r3.4HG0399970.1	0.8449133	1.1084163	1.05951791	cluster 3
HORVU.MOREX.r3.4HG0400520.1	0.9972842	1.3617709	1.26348373	cluster 3
HORVU.MOREX.r3.4HG0400530.1	0.9162412	1.3692997	1.26424739	cluster 3
HORVU.MOREX.r3.4HG0403620.1	0.8105203	1.6808756	1.53698126	cluster 3
HORVU.MOREX.r3.4HG0405860.1	0.7839534	2.4328059	2.05054853	cluster 3
HORVU.MOREX.r3.4HG0406670.1	0.4756937	0.8967279	0.81404402	cluster 3
HORVU.MOREX.r3.4HG0407230.1	0.6594467	1.4212745	1.02386225	cluster 3
HORVU.MOREX.r3.4HG0407310.1	0.6173735	0.9311402	0.72037621	cluster 3
HORVU.MOREX.r3.4HG0408270.1	1.5757383	2.186194	1.82641241	cluster 3
HORVU.MOREX.r3.4HG0409230.1	1.1281871	2.2149577	1.85850757	cluster 3
HORVU.MOREX.r3.4HG0409880.1	1.1842185	2.0855537	1.419768	cluster 3
HORVU.MOREX.r3.4HG0410830.1	0.4722377	1.2267372	1.08934367	cluster 3
HORVU.MOREX.r3.4HG0410910.1	0.6882354	2.2746247	0.9723833	cluster 3
HORVU.MOREX.r3.4HG0412140.1	0.7597879	1.2239557	1.10254828	cluster 3
HORVU.MOREX.r3.4HG0412370.1	1.289062	2.2483469	2.02792442	cluster 3
HORVU.MOREX.r3.4HG0413320.1	1.6092173	2.408495	1.85975722	cluster 3
HORVU.MOREX.r3.4HG0413740.1	1.3826066	2.3358491	2.06676432	cluster 3
HORVU.MOREX.r3.4HG0415330.1	1.7208855	2.2981548	2.20676924	cluster 3
HORVU.MOREX.r3.4HG0415490.1	1.3712582	2.2799411	1.91661429	cluster 3

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.4HG0417710.1	0.4850072	0.9575886	0.8932471	cluster 3
HORVU.MOREX.r3.5HG0420480.1	1.5142313	2.1727482	1.97952195	cluster 3
HORVU.MOREX.r3.5HG0420820.1	0.2361459	1.512927	1.18910008	cluster 3
HORVU.MOREX.r3.5HG0423820.1	0.6251739	0.9525042	0.87832373	cluster 3
HORVU.MOREX.r3.5HG0429180.1	1.1578838	1.5883447	1.51847088	cluster 3
HORVU.MOREX.r3.5HG0429900.1	0.8309484	1.5690068	1.29612079	cluster 3
HORVU.MOREX.r3.5HG0430050.1	0.3381948	0.6380405	0.55480978	cluster 3
HORVU.MOREX.r3.5HG0438460.1	1.0108142	1.6370994	1.2713	cluster 3
HORVU.MOREX.r3.5HG0458890.1	0.2821128	0.6130923	0.55484359	cluster 3
HORVU.MOREX.r3.5HG0462200.1	0.8685806	1.6681302	1.55919222	cluster 3
HORVU.MOREX.r3.5HG0467870.1	0.4080381	1.2350319	0.99358787	cluster 3
HORVU.MOREX.r3.5HG0468580.1	0.6477837	1.4170507	1.22714733	cluster 3
HORVU.MOREX.r3.5HG0469300.1	0.4322471	1.8371289	1.64450062	cluster 3
HORVU.MOREX.r3.5HG0469340.1	0.6755812	1.3640911	1.28897872	cluster 3
HORVU.MOREX.r3.5HG0470680.1	1.07089	1.8095719	1.34311909	cluster 3
HORVU.MOREX.r3.5HG0470700.1	1.1686656	1.7112834	1.62797996	cluster 3
HORVU.MOREX.r3.5HG0472770.1	0.3644496	0.9356928	0.66081951	cluster 3
HORVU.MOREX.r3.5HG0480130.1	2.2228809	2.7550735	2.36662323	cluster 3
HORVU.MOREX.r3.5HG0480980.1	2.1262608	2.8208384	2.46573355	cluster 3
HORVU.MOREX.r3.5HG0481580.1	0.1811226	0.7633795	0.58267162	cluster 3
HORVU.MOREX.r3.5HG0483980.1	0.4557283	1.4910701	1.16530945	cluster 3
HORVU.MOREX.r3.5HG0485780.1	1.6887318	3.0873953	2.53798604	cluster 3
HORVU.MOREX.r3.5HG0485790.1	0.5181595	0.7671405	0.56319019	cluster 3
HORVU.MOREX.r3.5HG0485940.1	1.324522	2.2839296	1.85733786	cluster 3
HORVU.MOREX.r3.5HG0486660.1	1.0465157	1.3277827	1.24955444	cluster 3
HORVU.MOREX.r3.5HG0488040.1	1.0923523	1.7732844	1.62325311	cluster 3
HORVU.MOREX.r3.5HG0488050.1	1.0785668	1.8958393	1.44670761	cluster 3
HORVU.MOREX.r3.5HG0488300.1	0.6213391	1.4837628	1.24871352	cluster 3
HORVU.MOREX.r3.5HG0488650.1	0.4018848	0.7007772	0.50270261	cluster 3
HORVU.MOREX.r3.5HG0493080.1	0.2535699	0.6497137	0.6015228	cluster 3
HORVU.MOREX.r3.5HG0493200.1	0.1955649	0.4277088	0.39170022	cluster 3
HORVU.MOREX.r3.5HG0493330.1	0.7777255	1.0852783	0.99429843	cluster 3
HORVU.MOREX.r3.5HG0498240.1	1.122667	2.6776854	2.35906406	cluster 3
HORVU.MOREX.r3.5HG0507680.1	0.7568425	1.5093324	1.28741254	cluster 3
HORVU.MOREX.r3.5HG0508880.1	1.0132383	1.7158097	1.50461804	cluster 3
HORVU.MOREX.r3.5HG0509120.1	0.9671099	1.3294133	1.03666518	cluster 3
HORVU.MOREX.r3.5HG0511820.1	1.3528892	2.8631742	2.27948748	cluster 3
HORVU.MOREX.r3.5HG0512210.1	2.4911558	3.3845249	2.9983563	cluster 3
HORVU.MOREX.r3.5HG0512230.1	0.6450639	1.4964435	1.18310829	cluster 3
HORVU.MOREX.r3.5HG0512250.1	0.5548324	1.4973299	1.30995135	cluster 3
HORVU.MOREX.r3.5HG0512490.1	0.8751636	1.7964817	1.66333167	cluster 3
HORVU.MOREX.r3.5HG0517760.1	1.3069569	2.0781906	1.69639787	cluster 3
HORVU.MOREX.r3.5HG0518560.1	1.8337137	2.7412758	2.22933652	cluster 3
HORVU.MOREX.r3.5HG0519120.1	1.3017572	1.7814097	1.49195287	cluster 3
HORVU.MOREX.r3.5HG0519660.1	0.2163523	0.466698	0.3453212	cluster 3
HORVU.MOREX.r3.5HG0521610.1	0.6700677	1.3505614	1.23466197	cluster 3
HORVU.MOREX.r3.5HG0522630.1	0.3678684	0.7218506	0.58376818	cluster 3

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.5HG0524350.1	1.2023506	2.2913521	2.05571947	cluster 3
HORVU.MOREX.r3.5HG0527570.1	1.8854684	2.1718098	2.04833397	cluster 3
HORVU.MOREX.r3.5HG0528570.1	0.9358814	1.0829495	0.96066106	cluster 3
HORVU.MOREX.r3.5HG0528910.1	0.3617325	0.9156462	0.85130311	cluster 3
HORVU.MOREX.r3.5HG0532140.1	1.5492928	2.1014358	1.95829789	cluster 3
HORVU.MOREX.r3.5HG0533430.1	0.9031022	1.446154	1.33072424	cluster 3
HORVU.MOREX.r3.6HG0540020.1	0.8588432	1.5402701	1.25319459	cluster 3
HORVU.MOREX.r3.6HG0542640.1	0.5218459	1.2641997	1.1800139	cluster 3
HORVU.MOREX.r3.6HG0548710.1	1.0982311	2.3994057	2.18060188	cluster 3
HORVU.MOREX.r3.6HG0558350.1	1.9940078	3.1572343	2.50428293	cluster 3
HORVU.MOREX.r3.6HG0558430.1	0.148306	2.2535914	1.13767428	cluster 3
HORVU.MOREX.r3.6HG0560140.1	1.4626424	2.1736853	1.98031687	cluster 3
HORVU.MOREX.r3.6HG0568170.1	0.1992469	0.8528938	0.46445861	cluster 3
HORVU.MOREX.r3.6HG0570230.1	0.6332285	1.1625092	0.84009985	cluster 3
HORVU.MOREX.r3.6HG0571750.1	0.4053088	1.1426233	0.94440251	cluster 3
HORVU.MOREX.r3.6HG0575530.1	0.2038005	0.4900524	0.37931383	cluster 3
HORVU.MOREX.r3.6HG0577040.1	0.7590438	2.1745454	2.01778438	cluster 3
HORVU.MOREX.r3.6HG0577220.1	0.737418	1.8475852	1.43370062	cluster 3
HORVU.MOREX.r3.6HG0579050.1	0.7332115	1.2562127	0.8746038	cluster 3
HORVU.MOREX.r3.6HG0593260.1	0.1786921	0.7811675	0.48834429	cluster 3
HORVU.MOREX.r3.6HG0595190.1	0.8667652	1.6978509	1.51950652	cluster 3
HORVU.MOREX.r3.6HG0600000.1	0.8610614	1.6195013	1.48165102	cluster 3
HORVU.MOREX.r3.6HG0600910.1	1.1219058	1.5254939	1.32431676	cluster 3
HORVU.MOREX.r3.6HG0607590.1	0.7460334	1.0357551	0.93750755	cluster 3
HORVU.MOREX.r3.6HG0608960.1	0.4282294	0.6753256	0.52999535	cluster 3
HORVU.MOREX.r3.6HG0609830.1	0.4477905	0.7712683	0.66177301	cluster 3
HORVU.MOREX.r3.6HG0610980.1	0.6627385	1.4841871	1.29351447	cluster 3
HORVU.MOREX.r3.6HG0611050.1	0.5382335	2.4658504	1.62772118	cluster 3
HORVU.MOREX.r3.6HG0612780.1	1.1300789	1.6260166	1.53359698	cluster 3
HORVU.MOREX.r3.6HG0613360.1	1.0940168	1.971445	1.36987849	cluster 3
HORVU.MOREX.r3.6HG0613430.1	1.2341802	1.9262015	1.68468874	cluster 3
HORVU.MOREX.r3.6HG0613460.1	0.9048869	1.1602723	1.0746214	cluster 3
HORVU.MOREX.r3.6HG0614100.1	0.335877	0.8316447	0.6733021	cluster 3
HORVU.MOREX.r3.6HG0615840.1	2.543944	3.0297172	2.78659421	cluster 3
HORVU.MOREX.r3.6HG0616240.1	0.5017971	0.8374594	0.74187336	cluster 3
HORVU.MOREX.r3.6HG0616450.1	0.4330728	1.3871709	1.12929946	cluster 3
HORVU.MOREX.r3.6HG0617970.1	1.0835867	1.7436559	1.57859963	cluster 3
HORVU.MOREX.r3.6HG0618180.1	0.854205	1.4432678	1.30328419	cluster 3
HORVU.MOREX.r3.6HG0620200.1	0.5097715	1.4024548	1.18997482	cluster 3
HORVU.MOREX.r3.6HG0621170.1	1.0628228	2.4977178	1.7546666	cluster 3
HORVU.MOREX.r3.6HG0622110.1	0.9349369	1.6219918	1.42377366	cluster 3
HORVU.MOREX.r3.6HG0622740.1	0.0651294	0.4522345	0.37215229	cluster 3
HORVU.MOREX.r3.6HG0624390.1	0.2569616	1.2637085	1.05390227	cluster 3
HORVU.MOREX.r3.6HG0626020.1	0.9358838	1.5998957	1.42864688	cluster 3
HORVU.MOREX.r3.6HG0626030.1	1.3209903	2.1629848	1.72243897	cluster 3
HORVU.MOREX.r3.6HG0629520.1	0.9316716	1.8149024	1.52849703	cluster 3
HORVU.MOREX.r3.6HG0629810.2	0.7057222	1.0147678	0.92128087	cluster 3

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.6HG0631660.1	0.3410089	0.6921533	0.559483	cluster 3
HORVU.MOREX.r3.6HG0633900.1	1.2350146	2.2505326	1.82618881	cluster 3
HORVU.MOREX.r3.6HG0633960.1	0.3834116	0.9775832	0.88169322	cluster 3
HORVU.MOREX.r3.7HG0636890.1	0.9542233	1.9684083	1.6790455	cluster 3
HORVU.MOREX.r3.7HG0637030.1	0.37647	1.1998429	0.97163466	cluster 3
HORVU.MOREX.r3.7HG0641180.1	0.2307557	0.4779287	0.36897876	cluster 3
HORVU.MOREX.r3.7HG0641860.1	1.520959	2.1056133	1.96930234	cluster 3
HORVU.MOREX.r3.7HG0644220.1	0.0606799	0.5812324	0.23246826	cluster 3
HORVU.MOREX.r3.7HG0647300.1	1.1971558	2.3443238	1.78520597	cluster 3
HORVU.MOREX.r3.7HG0647950.1	-0.159238	2.3282228	1.24488122	cluster 3
HORVU.MOREX.r3.7HG0648390.1	0.5570917	0.9313779	0.72074745	cluster 3
HORVU.MOREX.r3.7HG0649240.1	1.1203123	1.6543708	1.54596008	cluster 3
HORVU.MOREX.r3.7HG0655170.1	0.7339463	1.3564245	1.13663409	cluster 3
HORVU.MOREX.r3.7HG0656570.1	0.4039746	0.9104744	0.78599654	cluster 3
HORVU.MOREX.r3.7HG0658560.1	0.1447342	0.7394279	0.51293477	cluster 3
HORVU.MOREX.r3.7HG0660720.1	0.9043602	1.6722795	1.04166286	cluster 3
HORVU.MOREX.r3.7HG0663920.1	1.8027123	2.6206634	2.35411352	cluster 3
HORVU.MOREX.r3.7HG0663940.1	0.4773975	0.8353165	0.78775812	cluster 3
HORVU.MOREX.r3.7HG0667060.1	0.4364638	1.6455151	0.87384296	cluster 3
HORVU.MOREX.r3.7HG0668820.1	0.1926463	0.5634167	0.50029293	cluster 3
HORVU.MOREX.r3.7HG0669410.1	0.2278248	0.5083021	0.40417588	cluster 3
HORVU.MOREX.r3.7HG0670900.1	0.9578828	1.6657957	1.57099504	cluster 3
HORVU.MOREX.r3.7HG0671410.1	0.6661116	1.2920591	0.89859128	cluster 3
HORVU.MOREX.r3.7HG0675310.1	0.8329982	1.4561707	1.23997831	cluster 3
HORVU.MOREX.r3.7HG0676040.1	0.0551884	0.6571765	0.56005952	cluster 3
HORVU.MOREX.r3.7HG0680960.1	1.0264564	2.0012917	1.61550618	cluster 3
HORVU.MOREX.r3.7HG0683600.1	1.2594735	1.8515597	1.62245145	cluster 3
HORVU.MOREX.r3.7HG0688730.1	0.1733679	0.5156428	0.42665333	cluster 3
HORVU.MOREX.r3.7HG0688870.1	0.5712165	0.7818879	0.74855596	cluster 3
HORVU.MOREX.r3.7HG0701080.1	0.7074732	0.9843881	0.8755626	cluster 3
HORVU.MOREX.r3.7HG0706130.1	0.4785005	0.6950621	0.54304118	cluster 3
HORVU.MOREX.r3.7HG0711230.1	0.3609468	0.5896796	0.45582649	cluster 3
HORVU.MOREX.r3.7HG0712000.1	1.0152618	1.9992251	1.73022492	cluster 3
HORVU.MOREX.r3.7HG0714400.1	0.437687	0.8739298	0.78423884	cluster 3
HORVU.MOREX.r3.7HG0714660.1	0.1668459	1.5116325	1.15283434	cluster 3
HORVU.MOREX.r3.7HG0716640.1	0.5646628	0.8312807	0.60267475	cluster 3
HORVU.MOREX.r3.7HG0721320.1	0.3195789	1.3864357	0.75136531	cluster 3
HORVU.MOREX.r3.7HG0722260.1	1.1134465	1.8066255	1.63999031	cluster 3
HORVU.MOREX.r3.7HG0727650.1	1.4778651	2.7853943	2.62748075	cluster 3
HORVU.MOREX.r3.7HG0728000.1	0.3480905	0.6297342	0.58300689	cluster 3
HORVU.MOREX.r3.7HG0728080.1	0.3138312	0.8212387	0.4492996	cluster 3
HORVU.MOREX.r3.7HG0728480.1	1.0632378	1.5774043	1.40350588	cluster 3
HORVU.MOREX.r3.7HG0728820.1	0.6658363	1.7114571	1.42708304	cluster 3
HORVU.MOREX.r3.7HG0729000.1	0.5445362	1.0377436	0.97930677	cluster 3
HORVU.MOREX.r3.7HG0730530.1	0.4549969	1.3054203	1.00940735	cluster 3
HORVU.MOREX.r3.7HG0730660.1	1.1890454	1.6958903	1.50246046	cluster 3
HORVU.MOREX.r3.7HG0730870.1	0.2037409	0.3743778	0.35057178	cluster 3

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.7HG0737340.1	0.4232764	1.6567824	1.39201746	cluster 3
HORVU.MOREX.r3.7HG0739080.1	1.6079733	2.592859	2.34402343	cluster 3
HORVU.MOREX.r3.7HG0742370.1	0.5386573	1.3387466	1.24105096	cluster 3
HORVU.MOREX.r3.7HG0747230.1	0.6875564	0.9838461	0.74613293	cluster 3
HORVU.MOREX.r3.7HG0747720.1	0.3506165	1.0227787	0.69360431	cluster 3
HORVU.MOREX.r3.7HG0748270.1	1.2442207	1.9760816	1.72587828	cluster 3
HORVU.MOREX.r3.7HG0748670.1	0.9419249	2.3304367	1.69523928	cluster 3
HORVU.MOREX.r3.7HG0750000.1	1.7484813	2.3774016	2.11315091	cluster 3
HORVU.MOREX.r3.7HG0751450.1	1.0234693	2.0879019	1.42930168	cluster 3
HORVU.MOREX.r3.1HG0000050.1	-0.210564	-0.486688	-0.4453408	cluster 4
HORVU.MOREX.r3.1HG0000140.1	-0.057747	-0.364258	-0.353427	cluster 4
HORVU.MOREX.r3.1HG0002340.1	-0.090387	-0.30519	-0.2024824	cluster 4
HORVU.MOREX.r3.1HG0006230.1	-0.265836	-0.627234	-0.6510553	cluster 4
HORVU.MOREX.r3.1HG0014430.1	-0.117054	-0.198848	-0.2041247	cluster 4
HORVU.MOREX.r3.1HG0020270.1	-0.148247	-0.379992	-0.3739876	cluster 4
HORVU.MOREX.r3.1HG0037910.1	-0.171377	-0.704039	-0.6912778	cluster 4
HORVU.MOREX.r3.1HG0039370.1	-0.069398	-0.402941	-0.407958	cluster 4
HORVU.MOREX.r3.1HG0043520.1	-0.238147	-0.519477	-0.50014	cluster 4
HORVU.MOREX.r3.1HG0049450.1	-0.131521	-0.451091	-0.4273442	cluster 4
HORVU.MOREX.r3.1HG0049520.1	-0.13782	-0.732898	-0.7527107	cluster 4
HORVU.MOREX.r3.1HG0051960.1	-0.220278	-1.091	-1.1754849	cluster 4
HORVU.MOREX.r3.1HG0052940.1	-0.090563	-0.378274	-0.4074182	cluster 4
HORVU.MOREX.r3.1HG0053680.1	-0.078399	-0.302188	-0.2049298	cluster 4
HORVU.MOREX.r3.1HG0055560.1	-0.002046	-0.40991	-0.4294738	cluster 4
HORVU.MOREX.r3.1HG0057000.1	-0.154442	-1.170442	-1.2252833	cluster 4
HORVU.MOREX.r3.1HG0057030.1	-0.195214	-0.854579	-0.6987391	cluster 4
HORVU.MOREX.r3.1HG0058470.1	-0.134275	-0.379924	-0.2626498	cluster 4
HORVU.MOREX.r3.1HG0059340.1	-0.171788	-0.34212	-0.2890759	cluster 4
HORVU.MOREX.r3.1HG0063810.1	-0.087931	-0.413414	-0.2988521	cluster 4
HORVU.MOREX.r3.1HG0066260.1	-0.11812	-0.444257	-0.4658723	cluster 4
HORVU.MOREX.r3.1HG0069210.1	-0.028778	-0.703608	-0.4911704	cluster 4
HORVU.MOREX.r3.1HG0069570.1	-0.134462	-0.387142	-0.3771681	cluster 4
HORVU.MOREX.r3.1HG0072760.1	-0.139447	-0.819272	-0.9126195	cluster 4
HORVU.MOREX.r3.1HG0072840.1	-0.10212	-0.342829	-0.3691419	cluster 4
HORVU.MOREX.r3.1HG0072910.2	-0.222798	-0.514361	-0.5098969	cluster 4
HORVU.MOREX.r3.1HG0073520.1	-0.227209	-0.749321	-0.7818548	cluster 4
HORVU.MOREX.r3.1HG0081620.1	-0.44562	-0.670831	-0.6509182	cluster 4
HORVU.MOREX.r3.1HG0083040.1	-0.377981	-0.74817	-0.5874048	cluster 4
HORVU.MOREX.r3.1HG0087170.1	-0.246922	-0.540091	-0.543782	cluster 4
HORVU.MOREX.r3.1HG0090170.1	-0.274432	-0.587936	-0.5627546	cluster 4
HORVU.MOREX.r3.1HG0090200.1	-0.137066	-0.510105	-0.4726677	cluster 4
HORVU.MOREX.r3.1HG0090710.1	-0.225109	-0.39678	-0.3901458	cluster 4
HORVU.MOREX.r3.1HG0094770.1	-0.184493	-0.551202	-0.4861682	cluster 4
HORVU.MOREX.r3.1HG0094980.1	-0.227694	-0.595078	-0.4299233	cluster 4
HORVU.MOREX.r3.2HG0098090.1	-0.358358	-1.227477	-1.2327465	cluster 4
HORVU.MOREX.r3.2HG0102600.1	-0.164277	-0.410456	-0.3688374	cluster 4
HORVU.MOREX.r3.2HG0104520.1	-0.177553	-0.553732	-0.5874395	cluster 4

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.2HG0108780.1	-0.065142	-0.205477	-0.1530493	cluster 4
HORVU.MOREX.r3.2HG0112060.1	-0.280124	-0.780091	-0.7503091	cluster 4
HORVU.MOREX.r3.2HG0117980.1	-0.154248	-0.359594	-0.2791979	cluster 4
HORVU.MOREX.r3.2HG0121570.1	-0.21981	-0.507466	-0.4110998	cluster 4
HORVU.MOREX.r3.2HG0122500.2	-0.384472	-1.657488	-1.8314263	cluster 4
HORVU.MOREX.r3.2HG0124450.1	-0.119997	-0.549691	-0.5896555	cluster 4
HORVU.MOREX.r3.2HG0128240.1	-0.203944	-0.407351	-0.3836201	cluster 4
HORVU.MOREX.r3.2HG0128490.1	-0.094818	-0.347458	-0.3261412	cluster 4
HORVU.MOREX.r3.2HG0132590.1	-0.131936	-0.331505	-0.258935	cluster 4
HORVU.MOREX.r3.2HG0135510.1	-0.092381	-0.318173	-0.3435911	cluster 4
HORVU.MOREX.r3.2HG0140700.1	-0.135934	-0.314454	-0.2293707	cluster 4
HORVU.MOREX.r3.2HG0140970.1	-0.280162	-0.804431	-0.859195	cluster 4
HORVU.MOREX.r3.2HG0141980.1	-0.152674	-0.403651	-0.4324579	cluster 4
HORVU.MOREX.r3.2HG0144230.1	-0.093503	-0.303229	-0.3259337	cluster 4
HORVU.MOREX.r3.2HG0152430.1	-0.157479	-0.477822	-0.3368035	cluster 4
HORVU.MOREX.r3.2HG0152890.1	-0.480596	-0.656631	-0.6549707	cluster 4
HORVU.MOREX.r3.2HG0156810.1	0.1657929	-1.605093	-0.7460263	cluster 4
HORVU.MOREX.r3.2HG0161410.1	-0.124115	-0.33139	-0.3275692	cluster 4
HORVU.MOREX.r3.2HG0161580.1	-0.283235	-0.552608	-0.5039145	cluster 4
HORVU.MOREX.r3.2HG0164850.1	-0.306654	-0.837785	-0.6724567	cluster 4
HORVU.MOREX.r3.2HG0171810.1	-0.221987	-0.489077	-0.5187989	cluster 4
HORVU.MOREX.r3.2HG0182990.1	-0.179004	-0.792773	-0.6544065	cluster 4
HORVU.MOREX.r3.2HG0188490.1	-0.066109	-0.808051	-0.6820208	cluster 4
HORVU.MOREX.r3.2HG0192910.1	-0.109653	-0.787404	-0.7465992	cluster 4
HORVU.MOREX.r3.2HG0193000.1	-0.196324	-0.71756	-0.6826582	cluster 4
HORVU.MOREX.r3.2HG0196940.1	-0.053432	-0.341399	-0.2791273	cluster 4
HORVU.MOREX.r3.2HG0199550.1	-0.066644	-0.521988	-0.4085273	cluster 4
HORVU.MOREX.r3.2HG0200730.1	-0.067512	-0.196754	-0.1968357	cluster 4
HORVU.MOREX.r3.2HG0204340.1	-0.613565	-2.387041	-2.2924992	cluster 4
HORVU.MOREX.r3.2HG0208960.1	-0.332485	-0.850496	-0.8815784	cluster 4
HORVU.MOREX.r3.2HG0210680.1	-0.013726	-0.28563	-0.2724734	cluster 4
HORVU.MOREX.r3.2HG0211730.1	-0.139536	-0.501831	-0.3484092	cluster 4
HORVU.MOREX.r3.2HG0211880.1	-0.168738	-0.456205	-0.4618274	cluster 4
HORVU.MOREX.r3.2HG0214240.1	-0.330191	-0.720019	-0.63166	cluster 4
HORVU.MOREX.r3.3HG0219750.1	-0.694726	-1.735553	-1.523473	cluster 4
HORVU.MOREX.r3.3HG0221490.1	-0.11546	-0.349416	-0.2641155	cluster 4
HORVU.MOREX.r3.3HG0222130.1	-0.11536	-0.341379	-0.3573973	cluster 4
HORVU.MOREX.r3.3HG0222830.1	-0.229299	-0.48403	-0.41894	cluster 4
HORVU.MOREX.r3.3HG0228010.1	-0.205685	-0.397499	-0.3962321	cluster 4
HORVU.MOREX.r3.3HG0230880.1	-0.097587	-0.213501	-0.2081264	cluster 4
HORVU.MOREX.r3.3HG0235030.1	-0.184656	-0.516033	-0.5021107	cluster 4
HORVU.MOREX.r3.3HG0235720.1	-0.451454	-2.293505	-2.0720386	cluster 4
HORVU.MOREX.r3.3HG0237330.1	-0.88099	-1.616044	-1.6289269	cluster 4
HORVU.MOREX.r3.3HG0238250.1	-0.611268	-0.985374	-0.8984795	cluster 4
HORVU.MOREX.r3.3HG0239940.1	-0.106152	-0.564578	-0.605368	cluster 4
HORVU.MOREX.r3.3HG0240310.1	-0.369458	-1.122443	-1.1950132	cluster 4
HORVU.MOREX.r3.3HG0242950.1	-0.190897	-0.433324	-0.4367021	cluster 4

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.3HG0243130.1	-0.486099	-0.756778	-0.6823611	cluster 4
HORVU.MOREX.r3.3HG0246540.1	-0.304757	-0.834515	-0.8782421	cluster 4
HORVU.MOREX.r3.3HG0247440.1	-0.412838	-1.038788	-0.9144083	cluster 4
HORVU.MOREX.r3.3HG0250870.1	-0.162252	-0.503649	-0.5000841	cluster 4
HORVU.MOREX.r3.3HG0250940.1	-0.189537	-0.60542	-0.5773945	cluster 4
HORVU.MOREX.r3.3HG0253450.1	-0.011765	-0.368997	-0.3293449	cluster 4
HORVU.MOREX.r3.3HG0256400.1	0.0735805	-0.499938	-0.3785823	cluster 4
HORVU.MOREX.r3.3HG0257310.1	-0.098947	-0.273317	-0.2255739	cluster 4
HORVU.MOREX.r3.3HG0264700.1	-0.285675	-0.333653	-0.3400111	cluster 4
HORVU.MOREX.r3.3HG0274100.1	-1.067729	-1.297125	-1.2686463	cluster 4
HORVU.MOREX.r3.3HG0280630.1	-0.172824	-0.41087	-0.4177276	cluster 4
HORVU.MOREX.r3.3HG0280920.1	-0.416991	-0.733995	-0.6264072	cluster 4
HORVU.MOREX.r3.3HG0280970.1	-0.077547	-0.406923	-0.414523	cluster 4
HORVU.MOREX.r3.3HG0281730.1	-0.132377	-1.52473	-1.3651815	cluster 4
HORVU.MOREX.r3.3HG0288080.1	-0.066388	-0.254736	-0.2583273	cluster 4
HORVU.MOREX.r3.3HG0288360.1	-0.212077	-0.287403	-0.2583098	cluster 4
HORVU.MOREX.r3.3HG0288370.1	-0.486641	-0.972153	-1.0220741	cluster 4
HORVU.MOREX.r3.3HG0292080.1	-0.144733	-0.49333	-0.4810081	cluster 4
HORVU.MOREX.r3.3HG0293430.1	1.3180018	1.1773024	1.20780458	cluster 4
HORVU.MOREX.r3.3HG0293570.1	-0.215612	-2.422838	-1.605738	cluster 4
HORVU.MOREX.r3.3HG0294670.1	-0.848006	-1.583304	-1.383073	cluster 4
HORVU.MOREX.r3.3HG0297330.1	-0.257665	-0.634878	-0.5272362	cluster 4
HORVU.MOREX.r3.3HG0300950.1	-0.331933	-0.855851	-0.8120216	cluster 4
HORVU.MOREX.r3.3HG0302340.1	-0.961716	-2.742539	-2.4059971	cluster 4
HORVU.MOREX.r3.3HG0304780.1	-0.217809	-0.513246	-0.5397324	cluster 4
HORVU.MOREX.r3.3HG0306060.1	-0.108451	-0.40301	-0.373696	cluster 4
HORVU.MOREX.r3.3HG0307850.1	-0.204906	-0.693866	-0.7553537	cluster 4
HORVU.MOREX.r3.3HG0307950.1	-0.100394	-0.303004	-0.271704	cluster 4
HORVU.MOREX.r3.3HG0310460.1	-0.18705	-0.805496	-0.5478687	cluster 4
HORVU.MOREX.r3.3HG0313020.1	-0.155766	-0.357107	-0.332207	cluster 4
HORVU.MOREX.r3.3HG0314240.1	-0.180125	-0.417324	-0.4126967	cluster 4
HORVU.MOREX.r3.3HG0316130.1	-0.227113	-0.695321	-0.7369012	cluster 4
HORVU.MOREX.r3.3HG0322740.1	-0.227097	-0.902679	-0.6225242	cluster 4
HORVU.MOREX.r3.3HG0324180.1	-0.412241	-0.868378	-0.8212219	cluster 4
HORVU.MOREX.r3.3HG0325670.1	-0.125844	-0.621853	-0.6298433	cluster 4
HORVU.MOREX.r3.3HG0326430.1	-0.072333	-0.365205	-0.2748693	cluster 4
HORVU.MOREX.r3.4HG0331630.1	-0.032278	-0.369393	-0.3918205	cluster 4
HORVU.MOREX.r3.4HG0331730.1	-0.167803	-0.308637	-0.3063395	cluster 4
HORVU.MOREX.r3.4HG0335180.1	-0.316712	-0.622832	-0.6396912	cluster 4
HORVU.MOREX.r3.4HG0335700.1	-0.098305	-0.239357	-0.2007837	cluster 4
HORVU.MOREX.r3.4HG0337110.1	-0.119306	-0.40188	-0.3460329	cluster 4
HORVU.MOREX.r3.4HG0343540.1	-0.886864	-1.868205	-1.4943153	cluster 4
HORVU.MOREX.r3.4HG0344830.1	-0.094413	-0.449223	-0.328731	cluster 4
HORVU.MOREX.r3.4HG0345610.1	-0.137979	-0.285953	-0.2416721	cluster 4
HORVU.MOREX.r3.4HG0347400.1	-0.146166	-0.452852	-0.3028916	cluster 4
HORVU.MOREX.r3.4HG0349310.1	-0.142031	-0.410999	-0.2838386	cluster 4
HORVU.MOREX.r3.4HG0350900.1	-0.161247	-0.44244	-0.4339045	cluster 4

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.4HG0352540.1	-0.218739	-0.583265	-0.5703874	cluster 4
HORVU.MOREX.r3.4HG0355390.1	-0.152652	-0.745518	-0.7235153	cluster 4
HORVU.MOREX.r3.4HG0355460.1	-0.219534	-0.463683	-0.3953742	cluster 4
HORVU.MOREX.r3.4HG0378000.1	-0.114183	-0.285587	-0.2721397	cluster 4
HORVU.MOREX.r3.4HG0379290.1	-0.138201	-0.316911	-0.3198258	cluster 4
HORVU.MOREX.r3.4HG0379530.1	-0.234909	-0.402578	-0.4169981	cluster 4
HORVU.MOREX.r3.4HG0380330.1	-0.152072	-0.499123	-0.5291229	cluster 4
HORVU.MOREX.r3.4HG0381800.1	-0.120611	-0.279721	-0.2693879	cluster 4
HORVU.MOREX.r3.4HG0384230.1	-0.154127	-0.579808	-0.637713	cluster 4
HORVU.MOREX.r3.4HG0390700.1	-0.060572	-0.194416	-0.2085167	cluster 4
HORVU.MOREX.r3.4HG0391730.1	-0.124635	-0.317151	-0.2467658	cluster 4
HORVU.MOREX.r3.4HG0392590.1	-0.029707	-0.420046	-0.432657	cluster 4
HORVU.MOREX.r3.4HG0400740.1	-0.099135	-0.304881	-0.2874618	cluster 4
HORVU.MOREX.r3.4HG0401730.1	-0.246305	-0.713924	-0.7434039	cluster 4
HORVU.MOREX.r3.4HG0402000.1	-0.241346	-0.71102	-0.6381152	cluster 4
HORVU.MOREX.r3.4HG0403370.1	-0.130151	-0.402659	-0.3882804	cluster 4
HORVU.MOREX.r3.4HG0403510.1	-0.111716	-0.413298	-0.3832699	cluster 4
HORVU.MOREX.r3.4HG0403680.1	-0.225767	-1.264573	-1.3828257	cluster 4
HORVU.MOREX.r3.4HG0409180.1	-0.074596	-0.328478	-0.2718058	cluster 4
HORVU.MOREX.r3.4HG0410640.1	-0.124296	-0.378262	-0.3970308	cluster 4
HORVU.MOREX.r3.4HG0416090.1	-0.111536	-0.523653	-0.5069306	cluster 4
HORVU.MOREX.r3.4HG0416760.1	-0.239652	-0.586074	-0.5290765	cluster 4
HORVU.MOREX.r3.5HG0420460.1	3.0932412	2.6734724	2.79652069	cluster 4
HORVU.MOREX.r3.5HG0420630.1	-0.18813	-0.480883	-0.4727335	cluster 4
HORVU.MOREX.r3.5HG0434380.1	-0.191479	-0.482553	-0.3843015	cluster 4
HORVU.MOREX.r3.5HG0436660.1	-0.224065	-0.476557	-0.4550899	cluster 4
HORVU.MOREX.r3.5HG0446900.1	-0.036148	-0.218937	-0.2236596	cluster 4
HORVU.MOREX.r3.5HG0454660.1	-0.208314	-0.40023	-0.4169716	cluster 4
HORVU.MOREX.r3.5HG0458440.1	-0.042315	-1.067416	-0.9131093	cluster 4
HORVU.MOREX.r3.5HG0459320.1	-0.201293	-0.450674	-0.4424902	cluster 4
HORVU.MOREX.r3.5HG0460630.1	0.1977752	-0.980742	-0.6336549	cluster 4
HORVU.MOREX.r3.5HG0463000.1	-0.214065	-0.448239	-0.3731562	cluster 4
HORVU.MOREX.r3.5HG0466440.1	-0.253495	-0.496231	-0.3984102	cluster 4
HORVU.MOREX.r3.5HG0466510.1	-0.281459	-0.969587	-0.761974	cluster 4
HORVU.MOREX.r3.5HG0476690.1	0.0280055	-0.321602	-0.3075335	cluster 4
HORVU.MOREX.r3.5HG0480890.1	1.8701414	1.2649812	1.45109118	cluster 4
HORVU.MOREX.r3.5HG0481760.1	-0.061848	-0.290194	-0.2071981	cluster 4
HORVU.MOREX.r3.5HG0486960.1	-0.654483	-1.501356	-1.1381945	cluster 4
HORVU.MOREX.r3.5HG0489720.1	-0.177447	-0.431894	-0.4331791	cluster 4
HORVU.MOREX.r3.5HG0493380.1	-0.068113	-0.320081	-0.2420716	cluster 4
HORVU.MOREX.r3.5HG0495490.1	-0.201213	-0.423029	-0.4221545	cluster 4
HORVU.MOREX.r3.5HG0500120.1	-0.522798	-1.061761	-1.1050016	cluster 4
HORVU.MOREX.r3.5HG0500180.1	-0.129879	-0.41309	-0.3181799	cluster 4
HORVU.MOREX.r3.5HG0501500.1	1.1804435	1.1252077	1.12682132	cluster 4
HORVU.MOREX.r3.5HG0503200.1	-0.057395	-0.566785	-0.609787	cluster 4
HORVU.MOREX.r3.5HG0510160.1	-0.055237	-0.459951	-0.5016767	cluster 4
HORVU.MOREX.r3.5HG0510210.1	-0.150813	-0.356296	-0.3731947	cluster 4

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.5HG0519040.1	-0.148928	-0.368191	-0.3427753	cluster 4
HORVU.MOREX.r3.5HG0520650.1	-0.209542	-0.68725	-0.6756638	cluster 4
HORVU.MOREX.r3.5HG0520990.1	-0.35326	-0.741574	-0.6553458	cluster 4
HORVU.MOREX.r3.5HG0522130.1	-0.161695	-0.483941	-0.5132723	cluster 4
HORVU.MOREX.r3.5HG0524120.1	-0.152452	-0.366911	-0.3915019	cluster 4
HORVU.MOREX.r3.5HG0526140.1	-0.051704	-0.403299	-0.4518669	cluster 4
HORVU.MOREX.r3.5HG0526160.1	-0.230133	-0.497186	-0.3693641	cluster 4
HORVU.MOREX.r3.5HG0526200.1	-0.100757	-0.272216	-0.2658474	cluster 4
HORVU.MOREX.r3.5HG0527500.1	-0.195335	-0.51146	-0.5397168	cluster 4
HORVU.MOREX.r3.5HG0529660.1	-0.035728	-0.271686	-0.1610445	cluster 4
HORVU.MOREX.r3.5HG0533230.1	-0.265764	-0.528208	-0.5553388	cluster 4
HORVU.MOREX.r3.5HG0534100.1	-0.214006	-0.820121	-0.8873792	cluster 4
HORVU.MOREX.r3.5HG0537090.1	-0.119397	-0.327596	-0.3455348	cluster 4
HORVU.MOREX.r3.6HG0543390.1	1.5419602	0.9739213	1.22556774	cluster 4
HORVU.MOREX.r3.6HG0546140.1	-0.070897	-0.758392	-0.7023619	cluster 4
HORVU.MOREX.r3.6HG0548360.1	-0.021977	-0.595089	-0.401464	cluster 4
HORVU.MOREX.r3.6HG0550940.1	-0.189132	-0.390098	-0.3346286	cluster 4
HORVU.MOREX.r3.6HG0553150.1	-0.386615	-0.593359	-0.5321773	cluster 4
HORVU.MOREX.r3.6HG0555660.2	-0.228528	-0.430502	-0.4350808	cluster 4
HORVU.MOREX.r3.6HG0557070.1	-0.17213	-0.56379	-0.4946179	cluster 4
HORVU.MOREX.r3.6HG0558250.1	-0.094468	-0.551478	-0.5931937	cluster 4
HORVU.MOREX.r3.6HG0564910.1	-0.158965	-0.985196	-1.0100623	cluster 4
HORVU.MOREX.r3.6HG0572400.1	-0.235159	-0.413275	-0.3607975	cluster 4
HORVU.MOREX.r3.6HG0577360.1	-0.171359	-0.661974	-0.6563386	cluster 4
HORVU.MOREX.r3.6HG0599080.1	-0.121656	-0.386829	-0.3657578	cluster 4
HORVU.MOREX.r3.6HG0601670.1	-0.310073	-1.038854	-0.9143986	cluster 4
HORVU.MOREX.r3.6HG0602230.1	-0.231684	-0.514986	-0.5091945	cluster 4
HORVU.MOREX.r3.6HG0605090.1	-0.04292	-0.285138	-0.3172045	cluster 4
HORVU.MOREX.r3.6HG0606850.1	-0.155525	-0.459291	-0.3134643	cluster 4
HORVU.MOREX.r3.6HG0606930.1	-0.071743	-0.374522	-0.4077279	cluster 4
HORVU.MOREX.r3.6HG0613230.1	-0.113996	-0.367812	-0.3068486	cluster 4
HORVU.MOREX.r3.6HG0616890.1	-0.536575	-0.917484	-0.9478679	cluster 4
HORVU.MOREX.r3.6HG0617730.1	-0.078532	-0.339833	-0.3596403	cluster 4
HORVU.MOREX.r3.6HG0618760.1	-0.292818	-0.747648	-0.796672	cluster 4
HORVU.MOREX.r3.6HG0621190.1	-0.154558	-0.673173	-0.6018863	cluster 4
HORVU.MOREX.r3.6HG0622550.1	-0.15326	-0.349934	-0.2835664	cluster 4
HORVU.MOREX.r3.6HG0626650.1	-0.123334	-0.267557	-0.2501574	cluster 4
HORVU.MOREX.r3.6HG0632270.1	-0.201751	-0.511546	-0.4392241	cluster 4
HORVU.MOREX.r3.6HG0632320.1	-0.140583	-0.360637	-0.3880408	cluster 4
HORVU.MOREX.r3.6HG0633650.1	-0.187888	-1.172822	-1.176745	cluster 4
HORVU.MOREX.r3.6HG0634130.1	-0.228673	-0.344764	-0.3096888	cluster 4
HORVU.MOREX.r3.7HG0634430.1	-0.05789	-0.820241	-0.530186	cluster 4
HORVU.MOREX.r3.7HG0634470.1	-0.076647	-0.276924	-0.2886309	cluster 4
HORVU.MOREX.r3.7HG0639930.1	-0.145969	-0.513816	-0.3434781	cluster 4
HORVU.MOREX.r3.7HG0640560.1	-1.061191	-3.052375	-2.5346574	cluster 4
HORVU.MOREX.r3.7HG0643260.1	-0.082668	-0.639752	-0.4085841	cluster 4
HORVU.MOREX.r3.7HG0658270.1	-0.071725	-0.604362	-0.5618305	cluster 4

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.7HG0661490.1	-0.147876	-0.307367	-0.3085276	cluster 4
HORVU.MOREX.r3.7HG0666650.1	-0.609304	-1.748073	-1.6004303	cluster 4
HORVU.MOREX.r3.7HG0671360.1	-0.142628	-0.337151	-0.2559202	cluster 4
HORVU.MOREX.r3.7HG0674320.1	-0.262906	-0.368676	-0.3746705	cluster 4
HORVU.MOREX.r3.7HG0674990.1	-0.171202	-0.465086	-0.500011	cluster 4
HORVU.MOREX.r3.7HG0678160.1	-0.270922	-0.702624	-0.6451568	cluster 4
HORVU.MOREX.r3.7HG0680970.1	-0.361888	-0.798843	-0.6609786	cluster 4
HORVU.MOREX.r3.7HG0680990.1	-0.129828	-0.348204	-0.2598531	cluster 4
HORVU.MOREX.r3.7HG0682460.1	-0.164134	-0.35679	-0.3473942	cluster 4
HORVU.MOREX.r3.7HG0687540.1	-0.113748	-0.311866	-0.2900132	cluster 4
HORVU.MOREX.r3.7HG0693590.1	-0.197214	-0.409448	-0.3367645	cluster 4
HORVU.MOREX.r3.7HG0696770.1	-0.133347	-0.329911	-0.3385414	cluster 4
HORVU.MOREX.r3.7HG0700270.1	-0.143956	-0.39241	-0.4245597	cluster 4
HORVU.MOREX.r3.7HG0710170.1	-0.34057	-2.238231	-1.7983181	cluster 4
HORVU.MOREX.r3.7HG0717850.1	-0.119137	-0.348577	-0.3554462	cluster 4
HORVU.MOREX.r3.7HG0719830.1	-0.75286	-1.733023	-1.4829856	cluster 4
HORVU.MOREX.r3.7HG0722380.1	-0.149099	-0.503357	-0.3453409	cluster 4
HORVU.MOREX.r3.7HG0725290.1	-0.005522	-0.60065	-0.47921	cluster 4
HORVU.MOREX.r3.7HG0728870.1	-0.200143	-0.675879	-0.5988388	cluster 4
HORVU.MOREX.r3.7HG0731320.1	-0.118784	-0.341523	-0.2786513	cluster 4
HORVU.MOREX.r3.7HG0734380.1	-0.178956	-0.455402	-0.4756674	cluster 4
HORVU.MOREX.r3.7HG0739180.1	-0.138186	-0.30909	-0.2397068	cluster 4
HORVU.MOREX.r3.7HG0752940.1	-0.061403	-0.324838	-0.196665	cluster 4
HORVU.MOREX.r3.1HG0003820.1	0.1506945	0.1903632	0.34939377	cluster 5
HORVU.MOREX.r3.1HG0008510.2	0.1315153	0.2016694	0.54376722	cluster 5
HORVU.MOREX.r3.1HG0008640.1	0.3204557	0.345242	0.48963061	cluster 5
HORVU.MOREX.r3.1HG0016710.2	1.1890242	1.3376758	1.75589204	cluster 5
HORVU.MOREX.r3.1HG0020980.1	0.2916687	0.3662362	0.54445194	cluster 5
HORVU.MOREX.r3.1HG0025870.1	0.5108263	0.5636698	0.75828619	cluster 5
HORVU.MOREX.r3.1HG0042440.1	1.26164	1.2501095	1.3921203	cluster 5
HORVU.MOREX.r3.1HG0043640.1	0.1201616	0.2422031	0.42338664	cluster 5
HORVU.MOREX.r3.1HG0045770.1	1.5447	1.7458726	2.12094315	cluster 5
HORVU.MOREX.r3.1HG0049550.1	0.1576196	0.1479541	0.39915593	cluster 5
HORVU.MOREX.r3.1HG0057610.1	0.5288138	0.5805584	0.69813619	cluster 5
HORVU.MOREX.r3.1HG0059850.1	0.1454644	0.2951392	0.52413389	cluster 5
HORVU.MOREX.r3.1HG0064390.1	0.1071974	0.1965282	0.38205732	cluster 5
HORVU.MOREX.r3.1HG0067720.1	1.2160888	1.3105495	1.65738455	cluster 5
HORVU.MOREX.r3.1HG0069870.1	0.1767651	0.3193547	0.68052598	cluster 5
HORVU.MOREX.r3.1HG0070480.1	0.0244839	0.1380118	0.32689078	cluster 5
HORVU.MOREX.r3.1HG0075650.1	0.3233917	0.6804061	1.18634955	cluster 5
HORVU.MOREX.r3.1HG0079130.1	0.123639	0.1546145	0.36243892	cluster 5
HORVU.MOREX.r3.1HG0079140.1	0.2935846	0.4445291	0.69272931	cluster 5
HORVU.MOREX.r3.1HG0079950.1	0.0858294	0.1651136	0.31117409	cluster 5
HORVU.MOREX.r3.1HG0082550.1	0.8194643	1.0342348	1.50018093	cluster 5
HORVU.MOREX.r3.1HG0084890.1	0.3478786	0.34503	0.61071091	cluster 5
HORVU.MOREX.r3.1HG0092880.1	0.4749795	0.5257856	0.59948098	cluster 5
HORVU.MOREX.r3.2HG0097010.1	0.0877437	0.1815887	0.39799786	cluster 5

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.2HG0099010.1	0.5486596	0.6936151	1.17562956	cluster 5
HORVU.MOREX.r3.2HG0099160.1	0.6424212	0.686862	0.98464269	cluster 5
HORVU.MOREX.r3.2HG0100360.1	0.125064	0.1270412	0.39321359	cluster 5
HORVU.MOREX.r3.2HG0100750.1	1.2075072	1.4933226	2.00037087	cluster 5
HORVU.MOREX.r3.2HG0105050.1	0.8090145	1.1605794	1.85682601	cluster 5
HORVU.MOREX.r3.2HG0111570.1	-0.033407	0.1424131	0.73615542	cluster 5
HORVU.MOREX.r3.2HG0113660.1	0.1554899	0.2139374	0.35324822	cluster 5
HORVU.MOREX.r3.2HG0117030.1	0.5822317	0.6240572	0.72265079	cluster 5
HORVU.MOREX.r3.2HG0122080.1	0.2666389	0.3454356	0.59234208	cluster 5
HORVU.MOREX.r3.2HG0126380.1	0.2457761	0.3007804	0.47791978	cluster 5
HORVU.MOREX.r3.2HG0126440.1	0.3812549	0.6296109	1.16229679	cluster 5
HORVU.MOREX.r3.2HG0131280.1	-0.04178	0.3444847	0.89225606	cluster 5
HORVU.MOREX.r3.2HG0135650.1	1.2476173	1.5945768	2.770416	cluster 5
HORVU.MOREX.r3.2HG0137620.1	0.1669473	0.2071834	0.47432716	cluster 5
HORVU.MOREX.r3.2HG0142740.1	0.1788709	0.2082363	0.36584606	cluster 5
HORVU.MOREX.r3.2HG0153420.1	0.5183998	0.7413509	1.11738569	cluster 5
HORVU.MOREX.r3.2HG0155290.1	0.4689755	0.8772635	1.482062	cluster 5
HORVU.MOREX.r3.2HG0157260.1	0.8422643	1.0459764	1.44511468	cluster 5
HORVU.MOREX.r3.2HG0159580.1	0.2014004	0.3455338	0.65480766	cluster 5
HORVU.MOREX.r3.2HG0160130.1	0.5326993	0.5959193	0.79332848	cluster 5
HORVU.MOREX.r3.2HG0160760.1	0.6251605	0.6294764	0.66585156	cluster 5
HORVU.MOREX.r3.2HG0165200.1	0.334928	0.4551799	0.62889149	cluster 5
HORVU.MOREX.r3.2HG0172580.1	1.1213565	1.2401841	1.65259497	cluster 5
HORVU.MOREX.r3.2HG0173380.1	0.0191126	0.133931	0.41562246	cluster 5
HORVU.MOREX.r3.2HG0177830.1	0.2974003	0.4238256	0.62031522	cluster 5
HORVU.MOREX.r3.2HG0186980.1	0.4348704	0.7049726	1.09965889	cluster 5
HORVU.MOREX.r3.2HG0189110.1	0.8017171	0.8633209	1.06107648	cluster 5
HORVU.MOREX.r3.2HG0190620.1	0.7019473	0.6991351	0.95931523	cluster 5
HORVU.MOREX.r3.2HG0191510.1	0.5490179	0.5822354	0.84188673	cluster 5
HORVU.MOREX.r3.2HG0196630.1	0.1987878	0.2309701	0.96600749	cluster 5
HORVU.MOREX.r3.2HG0197260.1	0.0062804	0.1096589	0.2688385	cluster 5
HORVU.MOREX.r3.2HG0199330.1	0.2860455	0.3700994	0.62871499	cluster 5
HORVU.MOREX.r3.2HG0204020.1	0.2760942	0.4700435	0.7417162	cluster 5
HORVU.MOREX.r3.2HG0207790.1	1.0148165	1.1822833	1.61922448	cluster 5
HORVU.MOREX.r3.2HG0213430.1	0.5039028	0.544796	0.76088997	cluster 5
HORVU.MOREX.r3.3HG0218560.1	0.872263	1.0259185	1.41284311	cluster 5
HORVU.MOREX.r3.3HG0226110.1	0.5157394	0.7011145	1.86209217	cluster 5
HORVU.MOREX.r3.3HG0228660.1	0.0955271	0.1285591	0.33763937	cluster 5
HORVU.MOREX.r3.3HG0234210.1	0.5296158	0.5100511	0.98978648	cluster 5
HORVU.MOREX.r3.3HG0244240.1	0.8114471	0.8835885	1.22221518	cluster 5
HORVU.MOREX.r3.3HG0245400.1	0.2898759	0.4244746	0.61866946	cluster 5
HORVU.MOREX.r3.3HG0269960.1	0.2215019	0.3635156	0.56275935	cluster 5
HORVU.MOREX.r3.3HG0279110.1	0.9218836	1.296394	2.07713439	cluster 5
HORVU.MOREX.r3.3HG0280530.1	0.2267596	0.2403021	0.53280743	cluster 5
HORVU.MOREX.r3.3HG0283080.2	0.2793467	0.5406405	1.02444722	cluster 5
HORVU.MOREX.r3.3HG0284760.1	0.0894929	0.1566816	0.56866413	cluster 5
HORVU.MOREX.r3.3HG0289020.1	1.1492856	1.1769054	1.30557443	cluster 5

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.3HG0291570.1	0.0639497	0.1001521	0.40453683	cluster 5
HORVU.MOREX.r3.3HG0291670.1	0.6984078	0.7129584	1.29457936	cluster 5
HORVU.MOREX.r3.3HG0295680.1	0.3017542	0.3989332	0.6162365	cluster 5
HORVU.MOREX.r3.3HG0296010.1	0.9557079	1.3367467	1.96877264	cluster 5
HORVU.MOREX.r3.3HG0297000.1	0.7808635	0.9095607	1.16065524	cluster 5
HORVU.MOREX.r3.3HG0299990.1	0.1441051	0.2615899	0.50713829	cluster 5
HORVU.MOREX.r3.3HG0301000.1	0.5097699	0.590378	0.91653442	cluster 5
HORVU.MOREX.r3.3HG0304660.1	0.0208108	-0.032096	0.41942742	cluster 5
HORVU.MOREX.r3.3HG0305600.1	0.0859495	0.1762314	0.40739692	cluster 5
HORVU.MOREX.r3.3HG0309900.1	1.0254695	1.1486088	1.46368758	cluster 5
HORVU.MOREX.r3.3HG0316870.1	0.0681683	0.1493181	0.36697207	cluster 5
HORVU.MOREX.r3.3HG0320350.1	1.4726565	1.5749652	1.85992323	cluster 5
HORVU.MOREX.r3.3HG0320520.1	0.4376358	0.4291602	0.68054367	cluster 5
HORVU.MOREX.r3.3HG0324480.1	0.4735448	0.6441702	1.35677217	cluster 5
HORVU.MOREX.r3.4HG0333540.1	0.6643687	0.7770503	0.94212038	cluster 5
HORVU.MOREX.r3.4HG0333550.2	0.195438	0.3645787	0.70912011	cluster 5
HORVU.MOREX.r3.4HG0340650.1	0.2275561	0.2445699	0.39966237	cluster 5
HORVU.MOREX.r3.4HG0349980.1	0.1567483	0.2679095	0.61503478	cluster 5
HORVU.MOREX.r3.4HG0351440.1	0.2172212	0.2217873	0.46079846	cluster 5
HORVU.MOREX.r3.4HG0353200.1	0.1292698	0.223277	0.52468811	cluster 5
HORVU.MOREX.r3.4HG0353950.1	0.5221309	0.5084894	2.94704517	cluster 5
HORVU.MOREX.r3.4HG0358980.1	0.1653312	0.1892386	0.50206292	cluster 5
HORVU.MOREX.r3.4HG0378330.1	0.6500979	0.8954483	1.26116524	cluster 5
HORVU.MOREX.r3.4HG0384350.1	-0.004781	0.0987288	0.37871172	cluster 5
HORVU.MOREX.r3.4HG0385240.1	0.2914315	0.411096	0.62102358	cluster 5
HORVU.MOREX.r3.4HG0392690.1	0.3101105	0.3534756	0.44460083	cluster 5
HORVU.MOREX.r3.4HG0394830.1	0.6965264	0.824201	1.25434005	cluster 5
HORVU.MOREX.r3.4HG0397570.1	0.3785475	0.5006545	0.75817975	cluster 5
HORVU.MOREX.r3.4HG0398980.1	0.0802368	0.1704924	0.35305742	cluster 5
HORVU.MOREX.r3.4HG0401130.1	0.1270489	0.2114731	0.36245202	cluster 5
HORVU.MOREX.r3.4HG0403260.1	0.1030162	0.0944493	0.3463164	cluster 5
HORVU.MOREX.r3.4HG0403630.1	0.8573751	1.0227619	1.56282623	cluster 5
HORVU.MOREX.r3.4HG0407560.1	0.1921403	0.2773518	0.41498208	cluster 5
HORVU.MOREX.r3.4HG0409600.1	0.1887469	0.2941607	0.48745659	cluster 5
HORVU.MOREX.r3.4HG0414000.1	0.1665393	0.3454709	0.76980864	cluster 5
HORVU.MOREX.r3.5HG0420410.1	0.2534881	0.3710897	0.5507145	cluster 5
HORVU.MOREX.r3.5HG0421310.1	0.6414658	0.7966063	1.07325559	cluster 5
HORVU.MOREX.r3.5HG0426210.3	0.4977726	0.6222315	0.86104193	cluster 5
HORVU.MOREX.r3.5HG0430460.1	0.1856268	0.236529	0.48946727	cluster 5
HORVU.MOREX.r3.5HG0432360.1	0.28872	0.3754987	0.63714401	cluster 5
HORVU.MOREX.r3.5HG0436900.1	0.1760451	0.1861287	0.36513154	cluster 5
HORVU.MOREX.r3.5HG0444270.1	0.1056411	0.2175851	0.44586786	cluster 5
HORVU.MOREX.r3.5HG0454720.1	0.2017966	0.3520529	0.5693287	cluster 5
HORVU.MOREX.r3.5HG0460160.1	0.1634637	0.2742783	0.43094171	cluster 5
HORVU.MOREX.r3.5HG0462450.1	0.7964124	0.9036124	1.30469581	cluster 5
HORVU.MOREX.r3.5HG0464630.1	0.3210834	0.4123414	0.56749817	cluster 5
HORVU.MOREX.r3.5HG0470940.1	0.1503364	0.2760358	0.50070992	cluster 5

Table SП Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.5HG0472140.1	0.4155581	0.4014265	0.69239096	cluster 5
HORVU.MOREX.r3.5HG0478610.1	0.0949356	0.179812	0.39951234	cluster 5
HORVU.MOREX.r3.5HG0485760.1	1.2127406	1.3978826	1.66332866	cluster 5
HORVU.MOREX.r3.5HG0487910.1	1.743065	1.7830562	2.00123739	cluster 5
HORVU.MOREX.r3.5HG0493890.2	0.2756003	0.2539389	0.44122832	cluster 5
HORVU.MOREX.r3.5HG0495640.1	1.541128	1.5710812	1.90941616	cluster 5
HORVU.MOREX.r3.5HG0498320.1	0.0654798	0.0814044	0.42141937	cluster 5
HORVU.MOREX.r3.5HG0506230.1	0.1985123	0.2556131	0.52424111	cluster 5
HORVU.MOREX.r3.5HG0509390.1	0.7920428	0.8589774	1.09567221	cluster 5
HORVU.MOREX.r3.5HG0510320.1	0.2486342	0.3375388	0.72221946	cluster 5
HORVU.MOREX.r3.5HG0510500.1	0.0186906	0.1532601	0.46359741	cluster 5
HORVU.MOREX.r3.5HG0513810.1	0.2686357	0.3272462	0.62971808	cluster 5
HORVU.MOREX.r3.5HG0514020.1	0.2824591	0.3358146	0.44111193	cluster 5
HORVU.MOREX.r3.5HG0515610.1	0.354598	0.6985583	1.23595498	cluster 5
HORVU.MOREX.r3.5HG0522090.1	0.1003735	0.1869424	0.60113722	cluster 5
HORVU.MOREX.r3.5HG0531450.1	0.5936271	0.5556235	0.91417864	cluster 5
HORVU.MOREX.r3.5HG0537780.1	0.121621	0.2363552	0.41488425	cluster 5
HORVU.MOREX.r3.6HG0545460.1	0.1884398	0.2478194	0.50599213	cluster 5
HORVU.MOREX.r3.6HG0549520.1	0.1886624	0.3124328	0.634171	cluster 5
HORVU.MOREX.r3.6HG0564690.1	0.1434775	0.2110247	0.41003985	cluster 5
HORVU.MOREX.r3.6HG0565800.1	0.5641555	0.5657139	0.77030214	cluster 5
HORVU.MOREX.r3.6HG0568390.1	0.1456539	0.2871736	0.653533	cluster 5
HORVU.MOREX.r3.6HG0569990.1	0.0073052	0.1058387	0.27427454	cluster 5
HORVU.MOREX.r3.6HG0582950.1	0.1647378	0.1551424	0.27946176	cluster 5
HORVU.MOREX.r3.6HG0587460.1	0.3697823	0.4815205	0.95382752	cluster 5
HORVU.MOREX.r3.6HG0597640.1	0.4515542	0.5103614	0.76651863	cluster 5
HORVU.MOREX.r3.6HG0597790.1	0.4176998	0.5353106	0.73827734	cluster 5
HORVU.MOREX.r3.6HG0598750.1	0.4075013	0.6800884	1.17151566	cluster 5
HORVU.MOREX.r3.6HG0599450.1	1.1916244	1.2732576	1.72370577	cluster 5
HORVU.MOREX.r3.6HG0605130.1	0.1834353	0.3140859	1.024442	cluster 5
HORVU.MOREX.r3.6HG0608180.1	0.6316125	0.7255867	1.10985309	cluster 5
HORVU.MOREX.r3.6HG0608390.1	0.016203	0.1408953	0.37418566	cluster 5
HORVU.MOREX.r3.6HG0614470.2	0.3174888	0.3683412	0.50449019	cluster 5
HORVU.MOREX.r3.6HG0617240.1	0.2407525	0.3667786	0.56049813	cluster 5
HORVU.MOREX.r3.6HG0627090.1	0.4150708	0.377575	0.66252627	cluster 5
HORVU.MOREX.r3.6HG0631400.1	0.4495172	0.7629271	1.21136897	cluster 5
HORVU.MOREX.r3.6HG0634200.1	0.739161	0.9506689	1.28357549	cluster 5
HORVU.MOREX.r3.7HG0636030.1	0.7435151	0.8391918	1.40370231	cluster 5
HORVU.MOREX.r3.7HG0644240.1	0.6288995	0.8654318	1.20747996	cluster 5
HORVU.MOREX.r3.7HG0648460.1	0.3065913	0.4263577	0.62082676	cluster 5
HORVU.MOREX.r3.7HG0653740.1	0.1315017	0.2266617	0.45924945	cluster 5
HORVU.MOREX.r3.7HG0661450.1	0.1414274	0.3598007	0.66913788	cluster 5
HORVU.MOREX.r3.7HG0667150.1	0.4012188	0.585758	0.91635962	cluster 5
HORVU.MOREX.r3.7HG0667730.1	0.0317561	0.0615784	0.45914324	cluster 5
HORVU.MOREX.r3.7HG0669580.1	0.2534228	0.4093086	0.71139983	cluster 5
HORVU.MOREX.r3.7HG0669750.1	0.2169147	0.197497	0.4081658	cluster 5
HORVU.MOREX.r3.7HG0672400.1	0.6814586	0.758207	1.07071728	cluster 5

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.7HG0676610.1	0.0885464	0.1749045	0.37598996	cluster 5
HORVU.MOREX.r3.7HG0678940.1	0.1357469	0.2300726	0.36876502	cluster 5
HORVU.MOREX.r3.7HG0685350.1	0.3166707	0.4168246	0.60223185	cluster 5
HORVU.MOREX.r3.7HG0701640.1	0.3650906	0.5382216	0.80746439	cluster 5
HORVU.MOREX.r3.7HG0702050.1	0.104106	0.4031577	1.01586603	cluster 5
HORVU.MOREX.r3.7HG0702660.1	0.3179493	0.2673309	1.16124912	cluster 5
HORVU.MOREX.r3.7HG0704760.1	0.4325514	0.3761209	1.21235137	cluster 5
HORVU.MOREX.r3.7HG0716320.1	0.3082597	0.3601296	0.53056742	cluster 5
HORVU.MOREX.r3.7HG0729150.1	0.6630894	0.8021488	1.26014855	cluster 5
HORVU.MOREX.r3.7HG0745120.1	0.2089014	0.2337941	0.35355569	cluster 5
HORVU.MOREX.r3.7HG0751030.1	0.4365522	0.7805611	1.31887325	cluster 5
HORVU.MOREX.r3.1HG0003150.1	-0.210376	-0.205283	-0.6263923	cluster 6
HORVU.MOREX.r3.1HG0003280.1	-1.465937	-1.082383	-2.2260952	cluster 6
HORVU.MOREX.r3.1HG0005840.1	-0.519881	-0.266103	-1.4218761	cluster 6
HORVU.MOREX.r3.1HG0007570.1	-0.639076	-0.266017	-1.3606559	cluster 6
HORVU.MOREX.r3.1HG0007930.1	-0.173029	-0.174301	-0.766703	cluster 6
HORVU.MOREX.r3.1HG0018430.1	-0.46222	-0.441472	-1.0676984	cluster 6
HORVU.MOREX.r3.1HG0037920.1	-1.074663	-0.740293	-1.9231614	cluster 6
HORVU.MOREX.r3.1HG0041250.1	-0.092455	0.0016478	-0.3701922	cluster 6
HORVU.MOREX.r3.1HG0043350.1	-0.085053	-0.035176	-0.4948174	cluster 6
HORVU.MOREX.r3.1HG0045490.1	-0.211641	-0.189946	-0.4149042	cluster 6
HORVU.MOREX.r3.1HG0053530.1	-0.199408	-0.195196	-1.4522622	cluster 6
HORVU.MOREX.r3.1HG0053720.1	-0.425146	-0.297207	-0.9030535	cluster 6
HORVU.MOREX.r3.1HG0059870.1	-0.132292	-0.126445	-0.3775719	cluster 6
HORVU.MOREX.r3.1HG0063000.1	-0.086115	-0.078976	-0.4382613	cluster 6
HORVU.MOREX.r3.1HG0064610.1	-0.190379	-0.070031	-0.9729466	cluster 6
HORVU.MOREX.r3.1HG0069110.1	-0.157536	-0.140838	-0.4783552	cluster 6
HORVU.MOREX.r3.1HG0074650.2	-0.510431	-0.168715	-1.0294116	cluster 6
HORVU.MOREX.r3.1HG0079810.1	-0.278065	-0.161205	-0.5402787	cluster 6
HORVU.MOREX.r3.1HG0082750.1	-0.738823	-0.507772	-1.8998339	cluster 6
HORVU.MOREX.r3.1HG0083980.1	-0.275479	-0.275687	-0.9930048	cluster 6
HORVU.MOREX.r3.1HG0095000.1	-0.565694	-0.539614	-1.5807766	cluster 6
HORVU.MOREX.r3.2HG0097350.1	-1.005101	-0.924292	-2.0949814	cluster 6
HORVU.MOREX.r3.2HG0108490.1	-0.219808	-0.132454	-1.2703107	cluster 6
HORVU.MOREX.r3.2HG0111270.1	0.8853755	1.1046113	0.53938805	cluster 6
HORVU.MOREX.r3.2HG0117100.1	0.6704028	0.9147007	0.08654056	cluster 6
HORVU.MOREX.r3.2HG0119360.1	-0.662395	-0.383498	-2.1030955	cluster 6
HORVU.MOREX.r3.2HG0120830.1	2.006445	2.4275847	1.35478833	cluster 6
HORVU.MOREX.r3.2HG0121530.1	-0.586808	-0.276879	-1.0529693	cluster 6
HORVU.MOREX.r3.2HG0122720.1	-0.417898	-0.257733	-0.9808534	cluster 6
HORVU.MOREX.r3.2HG0124470.1	-0.872348	-0.664108	-2.277542	cluster 6
HORVU.MOREX.r3.2HG0134300.1	1.7005685	2.0693025	0.24289318	cluster 6
HORVU.MOREX.r3.2HG0135860.1	-0.237153	-0.166929	-0.3859966	cluster 6
HORVU.MOREX.r3.2HG0136010.1	-0.295066	-0.173897	-0.7129157	cluster 6
HORVU.MOREX.r3.2HG0142490.1	-0.085467	-0.058264	-0.2785315	cluster 6
HORVU.MOREX.r3.2HG0148170.1	-0.812555	-0.597135	-1.3169603	cluster 6
HORVU.MOREX.r3.2HG0154500.1	-0.610336	-0.59653	-1.0398242	cluster 6

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.2HG0167540.1	-0.172394	-0.165011	-0.2223481	cluster 6
HORVU.MOREX.r3.2HG0171100.1	-0.332299	-0.317458	-0.4414421	cluster 6
HORVU.MOREX.r3.2HG0171850.1	-0.255421	-0.146486	-0.4887234	cluster 6
HORVU.MOREX.r3.2HG0181550.1	0.0751298	0.1297928	-1.0106527	cluster 6
HORVU.MOREX.r3.2HG0182010.1	-0.476485	-0.414783	-0.8520016	cluster 6
HORVU.MOREX.r3.2HG0189970.1	-0.301055	-0.147908	-0.7152154	cluster 6
HORVU.MOREX.r3.2HG0190260.1	1.0366098	1.0486261	0.84157807	cluster 6
HORVU.MOREX.r3.2HG0196960.1	-0.967413	-0.511161	-2.6121341	cluster 6
HORVU.MOREX.r3.2HG0201250.1	-0.272512	-0.199863	-0.5651718	cluster 6
HORVU.MOREX.r3.2HG0205680.1	-0.035521	0.1972397	-1.9432136	cluster 6
HORVU.MOREX.r3.2HG0205760.1	-0.361271	-0.366731	-0.9134359	cluster 6
HORVU.MOREX.r3.2HG0208280.1	-0.25249	-0.234284	-0.4920429	cluster 6
HORVU.MOREX.r3.2HG0209030.1	-0.117056	-0.088912	-1.4886989	cluster 6
HORVU.MOREX.r3.2HG0209090.1	-0.222263	-0.15666	-0.6005596	cluster 6
HORVU.MOREX.r3.2HG0215060.1	2.4857767	2.5684304	2.22913008	cluster 6
HORVU.MOREX.r3.3HG0225640.1	-0.421046	-0.117874	-1.2981488	cluster 6
HORVU.MOREX.r3.3HG0231880.1	-0.614058	-0.576063	-1.0812871	cluster 6
HORVU.MOREX.r3.3HG0236000.1	-0.195667	-0.189929	-0.4465279	cluster 6
HORVU.MOREX.r3.3HG0243560.1	-0.134212	-0.115022	-0.4068952	cluster 6
HORVU.MOREX.r3.3HG0243920.1	-0.125523	-0.023681	-1.1859745	cluster 6
HORVU.MOREX.r3.3HG0244010.1	-0.067479	-0.051859	-0.6610377	cluster 6
HORVU.MOREX.r3.3HG0245320.1	-0.15354	-0.137279	-0.5011831	cluster 6
HORVU.MOREX.r3.3HG0253630.1	1.1990125	1.4139342	0.94401369	cluster 6
HORVU.MOREX.r3.3HG0277330.1	-0.168801	-0.172149	-0.6224506	cluster 6
HORVU.MOREX.r3.3HG0281860.1	0.0321565	0.0784197	-0.5930055	cluster 6
HORVU.MOREX.r3.3HG0289070.1	0.0018635	-0.00883	-1.2054247	cluster 6
HORVU.MOREX.r3.3HG0291340.1	-0.606158	-0.546952	-0.9681079	cluster 6
HORVU.MOREX.r3.3HG0300810.1	-0.275664	-0.221569	-0.4895947	cluster 6
HORVU.MOREX.r3.3HG0308980.1	-0.262001	-0.253071	-0.6935355	cluster 6
HORVU.MOREX.r3.3HG0319570.1	-0.360375	-0.351079	-1.1568333	cluster 6
HORVU.MOREX.r3.3HG0323810.1	-0.168794	-0.15391	-0.4772449	cluster 6
HORVU.MOREX.r3.3HG0329510.1	-0.404317	-0.279715	-0.9626113	cluster 6
HORVU.MOREX.r3.4HG0335450.1	2.7351032	2.8494273	1.80351533	cluster 6
HORVU.MOREX.r3.4HG0345810.1	-0.516735	-0.363656	-1.2604258	cluster 6
HORVU.MOREX.r3.4HG0362350.1	-0.389043	-0.258159	-1.2144725	cluster 6
HORVU.MOREX.r3.4HG0364210.1	2.183526	2.5067424	0.99266889	cluster 6
HORVU.MOREX.r3.4HG0364880.1	-1.012113	-0.854058	-1.255772	cluster 6
HORVU.MOREX.r3.4HG0370520.1	-0.271313	-0.260419	-0.7428434	cluster 6
HORVU.MOREX.r3.4HG0375440.1	-0.496671	-0.138871	-1.167625	cluster 6
HORVU.MOREX.r3.4HG0388470.1	-0.113298	0.0635349	-2.2735105	cluster 6
HORVU.MOREX.r3.4HG0395130.1	-0.570158	0.1452184	-1.6829943	cluster 6
HORVU.MOREX.r3.4HG0405830.1	-0.26024	-0.129966	-0.7898168	cluster 6
HORVU.MOREX.r3.4HG0405990.1	1.2352983	1.4902374	0.90794655	cluster 6
HORVU.MOREX.r3.4HG0412730.1	-0.087227	0.1044175	-0.422168	cluster 6
HORVU.MOREX.r3.4HG0417660.1	2.5850014	2.7906547	1.85509947	cluster 6
HORVU.MOREX.r3.5HG0420670.1	-0.30801	-0.144831	-0.7737035	cluster 6
HORVU.MOREX.r3.5HG0439090.1	-0.370212	-0.360967	-0.727011	cluster 6

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.5HG0455080.1	-0.482031	-0.088085	-0.957045	cluster 6
HORVU.MOREX.r3.5HG0459600.1	0.6656884	0.6719967	0.63974505	cluster 6
HORVU.MOREX.r3.5HG0460560.1	-0.601994	-0.21141	-2.3379839	cluster 6
HORVU.MOREX.r3.5HG0465810.1	2.4748372	2.5847967	2.27103236	cluster 6
HORVU.MOREX.r3.5HG0466020.1	-0.005802	0.0216804	-0.7626933	cluster 6
HORVU.MOREX.r3.5HG0476390.1	-0.439241	-0.367227	-0.85495	cluster 6
HORVU.MOREX.r3.5HG0480060.1	-0.439933	-0.412945	-1.1842657	cluster 6
HORVU.MOREX.r3.5HG0483880.1	-0.573398	-0.364214	-1.6012317	cluster 6
HORVU.MOREX.r3.5HG0489840.1	-0.47416	-0.381838	-1.1150172	cluster 6
HORVU.MOREX.r3.5HG0490960.1	-0.437415	-0.353481	-0.643194	cluster 6
HORVU.MOREX.r3.5HG0491230.1	-0.457861	-0.347093	-0.9233452	cluster 6
HORVU.MOREX.r3.5HG0504700.1	-0.590943	-0.362548	-0.9160539	cluster 6
HORVU.MOREX.r3.5HG0506290.1	-0.653223	-0.484077	-0.8812599	cluster 6
HORVU.MOREX.r3.5HG0510370.1	-0.13359	-0.125914	-0.3018527	cluster 6
HORVU.MOREX.r3.5HG0512350.1	-0.509796	-0.512041	-1.1280956	cluster 6
HORVU.MOREX.r3.5HG0530240.1	-0.499727	-0.448928	-1.1496825	cluster 6
HORVU.MOREX.r3.5HG0535780.1	-0.242318	-0.180728	-0.7112602	cluster 6
HORVU.MOREX.r3.6HG0539410.1	-0.802439	-0.71711	-1.7411792	cluster 6
HORVU.MOREX.r3.6HG0553310.1	-0.36968	-0.189265	-0.7856658	cluster 6
HORVU.MOREX.r3.6HG0553580.1	1.1866115	1.274208	0.98142484	cluster 6
HORVU.MOREX.r3.6HG0555810.1	-0.682413	-0.607668	-1.2217529	cluster 6
HORVU.MOREX.r3.6HG0566930.1	-0.22637	0.0490535	-0.7599335	cluster 6
HORVU.MOREX.r3.6HG0569480.1	-0.379795	-0.23017	-2.5324008	cluster 6
HORVU.MOREX.r3.6HG0583730.1	-0.169149	-0.166424	-0.3843065	cluster 6
HORVU.MOREX.r3.6HG0586570.1	-0.066396	0.1873834	-0.8643434	cluster 6
HORVU.MOREX.r3.6HG0594290.1	-0.37741	-0.143018	-1.0226001	cluster 6
HORVU.MOREX.r3.6HG0596240.1	-0.508059	-0.427754	-1.1653371	cluster 6
HORVU.MOREX.r3.6HG0597460.1	-0.531191	0.0172299	-1.840106	cluster 6
HORVU.MOREX.r3.6HG0604310.1	-0.588063	-0.520915	-1.1290382	cluster 6
HORVU.MOREX.r3.6HG0606940.1	-0.438108	-0.176777	-3.0814176	cluster 6
HORVU.MOREX.r3.6HG0622980.1	-0.072754	-0.050755	-0.3923796	cluster 6
HORVU.MOREX.r3.6HG0630650.1	-0.097713	0.2318769	-1.690516	cluster 6
HORVU.MOREX.r3.7HG0635160.1	-0.068051	-0.028414	-0.3964848	cluster 6
HORVU.MOREX.r3.7HG0644540.1	0.6256665	0.7559992	0.30281531	cluster 6
HORVU.MOREX.r3.7HG0655260.1	-0.312909	-0.293031	-0.9635639	cluster 6
HORVU.MOREX.r3.7HG0656330.1	-1.163553	-0.904951	-1.4923467	cluster 6
HORVU.MOREX.r3.7HG0656420.1	-0.123269	0.128882	-1.063885	cluster 6
HORVU.MOREX.r3.7HG0656440.1	-0.027168	0.0020899	-0.4591596	cluster 6
HORVU.MOREX.r3.7HG0663820.1	-0.363469	-0.315317	-0.8339684	cluster 6
HORVU.MOREX.r3.7HG0668450.1	-0.279607	-0.259426	-0.4965059	cluster 6
HORVU.MOREX.r3.7HG0668560.1	0.8654427	0.9760688	0.58199648	cluster 6
HORVU.MOREX.r3.7HG0676880.1	-0.200974	-0.159506	-0.3829243	cluster 6
HORVU.MOREX.r3.7HG0688770.1	0.002493	0.0578383	-0.688143	cluster 6
HORVU.MOREX.r3.7HG0689580.1	-0.242788	-0.237787	-0.6068275	cluster 6
HORVU.MOREX.r3.7HG0692070.1	-0.30171	-0.181181	-0.7256002	cluster 6
HORVU.MOREX.r3.7HG0697940.1	0.4916888	0.5754474	-1.3457295	cluster 6
HORVU.MOREX.r3.7HG0702190.1	-0.113268	-0.119335	-1.6389848	cluster 6

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.7HG0704060.1	0.3659122	0.5559675	0.0679357	cluster 6
HORVU.MOREX.r3.7HG0708050.1	-1.159545	-0.485533	-2.6356189	cluster 6
HORVU.MOREX.r3.7HG0709720.1	-0.045605	-0.048208	-0.4654158	cluster 6
HORVU.MOREX.r3.7HG0714900.1	-0.461434	-0.307175	-0.7230933	cluster 6
HORVU.MOREX.r3.7HG0720720.1	-0.327706	-0.213257	-0.4870422	cluster 6
HORVU.MOREX.r3.7HG0723240.1	3.3718803	3.5954892	3.03861644	cluster 6
HORVU.MOREX.r3.7HG0736860.1	-0.454611	-0.321158	-2.1718564	cluster 6
HORVU.MOREX.r3.7HG0737960.2	-0.191814	-0.136333	-0.6723185	cluster 6
HORVU.MOREX.r3.1HG0030290.1	3.2160988	2.9900065	3.26082502	cluster 7
HORVU.MOREX.r3.1HG0042120.1	-0.15605	-0.470082	-0.2554328	cluster 7
HORVU.MOREX.r3.1HG0042870.1	-0.170446	-0.246205	-0.1303301	cluster 7
HORVU.MOREX.r3.1HG0051110.1	-0.212994	-0.429426	-0.206373	cluster 7
HORVU.MOREX.r3.1HG0055320.1	-0.133147	-0.277538	-0.1776111	cluster 7
HORVU.MOREX.r3.1HG0056510.1	0.0287858	-1.460636	-0.3552398	cluster 7
HORVU.MOREX.r3.1HG0058140.1	-0.214192	-0.407669	-0.2639165	cluster 7
HORVU.MOREX.r3.1HG0062450.1	-0.427538	-0.820102	-0.6131836	cluster 7
HORVU.MOREX.r3.1HG0063020.1	1.2227825	0.9115231	1.29517293	cluster 7
HORVU.MOREX.r3.1HG0083250.1	-0.090481	-0.792259	-0.4232434	cluster 7
HORVU.MOREX.r3.2HG0105990.1	-0.198432	-0.412564	-0.3015049	cluster 7
HORVU.MOREX.r3.2HG0109580.1	-0.452354	-1.391812	-0.4661135	cluster 7
HORVU.MOREX.r3.2HG0115650.1	-0.269629	-1.041937	-0.4347862	cluster 7
HORVU.MOREX.r3.2HG0126960.1	-0.132265	-0.56668	-0.2388556	cluster 7
HORVU.MOREX.r3.2HG0137140.1	-0.120656	-1.13362	-0.2842848	cluster 7
HORVU.MOREX.r3.2HG0157710.1	-0.253123	-0.85214	-0.3936226	cluster 7
HORVU.MOREX.r3.2HG0158260.1	-0.624144	-0.99133	-0.7315255	cluster 7
HORVU.MOREX.r3.2HG0162300.1	-0.207332	-0.431563	-0.1364607	cluster 7
HORVU.MOREX.r3.2HG0168700.1	-0.169481	-1.93174	-0.7636944	cluster 7
HORVU.MOREX.r3.2HG0175350.1	2.6333297	1.7344105	2.26098474	cluster 7
HORVU.MOREX.r3.2HG0181880.1	-0.141264	-0.348116	-0.2230559	cluster 7
HORVU.MOREX.r3.2HG0190800.1	1.5459298	1.0077875	1.70810426	cluster 7
HORVU.MOREX.r3.2HG0193510.2	-0.201709	-0.360121	-0.1759317	cluster 7
HORVU.MOREX.r3.2HG0195600.1	-0.116421	-0.358898	-0.21699	cluster 7
HORVU.MOREX.r3.2HG0216470.1	-0.261736	-0.58313	-0.3678178	cluster 7
HORVU.MOREX.r3.3HG0219860.1	-0.160323	-0.444479	-0.248577	cluster 7
HORVU.MOREX.r3.3HG0228600.1	-0.217675	-0.838092	-0.253968	cluster 7
HORVU.MOREX.r3.3HG0234470.1	-0.244497	-0.562767	-0.2254953	cluster 7
HORVU.MOREX.r3.3HG0241320.1	-0.235043	-0.574987	-0.3063886	cluster 7
HORVU.MOREX.r3.3HG0246550.1	-0.378418	-0.792749	-0.3262336	cluster 7
HORVU.MOREX.r3.3HG0249430.1	0.4532392	-2.481498	-0.9514063	cluster 7
HORVU.MOREX.r3.3HG0257680.1	-0.20108	-0.506971	-0.2343225	cluster 7
HORVU.MOREX.r3.3HG0258280.1	-0.119148	-0.287422	-0.1490613	cluster 7
HORVU.MOREX.r3.3HG0264440.1	-0.171005	-0.653189	-0.4036477	cluster 7
HORVU.MOREX.r3.3HG0267430.2	-0.340256	-0.706942	-0.449371	cluster 7
HORVU.MOREX.r3.3HG0273730.1	-0.147686	-0.551093	-0.2891259	cluster 7
HORVU.MOREX.r3.3HG0293010.1	-0.212651	-0.411838	-0.3017727	cluster 7
HORVU.MOREX.r3.3HG0293420.1	1.1549496	0.9357247	1.06112938	cluster 7
HORVU.MOREX.r3.3HG0304230.1	2.0220451	1.5808034	2.17038351	cluster 7

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.3HG0307310.1	-0.067888	-0.307881	-0.1429791	cluster 7
HORVU.MOREX.r3.3HG0315130.1	-0.43211	-1.200566	-0.5473714	cluster 7
HORVU.MOREX.r3.3HG0324070.1	1.6702737	1.4062936	1.76382212	cluster 7
HORVU.MOREX.r3.3HG0330040.1	-0.120768	-0.658763	-0.3435413	cluster 7
HORVU.MOREX.r3.4HG0331520.1	-0.187311	-0.586644	-0.2447804	cluster 7
HORVU.MOREX.r3.4HG0332930.1	-0.822034	-1.615903	-1.0259526	cluster 7
HORVU.MOREX.r3.4HG0343710.1	-0.220913	-0.349295	-0.1657513	cluster 7
HORVU.MOREX.r3.4HG0348450.1	-0.717871	-1.243245	-0.8769814	cluster 7
HORVU.MOREX.r3.4HG0352760.1	-0.168049	-0.344307	-0.2394104	cluster 7
HORVU.MOREX.r3.4HG0356090.1	-0.295739	-0.622584	-0.4116669	cluster 7
HORVU.MOREX.r3.4HG0373800.1	-0.458263	-1.0656	-0.7512242	cluster 7
HORVU.MOREX.r3.4HG0383400.1	-0.18225	-0.355746	-0.231642	cluster 7
HORVU.MOREX.r3.4HG0389410.1	0.615519	0.2822746	0.75198528	cluster 7
HORVU.MOREX.r3.4HG0390140.1	-0.132516	-0.262139	-0.1947101	cluster 7
HORVU.MOREX.r3.4HG0396760.1	-0.106994	-0.400321	-0.2508712	cluster 7
HORVU.MOREX.r3.5HG0419520.1	-0.060643	-0.262126	-0.1109363	cluster 7
HORVU.MOREX.r3.5HG0423790.1	-0.169621	-0.545146	-0.1361613	cluster 7
HORVU.MOREX.r3.5HG0425880.1	-0.186934	-0.548493	-0.2320833	cluster 7
HORVU.MOREX.r3.5HG0426280.1	0.895911	0.8026891	0.91336719	cluster 7
HORVU.MOREX.r3.5HG0430480.1	-0.146778	-0.272973	-0.1370712	cluster 7
HORVU.MOREX.r3.5HG0438280.1	-0.47725	-1.805543	-0.9756747	cluster 7
HORVU.MOREX.r3.5HG0439190.1	-0.256617	-0.507693	-0.3533273	cluster 7
HORVU.MOREX.r3.5HG0441840.1	1.3633768	1.2209914	1.3181252	cluster 7
HORVU.MOREX.r3.5HG0448080.1	-0.208832	-0.556157	-0.3113608	cluster 7
HORVU.MOREX.r3.5HG0473900.1	0.3363969	0.2043496	0.39301885	cluster 7
HORVU.MOREX.r3.5HG0474540.1	-0.176849	-0.363756	-0.245905	cluster 7
HORVU.MOREX.r3.5HG0483860.1	-0.114833	-0.54771	-0.3128479	cluster 7
HORVU.MOREX.r3.5HG0486810.1	-0.377942	-1.001511	-0.4599156	cluster 7
HORVU.MOREX.r3.5HG0488950.1	-0.530402	-1.081169	-0.7442717	cluster 7
HORVU.MOREX.r3.5HG0491250.1	-0.056524	-0.439289	-0.2369434	cluster 7
HORVU.MOREX.r3.5HG0496980.1	-0.132492	-0.627109	-0.2096685	cluster 7
HORVU.MOREX.r3.5HG0497990.1	1.0351763	0.7722732	1.11838961	cluster 7
HORVU.MOREX.r3.5HG0527280.1	-0.064662	-0.251611	-0.1256452	cluster 7
HORVU.MOREX.r3.5HG0531390.1	-0.134208	-0.297476	-0.1909864	cluster 7
HORVU.MOREX.r3.5HG0537000.1	1.0746695	0.9108017	1.00821353	cluster 7
HORVU.MOREX.r3.6HG0549990.1	-0.134297	-0.91081	-0.41267	cluster 7
HORVU.MOREX.r3.6HG0552230.1	-0.34495	-0.528849	-0.4279295	cluster 7
HORVU.MOREX.r3.6HG0567780.1	-0.434157	-0.731683	-0.5097421	cluster 7
HORVU.MOREX.r3.6HG0569610.1	-0.29027	-0.723435	-0.3262721	cluster 7
HORVU.MOREX.r3.6HG0605120.1	-0.503633	-0.941651	-0.6142515	cluster 7
HORVU.MOREX.r3.6HG0616880.1	-0.235822	-1.496044	-0.5642134	cluster 7
HORVU.MOREX.r3.6HG0617750.1	-0.108153	-0.585285	-0.3302267	cluster 7
HORVU.MOREX.r3.6HG0628410.1	-0.107487	-0.322295	-0.1185619	cluster 7
HORVU.MOREX.r3.7HG0652820.1	-0.588486	-2.251526	-1.3184711	cluster 7
HORVU.MOREX.r3.7HG0667180.1	-0.556496	-0.798449	-0.4581096	cluster 7
HORVU.MOREX.r3.7HG0671470.1	-0.208542	-0.924604	-0.4782527	cluster 7
HORVU.MOREX.r3.7HG0674680.1	1.1070658	0.7065894	1.2363665	cluster 7

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.7HG0675770.1	-0.353457	-0.599998	-0.4555224	cluster 7
HORVU.MOREX.r3.7HG0680410.1	-0.206222	-0.647094	-0.3041446	cluster 7
HORVU.MOREX.r3.7HG0711200.1	-0.071671	-0.380001	-0.1717068	cluster 7
HORVU.MOREX.r3.7HG0714530.1	-0.385011	-1.361976	-0.3521423	cluster 7
HORVU.MOREX.r3.7HG0721080.1	-0.362552	-0.888793	-0.455568	cluster 7
HORVU.MOREX.r3.7HG0726170.1	-0.107939	-0.368825	-0.2214472	cluster 7
HORVU.MOREX.r3.7HG0729510.1	-0.38105	-0.660762	-0.4855394	cluster 7
HORVU.MOREX.r3.7HG0742720.1	-0.204679	-0.355489	-0.2419012	cluster 7
HORVU.MOREX.r3.7HG0745360.1	-0.120774	-0.317561	-0.1896039	cluster 7
HORVU.MOREX.r3.7HG0745700.1	-0.252755	-0.305338	-0.2583258	cluster 7
HORVU.MOREX.r3.7HG0751060.1	-0.049984	-0.386301	-0.1963032	cluster 7
HORVU.MOREX.r3.1HG0016560.1	-0.68839	0.0457791	-1.4256237	cluster 8
HORVU.MOREX.r3.1HG0033450.1	-1.370905	-0.973254	-1.6061167	cluster 8
HORVU.MOREX.r3.1HG0047250.1	-0.842719	-0.335649	-0.8617388	cluster 8
HORVU.MOREX.r3.1HG0052250.1	0.7624389	1.4813074	0.77029671	cluster 8
HORVU.MOREX.r3.1HG0055590.1	1.279564	1.4617378	1.22363957	cluster 8
HORVU.MOREX.r3.1HG0073460.1	0.2357812	0.4582906	0.25351407	cluster 8
HORVU.MOREX.r3.1HG0083550.1	1.005615	2.8081284	0.07977259	cluster 8
HORVU.MOREX.r3.1HG0083730.1	0.6875268	1.06344	0.69693972	cluster 8
HORVU.MOREX.r3.1HG0086480.1	0.9142496	1.3676222	0.79241127	cluster 8
HORVU.MOREX.r3.2HG0101220.2	-0.421702	-0.342134	-0.4980625	cluster 8
HORVU.MOREX.r3.2HG0151790.1	0.0187827	2.5871455	0.07610652	cluster 8
HORVU.MOREX.r3.2HG0156140.1	-1.001972	-0.789672	-1.146646	cluster 8
HORVU.MOREX.r3.2HG0165640.1	-1.879812	-1.097162	-2.4990806	cluster 8
HORVU.MOREX.r3.2HG0170210.1	1.0146391	1.7031544	0.85067223	cluster 8
HORVU.MOREX.r3.2HG0189780.1	0.9533907	1.6835911	0.92413746	cluster 8
HORVU.MOREX.r3.2HG0203080.1	1.6417226	2.0966103	1.67264528	cluster 8
HORVU.MOREX.r3.2HG0206920.1	0.7491963	0.9379036	0.73132938	cluster 8
HORVU.MOREX.r3.2HG0210650.1	1.4265372	1.7254115	1.43270808	cluster 8
HORVU.MOREX.r3.2HG0212990.1	-0.435296	-0.136573	-0.6607481	cluster 8
HORVU.MOREX.r3.2HG0213020.1	0.8360542	1.6698752	0.89323859	cluster 8
HORVU.MOREX.r3.2HG0213840.1	0.7932587	1.0372114	0.79750973	cluster 8
HORVU.MOREX.r3.3HG0256860.1	1.0448509	2.9093608	0.61511877	cluster 8
HORVU.MOREX.r3.3HG0275300.1	-0.756268	-0.330074	-0.9695207	cluster 8
HORVU.MOREX.r3.3HG0299020.1	0.8142026	1.221284	0.80736762	cluster 8
HORVU.MOREX.r3.3HG0307340.1	0.9516359	1.299012	0.82274733	cluster 8
HORVU.MOREX.r3.4HG0331420.1	0.6161197	1.3603997	0.29829575	cluster 8
HORVU.MOREX.r3.4HG0332710.1	-2.24356	-1.189108	-2.9250651	cluster 8
HORVU.MOREX.r3.4HG0337720.1	1.653155	2.7358164	1.55437631	cluster 8
HORVU.MOREX.r3.4HG0338290.1	0.6005137	0.8366727	0.56932138	cluster 8
HORVU.MOREX.r3.4HG0345840.1	1.0853304	1.4740281	0.77264726	cluster 8
HORVU.MOREX.r3.4HG0347840.1	0.3951563	0.4822898	0.31282058	cluster 8
HORVU.MOREX.r3.4HG0381620.1	1.0317313	1.2708755	0.96484377	cluster 8
HORVU.MOREX.r3.4HG0382280.1	0.3856754	1.2089321	0.2711101	cluster 8
HORVU.MOREX.r3.4HG0383340.1	-0.870385	-0.089032	-1.5932755	cluster 8
HORVU.MOREX.r3.4HG0391160.1	0.5692179	0.9617819	0.54210761	cluster 8
HORVU.MOREX.r3.4HG0391440.1	1.7641957	2.444945	1.76772557	cluster 8

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.4HG0395770.1	-0.631838	-0.472398	-0.7406453	cluster 8
HORVU.MOREX.r3.4HG0410820.1	0.3757779	1.2713538	0.25521382	cluster 8
HORVU.MOREX.r3.4HG0412650.1	1.8399537	2.405969	1.76125167	cluster 8
HORVU.MOREX.r3.4HG0417920.1	2.6693365	3.4513226	2.62403404	cluster 8
HORVU.MOREX.r3.5HG0426110.1	1.8031372	2.4005857	1.66149118	cluster 8
HORVU.MOREX.r3.5HG0439710.1	-1.381654	-0.486641	-1.972956	cluster 8
HORVU.MOREX.r3.5HG0441420.1	1.2605773	2.3016515	1.05034251	cluster 8
HORVU.MOREX.r3.5HG0447610.1	0.5047409	0.9429919	0.52926345	cluster 8
HORVU.MOREX.r3.5HG0470690.1	1.2429358	1.6905877	1.23651628	cluster 8
HORVU.MOREX.r3.5HG0471320.1	-1.346566	-0.79475	-1.7343734	cluster 8
HORVU.MOREX.r3.5HG0473970.1	1.4828238	2.2987644	1.5130937	cluster 8
HORVU.MOREX.r3.5HG0477750.1	2.1417084	2.4619085	1.98143426	cluster 8
HORVU.MOREX.r3.5HG0485960.1	1.3586954	1.7677775	1.06750445	cluster 8
HORVU.MOREX.r3.5HG0488200.1	0.4976283	1.1247694	0.34608666	cluster 8
HORVU.MOREX.r3.5HG0495910.1	1.4237489	1.9154817	1.0961816	cluster 8
HORVU.MOREX.r3.5HG0500360.1	3.0432371	3.3969682	2.91684266	cluster 8
HORVU.MOREX.r3.5HG0508610.1	0.7048323	1.2109206	0.58303996	cluster 8
HORVU.MOREX.r3.5HG0509350.1	0.4899925	2.0910094	0.56851341	cluster 8
HORVU.MOREX.r3.5HG0509460.1	-0.685116	-0.427906	-0.9448471	cluster 8
HORVU.MOREX.r3.5HG0512710.1	1.3515157	1.9535053	1.15738349	cluster 8
HORVU.MOREX.r3.5HG0517740.1	2.4264659	2.6794845	2.36584881	cluster 8
HORVU.MOREX.r3.5HG0527310.1	1.5258793	2.5036434	1.46706368	cluster 8
HORVU.MOREX.r3.5HG0532120.1	1.8178781	1.9583289	1.72602711	cluster 8
HORVU.MOREX.r3.6HG0543540.1	1.3863265	1.5053508	1.3537395	cluster 8
HORVU.MOREX.r3.6HG0554070.1	1.6818835	3.6687108	1.22141612	cluster 8
HORVU.MOREX.r3.6HG0576010.1	0.3679369	0.6885457	0.31848861	cluster 8
HORVU.MOREX.r3.6HG0595580.1	1.4276508	2.3878808	1.0853941	cluster 8
HORVU.MOREX.r3.6HG0606530.1	0.4428105	0.6577069	0.30875491	cluster 8
HORVU.MOREX.r3.6HG0607160.1	0.5753563	0.7585488	0.57609991	cluster 8
HORVU.MOREX.r3.6HG0609390.1	0.2668566	0.7232304	0.25618375	cluster 8
HORVU.MOREX.r3.6HG0609680.1	1.1862527	1.5598004	1.01676472	cluster 8
HORVU.MOREX.r3.6HG0613020.1	0.5524338	0.7327898	0.46253984	cluster 8
HORVU.MOREX.r3.7HG0634520.1	1.1504993	1.5528927	1.16398918	cluster 8
HORVU.MOREX.r3.7HG0636540.1	1.5695804	1.9686879	1.23916107	cluster 8
HORVU.MOREX.r3.7HG0638940.1	1.3386458	2.4034981	0.80305954	cluster 8
HORVU.MOREX.r3.7HG0642520.1	1.9370895	2.2840032	1.83025225	cluster 8
HORVU.MOREX.r3.7HG0650310.1	0.6615734	1.3406596	0.51987973	cluster 8
HORVU.MOREX.r3.7HG0654810.1	-1.942124	-0.260052	-2.4042506	cluster 8
HORVU.MOREX.r3.7HG0662370.1	1.3241722	1.7259933	1.21876266	cluster 8
HORVU.MOREX.r3.7HG0662420.1	0.7603474	1.0866451	0.67240873	cluster 8
HORVU.MOREX.r3.7HG0663750.1	1.7470975	2.3972216	1.42992263	cluster 8
HORVU.MOREX.r3.7HG0665040.1	2.4892506	3.1369681	1.92838846	cluster 8
HORVU.MOREX.r3.7HG0667260.1	0.5586346	0.8013911	0.52307275	cluster 8
HORVU.MOREX.r3.7HG0673330.1	1.2884278	1.6333472	1.31253661	cluster 8
HORVU.MOREX.r3.7HG0697980.1	-0.910687	-0.560554	-0.9376121	cluster 8
HORVU.MOREX.r3.7HG0708080.1	1.3750928	1.6864139	1.15384371	cluster 8
HORVU.MOREX.r3.7HG0710180.1	-0.960132	-0.461752	-1.3850899	cluster 8

Table Sп Continued.

ID	logFC_3 h	logFC_6 h	logFC_12 h	cluster No.
HORVU.MOREX.r3.7HG0731560.1	1.2332042	1.8283902	0.96734845	cluster 8
HORVU.MOREX.r3.7HG0735700.1	1.1785731	1.7513368	1.01796317	cluster 8
HORVU.MOREX.r3.7HG0739230.1	3.8556548	4.7252315	2.96062925	cluster 8
HORVU.MOREX.r3.1HG0072580.1	0.5504146	0.5074494	0.6826394	cluster 9
HORVU.MOREX.r3.1HG0076800.1	0.3709137	0.3121963	0.64710848	cluster 9
HORVU.MOREX.r3.1HG0084760.1	0.9694768	0.7509061	1.31581169	cluster 9
HORVU.MOREX.r3.2HG0101250.1	0.5952558	0.4208567	0.80339888	cluster 9
HORVU.MOREX.r3.2HG0194850.1	0.5105544	0.4560437	0.68449166	cluster 9
HORVU.MOREX.r3.2HG0204480.1	-0.341332	-0.630844	-0.0348636	cluster 9
HORVU.MOREX.r3.3HG0226150.1	1.3843313	1.0545768	1.69469367	cluster 9
HORVU.MOREX.r3.4HG0376720.1	2.8197207	2.748408	2.94486373	cluster 9
HORVU.MOREX.r3.4HG0378460.1	0.5557031	0.4984911	0.77886874	cluster 9
HORVU.MOREX.r3.4HG0388780.1	0.8159196	-0.05139	1.83722955	cluster 9
HORVU.MOREX.r3.5HG0442250.1	0.8581869	0.8140699	0.92212005	cluster 9
HORVU.MOREX.r3.5HG0475150.1	0.6894442	0.5314124	1.03057189	cluster 9
HORVU.MOREX.r3.5HG0485410.1	2.3398523	2.2335101	2.42992147	cluster 9
HORVU.MOREX.r3.5HG0509970.1	1.3142047	0.6687246	1.77801444	cluster 9
HORVU.MOREX.r3.5HG0527890.1	0.1545306	0.0248258	0.31949894	cluster 9
HORVU.MOREX.r3.6HG0570520.1	-0.193203	-0.251218	-0.1025166	cluster 9
HORVU.MOREX.r3.6HG0577770.1	-1.393416	-1.916621	-0.6306346	cluster 9
HORVU.MOREX.r3.6HG0606990.1	1.2102586	1.1073845	1.42794469	cluster 9
HORVU.MOREX.r3.7HG0674590.1	0.591647	0.4832687	1.1299294	cluster 9
HORVU.MOREX.r3.7HG0725440.1	0.4876101	0.2580707	0.8889395	cluster 9
HORVU.MOREX.r3.7HG0735210.1	1.5661608	1.5068382	1.6566023	cluster 9

Table Spa Enriched biological process terms among differentially expressed genes in the root cap (RC) of gravistimulated wild type roots.

No. cluster	**GO term**	**Description**	cluster 1			cluster 2			cluster 3		
			3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h
cluster 1	GO:0006635	fatty acid beta-oxidation			🟦						
	GO:0009408	response to heat			🟦						
	GO:0009409	response to cold			🟦						
	GO:0015976	carbon utilization			🟦						
	GO:0050881	musculoskeletal movement			🟦						
	GO:1903426	regulation of reactive oxygen species biosynthetic process			🟦						
	GO:0031122	cytoplasmic microtubule organization			🟦						
	GO:0044743	protein transmembrane import into intracellular organelle			🟦						
	GO:0065002	intracellular protein transmembrane transport			🟦						
	GO:0006470	protein dephosphorylation			🟦						
	GO:0006468	protein phosphorylation			🟦						
	GO:0006809	nitric oxide biosynthetic process			🟦						
	GO:0006629	lipid metabolic process			🟦						
	GO:0005975	carbohydrate metabolic process			🟦						
	GO:0055023	positive regulation of cardiac muscle tissue growth			🟦						
	GO:0050795	regulation of behavior			🟦						
	GO:0051726	regulation of cell cycle			🟦						
	GO:0061041	regulation of wound healing			🟦						
	GO:0006012	galactose metabolic process			🟦						
	GO:0010951	negative regulation of endopeptidase activity			🟦						
	GO:0010507	negative regulation of autophagy			🟦						
	GO:0006359	regulation of transcription by RNA polymerase III			🟦						
	GO:0006570	tyrosine metabolic process			🟦						
	GO:0046496	nicotinamide nucleotide metabolic process			🟦						
	GO:0014009	glial cell proliferation			🟦						
	GO:0010411	xyloglucan metabolic process			🟦						
	GO:0005978	glycogen biosynthetic process			🟦						
	GO:0005977	glycogen metabolic process			🟦						
	GO:0015866	ADP transport			🟦						
	GO:0034198	cellular response to amino acid starvation			🟦						
	GO:0002011	morphogenesis of an epithelial sheet			🟦						
	GO:0019673	GDP-mannose metabolic process			🟦						
	GO:0010717	regulation of epithelial to mesenchymal transition			🟦						
	GO:0016117	carotenoid biosynthetic process			🟦						
	GO:0006914	autophagy			🟦						
	GO:0035307	positive regulation of protein dephosphorylation			🟦						
	GO:0050848	regulation of calcium-mediated signaling			🟦						
cluster 2	GO:0009308	amine metabolic process						🟦			
cluster 3	GO:0051491	positive regulation of filopodium assembly									🟥
	GO:0030833	regulation of actin filament polymerization									🟥
	GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules									🟥
	GO:0019722	calcium-mediated signaling									🟥
	GO:0042176	regulation of protein catabolic process									🟥
	GO:0007411	axon guidance									🟥

🟥 up-regulated
🟦 down-regulated

Table Spb Enriched biological process terms among differentially expressed genes in the elongation zone (E) of gravistimulated wild type roots.

No. cluster	GO term	Description	cluster 1			cluster 2			cluster 3			cluster 4			cluster 5			cluster 6			cluster 7			cluster 8			cluster 9		
			3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h
cluster 1	GO:0009664	plant-type cell wall organization	🟥	🟪	🟪		🟥			🟥	🟥			🟥								🟦	🟪			🟥			
	GO:0006566	threonine metabolic process		🟥	🟦												🟥												
	GO:0006544	glycine metabolic process		🟥																									
	GO:1901606	alpha-amino acid catabolic process		🟥																									
	GO:0009063	cellular amino acid catabolic process		🟥																									
	GO:0016311	dephosphorylation		🟥																									
	GO:0006004	fucose metabolic process		🟦	🟦								🟦	🟦								🟦							
	GO:0019320	hexose catabolic process		🟦																									
	GO:0006012	galactose metabolic process		🟦	🟦			🟥																					
	GO:0007219	Notch signaling pathway		🟦	🟦																								
	GO:0010102	lateral root morphogenesis		🟦	🟦																								
	GO:0072595	maintenance of protein localization in organelle		🟦																									
	GO:0007020	microtubule nucleation		🟦	🟦																								
	GO:0098930	axonal transport		🟦																									
	GO:0045104	intermediate filament cytoskeleton organization		🟦																									
	GO:0047496	vesicle transport along microtubule		🟦																									
	GO:0006457	protein folding		🟦	🟦																								
	GO:0016485	protein processing		🟦																									
	GO:0006511	ubiquitin-dependent protein catabolic process		🟦	🟦																								
	GO:0030433	ubiquitin-dependent ERAD pathway		🟦																									
	GO:0008299	isoprenoid biosynthetic process		🟦																									
	GO:0006665	sphingolipid metabolic process		🟦																									
	GO:0005975	carbohydrate metabolic process		🟦	🟦												🟥												
	GO:1903036	positive regulation of response to wounding		🟦																									
	GO:0015780	nucleotide-sugar transmembrane transport		🟦	🟦			🟥																					
	GO:0033157	regulation of intracellular protein transport		🟦																									
	GO:0040008	regulation of growth		🟦																									
	GO:0006486	protein glycosylation		🟦	🟦								🟦	🟦															
	GO:0036065	fucosylation		🟦	🟦																				🟥	🟥			
	GO:0006493	protein O-linked glycosylation		🟦	🟦																								
	GO:0006487	protein N-linked glycosylation		🟦	🟦																								
	GO:0031529	ruffle organization		🟦																									
	GO:0031103	axon regeneration		🟦																									
	GO:0006082	organic acid metabolic process		🟦																									
	GO:0045489	pectin biosynthetic process		🟦	🟦																								
	GO:0070592	cell wall polysaccharide biosynthetic process		🟦	🟦								🟦																
	GO:0009734	auxin-activated signaling pathway		🟦																									
	GO:0008286	insulin receptor signaling pathway		🟦																									
	GO:0046686	response to cadmium ion		🟦	🟦																								
	GO:0009414	response to water deprivation		🟦	🟦																								
	GO:0009409	response to cold			🟦																								
	GO:0010039	response to iron ion			🟦												🟥												
	GO:0045773	positive regulation of axon extension		🟦																									
	GO:0022029	telencephalon cell migration		🟦																									
	GO:0021954	central nervous system neuron development		🟦																									
	GO:0001764	neuron migration		🟦																									
	GO:0021987	cerebral cortex development		🟦																									
	GO:0009311	oligosaccharide metabolic process		🟦	🟦																								
	GO:0032418	lysosome localization		🟦																									

🟥 up-regulated
🟦 down-regulated
🟪 up and down-regulation

Table Spb Continued.

No. cluster	GO term	Description	cluster 1			cluster 2			cluster 3			cluster 4			cluster 5			cluster 6			cluster 7			cluster 8			cluster 9		
			3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h
cluster 1	GO:0051303	establishment of chromosome localization		🟦																									
	GO:0005984	disaccharide metabolic process		🟦																									
	GO:0005992	trehalose biosynthetic process		🟦																									
	GO:0001824	blastocyst development		🟦																									
	GO:0016579	protein deubiquitination		🟦						🟥																			
	GO:1905393	plant organ formation		🟦	🟦																								
	GO:0006085	acetyl-CoA biosynthetic process		🟦																									
	GO:0048316	seed development			🟦																								
	GO:0007140	male meiotic nuclear division			🟦																								
	GO:0009832	plant-type cell wall biogenesis			🟦								🟦																
	GO:1990748	cellular detoxification			🟦																								
	GO:0036503	ERAD pathway			🟦																								
	GO:0009873	ethylene-activated signaling pathway			🟦																								
	GO:0009737	response to abscisic acid			🟦																								
	GO:0071369	cellular response to ethylene stimulus			🟦																								
	GO:0006099	tricarboxylic acid cycle			🟦																								
	GO:0006067	ethanol metabolic process			🟦												🟥												
	GO:0009206	purine ribonucleoside triphosphate biosynthetic process			🟦																								
	GO:0015936	coenzyme A metabolic process			🟦																								
	GO:0006165	nucleoside diphosphate phosphorylation			🟦																								
	GO:0046039	GTP metabolic process			🟦																								
	GO:0006633	fatty acid biosynthetic process			🟦																								
	GO:0046470	phosphatidylcholine metabolic process			🟦																								
	GO:0009800	cinnamic acid biosynthetic process			🟦																🟦									
	GO:0009059	macromolecule biosynthetic process			🟦																								
	GO:0006508	proteolysis			🟦																								
	GO:0006334	nucleosome assembly			🟦																								
	GO:0007010	cytoskeleton organization			🟦																								
	GO:0006073	cellular glucan metabolic process			🟦																								
	GO:0030244	cellulose biosynthetic process			🟦		🟥	🟥														🟦	🟦						
	GO:0006559	L-phenylalanine catabolic process			🟦																🟦									
	GO:1901575	organic substance catabolic process			🟦																								
	GO:0006997	nucleus organization			🟦																								
	GO:0000096	sulfur amino acid metabolic process			🟦																								
	GO:0009826	unidimensional cell growth			🟦																	🟦							
cluster 2	GO:0006979	response to oxidative stress					🟥	🟥		🟥	🟥													🟥	🟥	🟥			
	GO:0035377	transepithelial water transport					🟥																						
	GO:0042744	hydrogen peroxide catabolic process					🟥	🟥		🟥	🟥													🟥	🟥	🟥	🟥			
	GO:0048146	positive regulation of fibroblast proliferation					🟥																						
	GO:0030950	establishment or maintenance of actin cytoskeleton polarity					🟥																						
	GO:0045445	myoblast differentiation					🟥																						
	GO:0035914	skeletal muscle cell differentiation					🟥																						
	GO:0006468	protein phosphorylation					🟥	🟥		🟥	🟥					🟥	🟥			🟥		🟦							
	GO:0032941	secretion by tissue					🟥																						
	GO:0006687	glycosphingolipid metabolic process					🟥	🟥																					
	GO:0006672	ceramide metabolic process					🟥	🟥																					
	GO:0072488	ammonium transmembrane transport					🟥																		🟥				
	GO:0015791	polyol transport					🟥																						
	GO:0010411	xyloglucan metabolic process					🟥	🟥		🟥	🟥		🟦	🟦						🟦									

Table Spb Continued.

No. cluster	GO term	Description	cluster 1			cluster 2			cluster 3			cluster 4			cluster 5			cluster 6			cluster 7			cluster 8			cluster 9		
			3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h
cluster 2	GO:0005991	trehalose metabolic process					🟥	🟥																						
	GO:0042546	cell wall biogenesis					🟥			🟥	🟥		🟦																	
	GO:0071870	cellular response to catecholamine stimulus					🟥						🟦																	
	GO:0021670	lateral ventricle development					🟥																							
	GO:0022600	digestive system process					🟥																							
	GO:0046689	response to mercury ion					🟥																							
	GO:0046274	lignin catabolic process					🟥	🟥																						
	GO:0071474	cellular hyperosmotic response					🟥																							
	GO:0043171	peptide catabolic process					🟥																							
	GO:0042219	cellular modified amino acid catabolic process					🟥																							
	GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway						🟥			🟥																			
	GO:0046364	monosaccharide biosynthetic process						🟥																						
	GO:0008643	carbohydrate transport						🟥																						
	GO:0000160	phosphorelay signal transduction system						🟥																						
cluster3	GO:0006542	glutamine biosynthetic process							🟥	🟥	🟥																			
	GO:0015695	organic cation transport								🟥	🟥																			
	GO:0034220	ion transmembrane transport								🟥	🟥																			
	GO:0046856	phosphatidylinositol dephosphorylation								🟥																				
	GO:0032606	type I interferon production								🟥																				
	GO:0009690	cytokinin metabolic process								🟥																				
	GO:0001959	regulation of cytokine-mediated signaling pathway								🟥																				
	GO:2001233	regulation of apoptotic signaling pathway								🟥																				
	GO:1905477	positive regulation of protein localization to membrane								🟥	🟥																			
	GO:0032414	positive regulation of ion transmembrane transporter activity								🟥	🟥																			
	GO:0022408	negative regulation of cell-cell adhesion								🟥																				
	GO:0045582	positive regulation of T cell differentiation								🟥																				
	GO:0007041	lysosomal transport								🟥																				
	GO:0006741	NADP biosynthetic process								🟥	🟥																			
	GO:0016119	carotene metabolic process								🟥	🟥																			
	GO:0050866	negative regulation of cell activation								🟥																				
	GO:0048532	anatomical structure arrangement									🟥									🟦										
	GO:0050905	neuromuscular process									🟥																			
	GO:0010043	response to zinc ion									🟥																			
	GO:0030837	negative regulation of actin filament polymerization									🟥																			
	GO:0030834	regulation of actin filament depolymerization									🟥																			
	GO:1901880	negative regulation of protein depolymerization									🟥																			
	GO:0035315	hair cell differentiation									🟥																			
	GO:0006950	response to stress									🟥																			
cluster 4	GO:0006813	potassium ion transport											🟦																	
	GO:0070839	metal ion export											🟦																	
	GO:0035725	sodium ion transmembrane transport											🟦																	
	GO:0007006	mitochondrial membrane organization											🟦																	
	GO:0050848	regulation of calcium-mediated signaling											🟦																	
	GO:0071871	response to epinephrine											🟦																	
	GO:0006629	lipid metabolic process											🟦	🟦																
	GO:0051930	regulation of sensory perception of pain											🟦																	
	GO:0010611	regulation of cardiac muscle hypertrophy											🟦																	
	GO:0051453	regulation of intracellular pH											🟦																	

Table Spb Continued.

No. cluster	GO term	Description	cluster 1			cluster 2			cluster 3			cluster 4			cluster 5			cluster 6			cluster 7			cluster 8			cluster 9		
			3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h
cluster 4	GO:0048016	inositol phosphate-mediated signaling											🟦																
	GO:0009268	response to pH											🟦																
	GO:0051602	response to electrical stimulus											🟦																
	GO:0006972	hyperosmotic response											🟦	🟦															
	GO:0006303	double-strand break repair via nonhomologous end joining											🟦	🟦															
	GO:0009735	response to cytokinin											🟦	🟦															
	GO:2000028	regulation of photoperiodism, flowering											🟦	🟦															
	GO:0009100	glycoprotein metabolic process											🟦	🟦															
	GO:0006506	GPI anchor biosynthetic process											🟦	🟦								🟦							
	GO:0006888	endoplasmic reticulum to Golgi vesicle-mediated transport												🟦															
cluster 5	GO:0006536	glutamate metabolic process														🟥	🟥												
	GO:0009084	glutamine family amino acid biosynthetic process														🟥	🟥												
	GO:0043650	dicarboxylic acid biosynthetic process														🟥	🟥												
	GO:0009741	response to brassinosteroid															🟥												
	GO:0010923	negative regulation of phosphatase activity															🟥												
	GO:0043666	regulation of phosphoprotein phosphatase activity															🟥												
	GO:0006458	'de novo' protein folding															🟥												
	GO:1990542	mitochondrial transmembrane transport															🟥												
	GO:0007015	actin filament organization															🟥												
	GO:0007018	microtubule-based movement															🟥												
	GO:0009773	photosynthetic electron transport in photosystem I															🟥												
	GO:0006807	nitrogen compound metabolic process															🟥												
	GO:0046654	tetrahydrofolate biosynthetic process															🟥												
	GO:0072529	pyrimidine-containing compound catabolic process															🟥												
	GO:0008272	sulfate transport															🟥												
	GO:0044743	protein transmembrane import into intracellular organelle															🟥												
	GO:0006626	protein targeting to mitochondrion															🟥												
	GO:0065002	intracellular protein transmembrane transport															🟥												
	GO:0036092	phosphatidylinositol-3-phosphate biosynthetic process															🟥												
cluster 6	GO:0006086	acetyl-CoA biosynthetic process from pyruvate																	🟥										
	GO:0006431	methionyl-tRNA aminoacylation																	🟥										
	GO:0016024	CDP-diacylglycerol biosynthetic process																		🟦									
	GO:0045892	negative regulation of transcription, DNA-templated																		🟦									
	GO:0007031	peroxisome organization																		🟦									
	GO:0009056	catabolic process																		🟦									
	GO:0045292	mRNA cis splicing, via spliceosome																		🟦									
	GO:0009740	gibberellic acid mediated signaling pathway																		🟦									
	GO:0051781	positive regulation of cell division																		🟦									
	GO:0009411	response to UV																		🟦									
	GO:0009157	deoxyribonucleoside monophosphate biosynthetic process																		🟦									
	GO:0007131	reciprocal meiotic recombination																		🟦									
	GO:0019264	glycine biosynthetic process from serine																		🟦									
	GO:0048507	meristem development																		🟦									
	GO:0034728	nucleosome organization																		🟦									
	GO:0006333	chromatin assembly or disassembly																		🟦									
cluster 7	GO:0010015	root morphogenesis																				🟦							
	GO:0060560	developmental growth involved in morphogenesis																				🟦							
	GO:0048588	developmental cell growth																				🟦							
	GO:0048168	regulation of neuronal synaptic plasticity																				🟦							

Table Spb Continued.

No. cluster	GO term	Description	cluster 1			cluster 2			cluster 3			cluster 4			cluster 5			cluster 6			cluster 7			cluster 8			cluster 9		
			3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h	3 h	6 h	12 h
cluster 7	GO:0042545	cell wall modification																				🟦	🟦						
	GO:0046149	pigment catabolic process																				🟦							
	GO:0006787	porphyrin-containing compound catabolic process																				🟦							
	GO:0019511	peptidyl-proline hydroxylation																				🟦							
	GO:0007269	neurotransmitter secretion																				🟦							
	GO:0090558	plant epidermis development																				🟦							
	GO:0009103	lipopolysaccharide biosynthetic process																				🟦							
	GO:0030833	regulation of actin filament polymerization																				🟦							
	GO:0001558	regulation of cell growth																				🟦							
	GO:0048469	cell maturation																				🟦							
cluster 8	GO:0010228	vegetative to reproductive phase transition of meristem																							🟥				
	GO:0009809	lignin biosynthetic process																							🟥				
	GO:0035335	peptidyl-tyrosine dephosphorylation																							🟥				
	GO:0006367	transcription initiation from RNA polymerase II promoter																							🟥				
	GO:0015689	molybdate ion transport																							🟥	🟦			
	GO:0016042	lipid catabolic process																							🟥				
	GO:0009252	peptidoglycan biosynthetic process																								🟦			
	GO:0006298	mismatch repair																								🟦			
	GO:0008360	regulation of cell shape																								🟦			
cluster 9	GO:0006520	cellular amino acid metabolic process																										🟥	
	GO:0006352	DNA-templated transcription, initiation																											🟥
	GO:0009058	biosynthetic process																											🟥

Table Sc Overview of genes differentially expressed between wild type and *egt2* (false discovery rate (FDR) <5%) in a gravistimulation time-course experiment.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0078900.1	-1.929327809	5.8370464	-23.68173821	7.29E-30	1.50E-25	56.03841628	MATH domain-containing protein	root cap	0 h
HORVU.MOREX.r3.1HG0067040.1	-1.308404397	7.101906906	-11.15904817	1.58E-15	1.08E-11	25.11728876	NAC domain protein,	root cap	0 h
HORVU.MOREX.r3.1HG0067490.1	-6.554595547	-1.72649178	-12.74731843	8.95E-18	9.19E-14	18.16094389	Retrovirus-related Pol polyprotein from transposon TNT 1-94	root cap	0 h
HORVU.MOREX.r3.7HG0748980.1	3.493254047	-2.90728761	9.609202952	3.32E-13	1.70E-09	15.920196	11S seed storage globulin A	root cap	0 h
HORVU.MOREX.r3.3HG0280700.1	0.608457798	6.27769849	7.701208229	3.36E-10	7.66E-07	13.11387248	Katanin p60 ATPase-containing subunit A1	root cap	0 h
HORVU.MOREX.r3.5HG0475760.1	-4.962837145	-2.872794743	-8.551939863	1.48E-11	6.08E-08	11.97354268	Skp1	root cap	0 h
HORVU.MOREX.r3.7HG0727570.1	4.315861861	-0.569333422	8.16872267	6.01E-11	1.76E-07	11.34057257	ATP-dependent RNA helicase, putative	root cap	0 h
HORVU.MOREX.r3.1HG0007570.1	-4.739766406	-2.580123327	-8.313168127	3.54E-11	1.21E-07	9.983565255	Werner Syndrome-like exonuclease	root cap	0 h
HORVU.MOREX.r3.2HG0111680.1	-4.781564999	-2.082427636	-7.935560457	1.42E-10	3.63E-07	8.840158354	Formate--tetrahydrofolate ligase	root cap	0 h
HORVU.MOREX.r3.7HG0679070.1	-1.43967604	9.365871523	-6.345405901	5.08E-08	9.47E-05	8.104093549	Rab3 GTPase-activating protein catalytic subunit	root cap	0 h
HORVU.MOREX.r3.1HG0067030.1	-0.905505797	5.504670742	-6.131950615	1.11E-07	0.000190617	7.527487432	Protein trichome birefringence	root cap	0 h
HORVU.MOREX.r3.5HG0447830.1	-0.688518141	4.419279148	-5.9785554	1.96E-07	0.000308917	7.00166162	Sterile alpha motif (SAM) domain-containing protein	root cap	0 h
HORVU.MOREX.r3.6HG0629160.1	1.201077078	2.999097227	5.800628848	3.75E-07	0.000480882	6.390525245	Disease resistance protein RPM1	root cap	0 h
HORVU.MOREX.r3.6HG0559680.1	-2.865919207	0.573580493	-5.848088929	3.15E-07	0.000431402	6.058192839	NADPH:quinone oxidoreductase	root cap	0 h
HORVU.MOREX.r3.5HG0523890.1	-4.305158039	-2.93597984	-6.621856604	1.83E-08	3.75E-05	6.053215176	Protein FAR1-RELATED SEQUENCE 5	root cap	0 h
HORVU.MOREX.r3.2HG0170640.1	3.361663461	-0.509068665	5.677495016	5.87E-07	0.000692137	5.125097007	Protein FAR1-RELATED SEQUENCE 5	root cap	0 h
HORVU.MOREX.r3.5HG0523880.1	-3.723667717	-2.522148569	-5.887396499	2.73E-07	0.000400404	4.751039016	cryptochrome-interacting basic-helix-loop-helix 5	root cap	0 h
HORVU.MOREX.r3.7HG0739910.1	0.892656383	4.210713917	5.286844618	2.40E-06	0.002516764	4.661580015	Disease resistance protein (NBS-LRR class) family	root cap	0 h
HORVU.MOREX.r3.7HG0695920.1	1.276263915	2.660691655	5.266940332	2.58E-06	0.002516764	4.603056232	#N/A	root cap	0 h
HORVU.MOREX.r3.2HG0215060.1	4.98419157	-1.599980119	5.66814002	6.07E-07	0.000692137	4.059746903	WAT1-related protein	root cap	0 h
HORVU.MOREX.r3.4HG0343330.1	5.573085555	-0.333480115	5.277388614	2.48E-06	0.002516764	3.838588837	Endonuclease III homolog	root cap	0 h
HORVU.MOREX.r3.5HG0489790.1	1.891910844	-0.067483895	5.063576336	5.30E-06	0.00473253	3.557181376	SKP1-like protein 4	root cap	0 h
HORVU.MOREX.r3.7HG0720330.1	-2.199244835	-3.241254914	-5.220048657	3.04E-06	0.002839724	3.546752538	Phosphatidylinositol 4-phosphate 5-kinase 1	root cap	0 h
HORVU.MOREX.r3.7HG0663550.1	-2.348596099	0.15599737	-4.949164396	7.94E-06	0.006097532	3.488292383	Glycosyltransferase	root cap	0 h
HORVU.MOREX.r3.1HG0049550.1	0.544247115	3.543555344	4.900725739	9.40E-06	0.006892471	3.366511337	Protein BPS1, chloroplastic	root cap	0 h
HORVU.MOREX.r3.6HG0628890.1	-1.568007098	-2.722150267	-4.949769109	7.92E-06	0.006097532	3.356220853	Nicotianamine synthase	root cap	0 h
HORVU.MOREX.r3.1HG0068380.1	0.559201929	5.314485157	4.946074853	8.02E-06	0.006097532	3.332950369	#N/A	root cap	0 h
HORVU.MOREX.r3.6HG0559690.1	1.292974786	2.590055839	4.841196551	1.16E-05	0.00791968	3.210011071	Cell division cycle 5-like protein	root cap	0 h
HORVU.MOREX.r3.7HG0679060.1	-2.731993942	1.156648697	-5.024302698	6.09E-06	0.005209649	3.208114798	Nuclear transport factor 2 family protein, putative	root cap	0 h
HORVU.MOREX.r3.1HG0012570.1	-1.549175047	-1.556736336	-4.821807681	1.24E-05	0.008199768	3.144475753	Chymotrypsin inhibitor	root cap	0 h
HORVU.MOREX.r3.2HG0196720.1	1.344875712	-0.225277908	4.807586579	1.30E-05	0.008346514	3.102298545	XH/XS domain-containing protein	root cap	0 h
HORVU.MOREX.r3.3HG0229300.1	-1.500383909	1.779653302	-4.731243511	1.70E-05	0.010547776	2.717609275	Germin-like protein	root cap	0 h
HORVU.MOREX.r3.1HG0024020.1	0.64615229	5.072656773	4.673785933	2.07E-05	0.012484071	2.481014965	Heparan-alpha-glucosaminide N-acetyltransferase	root cap	0 h
HORVU.MOREX.r3.5HG0425000.1	-3.476618373	-0.918831697	-4.860106437	1.08E-05	0.007669821	2.36137305	Transposon protein, putative, Pong sub-class	root cap	0 h
HORVU.MOREX.r3.2HG0215830.1	0.909482307	2.436514446	4.433572634	4.70E-05	0.027159657	1.906518672	CsAtPR5	root cap	0 h
HORVU.MOREX.r3.4HG0343000.1	-0.734055922	2.745864292	-4.421209371	4.90E-05	0.027159657	1.776200143	Cyclin family protein	root cap	0 h
HORVU.MOREX.r3.1HG0060370.1	2.167139952	-0.902409718	4.268831162	8.16E-05	0.042958019	1.275393188	1,4-alpha-glucan branching enzyme GlgB	root cap	0 h
HORVU.MOREX.r3.UnG0765280.1	0.91177688	2.589811572	4.223060034	9.51E-05	0.047576893	1.191925829	F-box family protein	root cap	0 h
HORVU.MOREX.r3.6HG0630920.1	2.981017522	-2.009589986	4.410268098	5.08E-05	0.027439865	1.166346435	NBS-LRR disease resistance protein-like	root cap	0 h
HORVU.MOREX.r3.1HG0069090.1	2.855974492	-3.256645115	4.423482203	4.86E-05	0.027159657	1.052861777	Ribosomal protein S5/Elongation factor G/III/V family protein	root cap	0 h
HORVU.MOREX.r3.1HG0069420.1	0.509256845	7.626353217	4.257942902	8.47E-05	0.04343025	1.002512481	Cytochrome P450	root cap	0 h
HORVU.MOREX.r3.1HG0078900.1	-2.049158051	5.8370464	-25.5913251	1.65E-31	3.39E-27	59.40939911	MATH domain-containing protein	root cap	3 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0067490.1	-6.383840185	-1.72649178	-12.37876227	2.89E-17	2.96E-13	17.39549212	Retrovirus-related Pol polyprotein from transposon TNT 1-94	root cap	3 h
HORVU.MOREX.r3.1HG0067040.1	-0.948748924	7.101906906	-8.133925411	6.83E-11	2.00E-07	14.64438446	NAC domain protein,	root cap	3 h
HORVU.MOREX.r3.5HG0475760.1	-4.7787136	-2.872794743	-9.124845659	1.87E-12	1.28E-08	14.10459468	Skp1	root cap	3 h
HORVU.MOREX.r3.7HG0748980.1	2.574044815	-2.90728761	8.349935208	3.10E-11	1.06E-07	13.49933969	11S seed storage globulin A	root cap	3 h
HORVU.MOREX.r3.7HG0679070.1	-1.771150056	9.365871523	-7.760381157	2.70E-10	6.93E-07	13.26377351	Rab3 GTPase-activating protein catalytic subunit	root cap	3 h
HORVU.MOREX.r3.7HG0727570.1	4.301563852	-0.569333422	8.461585041	2.06E-11	8.45E-08	12.27770433	ATP-dependent RNA helicase, putative	root cap	3 h
HORVU.MOREX.r3.1HG0007570.1	-4.984701776	-2.580123327	-8.492081443	1.84E-11	8.45E-08	9.988247475	Werner Syndrome-like exonuclease	root cap	3 h
HORVU.MOREX.r3.5HG0447830.1	-0.765202966	4.419279148	-6.446617635	3.50E-08	7.17E-05	8.664763017	Sterile alpha motif (SAM) domain-containing protein	root cap	3 h
HORVU.MOREX.r3.2HG0111680.1	-4.451956379	-2.082427636	-7.310294255	1.43E-09	3.25E-06	7.313765456	Formate--tetrahydrofolate ligase	root cap	3 h
HORVU.MOREX.r3.3HG0280700.1	0.453504859	6.27769849	5.7487585	4.53E-07	0.000714932	6.090140023	Katanin p60 ATPase-containing subunit A1	root cap	3 h
HORVU.MOREX.r3.7HG0679060.1	-3.838166529	1.156648697	-6.030511322	1.62E-07	0.000301782	5.455380293	Nuclear transport factor 2 family protein, putative	root cap	3 h
HORVU.MOREX.r3.7HG0695920.1	1.355366476	2.660691655	5.460487952	1.29E-06	0.001649904	5.241127218	#N/A	root cap	3 h
HORVU.MOREX.r3.2HG0215060.1	4.959945214	-1.599980119	5.882627922	2.78E-07	0.000475349	4.727483489	WAT1-related protein	root cap	3 h
HORVU.MOREX.r3.3HG0306460.1	2.437108867	-3.648540528	5.472775832	1.23E-06	0.001649904	4.390093937	#N/A	root cap	3 h
HORVU.MOREX.r3.2HG0186210.1	-1.805650424	1.781727841	-5.314095923	2.18E-06	0.002626649	4.245888499	DUF1191 superfamily protein	root cap	3 h
HORVU.MOREX.r3.6HG0559680.1	-2.537697339	0.573580493	-5.188963938	3.40E-06	0.0038769	4.02962174	NADPH:quinone oxidoreductase	root cap	3 h
HORVU.MOREX.r3.5HG0523880.1	-3.666992223	-2.522148569	-5.578441515	8.40E-07	0.001231731	3.772507218	cryptochrome-interacting basic-helix-loop-helix 5	root cap	3 h
HORVU.MOREX.r3.7HG0718080.1	1.111041113	-3.103532351	5.125626538	4.26E-06	0.004369302	3.697404394	Amino acid permease	root cap	3 h
HORVU.MOREX.r3.2HG0170640.1	3.087621572	-0.509068665	5.168782711	3.65E-06	0.003946062	3.623831661	Protein FAR1-RELATED SEQUENCE 5	root cap	3 h
HORVU.MOREX.r3.6HG0628890.1	-1.552503511	-2.722150267	-4.945152987	8.05E-06	0.007865085	3.340133295	Nicotianamine synthase	root cap	3 h
HORVU.MOREX.r3.4HG0363330.1	1.15043771	2.648390841	4.853547214	1.11E-05	0.010344293	3.24056058	F-box/RNI-like superfamily protein	root cap	3 h
HORVU.MOREX.r3.6HG0629160.1	0.964971655	2.999097227	4.647292824	2.27E-05	0.019374489	2.483946442	Disease resistance protein RPM1	root cap	3 h
HORVU.MOREX.r3.6HG0559690.1	1.177159453	2.590055839	4.598857558	2.68E-05	0.020336863	2.436512865	Cell division cycle 5-like protein	root cap	3 h
HORVU.MOREX.r3.4HG0343330.1	3.794018323	-0.333480115	4.605535487	2.62E-05	0.020336863	2.299370177	Endonuclease III homolog	root cap	3 h
HORVU.MOREX.r3.3HG0260150.1	1.812591182	-0.115050093	4.722613126	1.75E-05	0.015592341	2.255830577	Acylamino-acid-releasing enzyme	root cap	3 h
HORVU.MOREX.r3.5HG0448120.1	1.262846698	1.313003386	4.501170221	3.73E-05	0.026427435	2.136736162	Polyol transporter	root cap	3 h
HORVU.MOREX.r3.7HG0649080.1	0.767022726	5.069910261	4.605261218	2.62E-05	0.020336863	2.091891208	Peroxidase	root cap	3 h
HORVU.MOREX.r3.2HG0135600.1	-2.229351087	-2.598497762	-4.517288548	3.54E-05	0.025910754	1.975692355	Chlorophyll a-b binding protein, chloroplastic	root cap	3 h
HORVU.MOREX.r3.1HG0024020.1	0.596143047	5.072656773	4.337732035	6.49E-05	0.044360004	1.393976869	Heparan-alpha-glucosaminide N-acetyltransferase	root cap	3 h
HORVU.MOREX.r3.1HG0078900.1	-1.905105788	5.8370464	-23.73087579	6.59E-30	1.35E-25	57.10526724	MATH domain-containing protein	root cap	6 h
HORVU.MOREX.r3.1HG0067490.1	-6.473047274	-1.72649178	-12.57987883	1.52E-17	1.56E-13	21.32052513	Retrovirus-related Pol polyprotein from transposon TNT 1-94	root cap	6 h
HORVU.MOREX.r3.7HG0748980.1	3.078420767	-2.90728761	9.576066553	3.73E-13	2.55E-09	18.03062108	11S seed storage globulin A	root cap	6 h
HORVU.MOREX.r3.1HG0067040.1	-1.060515911	7.101906906	-9.063050876	2.33E-12	9.57E-09	17.88324005	NAC domain protein,	root cap	6 h
HORVU.MOREX.r3.5HG0447830.1	-1.002200885	4.419279148	-8.565800294	1.41E-11	4.82E-08	16.21493576	Sterile alpha motif (SAM) domain-containing protein	root cap	6 h
HORVU.MOREX.r3.5HG0475760.1	-5.342607838	-2.872794743	-9.146451526	1.73E-12	8.86E-09	15.12050511	Skp1	root cap	6 h
HORVU.MOREX.r3.3HG0225800.1	2.77197395	-2.677835456	7.354417545	1.21E-09	3.55E-06	11.40915567	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase far	root cap	6 h
HORVU.MOREX.r3.7HG0727570.1	3.259990996	-0.569333422	7.306371149	1.45E-09	3.71E-06	10.79206579	ATP-dependent RNA helicase, putative	root cap	6 h
HORVU.MOREX.r3.1HG0007570.1	-3.855234082	-2.580123327	-7.091254218	3.21E-09	7.32E-06	8.857110138	Werner Syndrome-like exonuclease	root cap	6 h
HORVU.MOREX.r3.6HG0576610.1	1.42396027	3.781355355	6.435078271	3.65E-08	5.76E-05	8.626959924	LURP-one-like protein (DUF567)	root cap	6 h
HORVU.MOREX.r3.5HG0523890.1	-4.530447334	-2.93597984	-7.052336049	3.71E-09	7.61E-06	8.489291638	Protein FAR1-RELATED SEQUENCE 5	root cap	6 h
HORVU.MOREX.r3.5HG0523880.1	-4.368236389	-2.522148569	-6.849619152	7.87E-09	1.47E-05	8.286613515	cryptochrome-interacting basic-helix-loop-helix 5	root cap	6 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.2HG0111680.1	-4.144731809	-2.082427636	-6.726225566	1.24E-08	2.12E-05	7.333570058	Formate--tetrahydrofolate ligase	root cap	6 h
HORVU.MOREX.r3.6HG0559680.1	-3.143773538	0.573580493	-6.077871376	1.36E-07	0.00017438	7.07251255	NADPH:quinone oxidoreductase	root cap	6 h
HORVU.MOREX.r3.7HG0679070.1	-1.378115686	9.365871523	-6.080124984	1.35E-07	0.00017438	6.977712719	Rab3 GTPase-activating protein catalytic subunit	root cap	6 h
HORVU.MOREX.r3.6HG0552590.1	1.643000496	-2.145556214	5.909263246	2.52E-07	0.000304414	6.776063715	Phototropic-responsive NPH3 family protein	root cap	6 h
HORVU.MOREX.r3.2HG0215060.1	4.81737596	-1.599980119	6.122529353	1.15E-07	0.000169142	6.51244959	WAT1-related protein	root cap	6 h
HORVU.MOREX.r3.7HG0644170.1	1.029409495	-1.791009835	5.67257598	5.97E-07	0.000645235	5.902947131	Transposon protein, putative, CACTA, En/Spm sub-class	root cap	6 h
HORVU.MOREX.r3.7HG0649080.1	0.965171841	5.069910261	5.733061223	4.80E-07	0.000546688	5.80844451	Peroxidase	root cap	6 h
HORVU.MOREX.r3.1HG0060370.1	2.815729541	-0.902409718	5.432737203	1.42E-06	0.001389128	4.949288258	1,4-alpha-glucan branching enzyme GlgB	root cap	6 h
HORVU.MOREX.r3.7HG0723140.1	1.293486809	-2.014032702	5.341215776	1.97E-06	0.001761756	4.790818327	#N/A	root cap	6 h
HORVU.MOREX.r3.2HG0170640.1	3.9698512	-0.509068665	5.481843511	1.19E-06	0.001222164	4.621636959	Protein FAR1-RELATED SEQUENCE 5	root cap	6 h
HORVU.MOREX.r3.7HG0695920.1	1.291739565	2.660691655	5.255225341	2.69E-06	0.002041083	4.541485572	#N/A	root cap	6 h
HORVU.MOREX.r3.4HG0343330.1	6.268033718	-0.333480115	5.416526571	1.51E-06	0.001405587	4.539731684	Endonuclease III homolog	root cap	6 h
HORVU.MOREX.r3.3HG0280700.1	0.422045286	6.27769849	5.322885841	2.11E-06	0.001802915	4.434245491	Katanin p60 ATPase-containing subunit A1	root cap	6 h
HORVU.MOREX.r3.6HG0550820.2	5.104844661	-0.93362822	5.265526537	2.59E-06	0.002041083	4.373755268	GDSL esterase/lipase	root cap	6 h
HORVU.MOREX.r3.3HG0225830.1	1.202776609	-1.658623447	5.183301698	3.47E-06	0.002542992	4.2321717	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase fa	root cap	6 h
HORVU.MOREX.r3.1HG0076850.1	1.853257222	-2.352399703	5.144859825	3.98E-06	0.002814589	4.155886879	Avr9/Cf-9 rapidly elicited protein	root cap	6 h
HORVU.MOREX.r3.3HG0220770.1	-0.909853286	6.392414316	-5.284763285	2.42E-06	0.001983673	4.146893812	Dipeptidyl peptidase family member 6	root cap	6 h
HORVU.MOREX.r3.6HG0559690.1	1.235844928	2.590055839	4.975707487	7.23E-06	0.004495764	3.592677419	Cell division cycle 5-like protein	root cap	6 h
HORVU.MOREX.r3.1HG0003270.1	1.481880615	-2.891112437	4.955464158	7.76E-06	0.004685173	3.555318877	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase fa	root cap	6 h
HORVU.MOREX.r3.5HG0423130.1	2.044171189	-2.684878217	4.942810317	8.12E-06	0.004758	3.498680716	Thaumatin-like protein	root cap	6 h
HORVU.MOREX.r3.1HG0078890.1	2.618879091	-0.071217622	5.021417054	6.16E-06	0.004137923	3.493487467	Ubiquitin carboxyl-terminal hydrolase 2	root cap	6 h
HORVU.MOREX.r3.3HG0306460.1	2.408791676	-3.648540528	5.017035472	6.25E-06	0.004137923	3.415391408	#N/A	root cap	6 h
HORVU.MOREX.r3.5HG0479830.1	-1.885238911	-1.947529218	-4.900460761	9.41E-06	0.005365784	3.398538424	Cytochrome P450	root cap	6 h
HORVU.MOREX.r3.4HG0409190.1	2.740609543	1.165329523	4.993357397	6.79E-06	0.004357194	3.117221626	Glutathione S-transferase	root cap	6 h
HORVU.MOREX.r3.5HG0425000.1	-2.745319596	-0.918831697	-4.819566889	1.25E-05	0.006568806	3.000563542	Transposon protein, putative, Pong sub-class	root cap	6 h
HORVU.MOREX.r3.5HG0489790.1	1.729913955	-0.067483895	4.792584234	1.37E-05	0.007034697	2.997183911	SKP1-like protein 4	root cap	6 h
HORVU.MOREX.r3.4HG0403870.1	1.115887457	-2.784620446	4.76329599	1.52E-05	0.007597555	2.960366468	Cysteine proteinase inhibitor	root cap	6 h
HORVU.MOREX.r3.6HG0628890.1	-1.353334416	-2.722150267	-4.700587535	1.89E-05	0.00899955	2.759250428	Nicotianamine synthase	root cap	6 h
HORVU.MOREX.r3.7HG0676800.1	-0.440173088	6.777542145	-4.867072001	1.06E-05	0.005867065	2.756918908	formate dehydrogenase	root cap	6 h
HORVU.MOREX.r3.1HG0069420.1	0.588761032	7.626353217	4.822387998	1.24E-05	0.006568806	2.692197104	Cytochrome P450	root cap	6 h
HORVU.MOREX.r3.6HG0609250.1	1.551098974	-2.575857699	4.678834511	2.03E-05	0.009269715	2.685685375	Stigma-specific Stig1 family protein	root cap	6 h
HORVU.MOREX.r3.7HG0679060.1	-2.624088415	1.156648697	-4.693586671	1.93E-05	0.009010121	2.553271747	Nuclear transport factor 2 family protein, putative	root cap	6 h
HORVU.MOREX.r3.1HG0076760.1	0.739718445	3.88919764	4.708824294	1.83E-05	0.008955432	2.53375467	IQ domain-containing protein	root cap	6 h
HORVU.MOREX.r3.7HG0724080.1	1.505414211	2.23197157	4.623830511	2.46E-05	0.010500511	2.483291017	6,7-dimethyl-8-ribityllumazine synthase	root cap	6 h
HORVU.MOREX.r3.3HG0244320.1	-2.674012215	-2.865168374	-4.660187334	2.17E-05	0.009598564	2.451635624	Lachrymatory-factor synthase	root cap	6 h
HORVU.MOREX.r3.7HG0749060.1	1.729470321	0.00150025	4.516383674	3.55E-05	0.014554787	2.179762807	Transducin/WD40 repeat-like superfamily protein	root cap	6 h
HORVU.MOREX.r3.1HG0069100.1	1.846276758	-2.641840701	4.492769873	3.84E-05	0.015165223	2.056725151	BZIP transcription factor	root cap	6 h
HORVU.MOREX.r3.2HG0215830.1	0.926109433	2.436514446	4.506786099	3.66E-05	0.014743103	2.05260992	CsAtPR5	root cap	6 h
HORVU.MOREX.r3.2HG0191320.1	2.9640787	1.356813235	4.656086323	2.20E-05	0.009598564	1.911901745	Glucan endo-1,3-beta-glucosidase-like protein 3	root cap	6 h
HORVU.MOREX.r3.5HG0446460.1	1.613594534	0.590554613	4.424241984	4.85E-05	0.017854203	1.864622834	Mitochondrial carrier protein, expressed	root cap	6 h
HORVU.MOREX.r3.7HG0725700.1	-3.356564102	-1.181670666	-4.54949582	3.17E-05	0.013266691	1.772500128	Receptor-like protein kinase	root cap	6 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.2HG0175580.1	2.216988136	1.299950378	4.422707585	4.87E-05	0.017854203	1.676043836	Aldo/keto reductase family oxidoreductase	root cap	6 h
HORVU.MOREX.r3.2HG0132440.2	-0.498359392	4.455296999	-4.446445915	4.50E-05	0.017409918	1.612179926	#N/A	root cap	6 h
HORVU.MOREX.r3.5HG0502990.1	3.538883067	3.237955153	4.311887062	7.07E-05	0.024410973	1.459453342	NAC domain protein,	root cap	6 h
HORVU.MOREX.r3.1HG0034450.1	-1.311503219	0.621391691	-4.250713897	8.67E-05	0.028245893	1.369687759	Retrovirus-related Pol polyprotein from transposon TNT 1-94	root cap	6 h
HORVU.MOREX.r3.1HG0067030.1	-0.642872967	5.504670742	-4.357508726	6.07E-05	0.021471697	1.320329842	Protein trichome birefringence	root cap	6 h
HORVU.MOREX.r3.6HG0601210.1	2.959072381	-0.829190823	4.42327686	4.86E-05	0.017854203	1.248866905	En/Spm transposon protein-like	root cap	6 h
HORVU.MOREX.r3.6HG0544580.1	3.253885945	0.367989846	4.402636782	5.21E-05	0.018770204	1.225924613	Werner Syndrome-like exonuclease	root cap	6 h
HORVU.MOREX.r3.1HG0081920.1	0.922012939	-2.160509685	4.233961362	9.17E-05	0.029396124	1.223479246	Pollen Ole e 1 allergen/extensin	root cap	6 h
HORVU.MOREX.r3.2HG0113590.1	0.571972113	3.8003454	4.284378752	7.75E-05	0.026077776	1.171842723	Zinc finger CCCH domain protein, putative	root cap	6 h
HORVU.MOREX.r3.3HG0245590.1	1.127912611	-1.410291341	4.216621335	9.71E-05	0.03065756	1.132263772	Ring finger protein, putative	root cap	6 h
HORVU.MOREX.r3.6HG0572410.1	2.39959512	-1.952913174	4.176637771	0.00011	0.034462619	1.060234282	Peptidylprolyl isomerase	root cap	6 h
HORVU.MOREX.r3.7HG0745510.1	-0.401626073	5.787158675	-4.309105143	7.14E-05	0.024410973	0.952275663	Transcriptional corepressor SEUSS	root cap	6 h
HORVU.MOREX.r3.1HG0062030.1	1.228525962	-2.693593678	4.095262378	0.00014	0.040170981	0.912607799	Dehydration responsive element binding transcription factor	root cap	6 h
HORVU.MOREX.r3.7HG0739910.1	0.725625834	4.210713917	4.163210122	0.00012	0.034964133	0.911102394	Disease resistance protein (NBS-LRR class) family	root cap	6 h
HORVU.MOREX.r3.7HG0644060.1	4.132576443	3.296548784	4.266268571	8.23E-05	0.027253602	0.87667231	Starch synthase, chloroplastic/amyloplastic	root cap	6 h
HORVU.MOREX.r3.5HG0518370.1	0.848757546	-1.963228378	4.170237538	0.00011	0.03467297	0.866667165	BTB/POZ domain containing protein	root cap	6 h
HORVU.MOREX.r3.1HG0069580.1	2.380284628	-2.817290135	4.100231981	0.00014	0.040170981	0.835294348	Gag-Pol polyprotein	root cap	6 h
HORVU.MOREX.r3.7HG0678660.1	2.06524295	0.844122535	4.103859273	0.00014	0.040170981	0.830998435	Protein kinase family protein	root cap	6 h
HORVU.MOREX.r3.6HG0561420.1	1.5545289	-3.217292483	4.055437995	0.00016	0.045137355	0.736120328	Transposon protein, putative, Mutator sub-class	root cap	6 h
HORVU.MOREX.r3.3HG0298070.1	3.218684852	-2.093355386	4.132359661	0.00013	0.038140595	0.717396318	Amino acid permease	root cap	6 h
HORVU.MOREX.r3.5HG0509930.1	0.76678881	3.497515567	4.107053411	0.00014	0.040170981	0.66276904	Zinc-transporting ATPase	root cap	6 h
HORVU.MOREX.r3.5HG0520080.1	2.127642877	-2.977064176	4.025094675	0.00018	0.049167601	0.576853223	Kinase-like	root cap	6 h
HORVU.MOREX.r3.3HG0220340.1	0.878729448	2.953247644	4.095222952	0.00014	0.040170981	0.511634139	Disease resistance protein RPM1	root cap	6 h
HORVU.MOREX.r3.1HG0078900.1	-1.860688339	5.8370464	-22.36883507	1.14E-28	2.35E-24	54.25575787	MATH domain-containing protein	root cap	12 h
HORVU.MOREX.r3.1HG0067490.1	-7.017751104	-1.72649178	-13.807562	3.40E-19	3.48E-15	23.23124234	Retrovirus-related Pol polyprotein from transposon TNT 1-94	root cap	12 h
HORVU.MOREX.r3.7HG0748980.1	4.992720797	-2.90728761	11.79582486	1.91E-16	1.31E-12	21.50283895	11S seed storage globulin A	root cap	12 h
HORVU.MOREX.r3.1HG0067040.1	-1.107535402	7.101906906	-9.153177808	1.69E-12	8.65E-09	18.22984053	NAC domain protein,	root cap	12 h
HORVU.MOREX.r3.7HG0727570.1	4.231410401	-0.569333422	8.279332645	4.01E-11	1.65E-07	13.0655516	ATP-dependent RNA helicase, putative	root cap	12 h
HORVU.MOREX.r3.5HG0475760.1	-4.953424396	-2.872794743	-8.18757804	5.61E-11	1.92E-07	12.155674	Skp1	root cap	12 h
HORVU.MOREX.r3.2HG0175580.1	3.354116578	1.299950378	7.121002037	2.88E-09	6.56E-06	11.0508038	Aldo/keto reductase family oxidoreductase	root cap	12 h
HORVU.MOREX.r3.3HG0280700.1	0.550692265	6.27769849	6.918609376	6.09E-09	1.14E-05	10.18636156	Katanin p60 ATPase-containing subunit A1	root cap	12 h
HORVU.MOREX.r3.3HG0225800.1	2.932023177	-2.677835456	7.032958629	3.99E-09	8.18E-06	10.09410244	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase far	root cap	12 h
HORVU.MOREX.r3.1HG0007570.1	-4.400085394	-2.580123327	-7.348284787	1.24E-09	3.63E-06	8.859679054	Werner Syndrome-like exonuclease	root cap	12 h
HORVU.MOREX.r3.2HG0111680.1	-4.370135615	-2.082427636	-7.166342333	2.43E-09	6.24E-06	8.388492305	Formate--tetrahydrofolate ligase	root cap	12 h
HORVU.MOREX.r3.3HG0225830.1	1.640390941	-1.658623447	6.009233187	1.75E-07	0.000251122	7.136309612	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase far	root cap	12 h
HORVU.MOREX.r3.5HG0523880.1	-4.163324659	-2.522148569	-6.476266222	3.13E-08	5.36E-05	7.099554497	cryptochrome-interacting basic-helix-loop-helix 5	root cap	12 h
HORVU.MOREX.r3.4HG0382640.1	1.790785999	-2.507767436	5.996034154	1.84E-07	0.000251122	6.874460067	Mitochondrial import inner membrane translocase subunit Tim1	root cap	12 h
HORVU.MOREX.r3.5HG0447830.1	-0.686440852	4.419279148	-5.911403457	2.50E-07	0.00029337	6.68456388	Sterile alpha motif (SAM) domain-containing protein	root cap	12 h
HORVU.MOREX.r3.5HG0425000.1	-5.175252186	-0.918831697	-6.356427969	4.88E-08	7.70E-05	6.593019236	Transposon protein, putative, Pong sub-class	root cap	12 h
HORVU.MOREX.r3.7HG0679070.1	-1.389938158	9.365871523	-5.903737311	2.57E-07	0.00029337	6.392269163	Rab3 GTPase-activating protein catalytic subunit	root cap	12 h
HORVU.MOREX.r3.7HG0695920.1	1.313948132	2.660691655	5.76748266	4.23E-07	0.000456931	6.287331113	#N/A	root cap	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.6HG0559680.1	-2.805018916	0.573580493	-5.707287109	5.27E-07	0.000540359	5.903888502	NADPH:quinone oxidoreductase	root cap	12 h
HORVU.MOREX.r3.5HG0489790.1	1.908347936	-0.067483895	5.651049133	6.46E-07	0.000631218	5.748701508	SKP1-like protein 4	root cap	12 h
HORVU.MOREX.r3.5HG0523890.1	-3.89806797	-2.93597984	-5.924538516	2.38E-07	0.00029337	5.238937919	Protein FAR1-RELATED SEQUENCE 5	root cap	12 h
HORVU.MOREX.r3.2HG0113590.1	0.786254625	3.8003454	5.390998159	1.65E-06	0.001540615	4.93093729	Zinc finger CCCH domain protein, putative	root cap	12 h
HORVU.MOREX.r3.1HG0060370.1	3.217276087	-0.902409718	5.377109252	1.74E-06	0.001548973	4.541704472	1,4-alpha-glucan branching enzyme GlgB	root cap	12 h
HORVU.MOREX.r3.7HG0725940.1	-1.639235011	-1.945827342	-5.128839728	4.21E-06	0.003455844	4.140817413	protein kinase family protein	root cap	12 h
HORVU.MOREX.r3.4HG0343330.1	5.767619043	-0.333480115	5.205803365	3.20E-06	0.00273855	3.951141896	Endonuclease III homolog	root cap	12 h
HORVU.MOREX.r3.6HG0559690.1	1.278339865	2.590055839	4.989977941	6.88E-06	0.00542685	3.659731614	Cell division cycle 5-like protein	root cap	12 h
HORVU.MOREX.r3.6HG0540710.1	0.951452883	1.044028848	4.862110717	1.08E-05	0.00745542	3.263468096	Disease resistance protein (TIR-NBS-LRR class) family	root cap	12 h
HORVU.MOREX.r3.2HG0215060.1	3.287258171	-1.599980119	4.927538272	8.56E-06	0.006507102	3.240359655	WAT1-related protein	root cap	12 h
HORVU.MOREX.r3.7HG0724080.1	1.461771759	2.23197157	4.845016446	1.14E-05	0.007562815	3.185745841	6,7-dimethyl-8-ribityllumazine synthase	root cap	12 h
HORVU.MOREX.r3.UnG0783730.1	1.374590715	6.739233425	4.889572135	9.78E-06	0.007166702	2.981034384	Histone H2B	root cap	12 h
HORVU.MOREX.r3.5HG0511210.1	-1.672657715	1.506867328	-4.735462662	1.67E-05	0.010089164	2.861889321	MADS box transcription factor	root cap	12 h
HORVU.MOREX.r3.5HG0518370.1	1.241226206	-1.963228378	4.746033134	1.61E-05	0.010021345	2.861746518	BTB/POZ domain containing protein	root cap	12 h
HORVU.MOREX.r3.6HG0630920.1	3.184249492	-2.009589986	4.858516336	1.09E-05	0.00745542	2.797978419	NBS-LRR disease resistance protein-like	root cap	12 h
HORVU.MOREX.r3.5HG0498610.1	1.772925053	-3.32898876	4.788734549	1.39E-05	0.008911768	2.593032399	Protein Mei2	root cap	12 h
HORVU.MOREX.r3.1HG0070000.1	0.947071992	1.808570831	4.582695162	2.83E-05	0.015314464	2.368356651	Histone H3	root cap	12 h
HORVU.MOREX.r3.2HG0197550.1	1.009479028	-0.290355644	4.67852934	2.03E-05	0.011930748	2.321526759	Transmembrane protein, putative	root cap	12 h
HORVU.MOREX.r3.6HG0633910.1	1.705820626	-2.820374223	4.581885972	2.84E-05	0.015314464	2.318850106	Protein SAWADEE HOMEODOMAIN-like protein 2	root cap	12 h
HORVU.MOREX.r3.2HG0132820.1	-3.434720032	1.249014446	-4.627649298	2.42E-05	0.013818314	2.285329858	Phenylalanine ammonia-lyase	root cap	12 h
HORVU.MOREX.r3.7HG0749060.1	1.918352159	0.00150025	4.506366673	3.67E-05	0.017927897	2.114753098	Transducin/WD40 repeat-like superfamily protein	root cap	12 h
HORVU.MOREX.r3.2HG0178180.1	1.883069531	-3.517770368	4.539256759	3.28E-05	0.017260972	1.967631887	Proteasome subunit beta type-9	root cap	12 h
HORVU.MOREX.r3.7HG0635050.1	0.859260477	0.346305785	4.509043283	3.64E-05	0.017927897	1.846757133	NBS-LRR-like resistance protein	root cap	12 h
HORVU.MOREX.r3.1HG0095330.1	0.908300605	2.512196306	4.491379774	3.86E-05	0.018426154	1.774637506	Zinc finger CCCH domain protein	root cap	12 h
HORVU.MOREX.r3.6HG0629160.1	0.954897274	2.999097227	4.404505237	5.18E-05	0.023112653	1.595978201	Disease resistance protein RPM1	root cap	12 h
HORVU.MOREX.r3.6HG0614490.1	0.800966667	2.880979216	4.443934219	4.54E-05	0.020680043	1.51683545	Type I inositol-1,4,5-trisphosphate 5-phosphatase	root cap	12 h
HORVU.MOREX.r3.1HG0070730.1	-3.52859849	-0.4130893	-4.454534191	4.38E-05	0.020404574	1.41874584	Glycosyltransferase	root cap	12 h
HORVU.MOREX.r3.2HG0191320.1	-3.06833176	1.356813235	-4.52472845	3.45E-05	0.017683779	1.378952424	Glucan endo-1,3-beta-glucosidase-like protein 3	root cap	12 h
HORVU.MOREX.r3.2HG0215830.1	0.825847403	2.436514446	4.290078812	7.61E-05	0.031852538	1.342456969	CsAtPR5	root cap	12 h
HORVU.MOREX.r3.6HG0565970.1	0.78319336	4.099013656	4.308926272	7.14E-05	0.030531971	1.31008281	Early nodulin-like protein	root cap	12 h
HORVU.MOREX.r3.3HG0291580.1	0.686909508	2.805578274	4.221238262	9.56E-05	0.037739864	1.135751902	Lysosomal Pro-X carboxypeptidase	root cap	12 h
HORVU.MOREX.r3.1HG0092900.1	1.626394045	-2.962290826	4.200740505	0.0001	0.039629343	1.066277888	C3HC4-type RING finger-containing protein	root cap	12 h
HORVU.MOREX.r3.3HG0240580.1	0.969073804	2.986398292	4.272358538	8.07E-05	0.033115789	1.059836153	Glycosyltransferase	root cap	12 h
HORVU.MOREX.r3.6HG0548800.1	1.27034093	-1.579734173	4.180293118	0.00011	0.040252358	1.039195703	transcription factor IIIA	root cap	12 h
HORVU.MOREX.r3.3HG0220340.1	1.000045067	2.953247644	4.233693225	9.18E-05	0.036922107	1.038302764	Disease resistance protein RPM1	root cap	12 h
HORVU.MOREX.r3.6HG0552590.1	1.388142618	-2.145556214	4.12711859	0.00013	0.044608301	0.945928611	Phototropic-responsive NPH3 family protein	root cap	12 h
HORVU.MOREX.r3.2HG0099100.1	1.945926633	-3.276482409	4.180054467	0.00011	0.040252358	0.941271562	Serine/threonine-protein phosphatase 7 long form-like protein	root cap	12 h
HORVU.MOREX.r3.5HG0495750.1	2.159968158	-2.868788994	4.151707368	0.00012	0.043322914	0.914374044	B3 domain-containing protein	root cap	12 h
HORVU.MOREX.r3.4HG0363330.1	1.075073102	2.648390841	4.127755767	0.00013	0.044608301	0.898258513	F-box/RNI-like superfamily protein	root cap	12 h
HORVU.MOREX.r3.3HG0286140.1	1.000293083	3.423023169	4.335507385	6.53E-05	0.028526829	0.840601977	Pollen Ole e 1 allergen/extensin	root cap	12 h
HORVU.MOREX.r3.3HG0258640.1	1.069871576	-1.96360197	4.072865425	0.00016	0.04951996	0.83868399	Kelch repeat protein, putative	root cap	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0068380.1	0.486285361	5.314485157	4.179366439	0.00011	0.040252358	0.689411461	#N/A	root cap	12 h
HORVU.MOREX.r3.3HG0311610.1	1.596124021	-1.025604193	4.061610029	0.00016	0.04951996	0.661533667	Glutathione S-transferase	root cap	12 h
HORVU.MOREX.r3.4HG0353070.1	1.038153513	0.247089748	4.107219961	0.00014	0.04536637	0.607847918	Phototropic-responsive NPH3 family protein	root cap	12 h
HORVU.MOREX.r3.6HG0575750.1	3.449962273	-0.706156741	4.122189733	0.00013	0.044608301	0.554110927	Cytochrome P450 family protein	root cap	12 h
HORVU.MOREX.r3.7HG0728160.1	0.720644627	5.080435682	4.110797805	0.00014	0.04536637	0.457283644	Mitogen-activated protein kinase	root cap	12 h
HORVU.MOREX.r3.2HG0125600.1	0.841028064	-0.842945351	4.064614401	0.00016	0.04951996	0.401703192	DNA-directed RNA polymerase subunit alpha	root cap	12 h
HORVU.MOREX.r3.7HG0651330.1	0.933042619	5.54057482	4.145306698	0.00012	0.043482632	0.382147406	Apyrase	root cap	12 h
HORVU.MOREX.r3.5HG0455240.1	0.852403177	2.696541261	4.063246318	0.00016	0.04951996	0.323663583	O-fucosyltransferase family protein	root cap	12 h
HORVU.MOREX.r3.1HG0078900.1	-2.18941927	5.8370464	-24.93737725	5.88E-31	1.21E-26	57.7066814	MATH domain-containing protein	meristem	0 h
HORVU.MOREX.r3.3HG0280700.1	0.753498871	6.27769849	10.0313638	7.52E-14	5.14E-10	21.32651553	Katanin p60 ATPase-containing subunit A1	meristem	0 h
HORVU.MOREX.r3.5HG0447830.1	-1.109883294	4.419279148	-9.636797126	3.01E-13	1.54E-09	19.85482732	Sterile alpha motif (SAM) domain-containing protein	meristem	0 h
HORVU.MOREX.r3.1HG0067490.1	-6.929389502	-1.72649178	-13.54705862	7.49E-19	7.68E-15	19.12319322	Retrovirus-related Pol polyprotein from transposon TNT 1-94	meristem	0 h
HORVU.MOREX.r3.1HG0067040.1	-1.016390302	7.101906906	-8.9505017	3.50E-12	1.43E-08	17.55857713	NAC domain protein,	meristem	0 h
HORVU.MOREX.r3.7HG0727570.1	5.579475085	-0.569333422	8.809521826	5.82E-12	1.99E-08	11.2003243	ATP-dependent RNA helicase, putative	meristem	0 h
HORVU.MOREX.r3.7HG0695920.1	1.723301085	2.660691655	7.137694518	2.70E-09	6.94E-06	10.96505618	#N/A	meristem	0 h
HORVU.MOREX.r3.2HG0111680.1	-4.776616021	-2.082427636	-7.878325928	1.75E-10	5.13E-07	8.550309124	Formate--tetrahydrofolate ligase	meristem	0 h
HORVU.MOREX.r3.1HG0011440.1	-3.170933054	-1.581106574	-6.619075132	1.85E-08	4.21E-05	7.636262692	Glucan endo-1,3-beta-glucosidase, putative	meristem	0 h
HORVU.MOREX.r3.7HG0739910.1	0.835184976	4.210713917	6.140077736	1.08E-07	0.000181892	7.572146015	Disease resistance protein (NBS-LRR class) family	meristem	0 h
HORVU.MOREX.r3.6HG0559690.1	1.572989065	2.590055839	6.102748126	1.24E-07	0.000181892	7.405751997	Cell division cycle 5-like protein	meristem	0 h
HORVU.MOREX.r3.7HG0640470.1	0.489930266	6.260306545	5.833312239	3.33E-07	0.000426848	6.354846771	WPP domain-interacting tail-anchored protein 1	meristem	0 h
HORVU.MOREX.r3.2HG0170640.1	3.723898226	-0.509068665	5.994626223	1.85E-07	0.000252421	5.847058386	Protein FAR1-RELATED SEQUENCE 5	meristem	0 h
HORVU.MOREX.r3.6HG0546230.1	5.085801563	-1.679648171	6.366968932	4.69E-08	8.75E-05	5.558806213	Disease resistance protein RPM1	meristem	0 h
HORVU.MOREX.r3.1HG0007570.1	-4.032039242	-2.580123327	-6.559325583	2.30E-08	4.73E-05	5.460801058	Werner Syndrome-like exonuclease	meristem	0 h
HORVU.MOREX.r3.1HG0024020.1	0.741911468	5.072656773	5.425302687	1.46E-06	0.001762489	5.028488511	Heparan-alpha-glucosaminide N-acetyltransferase	meristem	0 h
HORVU.MOREX.r3.2HG0215830.1	1.087989707	2.436514446	5.344623867	1.95E-06	0.002223807	4.863223805	CsAtPR5	meristem	0 h
HORVU.MOREX.r3.5HG0523880.1	-4.277013001	-2.522148569	-6.115176206	1.19E-07	0.000181892	4.754025334	cryptochrome-interacting basic-helix-loop-helix 5	meristem	0 h
HORVU.MOREX.r3.1HG0026900.1	-1.247644411	1.690413985	-5.315417037	2.17E-06	0.002311762	4.702054786	Protein apaG	meristem	0 h
HORVU.MOREX.r3.2HG0216110.1	0.47731075	5.350102781	5.304364239	2.25E-06	0.002311762	4.58568552	#N/A	meristem	0 h
HORVU.MOREX.r3.3HG0220340.1	1.557242415	2.953247644	5.081125008	4.99E-06	0.004871474	3.989898487	Disease resistance protein RPM1	meristem	0 h
HORVU.MOREX.r3.1HG0068380.1	0.583137921	5.314485157	4.863947993	1.07E-05	0.009975551	3.102506262	#N/A	meristem	0 h
HORVU.MOREX.r3.1HG0049550.1	0.527322497	3.543555344	4.737558429	1.66E-05	0.01362209	2.836982872	Protein BPS1, chloroplastic	meristem	0 h
HORVU.MOREX.r3.6HG0559680.1	-2.33163652	0.573580493	-4.747859363	1.60E-05	0.01362209	2.707498062	NADPH:quinone oxidoreductase	meristem	0 h
HORVU.MOREX.r3.7HG0724080.1	1.482851842	2.23197157	4.511674398	3.60E-05	0.023854751	2.169251024	6,7-dimethyl-8-ribityllumazine synthase	meristem	0 h
HORVU.MOREX.r3.3HG0288140.1	0.412434522	6.173911395	4.616621976	2.52E-05	0.019871122	2.167480328	Golgin candidate 1	meristem	0 h
HORVU.MOREX.r3.1HG0060370.1	2.553201532	-0.902409718	4.601640437	2.65E-05	0.020143851	2.077762197	1,4-alpha-glucan branching enzyme GlgB	meristem	0 h
HORVU.MOREX.r3.1HG0067030.1	-0.62418381	5.504670742	-4.532564211	3.36E-05	0.022957163	2.010991743	Protein trichome birefringence	meristem	0 h
HORVU.MOREX.r3.5HG0502990.1	3.908091076	3.237955153	4.420153102	4.91E-05	0.029661712	1.886697685	NAC domain protein,	meristem	0 h
HORVU.MOREX.r3.6HG0568640.1	0.463735712	4.543924675	4.477023678	4.05E-05	0.025996858	1.863384785	Methyltransferase domain protein	meristem	0 h
HORVU.MOREX.r3.5HG0425000.1	-2.988900341	-0.918831697	-4.572067762	2.93E-05	0.021493761	1.7831053	Transposon protein, putative, Pong sub-class	meristem	0 h
HORVU.MOREX.r3.6HG0629160.1	1.106297761	2.999097227	4.39709699	5.31E-05	0.031144818	1.768107482	Disease resistance protein RPM1	meristem	0 h
HORVU.MOREX.r3.5HG0471070.1	-0.341124774	6.510820563	-4.467849354	4.18E-05	0.026005847	1.657009205	Oxidoreductase family, NAD-binding rossmann fold protein	meristem	0 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0285150.1	1.81137796	1.826068882	4.332369067	6.60E-05	0.037637117	1.568274079	Tryptophan aminotransferase	meristem	0 h
HORVU.MOREX.r3.5HG0523890.1	-3.412504681	-2.93597984	-4.810357757	1.29E-05	0.01150114	1.432936023	Protein FAR1-RELATED SEQUENCE 5	meristem	0 h
HORVU.MOREX.r3.5HG0516660.1	0.469172516	4.126867737	4.31814388	6.93E-05	0.03840644	1.405890637	LEM3 (Ligand-effect modulator 3) family protein	meristem	0 h
HORVU.MOREX.r3.1HG0086120.1	1.215770892	4.055301306	4.292834704	7.54E-05	0.04049761	1.302483156	Histone H2B	meristem	0 h
HORVU.MOREX.r3.1HG0044150.1	0.452833383	5.220215331	4.286522696	7.70E-05	0.04049761	1.21974384	Ran-binding protein in the microtubule-organising centre protei	meristem	0 h
HORVU.MOREX.r3.6HG0572410.1	3.500578192	-1.952913174	4.559597791	3.06E-05	0.021656115	1.168643326	Peptidylprolyl isomerase	meristem	0 h
HORVU.MOREX.r3.1HG0078900.1	-2.187273592	5.8370464	-24.75184593	8.47E-31	1.74E-26	56.49450737	MATH domain-containing protein	meristem	3 h
HORVU.MOREX.r3.5HG0447830.1	-1.334440822	4.419279148	-11.27170688	1.08E-15	7.40E-12	24.95374435	Sterile alpha motif (SAM) domain-containing protein	meristem	3 h
HORVU.MOREX.r3.1HG0067040.1	-1.069173544	7.101906906	-9.224199954	1.31E-12	6.71E-09	18.53434344	NAC domain protein,	meristem	3 h
HORVU.MOREX.r3.1HG0067490.1	-6.573128045	-1.72649178	-12.83803928	6.73E-18	6.90E-14	16.21875274	Retrovirus-related Pol polyprotein from transposon TNT 1-94	meristem	3 h
HORVU.MOREX.r3.3HG0280700.1	0.560771909	6.27769849	7.448451638	8.55E-10	2.51E-06	12.22075425	Katanin p60 ATPase-containing subunit A1	meristem	3 h
HORVU.MOREX.r3.7HG0727570.1	4.484418745	-0.569333422	8.255716277	4.37E-11	1.79E-07	10.36056584	ATP-dependent RNA helicase, putative	meristem	3 h
HORVU.MOREX.r3.1HG0026900.1	-1.674423898	1.690413985	-6.954094546	5.34E-09	1.37E-05	9.851473109	Protein apaG	meristem	3 h
HORVU.MOREX.r3.7HG0695920.1	1.514843807	2.660691655	6.691892865	1.41E-08	2.90E-05	9.395962711	#N/A	meristem	3 h
HORVU.MOREX.r3.2HG0111680.1	-4.821699509	-2.082427636	-8.067416399	8.72E-11	2.98E-07	8.043258442	Formate--tetrahydrofolate ligase	meristem	3 h
HORVU.MOREX.r3.6HG0559680.1	-3.65460718	0.573580493	-6.282987397	6.39E-08	0.000119268	6.464081395	NADPH:quinone oxidoreductase	meristem	3 h
HORVU.MOREX.r3.5HG0523880.1	-4.815067675	-2.522148569	-6.832129409	8.39E-09	1.91E-05	5.582442447	cryptochrome-interacting basic-helix-loop-helix 5	meristem	3 h
HORVU.MOREX.r3.1HG0067030.1	-0.763654599	5.504670742	-5.422627172	1.47E-06	0.0020168	5.073605184	Protein trichome birefringence	meristem	3 h
HORVU.MOREX.r3.7HG0739910.1	0.701562223	4.210713917	5.199965078	3.27E-06	0.003728078	4.342699681	Disease resistance protein (NBS-LRR class) family	meristem	3 h
HORVU.MOREX.r3.6HG0546230.1	5.188005922	-1.679648171	6.199783949	8.69E-08	0.00014853	4.258821364	Disease resistance protein RPM1	meristem	3 h
HORVU.MOREX.r3.2HG0170640.1	3.199505282	-0.509068665	5.440581317	1.38E-06	0.0020168	4.126352675	Protein FAR1-RELATED SEQUENCE 5	meristem	3 h
HORVU.MOREX.r3.5HG0478990.1	-1.133688844	3.637153099	-5.000159182	6.63E-06	0.006806588	3.710624046	Kinase family protein	meristem	3 h
HORVU.MOREX.r3.5HG0471070.1	-0.380360853	6.510820563	-4.985255031	6.99E-06	0.006831523	3.4600243	Oxidoreductase family, NAD-binding rossmann fold protein	meristem	3 h
HORVU.MOREX.r3.1HG0011440.1	-2.584902877	-1.581106574	-5.172151125	3.61E-06	0.003899108	3.1456579	Glucan endo-1,3-beta-glucosidase, putative	meristem	3 h
HORVU.MOREX.r3.3HG0223920.1	3.476345648	-2.112939632	5.271772231	2.53E-06	0.003055756	3.102856736	E3 ubiquitin-protein ligase	meristem	3 h
HORVU.MOREX.r3.1HG0049550.1	0.508661675	3.543555344	4.632014235	2.39E-05	0.022275341	2.525616419	Protein BPS1, chloroplastic	meristem	3 h
HORVU.MOREX.r3.1HG0007570.1	-3.409555231	-2.580123327	-5.463055643	1.27E-06	0.002011957	2.396128103	Werner Syndrome-like exonuclease	meristem	3 h
HORVU.MOREX.r3.5HG0523890.1	-3.678873668	-2.93597984	-5.318514045	2.14E-06	0.00274703	2.157912709	Protein FAR1-RELATED SEQUENCE 5	meristem	3 h
HORVU.MOREX.r3.1HG0017480.1	2.554456701	0.957708265	4.515443616	3.56E-05	0.031742252	2.129593347	Peroxidase	meristem	3 h
HORVU.MOREX.r3.6HG0559690.1	1.063940877	2.590055839	4.435813166	4.66E-05	0.038260777	1.932199372	Cell division cycle 5-like protein	meristem	3 h
HORVU.MOREX.r3.5HG0425000.1	-2.937718782	-0.918831697	-4.493478279	3.83E-05	0.032778993	1.348701347	Transposon protein, putative, Pong sub-class	meristem	3 h
HORVU.MOREX.r3.1HG0078900.1	-2.227245044	5.8370464	-25.10525122	4.23E-31	8.69E-27	58.88620202	MATH domain-containing protein	meristem	6 h
HORVU.MOREX.r3.1HG0067040.1	-1.236115214	7.101906906	-10.63411971	9.35E-15	6.40E-11	23.36988965	NAC domain protein,	meristem	6 h
HORVU.MOREX.r3.5HG0447830.1	-1.175827184	4.419279148	-10.00606528	8.22E-14	4.21E-10	21.19439009	Sterile alpha motif (SAM) domain-containing protein	meristem	6 h
HORVU.MOREX.r3.1HG0067490.1	-6.610847604	-1.72649178	-12.85971473	6.29E-18	6.45E-14	20.65873986	Retrovirus-related Pol polyprotein from transposon TNT 1-94	meristem	6 h
HORVU.MOREX.r3.3HG0280700.1	0.613176273	6.27769849	8.081329267	8.29E-11	2.83E-07	14.42197547	Katanin p60 ATPase-containing subunit A1	meristem	6 h
HORVU.MOREX.r3.1HG0067030.1	-1.085004777	5.504670742	-7.643174947	4.16E-10	1.07E-06	12.90352646	Protein trichome birefringence	meristem	6 h
HORVU.MOREX.r3.7HG0727570.1	5.25170781	-0.569333422	8.180207516	5.76E-11	2.37E-07	11.02020211	ATP-dependent RNA helicase, putative	meristem	6 h
HORVU.MOREX.r3.2HG0111680.1	-4.83556055	-2.082427636	-8.020814481	1.03E-10	3.03E-07	10.21321374	Formate--tetrahydrofolate ligase	meristem	6 h
HORVU.MOREX.r3.7HG0695920.1	1.595960863	2.660691655	6.642378699	1.69E-08	3.86E-05	9.344165472	#N/A	meristem	6 h
HORVU.MOREX.r3.5HG0471070.1	-0.472783869	6.510820563	-6.131912256	1.11E-07	0.000228773	7.311705316	Oxidoreductase family, NAD-binding rossmann fold protein	meristem	6 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.6HG0559680.1	-2.917450981	0.573580493	-5.446020584	1.36E-06	0.002139234	4.907623967	NADPH:quinone oxidoreductase	meristem	6 h
HORVU.MOREX.r3.6HG0559690.1	1.387729973	2.590055839	5.2743685	2.51E-06	0.003107881	4.626466926	Cell division cycle 5-like protein	meristem	6 h
HORVU.MOREX.r3.6HG0546230.1	4.655478069	-1.679648171	5.719925291	5.03E-07	0.000860158	4.586915689	Disease resistance protein RPM1	meristem	6 h
HORVU.MOREX.r3.5HG0523880.1	-4.184534518	-2.522148569	-5.740752464	4.66E-07	0.000860158	4.399657341	cryptochrome-interacting basic-helix-loop-helix 5	meristem	6 h
HORVU.MOREX.r3.7HG0739910.1	0.730435435	4.210713917	5.220261438	3.04E-06	0.003468143	4.302367512	Disease resistance protein (NBS-LRR class) family	meristem	6 h
HORVU.MOREX.r3.1HG0026900.1	-1.267020115	1.690413985	-5.148713981	3.92E-06	0.004025705	4.20242939	Protein apaG	meristem	6 h
HORVU.MOREX.r3.1HG0011440.1	-2.707612035	-1.581106574	-5.267036101	2.57E-06	0.003107881	4.020869579	Glucan endo-1,3-beta-glucosidase, putative	meristem	6 h
HORVU.MOREX.r3.5HG0425000.1	-3.88143041	-0.918831697	-5.313227343	2.18E-06	0.003107881	3.896764527	Transposon protein, putative, Pong sub-class	meristem	6 h
HORVU.MOREX.r3.5HG0489790.1	1.870434419	-0.067483895	5.09663292	4.72E-06	0.004307903	3.862876945	SKP1-like protein 4	meristem	6 h
HORVU.MOREX.r3.2HG0170640.1	3.205760675	-0.509068665	5.158560514	3.79E-06	0.004025705	3.819457129	Protein FAR1-RELATED SEQUENCE 5	meristem	6 h
HORVU.MOREX.r3.7HG0640470.1	0.434325274	6.260306545	5.13002745	4.19E-06	0.004096809	3.781484078	WPP domain-interacting tail-anchored protein 1	meristem	6 h
HORVU.MOREX.r3.1HG0024020.1	0.696729666	5.072656773	5.090163043	4.83E-06	0.004307903	3.777962551	Heparan-alpha-glucosaminide N-acetyltransferase	meristem	6 h
HORVU.MOREX.r3.2HG0215830.1	0.967978927	2.436514446	4.9904093	6.87E-06	0.005870172	3.646293647	CsAtPR5	meristem	6 h
HORVU.MOREX.r3.3HG0220340.1	1.433547088	2.953247644	4.922847986	8.70E-06	0.007144143	3.424124614	Disease resistance protein RPM1	meristem	6 h
HORVU.MOREX.r3.1HG0007570.1	-3.340096404	-2.580123327	-5.29140569	2.36E-06	0.003107881	3.132270009	Werner Syndrome-like exonuclease	meristem	6 h
HORVU.MOREX.r3.1HG0060370.1	2.945280259	-0.902409718	4.862312934	1.08E-05	0.008489167	2.919950252	1,4-alpha-glucan branching enzyme GlgB	meristem	6 h
HORVU.MOREX.r3.6HG0629160.1	1.240259326	2.999097227	4.683304963	2.00E-05	0.01456431	2.641039924	Disease resistance protein RPM1	meristem	6 h
HORVU.MOREX.r3.2HG0178600.1	-1.55256008	0.128064074	-4.672365139	2.08E-05	0.01456431	2.624451379	auxin canalization protein (DUF828)	meristem	6 h
HORVU.MOREX.r3.2HG0165670.1	-2.846409734	0.059715459	-4.795387704	1.36E-05	0.010320737	2.267923637	Cytochrome P450	meristem	6 h
HORVU.MOREX.r3.4HG0343330.1	5.692113458	-0.333480115	4.665379318	2.13E-05	0.01456431	2.156336471	Endonuclease III homolog	meristem	6 h
HORVU.MOREX.r3.5HG0502990.1	4.234823953	3.237955153	4.428004351	4.79E-05	0.029760706	1.902041287	NAC domain protein,	meristem	6 h
HORVU.MOREX.r3.6HG0614470.2	-1.516668008	0.971508223	-4.410237313	5.08E-05	0.03067127	1.849982946	Beta-xylosidase, putative	meristem	6 h
HORVU.MOREX.r3.2HG0120320.1	-2.228314567	1.685244219	-4.386755463	5.50E-05	0.032248892	1.768206866	Peroxidase	meristem	6 h
HORVU.MOREX.r3.2HG0181120.1	-2.430420067	-0.308323987	-4.475133889	4.08E-05	0.02700808	1.732342873	CheY-like two-component responsive regulator family protein	meristem	6 h
HORVU.MOREX.r3.2HG0190780.1	-2.941339907	0.027076117	-4.457271067	4.33E-05	0.027797407	1.515180368	Lectin protein kinase family protein	meristem	6 h
HORVU.MOREX.r3.1HG0046230.1	-1.800046565	-0.059533313	-4.325177321	6.76E-05	0.037512763	1.41805808	Chloroplast inner envelope protein, putative, expressed	meristem	6 h
HORVU.MOREX.r3.7HG0738460.1	-1.714850255	2.451203072	-4.281371669	7.83E-05	0.042283677	1.335424861	Cortical cell-delineating protein	meristem	6 h
HORVU.MOREX.r3.4HG0407340.1	-1.451619444	4.417710977	-4.358560748	6.05E-05	0.034471281	1.231992455	Receptor-like protein kinase	meristem	6 h
HORVU.MOREX.r3.3HG0297940.1	0.942706379	3.507795484	4.207508857	0.0001	0.049839617	1.060080699	Transcription initiation factor TFIID subunit 9	meristem	6 h
HORVU.MOREX.r3.7HG0723600.1	-1.780246331	3.100437987	-4.201762404	0.0001	0.049839617	0.986151857	Peroxidase	meristem	6 h
HORVU.MOREX.r3.6HG0615550.1	-0.520631395	6.486073771	-4.225619412	9.43E-05	0.049593927	0.764136131	Auxin efflux carrier component	meristem	6 h
HORVU.MOREX.r3.2HG0136150.1	3.558062051	-1.262543021	4.21427047	9.79E-05	0.049839617	0.751063599	Cyclin family protein	meristem	6 h
HORVU.MOREX.r3.1HG0078900.1	-2.356943162	5.8370464	-26.67159165	2.16E-32	4.42E-28	61.18748575	MATH domain-containing protein	meristem	12 h
HORVU.MOREX.r3.5HG0447830.1	-1.323993218	4.419279148	-11.57068945	4.00E-16	2.74E-12	26.28868029	Sterile alpha motif (SAM) domain-containing protein	meristem	12 h
HORVU.MOREX.r3.1HG0067040.1	-1.166006839	7.101906906	-10.21502612	3.97E-14	2.03E-10	21.9504842	NAC domain protein,	meristem	12 h
HORVU.MOREX.r3.1HG0067490.1	-6.64671345	-1.72649178	-12.99379168	4.13E-18	4.24E-14	20.05467657	Retrovirus-related Pol polyprotein from transposon TNT 1-94	meristem	12 h
HORVU.MOREX.r3.3HG0280700.1	0.604546298	6.27769849	8.150181955	6.44E-11	2.20E-07	14.68533822	Katanin p60 ATPase-containing subunit A1	meristem	12 h
HORVU.MOREX.r3.2HG0111680.1	-5.098858127	-2.082427636	-8.602040897	1.24E-11	5.07E-08	11.21508203	Formate--tetrahydrofolate ligase	meristem	12 h
HORVU.MOREX.r3.7HG0727570.1	4.174950339	-0.569333422	7.805185343	2.29E-10	6.71E-07	10.88033053	ATP-dependent RNA helicase, putative	meristem	12 h
HORVU.MOREX.r3.7HG0695920.1	1.622784768	2.660691655	6.878807223	7.06E-09	1.81E-05	10.15654296	#N/A	meristem	12 h
HORVU.MOREX.r3.1HG0067030.1	-0.862966737	5.504670742	-6.333594859	5.31E-08	9.90E-05	8.17836392	Protein trichome birefringence	meristem	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.6HG0546230.1	5.459334402	-1.679648171	6.842051948	8.09E-09	1.84E-05	7.30519672	Disease resistance protein RPM1	meristem	12 h
HORVU.MOREX.r3.3HG0260130.1	-1.599399816	3.376690694	-5.928102502	2.35E-07	0.000371577	6.843899026	Metal transporter, putative	meristem	12 h
HORVU.MOREX.r3.5HG0523880.1	-4.722789843	-2.522148569	-6.676633239	1.49E-08	3.06E-05	6.601525934	cryptochrome-interacting basic-helix-loop-helix 5	meristem	12 h
HORVU.MOREX.r3.6HG0559680.1	-3.215558858	0.573580493	-5.997855654	1.82E-07	0.000311814	6.518765098	NADPH:quinone oxidoreductase	meristem	12 h
HORVU.MOREX.r3.5HG0471070.1	-0.401247133	6.510820563	-5.297305196	2.31E-06	0.002943382	4.376261495	Oxidoreductase family, NAD-binding rossmann fold protein	meristem	12 h
HORVU.MOREX.r3.7HG0739910.1	0.71406699	4.210713917	5.233952919	2.90E-06	0.003302976	4.367441517	Disease resistance protein (NBS-LRR class) family	meristem	12 h
HORVU.MOREX.r3.5HG0425000.1	-4.319248879	-0.918831697	-5.574245672	8.53E-07	0.001250572	4.252879251	Transposon protein, putative, Pong sub-class	meristem	12 h
HORVU.MOREX.r3.3HG0297940.1	1.129542517	3.507795484	5.055647179	5.46E-06	0.005597007	3.846979247	Transcription initiation factor TFIID subunit 9	meristem	12 h
HORVU.MOREX.r3.1HG0067420.1	2.325264852	2.43369759	5.022866059	6.12E-06	0.005984115	3.7959806	Cyclic nucleotide-gated channel	meristem	12 h
HORVU.MOREX.r3.1HG0060370.1	3.279898541	-0.902409718	5.21807718	3.07E-06	0.003311276	3.762431345	1,4-alpha-glucan branching enzyme GlgB	meristem	12 h
HORVU.MOREX.r3.1HG0026900.1	-1.154634422	1.690413985	-4.945755063	8.03E-06	0.007166009	3.543833674	Protein apaG	meristem	12 h
HORVU.MOREX.r3.3HG0223800.1	2.63548691	-2.080959444	5.419661895	1.49E-06	0.002038419	3.527682514	E3 ubiquitin-protein ligase	meristem	12 h
HORVU.MOREX.r3.2HG0109620.1	-2.445135025	0.349033917	-4.967114766	7.45E-06	0.006950404	3.274846815	Retrotransposon protein, putative, Ty3-gypsy subclass	meristem	12 h
HORVU.MOREX.r3.5HG0523890.1	-3.65555498	-2.93597984	-5.282259871	2.44E-06	0.002943382	2.982928747	Protein FAR1-RELATED SEQUENCE 5	meristem	12 h
HORVU.MOREX.r3.5HG0502990.1	4.493857223	3.237955153	4.643211834	2.30E-05	0.018862338	2.580120455	NAC domain protein,	meristem	12 h
HORVU.MOREX.r3.6HG0559690.1	1.138810387	2.590055839	4.5844711	2.81E-05	0.021363852	2.362103233	Cell division cycle 5-like protein	meristem	12 h
HORVU.MOREX.r3.1HG0086120.1	1.367385604	4.055301306	4.631457791	2.39E-05	0.018884426	2.355806089	Histone H2B	meristem	12 h
HORVU.MOREX.r3.3HG0220340.1	1.363613788	2.953247644	4.472439375	4.12E-05	0.030176366	2.000332721	Disease resistance protein RPM1	meristem	12 h
HORVU.MOREX.r3.5HG0455140.1	3.789572114	-2.159476557	4.677506067	2.04E-05	0.017460482	1.503725036	tRNA (guanine(37)-N1)-methyltransferase	meristem	12 h
HORVU.MOREX.r3.4HG0343330.1	5.520532154	-0.333480115	4.432941053	4.71E-05	0.03330527	1.401491537	Endonuclease III homolog	meristem	12 h
HORVU.MOREX.r3.1HG0078900.1	-2.422614082	5.8370464	-28.51895383	7.77E-34	1.59E-29	64.98084387	MATH domain-containing protein	elongation zone	0 h
HORVU.MOREX.r3.5HG0447830.1	-1.739209628	4.419279148	-15.07217186	8.24E-21	8.45E-17	36.70962545	Sterile alpha motif (SAM) domain-containing protein	elongation zone	0 h
HORVU.MOREX.r3.1HG0067040.1	-1.148278282	7.101906906	-10.76607327	5.96E-15	3.62E-11	23.78021089	NAC domain protein,	elongation zone	0 h
HORVU.MOREX.r3.3HG0280700.1	0.77344826	6.27769849	10.71690425	7.05E-15	3.62E-11	23.64510567	Katanin p60 ATPase-containing subunit A1	elongation zone	0 h
HORVU.MOREX.r3.6HG0546230.1	5.587987042	-1.679648171	10.1529121	4.92E-14	2.02E-10	19.114336	Disease resistance protein RPM1	elongation zone	0 h
HORVU.MOREX.r3.1HG0070480.1	-0.999693512	6.291080843	-9.110723368	1.96E-12	5.76E-09	18.09361735	60 kDa chaperonin	elongation zone	0 h
HORVU.MOREX.r3.2HG0111680.1	-5.827259149	-2.082427636	-10.01921086	7.85E-14	2.68E-10	15.56820658	Formate--tetrahydrofolate ligase	elongation zone	0 h
HORVU.MOREX.r3.7HG0739910.1	0.970181061	4.210713917	7.839195746	2.02E-10	4.60E-07	13.59220078	Disease resistance protein (NBS-LRR class) family	elongation zone	0 h
HORVU.MOREX.r3.7HG0727570.1	4.344454469	-0.569333422	8.018617137	1.04E-10	2.68E-07	11.99875711	ATP-dependent RNA helicase, putative	elongation zone	0 h
HORVU.MOREX.r3.1HG0067420.1	2.113663726	2.43369759	7.255677299	1.75E-09	3.26E-06	11.49215906	Cyclic nucleotide-gated channel	elongation zone	0 h
HORVU.MOREX.r3.1HG0024020.1	0.881576746	5.072656773	6.611655844	1.90E-08	3.00E-05	9.126149482	Heparan-alpha-glucosaminide N-acetyltransferase	elongation zone	0 h
HORVU.MOREX.r3.1HG0067490.1	-4.109176405	-1.72649178	-7.351158696	1.23E-09	2.52E-06	8.734196801	Retrovirus-related Pol polyprotein from transposon TNT 1-94	elongation zone	0 h
HORVU.MOREX.r3.7HG0729150.1	-4.08685209	-2.071842766	-6.486030244	3.02E-08	4.43E-05	8.273992271	GDSL esterase/lipase	elongation zone	0 h
HORVU.MOREX.r3.1HG0067030.1	-0.70170823	5.504670742	-6.244083069	7.38E-08	0.000100942	7.671149471	Protein trichome birefringence	elongation zone	0 h
HORVU.MOREX.r3.1HG0007570.1	-4.176564388	-2.580123327	-6.871743302	7.25E-09	1.24E-05	7.532448969	Werner Syndrome-like exonuclease	elongation zone	0 h
HORVU.MOREX.r3.3HG0298020.1	1.559034982	3.677613517	6.089064833	1.30E-07	0.000167358	7.414162165	Transcription initiation factor TFIID subunit 9	elongation zone	0 h
HORVU.MOREX.r3.7HG0695920.1	1.655379288	2.660691655	5.881841045	2.79E-07	0.000336506	6.682821932	#N/A	elongation zone	0 h
HORVU.MOREX.r3.3HG0297940.1	1.681302659	3.507795484	5.84300731	3.21E-07	0.000366232	6.560477311	Transcription initiation factor TFIID subunit 9	elongation zone	0 h
HORVU.MOREX.r3.6HG0559680.1	-2.825403355	0.573580493	-5.537876655	9.73E-07	0.000998411	5.316461587	NADPH:quinone oxidoreductase	elongation zone	0 h
HORVU.MOREX.r3.1HG0011440.1	-2.432512003	-1.581106574	-5.503821648	1.10E-06	0.001075269	5.078537785	Glucan endo-1,3-beta-glucosidase, putative	elongation zone	0 h
HORVU.MOREX.r3.1HG0069040.1	2.736631601	0.814092704	5.552625688	9.23E-07	0.00099641	4.913083956	#N/A	elongation zone	0 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0026900.1	-1.537272869	1.690413985	-5.372606052	1.76E-06	0.001645764	4.894176493	Protein apaG	elongation zone	0 h
HORVU.MOREX.r3.7HG0713840.1	-1.729173965	-2.185081282	-5.323087466	2.11E-06	0.001879945	4.67913266	Cytochrome P450	elongation zone	0 h
HORVU.MOREX.r3.5HG0471070.1	-0.38511	6.510820563	-5.270083685	2.55E-06	0.002177587	4.16886943	Oxidoreductase family, NAD-binding rossmann fold protein	elongation zone	0 h
HORVU.MOREX.r3.1HG0008190.1	-2.015856807	-0.63381752	-5.145343793	3.97E-06	0.00325932	4.153817343	Cytochrome P450	elongation zone	0 h
HORVU.MOREX.r3.1HG0070000.1	1.18351875	1.808570831	4.968347796	7.42E-06	0.005728582	3.617173342	Histone H3	elongation zone	0 h
HORVU.MOREX.r3.5HG0456970.1	0.756861983	5.8820687	4.963852047	7.54E-06	0.005728582	3.297343114	Methylthioribose-1-phosphate isomerase	elongation zone	0 h
HORVU.MOREX.r3.5HG0502990.1	3.613022113	3.237955153	4.833050057	1.19E-05	0.008428702	3.110484948	NAC domain protein,	elongation zone	0 h
HORVU.MOREX.r3.5HG0425000.1	-3.369231289	-0.918831697	-4.879950122	1.01E-05	0.007411861	2.902544643	Transposon protein, putative, Pong sub-class	elongation zone	0 h
HORVU.MOREX.r3.7HG0642740.1	0.566304994	4.413737834	4.684904102	1.99E-05	0.013616628	2.478305116	SET domain-containing protein	elongation zone	0 h
HORVU.MOREX.r3.1HG0049550.1	0.507585192	3.543555344	4.647304544	2.27E-05	0.014999	2.433088554	Protein BPS1, chloroplastic	elongation zone	0 h
HORVU.MOREX.r3.1HG0070730.1	-1.966552983	-0.4130893	-4.569639661	2.96E-05	0.018963815	2.338886368	Glycosyltransferase	elongation zone	0 h
HORVU.MOREX.r3.6HG0559690.1	1.26091266	2.590055839	4.547933073	3.18E-05	0.019804371	2.2461328	Cell division cycle 5-like protein	elongation zone	0 h
HORVU.MOREX.r3.2HG0170640.1	2.884435418	-0.509068665	4.513814427	3.58E-05	0.021592098	1.979093494	Protein FAR1-RELATED SEQUENCE 5	elongation zone	0 h
HORVU.MOREX.r3.2HG0215830.1	1.269991868	2.436514446	4.389339633	5.45E-05	0.028690561	1.792378738	CsAtPR5	elongation zone	0 h
HORVU.MOREX.r3.1HG0070100.1	-0.529189266	4.109158355	-4.442367971	4.56E-05	0.025670408	1.660912197	Prolyl 4-hydroxylase alpha subunit, putative	elongation zone	0 h
HORVU.MOREX.r3.1HG0086120.1	1.87007834	4.055301306	4.352790109	6.17E-05	0.031631148	1.604095686	Histone H2B	elongation zone	0 h
HORVU.MOREX.r3.7HG0672900.1	2.368462875	0.425915719	4.410644072	5.08E-05	0.027405079	1.569048605	Pentatricopeptide repeat-containing protein	elongation zone	0 h
HORVU.MOREX.r3.5HG0462380.1	-0.804499194	3.998698155	-4.43789627	4.63E-05	0.025670408	1.558859351	LYR family of Fe/S cluster biogenesis protein	elongation zone	0 h
HORVU.MOREX.r3.3HG0222160.1	1.645322602	-1.846318567	4.264610651	8.28E-05	0.040454234	1.415475584	Nuclease S1	elongation zone	0 h
HORVU.MOREX.r3.UnG0765280.1	1.461373095	2.589811572	4.211707084	9.87E-05	0.045010155	1.249952442	F-box family protein	elongation zone	0 h
HORVU.MOREX.r3.5HG0485410.1	2.807732376	-0.444670009	4.448551505	4.46E-05	0.025670408	1.23452293	#N/A	elongation zone	0 h
HORVU.MOREX.r3.1HG0069380.1	-1.252691628	2.129642878	-4.222105907	9.54E-05	0.044473516	1.102014108	Cysteine proteinase inhibitor	elongation zone	0 h
HORVU.MOREX.r3.1HG0068410.1	-0.396632513	4.707522572	-4.227371005	9.37E-05	0.044473516	0.901219617	E3 ubiquitin-protein ligase	elongation zone	0 h
HORVU.MOREX.r3.7HG0640470.1	0.360908747	6.260306545	4.268354115	8.18E-05	0.040454234	0.863727652	WPP domain-interacting tail-anchored protein 1	elongation zone	0 h
HORVU.MOREX.r3.1HG0078900.1	-2.367787064	5.8370464	-27.16858464	8.65E-33	1.78E-28	61.4975963	MATH domain-containing protein	elongation zone	3 h
HORVU.MOREX.r3.3HG0280700.1	0.955350063	6.27769849	13.06592538	3.30E-18	3.38E-14	31.11992727	Katanin p60 ATPase-containing subunit A1	elongation zone	3 h
HORVU.MOREX.r3.5HG0447830.1	-1.385731994	4.419279148	-12.00606175	9.61E-17	6.57E-13	27.52191979	Sterile alpha motif (SAM) domain-containing protein	elongation zone	3 h
HORVU.MOREX.r3.1HG0070480.1	-1.055905972	6.291080843	-9.525129096	4.47E-13	1.84E-09	19.58432076	60 kDa chaperonin	elongation zone	3 h
HORVU.MOREX.r3.6HG0546230.1	8.223902991	-1.679648171	10.89599429	3.83E-15	1.97E-11	16.04555447	Disease resistance protein RPM1	elongation zone	3 h
HORVU.MOREX.r3.7HG0739910.1	1.058388899	4.210713917	8.463391419	2.05E-11	6.00E-08	15.84797849	Disease resistance protein (NBS-LRR class) family	elongation zone	3 h
HORVU.MOREX.r3.1HG0067040.1	-0.860334376	7.101906906	-8.072437153	8.56E-11	2.20E-07	14.37828129	NAC domain protein,	elongation zone	3 h
HORVU.MOREX.r3.1HG0024020.1	1.007859267	5.072656773	7.548999833	5.90E-10	1.10E-06	12.58535786	Heparan-alpha-glucosaminide N-acetyltransferase	elongation zone	3 h
HORVU.MOREX.r3.7HG0727570.1	4.507550537	-0.569333422	8.57418003	1.37E-11	4.67E-08	12.4573334	ATP-dependent RNA helicase, putative	elongation zone	3 h
HORVU.MOREX.r3.7HG0729150.1	-4.941180132	-2.071842766	-7.64021831	4.21E-10	8.64E-07	11.13257623	GDSL esterase/lipase	elongation zone	3 h
HORVU.MOREX.r3.2HG0111680.1	-4.589353007	-2.082427636	-7.886653376	1.70E-10	3.87E-07	9.094847114	Formate--tetrahydrofolate ligase	elongation zone	3 h
HORVU.MOREX.r3.7HG0640470.1	0.528792269	6.260306545	6.249446952	7.23E-08	0.000114194	7.835006347	WPP domain-interacting tail-anchored protein 1	elongation zone	3 h
HORVU.MOREX.r3.1HG0070000.1	1.471763849	1.808570831	6.201305183	8.64E-08	0.000126601	7.523035759	Histone H3	elongation zone	3 h
HORVU.MOREX.r3.1HG0067030.1	-0.681642754	5.504670742	-6.029899435	1.62E-07	0.000221804	7.029741265	Protein trichome birefringence	elongation zone	3 h
HORVU.MOREX.r3.1HG0067420.1	1.693409973	2.43369759	5.992921729	1.86E-07	0.000229369	7.013538098	Cyclic nucleotide-gated channel	elongation zone	3 h
HORVU.MOREX.r3.6HG0559690.1	1.701878582	2.590055839	5.986602932	1.90E-07	0.000229369	6.968088164	Cell division cycle 5-like protein	elongation zone	3 h
HORVU.MOREX.r3.1HG0067490.1	-3.871019017	-1.72649178	-6.885558721	6.89E-09	1.18E-05	6.35207369	Retrovirus-related Pol polyprotein from transposon TNT 1-94	elongation zone	3 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0069380.1	-1.723970494	2.129642878	-5.596127384	7.88E-07	0.000851314	5.714386819	Cysteine proteinase inhibitor	elongation zone	3 h
HORVU.MOREX.r3.6HG0559680.1	-3.241273008	0.573580493	-5.695060318	5.51E-07	0.000627676	5.288905706	NADPH:quinone oxidoreductase	elongation zone	3 h
HORVU.MOREX.r3.1HG0049550.1	0.553787039	3.543555344	5.202462527	3.24E-06	0.002994663	4.358235879	Protein BPS1, chloroplastic	elongation zone	3 h
HORVU.MOREX.r3.5HG0502990.1	3.912615301	3.237955153	5.192641224	3.36E-06	0.002994663	4.356523379	NAC domain protein,	elongation zone	3 h
HORVU.MOREX.r3.2HG0216110.1	0.462249853	5.350102781	5.139171845	4.06E-06	0.003470302	4.004733356	#N/A	elongation zone	3 h
HORVU.MOREX.r3.1HG0011440.1	-2.859919008	-1.581106574	-5.341069817	1.98E-06	0.001930552	3.787414724	Glucan endo-1,3-beta-glucosidase, putative	elongation zone	3 h
HORVU.MOREX.r3.5HG0471070.1	-0.36625879	6.510820563	-4.929120818	8.51E-06	0.006471105	3.155351816	Oxidoreductase family, NAD-binding rossmann fold protein	elongation zone	3 h
HORVU.MOREX.r3.1HG0007570.1	-3.437776806	-2.580123327	-5.489837761	1.16E-06	0.001187441	3.075820548	Werner Syndrome-like exonuclease	elongation zone	3 h
HORVU.MOREX.r3.1HG0008190.1	-1.885579918	-0.63381752	-4.751862413	1.58E-05	0.011175626	2.805536576	Cytochrome P450	elongation zone	3 h
HORVU.MOREX.r3.3HG0297940.1	1.409703042	3.507795484	4.699491836	1.89E-05	0.012530555	2.75751099	Transcription initiation factor TFIID subunit 9	elongation zone	3 h
HORVU.MOREX.r3.4HG0344830.1	0.618537725	4.535567699	4.732773499	1.69E-05	0.011541293	2.685874488	NBS-LRR disease resistance protein, putative, expressed	elongation zone	3 h
HORVU.MOREX.r3.2HG0170640.1	3.7419642	-0.509068665	4.987331845	6.94E-06	0.005477606	2.614080447	Protein FAR1-RELATED SEQUENCE 5	elongation zone	3 h
HORVU.MOREX.r3.1HG0069030.1	-2.774203235	1.480380355	-4.650823875	2.24E-05	0.014355463	2.553387438	Calcium-transporting ATPase	elongation zone	3 h
HORVU.MOREX.r3.2HG0131630.1	-3.211907792	-3.028166822	-4.765991826	1.50E-05	0.011021467	2.482398226	vacuolar sorting-associated protein (DUF946)	elongation zone	3 h
HORVU.MOREX.r3.6HG0581570.1	0.473463599	4.929735327	4.619585589	2.49E-05	0.015497632	2.320262592	Leucine-rich repeat-containing protein 1	elongation zone	3 h
HORVU.MOREX.r3.5HG0516660.1	0.484063951	4.126867737	4.578655188	2.87E-05	0.017306414	2.213175948	LEM3 (Ligand-effect modulator 3) family protein	elongation zone	3 h
HORVU.MOREX.r3.3HG0283300.1	0.864415145	2.473566507	4.516716492	3.54E-05	0.02076901	2.177606725	Farnesyl diphosphate synthase	elongation zone	3 h
HORVU.MOREX.r3.4HG0408780.1	3.311828691	0.649042183	5.099689871	4.67E-06	0.003831858	2.138941056	Pentatricopeptide repeat-containing protein	elongation zone	3 h
HORVU.MOREX.r3.1HG0026900.1	-1.314590096	1.690413985	-4.426931743	4.80E-05	0.025938662	1.834003757	Protein apaG	elongation zone	3 h
HORVU.MOREX.r3.2HG0101220.2	0.715197686	2.581198545	4.352859232	6.16E-05	0.030465058	1.641381682	Formin-like protein	elongation zone	3 h
HORVU.MOREX.r3.3HG0298020.1	1.093419967	3.677613517	4.31722943	6.95E-05	0.0323953	1.543507182	Transcription initiation factor TFIID subunit 9	elongation zone	3 h
HORVU.MOREX.r3.1HG0068410.1	-0.417149359	4.707522572	-4.376301115	5.70E-05	0.029977701	1.525312309	E3 ubiquitin-protein ligase	elongation zone	3 h
HORVU.MOREX.r3.5HG0490030.1	0.303902563	7.481265074	4.481675984	3.99E-05	0.022746333	1.521349586	Vacuolar protein sorting-associated protein 52	elongation zone	3 h
HORVU.MOREX.r3.4HG0413690.1	0.622272005	4.40336351	4.337224121	6.50E-05	0.03100158	1.470809108	26S proteasome non-ATPase regulatory subunit-like protein	elongation zone	3 h
HORVU.MOREX.r3.7HG0695920.1	1.148034454	2.660691655	4.277746903	7.93E-05	0.036140397	1.449527232	#N/A	elongation zone	3 h
HORVU.MOREX.r3.1HG0044150.1	0.429249479	5.220215331	4.349444765	6.24E-05	0.030465058	1.356020546	Ran-binding protein in the microtubule-organising centre protei	elongation zone	3 h
HORVU.MOREX.r3.7HG0635110.1	1.280557244	1.994165679	4.222670585	9.52E-05	0.042056332	1.289237533	NBS-LRR-like resistance protein	elongation zone	3 h
HORVU.MOREX.r3.4HG0374910.2	0.345737887	6.337717806	4.368329306	5.85E-05	0.030022376	1.278032186	Beta-adaptin-like protein	elongation zone	3 h
HORVU.MOREX.r3.5HG0515610.1	-2.401569095	-3.366672775	-4.44048086	4.59E-05	0.025446978	1.107059229	Collagen alpha chain	elongation zone	3 h
HORVU.MOREX.r3.5HG0443920.1	0.579301829	3.840341821	4.161039685	0.00012	0.048870078	0.940454887	Calmodulin-binding protein, putative, expressed	elongation zone	3 h
HORVU.MOREX.r3.7HG0685870.1	0.282506125	7.40990073	4.219067623	9.63E-05	0.042056332	0.714242914	Ankyrin repeat domain containing protein	elongation zone	3 h
HORVU.MOREX.r3.3HG0309270.1	0.357546443	8.53260482	4.179899551	0.00011	0.04687848	0.561145832	Proline--tRNA ligase	elongation zone	3 h
HORVU.MOREX.r3.1HG0078900.1	-2.455370206	5.8370464	-28.11453467	1.58E-33	3.25E-29	63.65412911	MATH domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0447830.1	-1.690771799	4.419279148	-14.01906786	1.80E-19	1.84E-15	33.53649068	Sterile alpha motif (SAM) domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0280700.1	0.95254549	6.27769849	12.9611432	4.57E-18	3.13E-14	30.85679699	Katanin p60 ATPase-containing subunit A1	elongation zone	6 h
HORVU.MOREX.r3.1HG0070480.1	-1.174994142	6.291080843	-10.68035051	7.98E-15	3.28E-11	23.53342025	60 kDa chaperonin	elongation zone	6 h
HORVU.MOREX.r3.6HG0546230.1	6.651659642	-1.679648171	10.71297343	7.14E-15	3.28E-11	18.94302896	Disease resistance protein RPM1	elongation zone	6 h
HORVU.MOREX.r3.1HG0067040.1	-0.981175584	7.101906906	-9.180873495	1.53E-12	5.22E-09	18.31447218	NAC domain protein,	elongation zone	6 h
HORVU.MOREX.r3.7HG0739910.1	1.19638186	4.210713917	9.0268823	2.66E-12	7.78E-09	17.83509786	Disease resistance protein (NBS-LRR class) family	elongation zone	6 h
HORVU.MOREX.r3.1HG0024020.1	1.079933311	5.072656773	7.891375987	1.67E-10	3.42E-07	13.80313715	Heparan-alpha-glucosaminide N-acetyltransferase	elongation zone	6 h
HORVU.MOREX.r3.7HG0729150.1	-5.192955515	-2.071842766	-7.905081967	1.58E-10	3.42E-07	12.28495143	GDSL esterase/lipase	elongation zone	6 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.7HG0727570.1	4.338282709	-0.569333422	7.775303779	2.56E-10	4.77E-07	10.67323007	ATP-dependent RNA helicase, putative	elongation zone	6 h
HORVU.MOREX.r3.3HG0297940.1	2.412350516	3.507795484	7.017407454	4.22E-09	6.67E-06	10.41416616	Transcription initiation factor TFIID subunit 9	elongation zone	6 h
HORVU.MOREX.r3.2HG0111680.1	-4.61053162	-2.082427636	-7.946881235	1.36E-10	3.42E-07	10.04730863	Formate--tetrahydrofolate ligase	elongation zone	6 h
HORVU.MOREX.r3.7HG0640470.1	0.58174285	6.260306545	6.794966612	9.63E-09	1.41E-05	9.759209171	WPP domain-interacting tail-anchored protein 1	elongation zone	6 h
HORVU.MOREX.r3.3HG0307310.1	0.614982179	5.321616586	6.774594255	1.04E-08	1.42E-05	9.723133442	magnesium transporter, putative (DUF803)	elongation zone	6 h
HORVU.MOREX.r3.1HG0069380.1	-1.763094232	2.129642878	-6.491279587	2.96E-08	3.58E-05	8.820532232	Cysteine proteinase inhibitor	elongation zone	6 h
HORVU.MOREX.r3.1HG0067030.1	-0.726019821	5.504670742	-6.539553565	2.48E-08	3.18E-05	8.794661825	Protein trichome birefringence	elongation zone	6 h
HORVU.MOREX.r3.2HG0121410.1	-2.139380697	3.844655715	-6.341546329	5.15E-08	5.87E-05	8.21376623	Cytochrome P450	elongation zone	6 h
HORVU.MOREX.r3.1HG0067490.1	-4.025300541	-1.72649178	-7.211767514	2.06E-09	3.51E-06	7.834831591	Retrovirus-related Pol polyprotein from transposon TNT 1-94	elongation zone	6 h
HORVU.MOREX.r3.1HG0067420.1	1.639056173	2.43369759	6.197460773	8.76E-08	8.99E-05	7.661526291	Cyclic nucleotide-gated channel	elongation zone	6 h
HORVU.MOREX.r3.7HG0713840.1	-1.835945375	-2.185081282	-6.139491032	1.08E-07	0.000105947	7.315556406	Cytochrome P450	elongation zone	6 h
HORVU.MOREX.r3.3HG0298020.1	1.532913962	3.677613517	5.884167085	2.76E-07	0.000246617	6.700175248	Transcription initiation factor TFIID subunit 9	elongation zone	6 h
HORVU.MOREX.r3.7HG0717610.1	-1.021543256	4.008622047	-5.780761256	4.03E-07	0.000330872	6.22234164	Pollen-specific protein SF21	elongation zone	6 h
HORVU.MOREX.r3.3HG0246300.1	-0.761004763	4.385187463	-5.749778683	4.51E-07	0.000356141	6.14000964	RNA-binding protein, putative	elongation zone	6 h
HORVU.MOREX.r3.7HG0721320.1	-2.888168968	-3.129421625	-6.054431513	1.48E-07	0.000138215	6.131854686	Auxin-responsive family protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0467870.1	-1.53632014	2.049337326	-5.669167377	6.05E-07	0.000459707	5.948759622	Kynurenine formamidase	elongation zone	6 h
HORVU.MOREX.r3.7HG0750000.1	-1.961665845	-2.120414367	-5.638396638	6.76E-07	0.000495644	5.84507816	Disease resistance protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0265690.1	2.604079702	0.540508683	5.854804527	3.08E-07	0.000263097	5.434526612	Oxidoreductase/transition metal ion-binding protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0045510.1	0.88273122	5.275918097	5.552347984	9.24E-07	0.000653476	5.43350822	Prefoldin subunit, putative	elongation zone	6 h
HORVU.MOREX.r3.1HG0007570.1	-3.810028916	-2.580123327	-6.205618112	8.50E-08	8.99E-05	5.345121288	Werner Syndrome-like exonuclease	elongation zone	6 h
HORVU.MOREX.r3.1HG0070000.1	1.31894142	1.808570831	5.450424803	1.33E-06	0.00091242	5.145583959	Histone H3	elongation zone	6 h
HORVU.MOREX.r3.6HG0576010.1	-0.862268712	4.663155786	-5.384744763	1.69E-06	0.001083225	4.915571494	Protein kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0559690.1	1.539799486	2.590055839	5.324074131	2.10E-06	0.001240485	4.789298387	Cell division cycle 5-like protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0751110.1	0.903579811	4.358148537	5.321938433	2.12E-06	0.001240485	4.686130966	Kinesin-like	elongation zone	6 h
HORVU.MOREX.r3.1HG0069030.1	-3.029787188	1.480380355	-5.297280366	2.31E-06	0.001281665	4.6572396	Calcium-transporting ATPase	elongation zone	6 h
HORVU.MOREX.r3.1HG0066800.1	-1.713700121	-2.502872481	-5.304873224	2.25E-06	0.001281665	4.648832848	Potassium channel	elongation zone	6 h
HORVU.MOREX.r3.3HG0257680.1	0.606888573	4.018531146	5.287662346	2.39E-06	0.001291596	4.58263926	GDSL esterase/lipase	elongation zone	6 h
HORVU.MOREX.r3.2HG0191490.1	-1.218138174	4.031252139	-5.271671375	2.53E-06	0.001324316	4.578022461	Protein kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0250060.1	-2.507206312	-2.506423371	-5.395287951	1.63E-06	0.001076624	4.536257979	CASP-like protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0234470.1	0.554525675	6.523252025	5.337159015	2.00E-06	0.001240485	4.492703754	Kinase interacting (KIP1-like) family protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0456970.1	0.821729809	5.8820687	5.266302155	2.58E-06	0.001324316	4.410059397	Methylthioribose-1-phosphate isomerase	elongation zone	6 h
HORVU.MOREX.r3.5HG0502990.1	4.9082101	3.237955153	5.187439488	3.42E-06	0.001670563	4.333541478	NAC domain protein,	elongation zone	6 h
HORVU.MOREX.r3.7HG0695920.1	1.447766581	2.660691655	5.173306978	3.60E-06	0.001710089	4.290523171	#N/A	elongation zone	6 h
HORVU.MOREX.r3.2HG0121570.1	0.750639648	4.65733005	5.204131254	3.22E-06	0.001612625	4.246480902	Protein LTV1	elongation zone	6 h
HORVU.MOREX.r3.1HG0003620.1	-1.057878604	2.573512603	-5.123715687	4.29E-06	0.001955112	4.073214787	Protein ZINC INDUCED FACILITATOR-LIKE 1	elongation zone	6 h
HORVU.MOREX.r3.2HG0096230.1	-1.969780166	-2.935502699	-5.16777579	3.67E-06	0.001710089	3.94862768	Phosphatidylinositol 3- and 4-kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0749460.1	0.74573892	5.222321052	5.089005984	4.85E-06	0.002125793	3.773305094	Thioredoxin	elongation zone	6 h
HORVU.MOREX.r3.6HG0549990.1	1.245683575	2.338995774	4.96765541	7.44E-06	0.002962634	3.611201186	Pentatricopeptide repeat-containing protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0472700.1	-0.583699361	4.865209235	-5.004481291	6.53E-06	0.002793246	3.532137528	Lipid phosphate phosphatase-like protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0082770.1	0.418014229	7.702552295	5.087803984	4.87E-06	0.002125793	3.527496667	Reticulon-like protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0513990.1	-1.907823345	-1.75785159	-4.99251821	6.81E-06	0.00285393	3.516572003	Nitrate transporter 1.1	elongation zone	6 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0280960.1	-1.085878314	1.80535629	-4.959397535	7.66E-06	0.002962634	3.483252383	Glycosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.7HG0636630.1	-1.615620741	-0.128553353	-4.934860399	8.34E-06	0.002991092	3.435965215	WAT1-related protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0546140.1	1.16624523	0.639454141	4.892027425	9.70E-06	0.003309051	3.373914025	F-box protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0518560.1	-2.120765461	2.148281347	-4.95423955	7.80E-06	0.002962634	3.356430992	Leucine-rich repeat protein kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0706100.1	0.454452673	5.89851201	4.964950579	7.51E-06	0.002962634	3.317552742	Survival of motor neuron-related-splicing factor 30	elongation zone	6 h
HORVU.MOREX.r3.7HG0649950.1	-0.814788896	3.836694774	-4.926479766	8.59E-06	0.002991092	3.297380017	Nudix hydrolase	elongation zone	6 h
HORVU.MOREX.r3.6HG0629160.1	1.937870345	2.999097227	4.874145492	1.03E-05	0.00335152	3.279240853	Disease resistance protein RPM1	elongation zone	6 h
HORVU.MOREX.r3.6HG0626030.1	-1.96809199	-0.562096779	-4.926270129	8.60E-06	0.002991092	3.26239866	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.3HG0278540.1	-0.579158692	6.253662754	-4.977925143	7.17E-06	0.00294416	3.261890915	Hydroxyacylglutathione hydrolase	elongation zone	6 h
HORVU.MOREX.r3.4HG0417920.1	-2.121932948	-1.699022369	-4.86825044	1.05E-05	0.00335152	3.249244029	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.1HG0068380.1	0.602322	5.314485157	4.926879574	8.58E-06	0.002991092	3.247150527	#N/A	elongation zone	6 h
HORVU.MOREX.r3.1HG0070730.1	-2.143795304	-0.4130893	-4.867084457	1.06E-05	0.00335152	3.209379901	Glycosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.2HG0217090.1	-1.775775231	-0.857487868	-4.887889031	9.84E-06	0.003309051	3.209130287	C2 calcium/lipid-binding and GRAM domain protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0010340.1	-1.651723824	-2.094132866	-4.825228968	1.22E-05	0.003693864	3.150066422	Non-specific lipid-transfer protein-like protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0302100.1	0.386270197	5.746504247	4.928421174	8.54E-06	0.002991092	3.142443404	Mannose-1-phosphate guanyltransferase 1	elongation zone	6 h
HORVU.MOREX.r3.5HG0504840.1	0.990941715	2.172085864	4.805590901	1.31E-05	0.003897807	3.092352702	transmembrane protein, putative (DUF594)	elongation zone	6 h
HORVU.MOREX.r3.7HG0748070.1	-1.973762015	-0.496958177	-4.796514172	1.35E-05	0.003955741	2.972546252	Heavy metal transport/detoxification superfamily protein, putati	elongation zone	6 h
HORVU.MOREX.r3.6HG0600000.1	-1.648680404	-0.219047099	-4.793127069	1.37E-05	0.003955741	2.891052276	Blue copper protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0680960.1	-2.642732462	0.61149754	-4.749076613	1.59E-05	0.004422113	2.884297231	electron transporter, putative (Protein of unknown function, DU	elongation zone	6 h
HORVU.MOREX.r3.5HG0468700.1	-1.511673438	1.52369506	-4.754597548	1.56E-05	0.004422113	2.874546671	#N/A	elongation zone	6 h
HORVU.MOREX.r3.3HG0270190.1	0.468703429	5.543138586	4.829850583	1.20E-05	0.003689135	2.865858569	dihydroflavonol 4-reductase/flavanone protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0207860.1	-2.002251609	-2.164021772	-4.741937003	1.63E-05	0.004446848	2.846789904	Serine/threonine-protein kinase	elongation zone	6 h
HORVU.MOREX.r3.5HG0519810.1	0.573419215	7.61792539	4.866061342	1.06E-05	0.00335152	2.776597205	Diphosphomevalonate decarboxylase	elongation zone	6 h
HORVU.MOREX.r3.5HG0532140.1	-1.781995241	-1.001133554	-4.750013417	1.59E-05	0.004422113	2.745681458	Expansin	elongation zone	6 h
HORVU.MOREX.r3.4HG0413320.1	-2.076701937	2.316272111	-4.739765317	1.65E-05	0.004446848	2.711744461	Subtilisin-like protease	elongation zone	6 h
HORVU.MOREX.r3.1HG0079800.1	0.612737305	7.794068	4.843388053	1.15E-05	0.003572457	2.670162339	Farnesyl diphosphate synthase	elongation zone	6 h
HORVU.MOREX.r3.3HG0329870.1	-1.626871202	-1.903215009	-4.679555651	2.03E-05	0.005267108	2.65195878	Pectin acetylesterase	elongation zone	6 h
HORVU.MOREX.r3.7HG0685920.1	-0.691070243	4.571683277	-4.726928497	1.72E-05	0.00458846	2.492304	Solute carrier family 35 protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0380950.1	-0.687805181	4.409828858	-4.701192657	1.88E-05	0.004950936	2.452080927	ABC(ATP-binding) family transporter	elongation zone	6 h
HORVU.MOREX.r3.7HG0634520.1	-1.65769725	-2.239871453	-4.603537684	2.63E-05	0.006432844	2.450305755	NBS-LRR-like resistance protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0034450.1	-1.866428293	0.621391691	-4.645227969	2.28E-05	0.005793016	2.407088615	Retrovirus-related Pol polyprotein from transposon TNT 1-94	elongation zone	6 h
HORVU.MOREX.r3.7HG0724080.1	1.764464637	2.23197157	4.581041349	2.84E-05	0.006612707	2.381617739	6,7-dimethyl-8-ribityllumazine synthase	elongation zone	6 h
HORVU.MOREX.r3.7HG0661290.1	-0.837154875	0.704847423	-4.633055835	2.38E-05	0.005954966	2.348395921	Inositol-tetrakisphosphate 1-kinase	elongation zone	6 h
HORVU.MOREX.r3.3HG0254260.1	-0.825521242	4.868531812	-4.644648949	2.29E-05	0.005793016	2.279995286	Kinesin, putative	elongation zone	6 h
HORVU.MOREX.r3.7HG0647950.1	-2.682472799	-1.041996542	-4.559469655	3.06E-05	0.006755938	2.255867347	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.1HG0026900.1	-1.412420154	1.690413985	-4.54195166	3.25E-05	0.006941783	2.204195351	Protein apaG	elongation zone	6 h
HORVU.MOREX.r3.1HG0038800.1	-0.796912567	2.879103431	-4.572879316	2.92E-05	0.006612707	2.187208787	Protein kinase	elongation zone	6 h
HORVU.MOREX.r3.2HG0196800.1	-2.258666615	-0.209944285	-4.540646951	3.27E-05	0.006941783	2.182634132	Multidrug resistance protein ABC transporter family	elongation zone	6 h
HORVU.MOREX.r3.4HG0408270.1	-1.422349983	-2.271186585	-4.51595474	3.55E-05	0.007361644	2.166218441	LOB domain-containing protein, putative	elongation zone	6 h
HORVU.MOREX.r3.2HG0210510.1	-1.067113774	-0.619193937	-4.573037577	2.92E-05	0.006612707	2.165181322	Rapid alkalinization factor 1	elongation zone	6 h
HORVU.MOREX.r3.1HG0068410.1	-0.43540793	4.707522572	-4.583131491	2.82E-05	0.006612707	2.124589145	E3 ubiquitin-protein ligase	elongation zone	6 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0069410.1	-1.737504924	3.463734972	-4.561018935	3.05E-05	0.006755938	2.056849284	Aldehyde dehydrogenase	elongation zone	6 h
HORVU.MOREX.r3.7HG0676040.1	-0.946662139	-0.533828415	-4.494385217	3.82E-05	0.007613546	2.052938204	Decaprenyl-phosphate N-acetylglucosaminephosphotransferase	elongation zone	6 h
HORVU.MOREX.r3.6HG0559680.1	-2.581853641	0.573580493	-4.527845665	3.41E-05	0.007141623	2.04209267	NADPH:quinone oxidoreductase	elongation zone	6 h
HORVU.MOREX.r3.4HG0393520.1	-1.081828956	3.798189813	-4.488754278	3.90E-05	0.007613546	1.957383638	Microtubule associated protein family protein, putative, express	elongation zone	6 h
HORVU.MOREX.r3.1HG0088530.1	-1.252124111	0.05264283	-4.440442789	4.59E-05	0.008407674	1.948881935	Cytochrome b561 domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0513020.1	0.430410759	6.516881897	4.58660244	2.79E-05	0.006612707	1.936110168	Transmembrane protein 147	elongation zone	6 h
HORVU.MOREX.r3.1HG0011440.1	-2.281968739	-1.581106574	-4.539180506	3.28E-05	0.006941783	1.931966525	Glucan endo-1,3-beta-glucosidase, putative	elongation zone	6 h
HORVU.MOREX.r3.3HG0297330.1	0.539603786	5.598321606	4.551018823	3.15E-05	0.006879758	1.911558133	Receptor-like kinase	elongation zone	6 h
HORVU.MOREX.r3.6HG0615840.1	-2.744951602	-2.27410401	-4.627031686	2.43E-05	0.00600621	1.910875403	Metalloendoproteinase 1	elongation zone	6 h
HORVU.MOREX.r3.2HG0191180.1	0.580323494	4.405018466	4.48919171	3.89E-05	0.007613546	1.902204661	Xanthine phosphoribosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.6HG0613230.1	0.476650804	6.00935735	4.572101272	2.93E-05	0.006612707	1.895853911	Allergen, putative	elongation zone	6 h
HORVU.MOREX.r3.3HG0329040.1	-2.146745974	-0.454710292	-4.440881524	4.58E-05	0.008407674	1.877809408	Vacuolar-processing enzyme	elongation zone	6 h
HORVU.MOREX.r3.6HG0599090.1	-1.310914408	-2.428665549	-4.409162925	5.10E-05	0.008964956	1.842611423	Vacuolar iron transporter	elongation zone	6 h
HORVU.MOREX.r3.3HG0291580.1	0.782303409	2.805578274	4.416594877	4.97E-05	0.008875539	1.831090662	Lysosomal Pro-X carboxypeptidase	elongation zone	6 h
HORVU.MOREX.r3.6HG0627570.1	0.718674028	4.766956665	4.483648763	3.96E-05	0.007673608	1.814434455	Immunoglobulin A1 protease autotransporter	elongation zone	6 h
HORVU.MOREX.r3.1HG0086370.1	-2.172626164	-3.209110522	-4.461466808	4.27E-05	0.008042578	1.810709604	Glyoxal oxidase	elongation zone	6 h
HORVU.MOREX.r3.1HG0091820.1	0.807918085	5.321522929	4.470272771	4.15E-05	0.00794144	1.778044025	Glutamyl-tRNA (Gln) amidotransferase subunit A	elongation zone	6 h
HORVU.MOREX.r3.4HG0342160.1	0.522337716	5.308472026	4.489007835	3.89E-05	0.007613546	1.768949566	Presenilin	elongation zone	6 h
HORVU.MOREX.r3.3HG0234970.1	-0.755117158	0.091121871	-4.458879424	4.31E-05	0.008042578	1.766942527	6,7-dimethyl-8-ribityllumazine synthase	elongation zone	6 h
HORVU.MOREX.r3.5HG0494040.1	-1.831724794	-3.000857515	-4.402406455	5.22E-05	0.009074007	1.738029167	Auxin efflux carrier component	elongation zone	6 h
HORVU.MOREX.r3.3HG0242880.1	-1.131554244	-0.890008185	-4.380148607	5.62E-05	0.009382875	1.732053631	Phloem protein 2-like protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0425000.1	-3.529383361	-0.918831697	-4.573038409	2.92E-05	0.006612707	1.700066573	Transposon protein, putative, Pong sub-class	elongation zone	6 h
HORVU.MOREX.r3.6HG0601830.1	-1.481295163	-2.059555704	-4.354773318	6.12E-05	0.00981914	1.657143854	C2 calcium/lipid-binding and GRAM domain protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0351750.1	-1.818178955	-1.823804439	-4.368974247	5.84E-05	0.009607858	1.649633027	BTB/POZ domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0624390.1	-1.524798697	1.652699025	-4.340103303	6.43E-05	0.010155862	1.630072027	Two-component response regulator	elongation zone	6 h
HORVU.MOREX.r3.7HG0655210.1	-1.841854981	-1.689922301	-4.365743885	5.90E-05	0.009607858	1.626060229	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.3HG0330200.1	-1.243251393	1.169812259	-4.468027223	4.18E-05	0.00794144	1.592256168	Aquaporin	elongation zone	6 h
HORVU.MOREX.r3.1HG0017280.1	-1.765314558	-0.330109732	-4.383406651	5.56E-05	0.009382875	1.571695713	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.3HG0275090.1	-2.036079506	-3.212508152	-4.389313057	5.45E-05	0.009325267	1.567163157	SWI/SNF-related matrix-associated actin-dependent regulator of	elongation zone	6 h
HORVU.MOREX.r3.1HG0072580.1	-0.653030101	5.490114394	-4.421404573	4.89E-05	0.008809167	1.555926018	Aminotransferase-related family protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0170230.1	-0.688713481	3.492538265	-4.343120367	6.37E-05	0.010131561	1.55421533	Smr domain containing protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0096800.1	-0.940855915	4.691800049	-4.408515067	5.11E-05	0.008964956	1.55195701	Flavin-containing monooxygenase	elongation zone	6 h
HORVU.MOREX.r3.5HG0483860.1	0.643096146	3.316156884	4.316997505	6.95E-05	0.010725562	1.49802978	RING/U-box superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0075440.1	-0.953320761	1.650312221	-4.366973554	5.88E-05	0.009607858	1.491539976	Protein NRT1/ PTR FAMILY 5.5	elongation zone	6 h
HORVU.MOREX.r3.4HG0350900.1	0.398899633	7.97599371	4.507261227	3.66E-05	0.007506841	1.488266334	UDP-glucose 6-dehydrogenase	elongation zone	6 h
HORVU.MOREX.r3.7HG0674720.1	-1.950135509	-1.463275625	-4.290977406	7.58E-05	0.011115	1.487489686	Epoxide hydrolase 2	elongation zone	6 h
HORVU.MOREX.r3.6HG0620820.1	-0.936220749	3.246758451	-4.298752377	7.39E-05	0.011107173	1.470768152	Pectin lyase-like superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0626650.1	0.326313709	8.259288679	4.493677457	3.83E-05	0.007613546	1.461863311	26S protease regulatory subunit-like protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0684940.1	-0.720838457	4.72025707	-4.392633116	5.39E-05	0.009299057	1.458140361	Zinc finger constans-like protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0510830.1	0.980424002	5.120306759	4.319319864	6.90E-05	0.010723158	1.406130191	#N/A	elongation zone	6 h
HORVU.MOREX.r3.2HG0136150.1	3.428126635	-1.262543021	4.432126313	4.72E-05	0.008570943	1.391408015	Cyclin family protein	elongation zone	6 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.7HG0648610.1	0.373099131	6.01586743	4.363584643	5.95E-05	0.009607858	1.29140352	Carboxypeptidase	elongation zone	6 h
HORVU.MOREX.r3.4HG0355210.1	-2.465957966	-0.137693228	-4.229300421	9.31E-05	0.012247977	1.277185858	transcription factor-like protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0655680.1	-2.026967996	-1.898894256	-4.238220662	9.04E-05	0.012075989	1.2730143	Serine/threonine-protein kinase	elongation zone	6 h
HORVU.MOREX.r3.4HG0354980.1	-0.873012559	2.412831318	-4.257532155	8.48E-05	0.011833919	1.266977237	#N/A	elongation zone	6 h
HORVU.MOREX.r3.1HG0025320.1	-1.57590765	0.572544846	-4.203541999	0.0001	0.012845495	1.233028551	Receptor-like kinase, putative	elongation zone	6 h
HORVU.MOREX.r3.3HG0330980.1	0.382819961	6.458067382	4.380404172	5.62E-05	0.009382875	1.224501131	Protein IQ-DOMAIN 1	elongation zone	6 h
HORVU.MOREX.r3.5HG0537150.1	-1.141844089	-2.246878812	-4.174842061	0.00011	0.013700934	1.147008989	Protein DETOXIFICATION	elongation zone	6 h
HORVU.MOREX.r3.4HG0337950.1	-2.281421129	-0.296307238	-4.286700326	7.69E-05	0.01119483	1.142024029	65-kDa microtubule-associated-like protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0390450.1	-2.322171728	-2.315588818	-4.181763093	0.00011	0.013472048	1.141178733	#N/A	elongation zone	6 h
HORVU.MOREX.r3.4HG0344830.1	0.590822337	4.535567699	4.263337935	8.32E-05	0.011767538	1.135671865	NBS-LRR disease resistance protein, putative, expressed	elongation zone	6 h
HORVU.MOREX.r3.4HG0372230.1	-2.125195208	-1.629808544	-4.246237208	8.80E-05	0.01204116	1.131489209	Transposon protein, putative, CACTA, En/Spm sub-class, expresse	elongation zone	6 h
HORVU.MOREX.r3.5HG0519120.1	-1.326655212	-0.875101352	-4.240277143	8.98E-05	0.012075989	1.122887799	CASP-like protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0550600.1	-1.046749539	1.720715964	-4.331227687	6.63E-05	0.010382654	1.113060496	Protein ROOT HAIR DEFECTIVE 3 homolog	elongation zone	6 h
HORVU.MOREX.r3.7HG0724090.1	3.11047028	0.704867316	4.237021147	9.08E-05	0.012075989	1.105027383	RING/U-box superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0619410.1	-1.017910577	1.820333919	-4.235497898	9.12E-05	0.012075989	1.104114927	Flavonol synthase	elongation zone	6 h
HORVU.MOREX.r3.4HG0407230.1	-1.748100229	-0.944900136	-4.164125519	0.00012	0.013781372	1.082116014	Flowering-promoting factor 1-like protein 1	elongation zone	6 h
HORVU.MOREX.r3.1HG0050700.1	-1.382940743	2.994863261	-4.264135513	8.29E-05	0.011767538	1.076018524	ATP-dependent zinc metalloprotease FtsH	elongation zone	6 h
HORVU.MOREX.r3.1HG0055240.1	-1.931442357	-3.14720018	-4.186154225	0.00011	0.013427958	1.052779012	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	elongation zone	6 h
HORVU.MOREX.r3.5HG0511820.1	-2.949386381	-3.38085013	-4.222424557	9.53E-05	0.012294138	1.049066927	Cyclic nucleotide-gated channel	elongation zone	6 h
HORVU.MOREX.r3.3HG0329950.1	-1.399744779	1.75889036	-4.148155103	0.00012	0.014195784	1.032670336	Pectin acetylesterase	elongation zone	6 h
HORVU.MOREX.r3.3HG0293570.1	2.45269119	-0.387941199	4.242544469	8.91E-05	0.012075989	1.005691981	BTB/POZ domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0540020.1	-2.305406832	-2.701095093	-4.119142437	0.00013	0.015184882	0.976942379	Ubiquitin carboxyl-terminal hydrolase 2	elongation zone	6 h
HORVU.MOREX.r3.2HG0161630.1	-1.020148712	1.307163675	-4.131270819	0.00013	0.01483784	0.97498662	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0272430.1	0.478577692	5.817079707	4.252535379	8.62E-05	0.011950976	0.919624673	Pectin lyase-like superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0131630.1	-2.665484743	-3.028166822	-4.132888102	0.00013	0.01483784	0.910190016	vacuolar sorting-associated protein (DUF946)	elongation zone	6 h
HORVU.MOREX.r3.7HG0661480.1	0.335871265	7.365151763	4.29333575	7.52E-05	0.011107173	0.887681238	Alpha-amylase 2	elongation zone	6 h
HORVU.MOREX.r3.4HG0378580.1	0.539006381	5.353083837	4.224416317	9.46E-05	0.01229049	0.876971332	Transcription factor	elongation zone	6 h
HORVU.MOREX.r3.7HG0737450.1	1.000026479	2.956707885	4.090076162	0.00015	0.015995535	0.876334311	Phosphoglycerate kinase	elongation zone	6 h
HORVU.MOREX.r3.3HG0246670.1	-1.447321914	-1.917828013	-4.08210546	0.00015	0.016166055	0.873698317	DUF4228 domain protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0707700.1	-1.269395343	-2.42616811	-4.081352052	0.00015	0.016166055	0.872980507	Late embryogenesis abundant (LEA) hydroxyproline-rich glycopro	elongation zone	6 h
HORVU.MOREX.r3.2HG0142850.1	0.310553124	6.438473516	4.249259576	8.71E-05	0.012000787	0.872282947	Organic solute transporter-like	elongation zone	6 h
HORVU.MOREX.r3.6HG0575710.1	0.521056028	4.807664746	4.184584419	0.00011	0.013427958	0.863389314	Kynurenine formamidase	elongation zone	6 h
HORVU.MOREX.r3.2HG0120320.1	-0.877368159	1.685244219	-4.271644222	8.09E-05	0.011606539	0.858856116	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.7HG0744040.1	-1.057940304	1.177534674	-4.080591753	0.00015	0.016166055	0.858414615	Transcription factor	elongation zone	6 h
HORVU.MOREX.r3.7HG0684880.1	-0.853998862	3.761266823	-4.158815352	0.00012	0.013943663	0.842152766	meiosis chromosome segregation family protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0081950.1	-2.141802047	-2.05546379	-4.068492722	0.00016	0.016551728	0.830369243	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.3HG0253860.1	-2.836916007	-0.092758097	-4.097648553	0.00014	0.015896607	0.820722141	Rapid alkalinization factor (RALF) family protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0065130.1	-1.554171213	1.689963316	-4.090138529	0.00015	0.015995535	0.810438353	NAC domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0344370.1	-1.430817839	-2.722566782	-4.061756204	0.00016	0.0166646	0.8087306	Glucuronoxylan 4-O-methyltransferase	elongation zone	6 h
HORVU.MOREX.r3.5HG0426110.1	-2.085521811	-3.224786885	-4.104777158	0.00014	0.015743485	0.797852564	NBS-LRR class disease resistance protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0403620.1	-1.524790505	0.126434613	-4.226188264	9.41E-05	0.01229049	0.78400056	#N/A	elongation zone	6 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0075590.1	0.32236971	8.23086424	4.293977264	7.51E-05	0.011107173	0.772006037	Coiled-coil domain-containing protein 47	elongation zone	6 h
HORVU.MOREX.r3.4HG0402730.1	-1.733601611	-1.081620137	-4.112811115	0.00014	0.01541845	0.738749119	Homeobox protein BEL1 like	elongation zone	6 h
HORVU.MOREX.r3.6HG0552040.1	0.237654174	8.106568618	4.276364677	7.96E-05	0.011505838	0.738357035	#N/A	elongation zone	6 h
HORVU.MOREX.r3.1HG0006230.1	0.526358707	5.574000008	4.16887669	0.00011	0.013703395	0.727987234	Disease resistance protein RPM1	elongation zone	6 h
HORVU.MOREX.r3.3HG0222130.1	0.363013413	8.795276054	4.29700533	7.43E-05	0.011107173	0.721759669	Transmembrane protein 214	elongation zone	6 h
HORVU.MOREX.r3.7HG0721650.1	0.374062496	5.578373097	4.190751872	0.00011	0.013318454	0.716487556	Novel plant snare, putative	elongation zone	6 h
HORVU.MOREX.r3.3HG0313090.1	-0.973454075	2.944420659	-4.080430752	0.00015	0.016166055	0.707330289	Thiamin pyrophosphokinase 1	elongation zone	6 h
HORVU.MOREX.r3.2HG0181680.1	-1.917355076	-1.908817715	-4.054967922	0.00017	0.016720589	0.707040615	CASP-like protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0466320.1	-0.391907084	6.324949057	-4.204694022	0.0001	0.012845495	0.697018543	Phosphoinositide phospholipase C	elongation zone	6 h
HORVU.MOREX.r3.6HG0612180.1	0.675229267	6.264662645	4.169267023	0.00011	0.013703395	0.677123183	NHL repeat-containing protein-like	elongation zone	6 h
HORVU.MOREX.r3.1HG0094770.1	0.715074383	3.670278309	4.053118196	0.00017	0.016720589	0.667316171	Transmembrane protein, putative	elongation zone	6 h
HORVU.MOREX.r3.4HG0337110.1	0.349044245	7.514078085	4.219504648	9.62E-05	0.012336161	0.642767094	Coatomer subunit alpha	elongation zone	6 h
HORVU.MOREX.r3.6HG0589860.1	-0.936026482	4.121931249	-4.09685916	0.00014	0.015896607	0.632999008	Kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0667060.1	-1.308924041	2.126304133	-4.007883844	0.00019	0.018284709	0.619126833	target of early activation tagged (EAT) 2	elongation zone	6 h
HORVU.MOREX.r3.7HG0641750.1	-2.672995114	-2.739012037	-3.996522601	0.0002	0.018702211	0.614380054	Aspartic proteinase nepenthesin-2	elongation zone	6 h
HORVU.MOREX.r3.4HG0415490.1	-1.836030917	-1.784637332	-4.054821235	0.00017	0.016720589	0.611857737	14 kDa proline-rich protein DC2.15	elongation zone	6 h
HORVU.MOREX.r3.4HG0412370.1	-2.127962639	-1.425115928	-4.010430538	0.00019	0.018284709	0.605327166	Homeobox protein knotted-1, putative	elongation zone	6 h
HORVU.MOREX.r3.3HG0313320.1	-2.109205885	-2.456522524	-3.983412742	0.00021	0.018906489	0.58880125	Potassium transporter	elongation zone	6 h
HORVU.MOREX.r3.6HG0610980.1	-1.396593689	-1.883261679	-4.008762756	0.00019	0.018284709	0.586320574	Nucleotide/sugar transporter family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0722360.1	-1.607779447	0.66493112	-4.038013658	0.00017	0.017309173	0.584736752	Receptor-like protein kinase	elongation zone	6 h
HORVU.MOREX.r3.2HG0187430.1	0.526471942	5.203928279	4.12778367	0.00013	0.01492498	0.576617883	Transmembrane emp24 domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0252610.1	0.43712499	7.233438842	4.167794809	0.00011	0.013703395	0.573042954	Protein kinase	elongation zone	6 h
HORVU.MOREX.r3.7HG0679050.1	-0.692966191	4.002867978	-4.047329903	0.00017	0.016955841	0.550752884	Upstream activation factor subunit spp27	elongation zone	6 h
HORVU.MOREX.r3.2HG0168110.1	-3.142973101	-1.271051778	-4.260614149	8.39E-05	0.011793388	0.548390176	Protein SET DOMAIN GROUP 41	elongation zone	6 h
HORVU.MOREX.r3.4HG0369570.1	0.242070995	10.41352761	4.312996419	7.05E-05	0.010788971	0.546739372	Alpha-1,4-glucan-protein synthase [UDP-forming]	elongation zone	6 h
HORVU.MOREX.r3.2HG0194620.1	-2.514314519	-2.147983455	-4.009796329	0.00019	0.018284709	0.524522797	F-box protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0567780.1	0.716660177	3.016752833	3.992282346	0.0002	0.018702211	0.514919098	disease resistance protein (TIR-NBS-LRR class)	elongation zone	6 h
HORVU.MOREX.r3.3HG0245250.1	-2.379427167	-1.643307554	-3.996452879	0.0002	0.018702211	0.489587225	Cysteine protease, putative	elongation zone	6 h
HORVU.MOREX.r3.7HG0694090.1	0.353560018	5.778504944	4.123141007	0.00013	0.015070113	0.483992615	Rer1 protein, putative	elongation zone	6 h
HORVU.MOREX.r3.6HG0541250.1	0.273508196	7.143194567	4.149322056	0.00012	0.014195784	0.469710791	Acetate kinase	elongation zone	6 h
HORVU.MOREX.r3.2HG0205990.1	-2.146107509	-2.557658252	-3.951496218	0.00023	0.020527378	0.46736824	Glutaredoxin family protein, putative	elongation zone	6 h
HORVU.MOREX.r3.5HG0526250.1	0.345237407	12.0381843	4.304781961	7.24E-05	0.011007254	0.461181975	70 kDa heat shock protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0309270.1	0.356544664	8.53260482	4.167614186	0.00011	0.013703395	0.433361136	Proline--tRNA ligase	elongation zone	6 h
HORVU.MOREX.r3.4HG0342080.1	-0.842240504	4.067325035	-4.07310794	0.00016	0.016387742	0.427787963	Adenine/guanine permease	elongation zone	6 h
HORVU.MOREX.r3.6HG0581570.1	0.419759835	4.929735327	4.043151288	0.00017	0.017104733	0.421590684	Leucine-rich repeat-containing protein 1	elongation zone	6 h
HORVU.MOREX.r3.2HG0218010.1	0.401955758	8.228324079	4.154422105	0.00012	0.01406566	0.362793053	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase s	elongation zone	6 h
HORVU.MOREX.r3.3HG0305440.1	-1.669627587	-2.501750371	-3.902353607	0.00027	0.021949523	0.357981485	Late embryogenesis abundant protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0632270.1	0.570025075	3.993704775	3.987539398	0.00021	0.018842535	0.356438417	Leucine-rich repeat family protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0485610.1	-1.500600981	0.794719635	-3.933336494	0.00024	0.021333038	0.355238729	Cytochrome P450, putative	elongation zone	6 h
HORVU.MOREX.r3.3HG0311410.1	-0.49145949	5.699117557	-4.031450942	0.00018	0.017513475	0.347655058	F box protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0458010.1	-0.393277383	5.942045141	-4.062742441	0.00016	0.0166646	0.336334701	Protein kinase, putative	elongation zone	6 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.6HG0605940.1	-0.868259182	3.17964847	-3.991464562	0.0002	0.018702211	0.328231967	Xyloglucan endotransglucosylase/hydrolase	elongation zone	6 h
HORVU.MOREX.r3.6HG0541940.1	0.39006774	6.76425912	4.094472053	0.00015	0.015935666	0.324753005	S-adenosyl-L-methionine-dependent methyltransferases superfa	elongation zone	6 h
HORVU.MOREX.r3.7HG0658560.1	-0.963861332	3.664515124	-3.905393734	0.00027	0.021822902	0.284550176	Kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0631040.1	-0.92405237	2.526682694	-3.93830977	0.00024	0.021271955	0.278154919	Mesoderm induction early response protein 1, putative isoform	elongation zone	6 h
HORVU.MOREX.r3.2HG0178160.1	0.666237379	7.879945441	4.099295252	0.00014	0.015896607	0.274563851	HTH-type transcriptional regulator YidZ	elongation zone	6 h
HORVU.MOREX.r3.2HG0213020.1	-1.229744423	3.221450174	-3.893688323	0.00028	0.022216127	0.269418936	Protein F12F1.11-, putative	elongation zone	6 h
HORVU.MOREX.r3.6HG0561180.1	-1.669539359	-0.688407242	-3.886100072	0.00029	0.02238184	0.267984347	Receptor kinase	elongation zone	6 h
HORVU.MOREX.r3.6HG0615600.1	-2.016650283	-2.882863566	-3.912004746	0.00026	0.021709616	0.263883037	Cytochrome P450, putative	elongation zone	6 h
HORVU.MOREX.r3.6HG0606930.1	0.423800413	5.680326244	4.029103626	0.00018	0.017563621	0.259367434	3-ketodihydrosphingosine reductase	elongation zone	6 h
HORVU.MOREX.r3.6HG0573150.1	-0.522561598	5.184389048	-3.982859121	0.00021	0.018906489	0.248353199	Copper-transporting ATPase	elongation zone	6 h
HORVU.MOREX.r3.7HG0649240.1	-1.639045242	-2.995715777	-3.906493893	0.00027	0.021822902	0.240879612	protein kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0180010.1	-1.330955496	1.125047742	-4.011410437	0.00019	0.018284709	0.221892077	#N/A	elongation zone	6 h
HORVU.MOREX.r3.7HG0737340.1	-1.545629428	-0.106662143	-4.032281836	0.00018	0.017513475	0.212505384	GDA1/CD39 nucleoside phosphatase family protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0162900.2	0.80856924	2.320158811	3.869265595	0.0003	0.023276244	0.20541253	Aldo-keto reductase	elongation zone	6 h
HORVU.MOREX.r3.2HG0214070.1	-1.744830889	-2.623970249	-3.850904434	0.00032	0.02415331	0.20528132	AT hook motif DNA-binding family protein, putative	elongation zone	6 h
HORVU.MOREX.r3.2HG0171550.1	0.790489854	4.111529363	3.919551005	0.00026	0.021417658	0.202629984	Major facilitator superfamily transporter	elongation zone	6 h
HORVU.MOREX.r3.4HG0374910.2	0.324275456	6.337717806	4.053576916	0.00017	0.016720589	0.201981915	Beta-adaptin-like protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0241320.1	0.568118576	3.585417651	3.931494927	0.00025	0.021333038	0.192702002	Prolyl 4-hydroxylase alpha subunit, putative	elongation zone	6 h
HORVU.MOREX.r3.3HG0239980.1	-1.334910759	1.292153679	-3.928287338	0.00025	0.021333038	0.192548623	Alpha/beta-Hydrolases superfamily protein, putative	elongation zone	6 h
HORVU.MOREX.r3.1HG0039670.1	0.289079396	7.408424513	4.075040613	0.00015	0.016368541	0.191788058	Calcium ion-binding protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0718170.1	-1.209497807	1.273374933	-3.845474054	0.00032	0.024305588	0.187861058	Pleiotropic drug resistance ABC transporter	elongation zone	6 h
HORVU.MOREX.r3.4HG0370380.1	0.47958889	5.905711064	4.009024064	0.00019	0.018284709	0.185123738	Erlin-2	elongation zone	6 h
HORVU.MOREX.r3.4HG0383780.1	-2.419761971	-0.062687302	-3.881835714	0.00029	0.022463016	0.183864602	Laccase	elongation zone	6 h
HORVU.MOREX.r3.4HG0380430.1	-0.42600792	3.638981565	-3.924639025	0.00025	0.021375796	0.177321242	Membrane steroid-binding protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0523860.1	-0.679560428	4.167580678	-3.965166912	0.00022	0.019727211	0.159267997	Calcium-dependent protein kinase	elongation zone	6 h
HORVU.MOREX.r3.3HG0257310.1	0.324842068	7.69321866	4.065720413	0.00016	0.016617419	0.126582353	Glucosidase 2 subunit beta	elongation zone	6 h
HORVU.MOREX.r3.6HG0581020.1	0.391806348	5.648770754	3.991230852	0.0002	0.018702211	0.119704078	Xyloglucan 6-xylosyltransferase 1	elongation zone	6 h
HORVU.MOREX.r3.6HG0557550.1	-0.94365046	1.605488567	-3.815945699	0.00036	0.025487626	0.113231556	CRS2-associated factor 1	elongation zone	6 h
HORVU.MOREX.r3.5HG0462220.1	-1.097383812	1.070356343	-3.932592536	0.00025	0.021333038	0.112529195	Calmodulin protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0664780.1	-0.859211583	4.573395079	-4.054149436	0.00017	0.016720589	0.110526867	Patatin	elongation zone	6 h
HORVU.MOREX.r3.6HG0595190.1	-1.711180164	-2.072106303	-3.809083482	0.00036	0.025778846	0.095865769	GDSL esterase/lipase	elongation zone	6 h
HORVU.MOREX.r3.3HG0293130.1	-1.124496679	3.772343167	-3.923174218	0.00025	0.021375796	0.075048991	Eukaryotic aspartyl protease family protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0334360.1	-0.924191945	4.121321037	-3.982380184	0.00021	0.018906489	0.073898099	Homeobox protein BEL1 like	elongation zone	6 h
HORVU.MOREX.r3.3HG0276120.1	-2.051419046	-1.330753495	-3.788007048	0.00039	0.026638848	0.035650793	Phospholipase A1	elongation zone	6 h
HORVU.MOREX.r3.5HG0483980.1	-1.424145581	-1.844541926	-3.78294743	0.0004	0.026712078	0.019506026	Cinnamoyl CoA reductase	elongation zone	6 h
HORVU.MOREX.r3.4HG0416170.1	-0.703163406	3.384356338	-3.935850914	0.00024	0.021311375	0.019177217	Methionyl-tRNA formyltransferase	elongation zone	6 h
HORVU.MOREX.r3.2HG0141140.1	-1.286792871	-2.857994565	-3.783448513	0.0004	0.026712078	0.016069937	DUF4228 domain protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0190560.1	-1.205550001	-0.224848231	-3.868342361	0.0003	0.023276244	0.014443599	#N/A	elongation zone	6 h
HORVU.MOREX.r3.2HG0197920.1	2.857684379	-1.098587388	3.847341169	0.00032	0.024250025	-0.00147563	BTB/POZ domain containing protein, expressed	elongation zone	6 h
HORVU.MOREX.r3.4HG0346830.1	-1.425774146	-2.756213705	-3.770713393	0.00041	0.027115872	-0.01269217	WEB family protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0419590.1	-0.566743523	6.133126066	-4.006614848	0.00019	0.018284709	-0.03148458	#N/A	elongation zone	6 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.5HG0527310.1	-1.840336786	-3.15597805	-3.778567267	0.0004	0.026862598	-0.03817673	Protein NRT1/ PTR FAMILY 5.5	elongation zone	6 h
HORVU.MOREX.r3.2HG0144000.1	-0.410227815	5.798118458	-3.937757137	0.00024	0.021271955	-0.04164743	Zeta-carotene desaturase	elongation zone	6 h
HORVU.MOREX.r3.1HG0081120.1	1.63134628	1.005476641	3.757974735	0.00043	0.027892198	-0.04594231	DNA mismatch repair protein MutL	elongation zone	6 h
HORVU.MOREX.r3.5HG0472810.1	-1.006116412	2.371977796	-3.977873609	0.00021	0.019099888	-0.04710299	Aquaporin	elongation zone	6 h
HORVU.MOREX.r3.3HG0312780.1	0.69776507	3.639594263	3.828028142	0.00034	0.024875194	-0.04726394	NBS-LRR disease resistance protein, putative, expressed	elongation zone	6 h
HORVU.MOREX.r3.2HG0130960.1	-0.838721146	1.762022677	-3.770976152	0.00041	0.027115872	-0.06646704	Benzene 1,2-dioxygenase subunit alpha	elongation zone	6 h
HORVU.MOREX.r3.1HG0015750.1	-1.893034039	-2.912149854	-3.750892135	0.00044	0.028211116	-0.06888109	transcription factor, putative (Protein of unknown function, DUF	elongation zone	6 h
HORVU.MOREX.r3.3HG0299740.1	-0.455980635	5.806671811	-3.927662719	0.00025	0.021333038	-0.06929315	Tubby-like F-box protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0050920.1	-1.023400497	2.478719451	-3.924456478	0.00025	0.021375796	-0.08119197	Trehalase	elongation zone	6 h
HORVU.MOREX.r3.5HG0469300.1	-1.57608715	0.250215668	-3.796291663	0.00038	0.026284234	-0.08800144	CCCH-type zinc finger protein with ARM repeat domain-containir	elongation zone	6 h
HORVU.MOREX.r3.4HG0388310.1	-0.459123738	3.870759069	-3.901117138	0.00027	0.021949918	-0.09417258	Protein kinase	elongation zone	6 h
HORVU.MOREX.r3.6HG0622740.1	-0.566048291	4.313476147	-3.918745153	0.00026	0.021417658	-0.09633858	Protein DETOXIFICATION	elongation zone	6 h
HORVU.MOREX.r3.2HG0152530.1	-0.458855554	4.851529635	-3.912345687	0.00026	0.021709616	-0.09671932	Fasciclin-like arabinogalactan protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0027200.1	-0.971650424	4.502879298	-3.858019392	0.00031	0.023872158	-0.1073209	Auxin-responsive protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0248480.1	-1.700583687	-1.004527296	-3.743242814	0.00045	0.028496623	-0.12054271	Cytochrome P450	elongation zone	6 h
HORVU.MOREX.r3.2HG0170640.1	2.802997303	-0.509068665	3.810867568	0.00036	0.025722162	-0.12998571	Protein FAR1-RELATED SEQUENCE 5	elongation zone	6 h
HORVU.MOREX.r3.7HG0640410.1	-2.963594707	-2.747397168	-3.77009813	0.00041	0.027115872	-0.13863515	Cytochrome P450	elongation zone	6 h
HORVU.MOREX.r3.5HG0488050.1	-1.401771625	-2.926199569	-3.7255621	0.00047	0.029390657	-0.14268426	Blue copper protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0641230.1	-1.297823001	-1.229188244	-3.823029539	0.00035	0.025184263	-0.15373962	Retrovirus-related Pol polyprotein from transposon TNT 1-94	elongation zone	6 h
HORVU.MOREX.r3.1HG0053060.1	-1.032894535	4.011377898	-3.829500534	0.00034	0.024875194	-0.1577276	PLATZ transcription factor	elongation zone	6 h
HORVU.MOREX.r3.2HG0165250.1	0.452839604	6.077437333	3.908426596	0.00027	0.021784575	-0.17968031	OJ000315_02.19 protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0254950.1	-1.160163954	1.019759768	-3.890488091	0.00028	0.022218304	-0.17975102	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.5HG0459320.1	0.587882775	4.812268395	3.839517452	0.00033	0.02468067	-0.19106983	Peptidylprolyl isomerase	elongation zone	6 h
HORVU.MOREX.r3.3HG0248540.2	-0.547608481	3.626501132	-3.789221256	0.00039	0.026638848	-0.19375322	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0333450.1	-0.638331526	3.618972788	-3.797819768	0.00038	0.026284234	-0.20059046	Type I inositol-1,4,5-trisphosphate 5-phosphatase CVP2	elongation zone	6 h
HORVU.MOREX.r3.7HG0639300.1	0.626346912	3.626615674	3.7787741	0.0004	0.026862598	-0.20692234	F-box protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0511090.1	-0.638230452	5.583411147	-3.85994922	0.00031	0.023818477	-0.20702057	Phytochrome	elongation zone	6 h
HORVU.MOREX.r3.3HG0278170.1	-1.651193094	0.346838504	-3.705523556	0.0005	0.030363091	-0.21208383	CCCH-type zinc fingerfamily protein with RNA-binding domain-co	elongation zone	6 h
HORVU.MOREX.r3.2HG0140700.1	0.347921757	5.904167686	3.890032383	0.00028	0.022218304	-0.21274615	#N/A	elongation zone	6 h
HORVU.MOREX.r3.4HG0354010.1	-2.332775953	-0.997515384	-3.696415728	0.00052	0.030363091	-0.2142125	LURP-one-like protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0379290.1	0.349308761	5.287980079	3.851134773	0.00032	0.02415331	-0.23622023	COP1-interacting-like protein, putative	elongation zone	6 h
HORVU.MOREX.r3.5HG0470030.1	0.514512176	7.999201135	3.967759405	0.00022	0.019648199	-0.23766636	3-ketoacyl-CoA thiolase	elongation zone	6 h
HORVU.MOREX.r3.5HG0430050.1	-0.664882426	4.495639375	-3.828167793	0.00034	0.024875194	-0.23920045	Stomatal closure-related actin-binding protein 1	elongation zone	6 h
HORVU.MOREX.r3.3HG0269810.1	0.693680639	4.116724617	3.798381617	0.00038	0.026284234	-0.24160016	Aspartyl protease family protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0558430.1	-2.918678757	-1.969157859	-3.698319925	0.00052	0.030363091	-0.26003925	SAUR-like auxin-responsive protein family, putative	elongation zone	6 h
HORVU.MOREX.r3.1HG0056620.1	-1.589470634	0.189161761	-3.892462406	0.00028	0.022217049	-0.26192557	Expansin protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0405920.1	-1.252631866	0.085137287	-3.828240129	0.00034	0.024875194	-0.2652035	Hexosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.4HG0387180.1	-0.933286469	1.821336783	-3.682540464	0.00054	0.030744687	-0.26576925	Proton pump-interactor 1	elongation zone	6 h
HORVU.MOREX.r3.4HG0391330.1	0.43530433	6.457455724	3.885345551	0.00029	0.02238184	-0.27199816	Phosphomevalonate kinase	elongation zone	6 h
HORVU.MOREX.r3.2HG0126550.1	-1.618153587	1.396372437	-3.678957948	0.00055	0.031004434	-0.27281395	Alpha/beta hydrolase, putative	elongation zone	6 h
HORVU.MOREX.r3.3HG0264440.1	0.748483772	2.161098312	3.691094948	0.00053	0.030429659	-0.27487653	Condensin complex subunit 2	elongation zone	6 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.4HG0343050.1	-0.56982995	6.230075431	-3.894244508	0.00028	0.022216127	-0.27831619	N-acetyl-gamma-glutamyl-phosphate reductase	elongation zone	6 h
HORVU.MOREX.r3.4HG0335450.1	-2.457946646	-2.959169593	-3.692737263	0.00053	0.03036885	-0.27885736	Nucleobase ascorbate transporter	elongation zone	6 h
HORVU.MOREX.r3.5HG0420480.1	-2.100792208	1.423524837	-3.693701107	0.00052	0.030363091	-0.29138024	BEL1-like homeodomain protein 6	elongation zone	6 h
HORVU.MOREX.r3.2HG0195690.1	-1.08462304	-2.810433048	-3.666669525	0.00057	0.031690477	-0.29505302	filamentous hemagglutinin transporter	elongation zone	6 h
HORVU.MOREX.r3.1HG0080180.1	-1.339686867	-2.352460779	-3.687901429	0.00053	0.030483629	-0.30078029	Jacalin lectin family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0666740.1	-1.042417761	1.938696651	-3.773454641	0.00041	0.027115872	-0.30648019	Glycosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.6HG0628790.1	-0.927189607	2.686977072	-3.694667111	0.00052	0.030363091	-0.32305914	Myb-like transcription factor family protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0112690.1	-0.952480116	1.247172627	-3.894301923	0.00028	0.022216127	-0.32372335	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.2HG0195020.1	1.090477608	2.396301121	3.65352303	0.00059	0.032312416	-0.33052753	tRNA (Guanine-N(7)-)-methyltransferase	elongation zone	6 h
HORVU.MOREX.r3.3HG0307630.1	2.051403981	2.923305984	3.665506728	0.00057	0.031719413	-0.33099415	SET-domain protein lysine methyltransferase family protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0284780.1	-0.427976595	5.323435331	-3.828892723	0.00034	0.024875194	-0.33302062	Protein PLASTID MOVEMENT IMPAIRED 1-RELATED 1	elongation zone	6 h
HORVU.MOREX.r3.3HG0303380.1	-0.900310102	-0.867377041	-3.723517822	0.00048	0.029402036	-0.33883151	Zinc finger protein CONSTANS	elongation zone	6 h
HORVU.MOREX.r3.1HG0094110.1	-1.723953107	0.561026983	-3.734174008	0.00046	0.029138607	-0.34109787	Sigma factor sigB regulation protein rsbQ	elongation zone	6 h
HORVU.MOREX.r3.4HG0413690.1	0.538253757	4.40336351	3.769966532	0.00041	0.027115872	-0.34376599	26S proteasome non-ATPase regulatory subunit-like protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0716900.1	0.384875417	8.192568258	3.918867731	0.00026	0.021417658	-0.35974345	Transmembrane 9 superfamily member	elongation zone	6 h
HORVU.MOREX.r3.3HG0234000.1	-1.578710628	-0.274430722	-3.837001274	0.00033	0.024767988	-0.35991519	Xyloglucan endotransglucosylase/hydrolase	elongation zone	6 h
HORVU.MOREX.r3.7HG0712850.1	0.414444229	4.698390518	3.783720401	0.00039	0.026712078	-0.36713344	Fiber protein Fb34	elongation zone	6 h
HORVU.MOREX.r3.6HG0614970.1	-0.422492877	5.579922669	-3.836128908	0.00033	0.024767988	-0.36936213	Kelch repeat-containing protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0248280.1	0.403275481	8.506150471	3.928980425	0.00025	0.021333038	-0.37002643	Reticulon-like protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0287000.1	-0.944549102	3.76861142	-3.778059237	0.0004	0.026862598	-0.37571845	Respiratory burst oxidase	elongation zone	6 h
HORVU.MOREX.r3.2HG0165110.1	-0.983853664	3.128473967	-3.745545292	0.00045	0.028496623	-0.37936024	Acetyl-coenzyme A synthetase	elongation zone	6 h
HORVU.MOREX.r3.2HG0179560.1	-0.949413077	1.523229319	-3.764365667	0.00042	0.027510832	-0.38486509	Nodulin-like / Major Facilitator Superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0518640.1	1.156564549	2.499571845	3.658649333	0.00058	0.031886221	-0.39063303	Methionine S-methyltransferase	elongation zone	6 h
HORVU.MOREX.r3.2HG0216110.1	0.347778795	5.350102781	3.798219655	0.00038	0.026284234	-0.39295764	#N/A	elongation zone	6 h
HORVU.MOREX.r3.4HG0354140.1	-1.358408329	-2.197267006	-3.627412003	0.00064	0.033489087	-0.40152952	CheY-like two-component responsive regulator family protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0189800.1	0.706385586	3.770834829	3.732655821	0.00046	0.029138607	-0.40488431	ethylene-responsive transcription factor	elongation zone	6 h
HORVU.MOREX.r3.5HG0471070.1	-0.288264241	6.510820563	-3.847725377	0.00032	0.024250025	-0.41521631	Oxidoreductase family, NAD-binding rossmann fold protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0133220.1	-0.852435556	3.407204844	-3.831540632	0.00034	0.024875194	-0.41732151	Blue copper protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0728060.1	-0.550522633	5.512336647	-3.79689628	0.00038	0.026284234	-0.4262837	Aminodeoxychorismate synthase	elongation zone	6 h
HORVU.MOREX.r3.2HG0182150.1	0.819024346	4.062913174	3.694669058	0.00052	0.030363091	-0.4300998	Charged multivesicular body protein 7	elongation zone	6 h
HORVU.MOREX.r3.7HG0679350.1	0.598814537	3.668407943	3.797777138	0.00038	0.026284234	-0.43805717	Leucine-rich repeat receptor-like protein kinase family	elongation zone	6 h
HORVU.MOREX.r3.2HG0113590.1	0.496439718	3.8003454	3.728199413	0.00047	0.029236824	-0.44983752	Zinc finger CCCH domain protein, putative	elongation zone	6 h
HORVU.MOREX.r3.3HG0245120.1	-3.163524487	-2.694279726	-3.643811494	0.00061	0.032525759	-0.45584644	Cysteine protease, putative	elongation zone	6 h
HORVU.MOREX.r3.3HG0294740.1	0.963770586	3.043041266	3.643440809	0.00061	0.032525759	-0.45918477	HTH-type transcriptional activator RhaR	elongation zone	6 h
HORVU.MOREX.r3.5HG0500680.1	0.717233715	6.785876601	3.819409787	0.00035	0.025297158	-0.4591963	Acyl carrier protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0114290.1	0.342421226	6.856362561	3.820931096	0.00035	0.025263639	-0.45995938	#N/A	elongation zone	6 h
HORVU.MOREX.r3.3HG0316280.1	0.954495209	4.501603233	3.696277107	0.00052	0.030363091	-0.46557911	Transcription initiation factor TFIID subunit 9	elongation zone	6 h
HORVU.MOREX.r3.5HG0504520.1	-1.196472882	0.68442194	-3.664415445	0.00057	0.031741526	-0.4688817	Phytoene synthase	elongation zone	6 h
HORVU.MOREX.r3.7HG0723060.1	-2.459985507	-1.228512714	-3.659185966	0.00058	0.031886221	-0.47135088	4-hydroxy-3-methylbut-2-enyl diphosphate synthase	elongation zone	6 h
HORVU.MOREX.r3.6HG0545620.1	0.388113795	11.02319041	3.992994465	0.0002	0.018702211	-0.48035237	Heat shock 70 kDa protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0415130.1	-1.642907647	-1.494103874	-3.630040661	0.00064	0.033339257	-0.49324883	rRNA N-glycosidase	elongation zone	6 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.5HG0491230.1	1.006784728	2.284227707	3.61856007	0.00066	0.033752681	-0.49364031	Dihydroflavonol-4-reductase	elongation zone	6 h
HORVU.MOREX.r3.5HG0474540.1	0.39529092	7.609555508	3.856902765	0.00031	0.023872158	-0.49561125	Protein transport protein Sec61 subunit alpha	elongation zone	6 h
HORVU.MOREX.r3.7HG0736960.1	0.718182229	3.878659947	3.669247569	0.00057	0.031591904	-0.4973797	BTB/POZ domain containing protein, expressed	elongation zone	6 h
HORVU.MOREX.r3.7HG0748670.1	-2.591030527	-1.854958195	-3.58887907	0.00073	0.0350911	-0.50467662	GDSL esterase/lipase	elongation zone	6 h
HORVU.MOREX.r3.1HG0076980.1	0.373230846	8.500485602	3.883703439	0.00029	0.022414154	-0.50539665	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase s	elongation zone	6 h
HORVU.MOREX.r3.3HG0307240.1	-2.09381985	-3.376882233	-3.603992908	0.00069	0.033986772	-0.50835229	Amino acid permease	elongation zone	6 h
HORVU.MOREX.r3.5HG0490760.1	0.632810261	4.107029811	3.690297667	0.00053	0.030429659	-0.50896684	Glucosamine 6-phosphate N-acetyltransferase	elongation zone	6 h
HORVU.MOREX.r3.3HG0283300.1	0.722989541	2.473566507	3.626440182	0.00065	0.033489087	-0.50896878	Farnesyl diphosphate synthase	elongation zone	6 h
HORVU.MOREX.r3.3HG0235030.1	0.532422271	3.06592017	3.643892372	0.00061	0.032525759	-0.51204366	Dehydration-responsive element binding protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0428840.1	0.728581537	5.358223693	3.719947148	0.00048	0.029555507	-0.51595812	BTB/POZ domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0664720.1	-1.177477733	0.421259005	-3.788989372	0.00039	0.026638848	-0.51793575	Blue copper protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0000050.1	0.441729568	5.048249047	3.744159449	0.00045	0.028496623	-0.53205209	RING-finger ubiquitin ligase	elongation zone	6 h
HORVU.MOREX.r3.3HG0321700.1	-0.63411323	3.776225864	-3.68628843	0.00054	0.030483629	-0.53690083	FMN-dependent NADPH-azoreductase	elongation zone	6 h
HORVU.MOREX.r3.4HG0348800.1	-0.971944539	2.044228231	-3.644323952	0.00061	0.032525759	-0.53751171	TCP transcription factor	elongation zone	6 h
HORVU.MOREX.r3.4HG0364210.1	-2.68297036	-2.342478207	-3.731323783	0.00047	0.029138607	-0.54538209	#N/A	elongation zone	6 h
HORVU.MOREX.r3.2HG0156390.1	0.327521307	6.734888733	3.795421762	0.00038	0.026284234	-0.54741284	Protein kinase	elongation zone	6 h
HORVU.MOREX.r3.6HG0560140.1	-2.494514576	-1.916702632	-3.573884082	0.00076	0.035856081	-0.54896686	Endoglucanase	elongation zone	6 h
HORVU.MOREX.r3.1HG0000030.1	1.360598273	0.806284125	3.56865402	0.00077	0.035934872	-0.56838418	Serine/threonine-protein kinase ATM	elongation zone	6 h
HORVU.MOREX.r3.1HG0024040.1	0.369160348	9.734967723	3.910725207	0.00026	0.02171138	-0.57237238	Disulfide-isomerase	elongation zone	6 h
HORVU.MOREX.r3.2HG0204820.1	-0.76047504	3.904121549	-3.706778099	0.0005	0.030363091	-0.5804904	Ethylene-responsive transcription factor	elongation zone	6 h
HORVU.MOREX.r3.5HG0465260.1	0.74295925	2.270828878	3.572646327	0.00076	0.035872795	-0.58904827	Zinc finger HIT domain-containing protein 1	elongation zone	6 h
HORVU.MOREX.r3.6HG0570230.1	-1.000381402	0.733369112	-3.558218256	0.0008	0.035982407	-0.61064421	Aldose 1-epimerase family protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0140170.1	-0.68427086	2.981208713	-3.638962134	0.00062	0.032755332	-0.61886727	Ras-related protein Rab-21	elongation zone	6 h
HORVU.MOREX.r3.6HG0607590.1	-1.193495013	1.682477401	-3.567888833	0.00077	0.035934872	-0.62609016	U-box domain-containing family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0731370.1	2.689394922	0.369074602	3.703249293	0.00051	0.030363091	-0.63027933	#N/A	elongation zone	6 h
HORVU.MOREX.r3.6HG0625340.1	1.048708262	1.518599241	3.542127047	0.00084	0.036935434	-0.64307007	GPI transamidase component PIG-T	elongation zone	6 h
HORVU.MOREX.r3.4HG0397940.1	0.793378071	3.598811101	3.61197521	0.00068	0.033870225	-0.64427415	Alpha-L-fucosidase 2	elongation zone	6 h
HORVU.MOREX.r3.2HG0170120.1	-0.840175754	2.445884193	-3.596547714	0.00071	0.034460123	-0.65222647	Protein NRT1/ PTR FAMILY 1.2	elongation zone	6 h
HORVU.MOREX.r3.7HG0674250.1	0.889694467	0.727477133	3.606543226	0.00069	0.033986772	-0.6548979	hydroxysteroid dehydrogenase 3	elongation zone	6 h
HORVU.MOREX.r3.5HG0536200.1	-1.056301773	-0.55460225	-3.69671955	0.00052	0.030363091	-0.65989239	Xyloglucan endotransglucosylase/hydrolase	elongation zone	6 h
HORVU.MOREX.r3.5HG0472770.1	-0.692807154	4.33132919	-3.67525642	0.00055	0.031192351	-0.66400056	SIN3-like 2	elongation zone	6 h
HORVU.MOREX.r3.4HG0402000.1	0.684436036	8.180685451	3.813120715	0.00036	0.02562773	-0.6643136	Kinase interacting (KIP1-like) family protein, putative	elongation zone	6 h
HORVU.MOREX.r3.4HG0351790.1	-1.686942525	0.588108997	-3.532894505	0.00086	0.037429607	-0.66442234	Calcium-activated potassium channel subunit alpha-1	elongation zone	6 h
HORVU.MOREX.r3.2HG0203080.1	-2.08098082	0.039802538	-3.527511402	0.00088	0.037809868	-0.66675358	NA	elongation zone	6 h
HORVU.MOREX.r3.3HG0296140.1	-1.842794583	2.111797459	-3.540115325	0.00084	0.036941016	-0.67336962	F-box protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0383070.1	0.703084535	5.44858875	3.696120929	0.00052	0.030363091	-0.6740717	Calmodulin-binding protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0192000.1	-0.928972045	0.357063756	-3.699565237	0.00051	0.030363091	-0.67463474	HXXXD-type acyl-transferase family protein, putative	elongation zone	6 h
HORVU.MOREX.r3.3HG0222660.1	1.45576785	1.364356123	3.525669448	0.00088	0.037863675	-0.67573833	F-box family protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0178990.1	0.583066437	4.094270236	3.611790956	0.00068	0.033870225	-0.67730136	DNA-3-methyladenine glycosylase, putative	elongation zone	6 h
HORVU.MOREX.r3.7HG0677270.1	0.958468865	2.721723616	3.560056717	0.00079	0.035972648	-0.6781955	Glycosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.5HG0513980.1	-1.294486606	-0.364729073	-3.568674049	0.00077	0.035934872	-0.68041604	Auxin-responsive protein	elongation zone	6 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.2HG0165840.1	0.634056901	6.204491334	3.696444482	0.00052	0.030363091	-0.69413382	Protein kinase	elongation zone	6 h
HORVU.MOREX.r3.5HG0480410.1	-1.051496101	3.257253448	-3.624739494	0.00065	0.033489087	-0.69619772	Copper transporter	elongation zone	6 h
HORVU.MOREX.r3.1HG0082240.1	0.366360194	5.659889983	3.71771623	0.00049	0.029586232	-0.6977039	ER lumen protein-retaining receptor	elongation zone	6 h
HORVU.MOREX.r3.7HG0731320.1	0.374477594	5.022738423	3.70762296	0.0005	0.030363091	-0.69843493	O-fucosyltransferase family protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0323600.1	-0.583734233	4.35559343	-3.700742657	0.00051	0.030363091	-0.70277397	Phosphatidylserine decarboxylase proenzyme 2	elongation zone	6 h
HORVU.MOREX.r3.6HG0575530.1	-0.566987084	6.131400028	-3.743191102	0.00045	0.028496623	-0.70369773	Alcohol dehydrogenase, putative	elongation zone	6 h
HORVU.MOREX.r3.6HG0601260.1	-1.051180842	3.05036359	-3.721457477	0.00048	0.029503984	-0.71122968	Sulfotransferase	elongation zone	6 h
HORVU.MOREX.r3.5HG0513810.1	-0.615029302	4.245645455	-3.686160405	0.00054	0.030483629	-0.71724418	Malate dehydrogenase	elongation zone	6 h
HORVU.MOREX.r3.3HG0282320.1	2.080196058	-0.605168808	3.61112935	0.00068	0.033870225	-0.71994872	Fatty acid desaturase 1	elongation zone	6 h
HORVU.MOREX.r3.7HG0735840.1	0.946956833	4.848168125	3.630224652	0.00064	0.033339257	-0.72108942	serine/arginine repetitive matrix-like protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0175420.1	0.358964588	6.198454241	3.754375615	0.00043	0.028032118	-0.73036186	Leucine-rich repeat (LRR) family protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0108450.1	-0.549824363	5.259081061	-3.731404575	0.00047	0.029138607	-0.73210624	Protein kinase family protein, putative, expressed	elongation zone	6 h
HORVU.MOREX.r3.5HG0443920.1	0.522928884	3.840341821	3.61670286	0.00067	0.033798115	-0.73308867	Calmodulin-binding protein, putative, expressed	elongation zone	6 h
HORVU.MOREX.r3.2HG0176960.1	0.363367851	4.988465286	3.674100112	0.00056	0.031219405	-0.73550279	Kelch repeat-containing protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0171780.1	-1.701302517	-1.262454147	-3.500850504	0.00095	0.039256264	-0.74702175	transcription repressor	elongation zone	6 h
HORVU.MOREX.r3.4HG0332930.1	1.522278035	0.588837805	3.545192731	0.00083	0.036748557	-0.74950134	Short-chain dehydrogenase/reductase family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0731560.1	-1.405468965	-0.874013134	-3.49580604	0.00096	0.039433228	-0.75032113	Regulator of Vps4 activity in the MVB pathway protein, putative	elongation zone	6 h
HORVU.MOREX.r3.2HG0119030.1	-0.698232704	3.539432921	-3.571709606	0.00076	0.035893875	-0.75266859	Protein phosphatase 2c, putative	elongation zone	6 h
HORVU.MOREX.r3.6HG0609720.1	0.682038548	3.853973881	3.579837988	0.00075	0.035624994	-0.76587547	Glucosamine 6-phosphate N-acetyltransferase	elongation zone	6 h
HORVU.MOREX.r3.6HG0614830.1	0.30840065	6.98068667	3.761610612	0.00042	0.027662361	-0.77935148	Exocyst complex component SEC6	elongation zone	6 h
HORVU.MOREX.r3.5HG0441420.1	-2.585222576	-0.428611158	-3.603872772	0.00069	0.033986772	-0.78230944	Ankyrin repeat-containing protein, putative	elongation zone	6 h
HORVU.MOREX.r3.6HG0610500.1	-0.957271298	1.298618032	-3.730238866	0.00047	0.029138607	-0.79337631	Eukaryotic aspartyl protease family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0663940.1	-0.900157677	0.764913385	-3.647889889	0.0006	0.032525759	-0.79541432	Alpha/beta-Hydrolases superfamily protein, putative	elongation zone	6 h
HORVU.MOREX.r3.5HG0487070.1	-0.516555601	4.654929378	-3.659515179	0.00058	0.031886221	-0.80031021	Alpha/beta-Hydrolases superfamily protein, putative	elongation zone	6 h
HORVU.MOREX.r3.6HG0631710.1	-0.959376174	2.878977233	-3.783375877	0.0004	0.026712078	-0.80057324	Aquaporin	elongation zone	6 h
HORVU.MOREX.r3.1HG0062110.1	-1.259960551	0.941666543	-3.474226753	0.00103	0.040615136	-0.80969219	Pentatricopeptide repeat-containing protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0477750.1	-1.444196348	0.65835179	-3.515556988	0.00091	0.038564824	-0.81277538	Homeobox protein, putative	elongation zone	6 h
HORVU.MOREX.r3.4HG0363330.1	0.910417121	2.648390841	3.528949615	0.00087	0.037723585	-0.81637404	F-box/RNI-like superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0742080.1	-1.06199179	-1.326097459	-3.561850966	0.00079	0.035934872	-0.8261079	Receptor-like kinase	elongation zone	6 h
HORVU.MOREX.r3.1HG0086480.1	-1.447292219	0.131690052	-3.480074337	0.00101	0.040367299	-0.82923389	UV-B-induced protein, chloroplastic	elongation zone	6 h
HORVU.MOREX.r3.4HG0378450.1	-1.291613682	0.244687178	-3.465269268	0.00106	0.040858317	-0.82966076	#N/A	elongation zone	6 h
HORVU.MOREX.r3.7HG0674320.1	0.402260818	4.709886156	3.658876055	0.00058	0.031886221	-0.83327215	Vesicle transport protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0666340.1	0.537842407	4.728875506	3.613710367	0.00067	0.033870225	-0.83648536	Hexosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.5HG0462450.1	-1.394727884	-0.846663356	-3.461772173	0.00107	0.040858317	-0.83838501	S-acyltransferase	elongation zone	6 h
HORVU.MOREX.r3.7HG0641890.1	-3.630607398	-3.164564754	-3.499499842	0.00095	0.039256264	-0.83933149	Aspartic proteinase nepenthesin-2	elongation zone	6 h
HORVU.MOREX.r3.7HG0665990.1	-0.652882016	6.15668184	-3.756723745	0.00043	0.027913688	-0.84302483	Shikimate kinase	elongation zone	6 h
HORVU.MOREX.r3.2HG0120830.1	-1.628373815	-3.157076886	-3.465788933	0.00106	0.040858317	-0.846427	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.2HG0096710.1	-1.393826839	-1.753677392	-3.49030699	0.00098	0.039681075	-0.84744167	Cytochrome P450	elongation zone	6 h
HORVU.MOREX.r3.2HG0158180.1	-1.185681008	3.620949743	-3.565858465	0.00078	0.035934872	-0.84890612	Proline transporter	elongation zone	6 h
HORVU.MOREX.r3.7HG0714660.1	-1.422186979	-2.488173436	-3.456992539	0.00108	0.040886579	-0.85015479	Retrovirus-related Pol polyprotein from transposon TNT 1-94	elongation zone	6 h
HORVU.MOREX.r3.5HG0473030.1	-1.059884994	0.923732427	-3.457801879	0.00108	0.040886579	-0.85267083	2-aminoethanethiol dioxygenase	elongation zone	6 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.2HG0187450.1	-1.304715428	0.03595626	-3.648391175	0.0006	0.032525759	-0.85559221	Rhomboid-like protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0544290.1	-1.268733394	-0.109959598	-3.538990002	0.00085	0.036941016	-0.85561716	Glycerol-3-phosphate acyltransferase	elongation zone	6 h
HORVU.MOREX.r3.4HG0395540.1	-1.166388737	4.838553225	-3.717960741	0.00049	0.029586232	-0.85807641	Glutamine synthetase	elongation zone	6 h
HORVU.MOREX.r3.5HG0493850.1	0.498347115	7.419096029	3.72418554	0.00048	0.029402036	-0.86904307	Acyl-[acyl-carrier-protein] hydrolase	elongation zone	6 h
HORVU.MOREX.r3.2HG0165300.1	0.904904533	2.849287283	3.495565925	0.00096	0.039433228	-0.88626077	UPF0496 protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0632320.1	0.418590435	5.523777089	3.642972055	0.00061	0.032525759	-0.88952204	Leucine-rich repeat protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0616850.1	-3.754573666	-2.90585403	-3.511515923	0.00092	0.038757609	-0.89250604	Blue copper protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0285440.1	-1.107104217	-1.285046886	-3.50492844	0.00094	0.039105108	-0.89527843	#N/A	elongation zone	6 h
HORVU.MOREX.r3.3HG0241360.1	-1.993906581	-0.960116855	-3.547700149	0.00082	0.036546446	-0.90061759	ATPase E1-E2 type family protein / haloacid dehalogenase-like hy	elongation zone	6 h
HORVU.MOREX.r3.7HG0665040.1	-2.217504527	-3.452636637	-3.479239655	0.00101	0.040391023	-0.90215185	Protein EXORDIUM-like 1	elongation zone	6 h
HORVU.MOREX.r3.1HG0073430.1	-0.471739597	3.344558802	-3.538581471	0.00085	0.036941016	-0.91328672	O-fucosyltransferase family protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0500590.1	-0.994355921	1.729937267	-3.459786133	0.00108	0.040858317	-0.91421064	Receptor-like kinase	elongation zone	6 h
HORVU.MOREX.r3.7HG0706310.1	-0.550087908	5.228140664	-3.611910418	0.00068	0.033870225	-0.91854111	Alcohol dehydrogenase	elongation zone	6 h
HORVU.MOREX.r3.2HG0168700.1	1.549193918	0.03517856	3.46325728	0.00106	0.040858317	-0.92097701	ADP-ribosylation factor GTPase-activating protein AGD4	elongation zone	6 h
HORVU.MOREX.r3.3HG0273790.2	-0.81426197	2.302444592	-3.465564406	0.00106	0.040858317	-0.92147104	CTD small phosphatase-like protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0344640.1	0.462989296	3.700508827	3.556327339	0.0008	0.035982407	-0.92260367	Glycerophosphodiester phosphodiesterase	elongation zone	6 h
HORVU.MOREX.r3.7HG0726360.1	-0.324310801	5.450154375	-3.649467232	0.0006	0.032525759	-0.92782625	12-oxophytodienoate reductase	elongation zone	6 h
HORVU.MOREX.r3.5HG0469340.1	-1.193268551	0.552227437	-3.52567578	0.00088	0.037863675	-0.93868516	Fasciclin-like arabinogalactan-protein-like	elongation zone	6 h
HORVU.MOREX.r3.2HG0190710.1	0.371257775	4.642344889	3.577699835	0.00075	0.035692712	-0.94334853	#N/A	elongation zone	6 h
HORVU.MOREX.r3.7HG0720790.1	0.946175021	3.444490231	3.460103171	0.00107	0.040858317	-0.94644246	Myb family transcription factor family protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0189670.1	-1.073772461	0.283223271	-3.604750059	0.00069	0.033986772	-0.95031813	Aquaporin-like protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0714400.1	-0.991274792	2.70239141	-3.492481004	0.00097	0.039646685	-0.95441574	Auxin-responsive protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0721580.1	-1.515038816	-1.146006065	-3.416245266	0.00123	0.043449664	-0.95634402	Ras-related protein Rab-25	elongation zone	6 h
HORVU.MOREX.r3.6HG0626020.1	-1.231138459	1.680187154	-3.687830054	0.00053	0.030483629	-0.95645817	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.1HG0079870.1	0.934129884	5.830169089	3.643051603	0.00061	0.032525759	-0.96063528	Pectin lyase-like superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0087170.1	0.425257402	5.424188381	3.607381734	0.00068	0.033986772	-0.96750056	3-deoxy-manno-octulosonate cytidylyltransferase	elongation zone	6 h
HORVU.MOREX.r3.4HG0418460.1	-0.51671108	1.75953737	-3.625547656	0.00065	0.033489087	-0.97573261	Cysteine protease	elongation zone	6 h
HORVU.MOREX.r3.2HG0173040.1	-0.485780804	4.911334977	-3.624509234	0.00065	0.033489087	-0.97932127	Loricrin-like protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0609210.1	-1.26804156	1.030285608	-3.407881803	0.00126	0.043818088	-0.97942582	RNA binding protein, putative	elongation zone	6 h
HORVU.MOREX.r3.5HG0532120.1	-1.623815914	-1.755607472	-3.484974076	0.001	0.039927046	-0.98211399	Expansin	elongation zone	6 h
HORVU.MOREX.r3.5HG0524060.1	-1.343682815	3.909293568	-3.567210384	0.00078	0.035934872	-0.98473941	Remorin	elongation zone	6 h
HORVU.MOREX.r3.4HG0404530.1	-1.393158917	-1.741402323	-3.405694845	0.00127	0.043818088	-0.98727692	Transmembrane protein, putative	elongation zone	6 h
HORVU.MOREX.r3.2HG0168090.1	0.385930594	5.385495042	3.608058076	0.00068	0.033986772	-0.98973551	Sphingomyelin synthase-like domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0125330.1	-0.38679831	4.679437814	-3.583008571	0.00074	0.035480233	-0.98996649	RNA-binding protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0244040.1	-1.278156136	-2.293841422	-3.43082716	0.00117	0.042465578	-0.99026365	ethylene-responsive transcription factor	elongation zone	6 h
HORVU.MOREX.r3.4HG0368770.2	1.469603179	2.047876559	3.406129094	0.00126	0.043818088	-0.99334241	ATP-dependent Clp protease proteolytic subunit	elongation zone	6 h
HORVU.MOREX.r3.3HG0311870.1	1.933191096	0.203024233	3.443659131	0.00113	0.04173815	-1.00169377	EamA-like transporter family protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0545970.1	0.426895373	5.654969195	3.613211486	0.00067	0.033870225	-1.00206576	Short-chain dehydrogenase/reductase family protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0512230.1	-1.108969121	2.048290165	-3.46497461	0.00106	0.040858317	-1.00515546	Protein ENHANCED DISEASE RESISTANCE 2-like	elongation zone	6 h
HORVU.MOREX.r3.1HG0060370.1	3.203141388	-0.902409718	3.566632158	0.00078	0.035934872	-1.00526719	1,4-alpha-glucan branching enzyme GlgB	elongation zone	6 h
HORVU.MOREX.r3.2HG0160690.1	-1.204767415	-0.418955769	-3.490105445	0.00098	0.039681075	-1.01013463	RALF	elongation zone	6 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.5HG0526200.1	0.288792942	5.48572856	3.59290839	0.00072	0.034740116	-1.0152164	Sec14 cytosolic factor	elongation zone	6 h
HORVU.MOREX.r3.3HG0307120.1	0.512115268	8.36463409	3.706192838	0.0005	0.030363091	-1.01550934	S-adenosyl-L-methionine-dependent methyltransferases superfa	elongation zone	6 h
HORVU.MOREX.r3.4HG0394460.1	-1.206231266	0.734389124	-3.41876347	0.00122	0.043346752	-1.02179996	Protein DETOXIFICATION	elongation zone	6 h
HORVU.MOREX.r3.3HG0246500.1	-0.864018577	3.040521827	-3.644179625	0.00061	0.032525759	-1.02829179	Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A	elongation zone	6 h
HORVU.MOREX.r3.5HG0477980.1	-0.607312768	3.756005664	-3.556936486	0.0008	0.035982407	-1.02981776	Acetyl-coenzyme A synthetase	elongation zone	6 h
HORVU.MOREX.r3.4HG0364050.1	-0.739879198	2.580176455	-3.468885514	0.00105	0.040858317	-1.03252295	Sodium/hydrogen exchanger	elongation zone	6 h
HORVU.MOREX.r3.7HG0678020.1	0.99519063	1.442697113	3.430070132	0.00118	0.042487533	-1.03271959	WPP domain-interacting protein 1	elongation zone	6 h
HORVU.MOREX.r3.3HG0280630.1	0.34881626	5.914468206	3.610454703	0.00068	0.033870225	-1.03381986	Glycosylphosphatidylinositol anchor attachment 1 protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0480980.1	-1.803200929	-1.63821174	-3.435979877	0.00116	0.042177981	-1.03969479	Spermidine/putrescine import ATP-binding protein PotA	elongation zone	6 h
HORVU.MOREX.r3.5HG0516660.1	0.381593632	4.126867737	3.53898501	0.00085	0.036941016	-1.04134984	LEM3 (Ligand-effect modulator 3) family protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0461950.1	-0.783808851	2.971610109	-3.518334502	0.0009	0.038318953	-1.04145443	2-isopropylmalate synthase 2	elongation zone	6 h
HORVU.MOREX.r3.5HG0458300.1	1.70854909	0.796200207	3.406250817	0.00126	0.043818088	-1.04180535	transcription repressor	elongation zone	6 h
HORVU.MOREX.r3.2HG0117880.1	-2.863040425	-0.66122785	-3.389228939	0.00133	0.045015937	-1.0542159	GDSL esterase/lipase	elongation zone	6 h
HORVU.MOREX.r3.5HG0462880.1	-2.02694221	-1.070584552	-3.496708272	0.00096	0.039433228	-1.05478873	Serine/threonine-protein phosphatase 7 long form-like protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0582480.1	-0.728474771	2.535480373	-3.463267635	0.00106	0.040858317	-1.05481458	Ethylene-responsive transcription factor-like protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0330150.1	-2.128516404	-0.302066567	-3.376170856	0.00138	0.046197603	-1.05692469	MYB transcription factor	elongation zone	6 h
HORVU.MOREX.r3.3HG0297870.1	-2.494816956	-0.912086094	-3.395964009	0.0013	0.044484558	-1.05777805	BAG family molecular chaperone regulator 2	elongation zone	6 h
HORVU.MOREX.r3.3HG0292680.1	-0.764760996	2.459132616	-3.559836052	0.00079	0.035972648	-1.0693981	Replicase polyprotein 1a	elongation zone	6 h
HORVU.MOREX.r3.5HG0515030.1	0.620798381	4.511137793	3.492575917	0.00097	0.039646685	-1.07204352	Obg-like ATPase 1	elongation zone	6 h
HORVU.MOREX.r3.3HG0280060.1	-1.561307679	-2.863950573	-3.368182939	0.00142	0.046697345	-1.07712742	Heavy metal transport/detoxification superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0736150.1	-1.017119524	8.171407337	-3.730428017	0.00047	0.029138607	-1.07832428	Phosphatidylinositol transfer protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0486660.1	-1.069270516	-2.069765734	-3.413251048	0.00124	0.043691234	-1.0797734	Calcium-binding protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0096600.1	0.526825678	8.083914516	3.677340916	0.00055	0.031075507	-1.08052466	Pyruvate dehydrogenase E1 component subunit alpha	elongation zone	6 h
HORVU.MOREX.r3.4HG0398070.1	0.688446993	3.523000734	3.429443814	0.00118	0.042490959	-1.08128542	Protein kinase	elongation zone	6 h
HORVU.MOREX.r3.5HG0493070.1	0.430186531	6.006757924	3.605737926	0.00069	0.033986772	-1.08318631	Peptidylprolyl isomerase	elongation zone	6 h
HORVU.MOREX.r3.7HG0704450.1	-0.487948587	5.126566504	-3.579407991	0.00075	0.035624994	-1.08334799	Hexosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.6HG0601670.1	0.911809891	2.45037985	3.392503188	0.00132	0.044798804	-1.08476692	Phosphatidic acid phosphatase	elongation zone	6 h
HORVU.MOREX.r3.3HG0219380.1	-1.008140873	4.367645105	-3.640953483	0.00062	0.032645728	-1.08733599	Glutamate receptor ionotropic, NMDA 3A	elongation zone	6 h
HORVU.MOREX.r3.3HG0302570.1	-2.508745825	-3.210356093	-3.367652034	0.00142	0.046697345	-1.09062584	Laccase	elongation zone	6 h
HORVU.MOREX.r3.6HG0577220.1	-1.96185772	-2.233904068	-3.362637819	0.00144	0.046971179	-1.09188501	Glycosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.1HG0046180.1	-0.463043475	5.918664759	-3.630207163	0.00064	0.033339257	-1.09701758	Ser/Thr protein phosphatase family protein, expressed	elongation zone	6 h
HORVU.MOREX.r3.4HG0380540.1	-0.617719899	3.365321911	-3.506978351	0.00093	0.039007436	-1.09899924	Aquaporin-1	elongation zone	6 h
HORVU.MOREX.r3.1HG0077950.1	0.363648708	4.840037428	3.542765721	0.00084	0.036935434	-1.10307781	BSD domain containing protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0204940.1	0.531883725	6.058216754	3.565556499	0.00078	0.035934872	-1.10327728	Crossover junction endonuclease EME1	elongation zone	6 h
HORVU.MOREX.r3.3HG0222830.1	0.327945155	7.515891005	3.668542031	0.00057	0.031591904	-1.10427142	Heavy metal transport/detoxification superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0473970.1	-2.387634429	-3.048444071	-3.377725252	0.00138	0.04605869	-1.10640124	Glycosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.3HG0321140.1	-2.032977367	-2.331879343	-3.374358192	0.00139	0.046297461	-1.1071247	Glutamate-1-semialdehyde 2,1-aminomutase 2	elongation zone	6 h
HORVU.MOREX.r3.5HG0518390.1	-2.60642644	-0.172193667	-3.499203216	0.00095	0.039256264	-1.10790825	BTB/POZ domain containing protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0415420.1	0.6046561	6.947213857	3.618530517	0.00066	0.033752681	-1.11775158	Tubulin beta chain	elongation zone	6 h
HORVU.MOREX.r3.7HG0727350.1	0.461459796	10.95622204	3.750354884	0.00044	0.028211116	-1.1187487	#N/A	elongation zone	6 h
HORVU.MOREX.r3.6HG0564590.1	0.482683245	6.449269546	3.576529748	0.00075	0.035692712	-1.1214732	O-fucosyltransferase family protein	elongation zone	6 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.6HG0573930.1	-0.423991807	3.609831823	-3.477204752	0.00102	0.04048377	-1.12530013	Mediator of RNA polymerase II transcription subunit 18	elongation zone	6 h
HORVU.MOREX.r3.6HG0627380.3	-1.669154308	1.232115316	-3.402710744	0.00128	0.043833962	-1.12727549	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfami	elongation zone	6 h
HORVU.MOREX.r3.4HG0410640.1	0.387804262	8.151713261	3.659867614	0.00058	0.031886221	-1.12878455	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase s	elongation zone	6 h
HORVU.MOREX.r3.5HG0532150.1	-1.551110063	-2.26204476	-3.387437424	0.00134	0.04518326	-1.13462054	Expansin	elongation zone	6 h
HORVU.MOREX.r3.5HG0536710.1	0.483148693	6.624728725	3.619464838	0.00066	0.033752681	-1.134657	NAD/NADP-dependent betaine aldehyde dehydrogenase	elongation zone	6 h
HORVU.MOREX.r3.2HG0215830.1	0.948562118	2.436514446	3.362510313	0.00144	0.046971179	-1.1379331	CsAtPR5	elongation zone	6 h
HORVU.MOREX.r3.2HG0107960.1	-0.550273195	3.123366617	-3.460354707	0.00107	0.040858317	-1.13869949	Phosphoinositide phospholipase C	elongation zone	6 h
HORVU.MOREX.r3.3HG0220360.1	0.851891693	4.616464522	3.458617057	0.00108	0.040886579	-1.13958331	Disease resistance protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0615130.1	-0.745681479	3.141376461	-3.565193759	0.00078	0.035934872	-1.14154508	TCP transcription factor	elongation zone	6 h
HORVU.MOREX.r3.4HG0417010.1	-1.06888801	-1.713964929	-3.40506063	0.00127	0.043818088	-1.14272089	Receptor protein kinase, putative	elongation zone	6 h
HORVU.MOREX.r3.7HG0747230.1	-0.591534859	2.606944875	-3.438354855	0.00115	0.041957464	-1.14391566	Non-specific serine/threonine protein kinase	elongation zone	6 h
HORVU.MOREX.r3.7HG0652950.1	1.188317314	1.220754935	3.353216324	0.00148	0.047599823	-1.14555958	NBS-LRR-like resistance protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0026080.1	-0.627323442	4.010773585	-3.488945486	0.00098	0.039681075	-1.15197786	RING finger protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0214240.1	0.591760427	3.183258219	3.420927059	0.00121	0.043205753	-1.15214231	Disease resistance protein (NBS-LRR class) family	elongation zone	6 h
HORVU.MOREX.r3.2HG0168770.1	-0.60205077	3.537711265	-3.490154737	0.00098	0.039681075	-1.16276627	Scarecrow transcription factor family protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0298680.1	-0.778583864	1.911503731	-3.445868675	0.00112	0.041610797	-1.16431576	Myb transcription factor	elongation zone	6 h
HORVU.MOREX.r3.1HG0086120.1	1.659779471	4.055301306	3.370417593	0.00141	0.046697345	-1.16826027	Histone H2B	elongation zone	6 h
HORVU.MOREX.r3.1HG0086390.1	-0.906213328	-0.260888993	-3.444991364	0.00112	0.041645779	-1.17445583	#N/A	elongation zone	6 h
HORVU.MOREX.r3.5HG0513340.1	-1.599288247	-3.018568987	-3.338593156	0.00155	0.048879452	-1.17573303	Basic-leucine zipper (bZIP) transcription factor family protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0072910.2	0.405567947	4.342104799	3.460615287	0.00107	0.040858317	-1.18214329	Serine/threonine-protein kinase ATM	elongation zone	6 h
HORVU.MOREX.r3.5HG0470170.1	0.552753579	3.126834047	3.40833289	0.00126	0.043818088	-1.19137647	F-box family protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0091360.1	0.490690398	6.214276876	3.557310498	0.0008	0.035982407	-1.19657145	Delta(14)-sterol reductase	elongation zone	6 h
HORVU.MOREX.r3.4HG0342000.1	-0.717688692	0.190754791	-3.416497126	0.00123	0.043449664	-1.20642895	4-coumarate:CoA ligase-like protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0476380.1	0.590576758	4.634572865	3.466944592	0.00105	0.040858317	-1.21230453	Major facilitator superfamily transporter	elongation zone	6 h
HORVU.MOREX.r3.5HG0501980.1	0.406622867	5.561069419	3.522936604	0.00089	0.038100943	-1.2137628	Rop guanine nucleotide exchange factor, putative	elongation zone	6 h
HORVU.MOREX.r3.7HG0739230.1	-2.284631643	-3.450977617	-3.326417649	0.0016	0.049756476	-1.21437207	Jacalin-like lectin	elongation zone	6 h
HORVU.MOREX.r3.5HG0461280.1	-0.488690851	6.014759518	-3.552695926	0.00081	0.036184546	-1.21476499	Calcium-binding EF-hand protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0554050.1	-0.910612159	-1.569574336	-3.381902507	0.00136	0.045711209	-1.216031	cyclin-dependent kinase inhibitor	elongation zone	6 h
HORVU.MOREX.r3.2HG0156810.1	1.708782825	1.309433717	3.324454835	0.00161	0.049971	-1.22382897	Sodium/potassium/calcium exchanger 3	elongation zone	6 h
HORVU.MOREX.r3.5HG0517740.1	-1.190237811	-0.307208015	-3.533567508	0.00086	0.037429607	-1.22712874	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.3HG0245440.1	-0.99505647	0.700858326	-3.39082436	0.00132	0.044875615	-1.22935823	Cellulose synthase	elongation zone	6 h
HORVU.MOREX.r3.1HG0079750.1	-1.123857566	-1.155378593	-3.364004037	0.00143	0.046971179	-1.23041424	MYB transcription factor	elongation zone	6 h
HORVU.MOREX.r3.3HG0254940.1	-0.88368612	2.451212431	-3.601933452	0.0007	0.034109179	-1.23159154	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.3HG0288140.1	0.311331045	6.173911395	3.563158785	0.00078	0.035934872	-1.23653531	Golgin candidate 1	elongation zone	6 h
HORVU.MOREX.r3.2HG0172110.1	-0.577920929	5.282401422	-3.561790827	0.00079	0.035934872	-1.24485477	Dihydrofolate reductase	elongation zone	6 h
HORVU.MOREX.r3.1HG0067720.1	-1.073963716	-2.106023761	-3.350940847	0.00149	0.047781359	-1.24906573	#N/A	elongation zone	6 h
HORVU.MOREX.r3.4HG0348670.1	0.32495001	7.764170114	3.638214948	0.00062	0.032755332	-1.24995178	#N/A	elongation zone	6 h
HORVU.MOREX.r3.1HG0061710.1	-0.490520508	5.632385509	-3.577179121	0.00075	0.035692712	-1.25831528	Trichome birefringence-like protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0002960.1	-0.907623908	0.278872787	-3.502006835	0.00095	0.039256264	-1.26945082	NBS-LRR disease resistance protein, putative, expressed	elongation zone	6 h
HORVU.MOREX.r3.3HG0275910.1	3.05451757	-0.86003395	3.442746676	0.00113	0.041777902	-1.2728986	Transcription factor GTE4-like protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0420630.1	0.513343995	3.720926699	3.447817025	0.00111	0.041517003	-1.27366929	Ankyrin repeat family protein	elongation zone	6 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0224680.1	0.378954852	5.580543005	3.514757053	0.00091	0.038579099	-1.27368031	Ferredoxin reductase-like protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0734670.1	0.481562973	6.626504106	3.57354513	0.00076	0.035856081	-1.27401052	L-ascorbate oxidase	elongation zone	6 h
HORVU.MOREX.r3.7HG0751060.1	0.406171284	4.948457618	3.503663188	0.00094	0.039176352	-1.27432509	Disease resistance protein (NBS-LRR class) family	elongation zone	6 h
HORVU.MOREX.r3.4HG0349310.1	0.368968984	5.375878972	3.499016835	0.00095	0.039256264	-1.27626465	Sec1 family domain-containing protein 2	elongation zone	6 h
HORVU.MOREX.r3.4HG0354970.1	0.580167076	6.732308281	3.55928249	0.00079	0.035972648	-1.27643003	Omega-3 fatty acid desaturase	elongation zone	6 h
HORVU.MOREX.r3.7HG0718190.1	-0.737788924	6.009060521	-3.617939424	0.00066	0.033752681	-1.28265013	ABC transporter family protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0192610.1	-0.56292893	5.913188646	-3.46943483	0.00104	0.040858317	-1.28514394	DNA ligase	elongation zone	6 h
HORVU.MOREX.r3.1HG0073460.1	-0.492927168	2.975475398	-3.398807763	0.00129	0.044254508	-1.2878058	Microneme/rhoptry antigen	elongation zone	6 h
HORVU.MOREX.r3.4HG0389250.1	-1.39026176	3.018685792	-3.352746352	0.00148	0.047599823	-1.29554757	lipase, putative (DUF620)	elongation zone	6 h
HORVU.MOREX.r3.6HG0616240.1	-0.913902885	-0.522759558	-3.465007106	0.00106	0.040858317	-1.30130591	Endoglucanase	elongation zone	6 h
HORVU.MOREX.r3.2HG0187940.1	-0.732937167	5.04269045	-3.499592904	0.00095	0.039256264	-1.30288943	Niemann-Pick C1 protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0739030.1	-0.562701519	5.253411819	-3.51993301	0.0009	0.038291477	-1.30478675	Kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0642520.1	-1.37787495	-0.871699978	-3.474361026	0.00103	0.040615136	-1.30806933	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.3HG0312490.1	0.660330948	2.855498414	3.334247866	0.00157	0.049210449	-1.30856954	Short-chain dehydrogenase/reductase family protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0346720.1	0.475678784	10.60860825	3.694266969	0.00052	0.030363091	-1.31381815	Protein disulfide-isomerase	elongation zone	6 h
HORVU.MOREX.r3.4HG0384390.1	-0.898818765	1.57490258	-3.391797497	0.00132	0.044819198	-1.32193356	Protein kinase family protein, putative, expressed	elongation zone	6 h
HORVU.MOREX.r3.1HG0023970.1	-1.093184483	0.759180505	-3.368641305	0.00141	0.046697345	-1.33028324	GATA transcription factor, putative	elongation zone	6 h
HORVU.MOREX.r3.1HG0057030.1	0.67712633	6.546045506	3.511214245	0.00092	0.038757609	-1.33666601	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.1HG0063810.1	0.400247305	4.973905479	3.451084979	0.0011	0.041410027	-1.34007455	Cyclin family protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0008200.1	1.528341759	1.354368368	3.386105239	0.00134	0.045289016	-1.34512433	Cytochrome P450	elongation zone	6 h
HORVU.MOREX.r3.7HG0711890.1	-1.024141786	2.553034049	-3.448104206	0.00111	0.041517003	-1.34543805	O-methyltransferase	elongation zone	6 h
HORVU.MOREX.r3.7HG0715570.1	0.394750591	6.466382964	3.520264115	0.00089	0.038291477	-1.35382994	Transmembrane protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0525700.1	0.366859152	7.295514432	3.530427997	0.00087	0.037633014	-1.35605801	Leukotriene a-4 hydrolase aminopeptidase	elongation zone	6 h
HORVU.MOREX.r3.4HG0332920.1	0.30273669	7.313310024	3.55236508	0.00081	0.036184546	-1.3578162	26S proteasome non-atpase regulatory subunit, putative	elongation zone	6 h
HORVU.MOREX.r3.6HG0568640.1	0.365740231	4.543924675	3.440499803	0.00114	0.041925776	-1.35959638	Methyltransferase domain protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0688870.1	-0.678369579	6.011072385	-3.540228487	0.00084	0.036941016	-1.36162601	Monodehydroascorbate reductase	elongation zone	6 h
HORVU.MOREX.r3.6HG0574990.1	-0.585422916	7.228108567	-3.584936172	0.00073	0.035436154	-1.36498367	ABC transporter B family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0668820.1	-0.584137731	4.620228035	-3.562845071	0.00079	0.035934872	-1.3683326	Endoglucanase	elongation zone	6 h
HORVU.MOREX.r3.3HG0298750.1	0.54170438	5.760333104	3.489058941	0.00098	0.039681075	-1.36976485	magnesium transporter NIPA (DUF803)	elongation zone	6 h
HORVU.MOREX.r3.4HG0400740.1	0.23990593	8.244974267	3.582253051	0.00074	0.035480233	-1.37074328	Cell division cycle protein 48-like protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0238180.1	0.422413375	4.144586965	3.407385077	0.00126	0.043818088	-1.37129481	#N/A	elongation zone	6 h
HORVU.MOREX.r3.6HG0555700.1	0.376158393	8.875975145	3.618782469	0.00066	0.033752681	-1.37820655	Calreticulin/calnexin	elongation zone	6 h
HORVU.MOREX.r3.7HG0654330.1	-0.520051316	7.269216004	-3.562970179	0.00079	0.035934872	-1.38182486	ABC transporter, putative	elongation zone	6 h
HORVU.MOREX.r3.3HG0326430.1	0.317758576	5.095188036	3.456508471	0.00109	0.040886579	-1.38687321	Diphosphomevalonate decarboxylase	elongation zone	6 h
HORVU.MOREX.r3.7HG0688040.1	0.721205581	2.581060956	3.327645305	0.0016	0.049650942	-1.39067514	DUF241 domain protein, putative (DUF241)	elongation zone	6 h
HORVU.MOREX.r3.5HG0527650.1	0.637056037	4.818573339	3.420425644	0.00121	0.043205753	-1.39463394	Succinate--CoA ligase [ADP-forming] subunit alpha-1, mitochond	elongation zone	6 h
HORVU.MOREX.r3.1HG0073170.1	0.624287957	5.178735655	3.407966884	0.00126	0.043818088	-1.39670533	F-box protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0482570.1	-0.321675158	4.680679207	-3.402551342	0.00128	0.043833962	-1.40711225	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyr	elongation zone	6 h
HORVU.MOREX.r3.5HG0533230.1	0.487085107	5.643176833	3.47511291	0.00103	0.040615136	-1.40969915	Pirin-like protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0079140.1	-0.554467319	4.43581546	-3.456581276	0.00109	0.040886579	-1.41177469	Kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0307850.1	0.652468311	6.891758697	3.555567126	0.0008	0.035987623	-1.41423869	Basic 7S globulin	elongation zone	6 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.7HG0730510.1	-0.92235097	-1.831161525	-3.329009471	0.00159	0.049525669	-1.42151805	Germin-like protein 1	elongation zone	6 h
HORVU.MOREX.r3.2HG0117980.1	0.380715929	6.65430886	3.507293776	0.00093	0.039007436	-1.42154302	Transmembrane protein 115	elongation zone	6 h
HORVU.MOREX.r3.5HG0488040.1	-1.312871965	-1.230138021	-3.378883603	0.00137	0.045974621	-1.43006309	Blue copper protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0094980.1	0.486850051	4.287158731	3.374791352	0.00139	0.046297461	-1.43033665	Mitochondrial outer membrane porin	elongation zone	6 h
HORVU.MOREX.r3.2HG0213250.1	0.542454716	6.347478748	3.506418383	0.00093	0.039007436	-1.43203225	Choline transporter-related family protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0363180.1	0.258002357	9.157327695	3.596301548	0.00071	0.034460123	-1.43222046	Translationally-controlled tumor protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0070340.1	-0.999266551	4.307026595	-3.486595093	0.00099	0.039808834	-1.43395633	Protein kinase-like protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0674990.1	0.4790589	3.286294703	3.34356581	0.00152	0.048382678	-1.43598953	Mannan endo-1,4-beta-mannosidase-like protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0490030.1	0.243342609	7.481265074	3.547777977	0.00082	0.036546446	-1.45729909	Vacuolar protein sorting-associated protein 52	elongation zone	6 h
HORVU.MOREX.r3.2HG0134400.1	-0.370541306	6.098222844	-3.478229521	0.00102	0.040436406	-1.45938479	Protein DETOXIFICATION	elongation zone	6 h
HORVU.MOREX.r3.4HG0382500.1	0.419481917	5.221396135	3.422721373	0.0012	0.043133621	-1.46115554	Seed maturation protein PM36, putative, expressed	elongation zone	6 h
HORVU.MOREX.r3.6HG0555660.2	0.386082859	7.208637701	3.513993449	0.00091	0.038589259	-1.46352661	Calreticulin/calnexin	elongation zone	6 h
HORVU.MOREX.r3.7HG0726770.1	-0.912777323	2.292249938	-3.370036361	0.00141	0.046697345	-1.47054762	Glycine-rich protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0050780.1	0.319692238	6.71627124	3.518659058	0.0009	0.038318953	-1.47234215	Major facilitator superfamily domain-containing protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0411870.1	0.737951282	4.541599175	3.367149856	0.00142	0.046697345	-1.47706039	Cysteine-rich repeat secretory protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0111880.1	2.361155522	-1.175412118	3.364418186	0.00143	0.046971179	-1.48260999	DNA/RNA helicase	elongation zone	6 h
HORVU.MOREX.r3.6HG0604210.1	0.365611674	6.058555923	3.451678315	0.0011	0.041410027	-1.48362219	Protease HtpX	elongation zone	6 h
HORVU.MOREX.r3.4HG0405400.1	-1.240438052	2.976905729	-3.393652076	0.00131	0.044719161	-1.49830958	DUF936 family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0661490.1	0.306509178	6.094894031	3.463143467	0.00106	0.040858317	-1.50090614	Stromal cell-derived factor 2	elongation zone	6 h
HORVU.MOREX.r3.7HG0749870.1	-0.585558346	4.569999785	-3.464286228	0.00106	0.040858317	-1.50914651	Glucuronoxylan 4-O-methyltransferase	elongation zone	6 h
HORVU.MOREX.r3.7HG0677510.1	0.443940306	5.971823823	3.446115077	0.00112	0.041610797	-1.52115952	Glycosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.2HG0185340.1	-0.848064	1.427350358	-3.354002437	0.00148	0.047599823	-1.53081582	Cationic amino acid transporter, putative	elongation zone	6 h
HORVU.MOREX.r3.7HG0728190.1	0.438885105	4.089813032	3.358257464	0.00146	0.047382603	-1.53391466	Purple acid phosphatase	elongation zone	6 h
HORVU.MOREX.r3.1HG0085380.1	-0.465559834	4.053078396	-3.348340733	0.0015	0.048034173	-1.53404288	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfami	elongation zone	6 h
HORVU.MOREX.r3.2HG0177290.1	2.196059937	-1.308802463	3.342778792	0.00153	0.048382678	-1.53801593	C3H4 type zinc finger protein (DUF23)	elongation zone	6 h
HORVU.MOREX.r3.2HG0127260.1	-1.06885664	-1.061970634	-3.355454706	0.00147	0.047574989	-1.54274819	COBRA-like protein	elongation zone	6 h
HORVU.MOREX.r3.5HG0513440.1	0.357121751	5.701505149	3.431055316	0.00117	0.042465578	-1.54893642	#N/A	elongation zone	6 h
HORVU.MOREX.r3.3HG0280970.1	0.456301625	5.971205795	3.420887364	0.00121	0.043205753	-1.55811501	Protein methyltransferase	elongation zone	6 h
HORVU.MOREX.r3.1HG0093710.1	0.233333322	6.865906621	3.466695224	0.00105	0.040858317	-1.55946627	dihydroflavonol 4-reductase/flavanone protein	elongation zone	6 h
HORVU.MOREX.r3.4HG0404740.1	-0.702204995	2.889075204	-3.412341999	0.00124	0.04373537	-1.57021574	Hydrolase, alpha/beta fold family protein, expressed	elongation zone	6 h
HORVU.MOREX.r3.2HG0212570.1	0.383682747	10.53927453	3.599788197	0.0007	0.03425392	-1.57479522	Calreticulin	elongation zone	6 h
HORVU.MOREX.r3.7HG0736930.1	0.253405497	7.557950747	3.50834383	0.00093	0.039007436	-1.57740298	Embryo yellow protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0107900.1	0.38593915	7.940344995	3.48736894	0.00099	0.039793297	-1.57988236	Elongation factor 1-alpha	elongation zone	6 h
HORVU.MOREX.r3.4HG0352200.1	-0.676587684	3.627838098	-3.342552995	0.00153	0.048382678	-1.59052589	Methyltransferase-related protein, putative	elongation zone	6 h
HORVU.MOREX.r3.4HG0406140.1	-0.478817603	5.424724713	-3.402773487	0.00128	0.043833962	-1.59164637	Transmembrane protein 131	elongation zone	6 h
HORVU.MOREX.r3.2HG0182400.1	-0.757431318	5.649464396	-3.449697557	0.00111	0.041507984	-1.59662405	Aquaporin	elongation zone	6 h
HORVU.MOREX.r3.4HG0416190.1	0.267107679	9.750154012	3.582246804	0.00074	0.035480233	-1.61030611	Coatomer subunit alpha	elongation zone	6 h
HORVU.MOREX.r3.2HG0124660.1	-0.343600778	4.762294428	-3.368817039	0.00141	0.046697345	-1.61109905	Dihydropteroate synthase, putative	elongation zone	6 h
HORVU.MOREX.r3.1HG0067410.1	0.362918449	5.64638285	3.385052511	0.00135	0.045357194	-1.61633554	1-acyl-sn-glycerol-3-phosphate acyltransferase	elongation zone	6 h
HORVU.MOREX.r3.6HG0616300.1	-0.521691506	5.182691489	-3.431754011	0.00117	0.042465578	-1.61857136	Histidine kinase	elongation zone	6 h
HORVU.MOREX.r3.3HG0329760.1	-0.583435797	4.295442546	-3.346474417	0.00151	0.048194138	-1.63224842	Ankyrin repeat family protein	elongation zone	6 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0326240.1	0.502747604	5.727778629	3.369659365	0.00141	0.046697345	-1.63722507	Beta-fructofuranosidase, insoluble protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0591570.1	0.313338275	7.825511756	3.468402619	0.00105	0.040858317	-1.63766134	26S proteasome non-atpase regulatory subunit, putative	elongation zone	6 h
HORVU.MOREX.r3.2HG0200920.1	-0.689918431	3.047317061	-3.435434301	0.00116	0.042177981	-1.65165954	Agmatine coumaroyltransferase-2	elongation zone	6 h
HORVU.MOREX.r3.5HG0511450.1	-0.341933839	5.650127206	-3.398241577	0.00129	0.044255756	-1.65308296	ABC transporter B family protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0685870.1	0.234160522	7.40990073	3.46249263	0.00107	0.040858317	-1.65881293	Ankyrin repeat domain containing protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0054010.1	-0.561367347	5.84165697	-3.448003074	0.00111	0.041517003	-1.65896447	zinc finger B-box protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0728000.1	-0.571629244	5.007313233	-3.418074448	0.00122	0.043361315	-1.66557838	Glycosyltransferase	elongation zone	6 h
HORVU.MOREX.r3.5HG0529780.1	0.400934389	6.056073639	3.42843689	0.00118	0.042490959	-1.6680417	Pectin lyase-like superfamily protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0566940.1	-0.559709745	4.63219243	-3.33370285	0.00157	0.049214696	-1.68170997	Sulfurtransferase	elongation zone	6 h
HORVU.MOREX.r3.1HG0093050.1	-0.806018447	4.062497425	-3.329621542	0.00159	0.049511037	-1.6867662	Indole-3-acetic acid-amido synthetase GH3.3	elongation zone	6 h
HORVU.MOREX.r3.6HG0600910.1	-1.106033705	1.060688972	-3.405701632	0.00127	0.043818088	-1.68952789	Aquaporin	elongation zone	6 h
HORVU.MOREX.r3.6HG0557920.1	-0.830719314	4.693871457	-3.335785062	0.00156	0.04913705	-1.69248614	Auxin response factor	elongation zone	6 h
HORVU.MOREX.r3.6HG0611250.1	0.2039617	6.631497812	3.428293185	0.00118	0.042490959	-1.70104563	BSD domain containing protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0075730.1	-0.837858635	1.539739381	-3.438983634	0.00114	0.041952802	-1.70506589	Subtilisin-like protease	elongation zone	6 h
HORVU.MOREX.r3.2HG0119160.1	0.464707348	6.243872664	3.33508557	0.00156	0.049163604	-1.74308926	#N/A	elongation zone	6 h
HORVU.MOREX.r3.1HG0028150.1	-0.821982076	4.589078583	-3.345426561	0.00151	0.048269373	-1.76276913	Leucine-rich repeat-containing protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0687630.1	0.540226522	7.969316852	3.434823879	0.00116	0.042180694	-1.7672578	Acyl carrier protein	elongation zone	6 h
HORVU.MOREX.r3.3HG0318700.1	-0.475844535	6.088388292	-3.404910549	0.00127	0.043818088	-1.76963284	Phosphotransferase	elongation zone	6 h
HORVU.MOREX.r3.2HG0172730.1	0.416197187	7.54861275	3.403443169	0.00127	0.043833962	-1.79656365	Alpha-ketoglutarate-dependent dioxygenase alkB-like protein 2	elongation zone	6 h
HORVU.MOREX.r3.7HG0721760.1	0.323215645	8.421100262	3.440384213	0.00114	0.041925776	-1.82924354	Translocon-associated protein subunit alpha	elongation zone	6 h
HORVU.MOREX.r3.6HG0597590.1	0.357031684	6.568013907	3.357453481	0.00146	0.047382603	-1.84109689	Protein disulfide-isomerase	elongation zone	6 h
HORVU.MOREX.r3.3HG0233990.1	-0.988127748	1.6033308	-3.411160726	0.00124	0.043815453	-1.85735123	Xyloglucan endotransglucosylase/hydrolase	elongation zone	6 h
HORVU.MOREX.r3.2HG0160130.1	-0.553722704	3.662810319	-3.331517994	0.00158	0.049383572	-1.86644381	Basic helix-loop-helix transcription factor	elongation zone	6 h
HORVU.MOREX.r3.3HG0287690.1	-0.784211902	2.64681478	-3.331711403	0.00158	0.049383572	-1.86824124	Profilin	elongation zone	6 h
HORVU.MOREX.r3.3HG0255020.1	-0.800215572	3.485610317	-3.415129866	0.00123	0.043520317	-1.87307188	Peroxidase	elongation zone	6 h
HORVU.MOREX.r3.2HG0150450.1	0.575217754	7.245663801	3.355032254	0.00147	0.047574989	-1.87619477	Pyruvate kinase	elongation zone	6 h
HORVU.MOREX.r3.2HG0170160.1	0.305417895	8.212366788	3.408198121	0.00126	0.043818088	-1.88485399	Cleft lip and palate transmembrane 1	elongation zone	6 h
HORVU.MOREX.r3.6HG0624650.1	0.330061968	8.612307726	3.439772286	0.00114	0.041928054	-1.89889949	Transmembrane 9 superfamily member	elongation zone	6 h
HORVU.MOREX.r3.5HG0425110.1	-0.616496562	6.461930984	-3.348116638	0.0015	0.048034173	-1.906502	Cationic amino acid transporter, putative	elongation zone	6 h
HORVU.MOREX.r3.7HG0661890.1	0.490000707	7.9160487	3.381256402	0.00136	0.045724589	-1.92201615	3-oxoacyl-[acyl-carrier-protein] synthase	elongation zone	6 h
HORVU.MOREX.r3.1HG0067630.1	-0.387958686	5.282271317	-3.330596087	0.00158	0.049443359	-1.95208936	Serine/threonine-protein kinase	elongation zone	6 h
HORVU.MOREX.r3.3HG0299220.1	-0.46464755	5.799007839	-3.353096602	0.00148	0.047599823	-1.96161521	Kinase family protein	elongation zone	6 h
HORVU.MOREX.r3.6HG0608780.1	0.432310842	7.822442469	3.363336781	0.00144	0.046971179	-1.96503675	Heat shock 70 kDa protein, putative	elongation zone	6 h
HORVU.MOREX.r3.5HG0472960.1	0.327077857	10.61648489	3.48385005	0.001	0.039985373	-1.98938514	Phosphoenolpyruvate carboxylase	elongation zone	6 h
HORVU.MOREX.r3.2HG0206470.1	-0.461365836	6.277699834	-3.336479466	0.00156	0.049111355	-1.99955379	Loricrin-like protein	elongation zone	6 h
HORVU.MOREX.r3.7HG0700270.1	0.336032051	7.724734938	3.34441238	0.00152	0.04833998	-2.01023999	Transaldolase	elongation zone	6 h
HORVU.MOREX.r3.7HG0746770.1	0.433597928	10.27031467	3.35784766	0.00146	0.047382603	-2.24500156	Chaperone protein htpG family protein	elongation zone	6 h
HORVU.MOREX.r3.2HG0134530.1	0.499993384	9.627861055	3.357656866	0.00146	0.047382603	-2.26664854	Brefeldin A-inhibited guanine nucleotide-exchange protein	elongation zone	6 h
HORVU.MOREX.r3.1HG0078900.1	-2.540241299	5.8370464	-28.86545308	4.26E-34	8.73E-30	65.7525437	MATH domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0447830.1	-1.596342521	4.419279148	-13.40207822	1.17E-18	1.20E-14	32.05124676	Sterile alpha motif (SAM) domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0070480.1	-1.337952657	6.291080843	-12.26785472	4.12E-17	2.82E-13	28.72182961	60 kDa chaperonin	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0280700.1	0.85887016	6.27769849	11.60700024	3.55E-16	1.82E-12	26.5911742	Katanin p60 ATPase-containing subunit A1	elongation zone	12 h
HORVU.MOREX.r3.1HG0067040.1	-1.091220419	7.101906906	-10.16812717	4.67E-14	1.60E-10	21.70255432	NAC domain protein,	elongation zone	12 h
HORVU.MOREX.r3.6HG0546230.1	5.950588965	-1.679648171	10.63420577	9.35E-15	3.84E-11	20.82196479	Disease resistance protein RPM1	elongation zone	12 h
HORVU.MOREX.r3.7HG0739910.1	1.271815913	4.210713917	9.222405424	1.32E-12	3.86E-09	18.52866828	Disease resistance protein (NBS-LRR class) family	elongation zone	12 h
HORVU.MOREX.r3.7HG0729150.1	-5.401087623	-2.071842766	-8.638439118	1.08E-11	2.47E-08	15.34778252	GDSL esterase/lipase	elongation zone	12 h
HORVU.MOREX.r3.2HG0111680.1	-5.398840898	-2.082427636	-9.151045792	1.70E-12	4.36E-09	14.14453901	Formate--tetrahydrofolate ligase	elongation zone	12 h
HORVU.MOREX.r3.1HG0067030.1	-0.856183796	5.504670742	-7.670438386	3.76E-10	7.02E-07	12.82369273	Protein trichome birefringence	elongation zone	12 h
HORVU.MOREX.r3.7HG0727570.1	3.835277904	-0.569333422	7.693927943	3.45E-10	7.02E-07	11.7838467	ATP-dependent RNA helicase, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0024020.1	1.005817158	5.072656773	7.319316428	1.38E-09	2.36E-06	11.67339862	Heparan-alpha-glucosaminide N-acetyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0297940.1	2.581895273	3.507795484	7.160235006	2.49E-09	3.93E-06	11.0374204	Transcription initiation factor TFIID subunit 9	elongation zone	12 h
HORVU.MOREX.r3.3HG0298020.1	2.037662695	3.677613517	6.710096779	1.32E-08	1.93E-05	9.568584072	Transcription initiation factor TFIID subunit 9	elongation zone	12 h
HORVU.MOREX.r3.1HG0067420.1	1.84151765	2.43369759	6.374136726	4.57E-08	6.25E-05	8.253160805	Cyclic nucleotide-gated channel	elongation zone	12 h
HORVU.MOREX.r3.7HG0713840.1	-1.832686304	-2.185081282	-6.306367795	5.87E-08	7.52E-05	8.070272429	Cytochrome P450	elongation zone	12 h
HORVU.MOREX.r3.7HG0751110.1	1.059820126	4.358148537	6.129681947	1.12E-07	0.000128142	7.451255415	Kinesin-like	elongation zone	12 h
HORVU.MOREX.r3.5HG0456970.1	0.990795929	5.8820687	6.147814613	1.05E-07	0.000126931	7.440748241	Methylthioribose-1-phosphate isomerase	elongation zone	12 h
HORVU.MOREX.r3.3HG0307630.1	3.377981627	2.923305984	5.930290449	2.34E-07	0.000239599	6.484933655	SET-domain protein lysine methyltransferase family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0526250.1	0.489819837	12.0381843	6.038535948	1.57E-07	0.000169649	6.336778005	70 kDa heat shock protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0510830.1	1.353050301	5.120306759	5.795042125	3.83E-07	0.000341408	6.308574636	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0216110.1	0.534201675	5.350102781	5.823024013	3.46E-07	0.000327709	6.236049967	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0254260.1	-1.024300514	4.868531812	-5.818467545	3.51E-07	0.000327709	6.20842364	Kinesin, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0109590.1	-2.395378782	-0.155486123	-5.503521966	1.10E-06	0.000934091	5.178525478	Retrotransposon protein, putative, unclassified	elongation zone	12 h
HORVU.MOREX.r3.7HG0640470.1	0.46879748	6.260306545	5.480749813	1.20E-06	0.000943673	4.912110149	WPP domain-interacting tail-anchored protein 1	elongation zone	12 h
HORVU.MOREX.r3.6HG0559680.1	-3.320513025	0.573580493	-5.437616958	1.40E-06	0.001023714	4.879594033	NADPH:quinone oxidoreductase	elongation zone	12 h
HORVU.MOREX.r3.4HG0404760.1	1.896274552	6.564561937	5.339261959	1.99E-06	0.001316292	4.67332883	Tubulin-tyrosine ligase family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0606940.1	3.732215166	2.180676744	5.470326841	1.24E-06	0.000943673	4.62123451	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0069380.1	-1.371913292	2.129642878	-5.322865985	2.11E-06	0.001352282	4.614832683	Cysteine proteinase inhibitor	elongation zone	12 h
HORVU.MOREX.r3.2HG0170640.1	4.636531871	-0.509068665	5.494507009	1.14E-06	0.000934091	4.393312442	Protein FAR1-RELATED SEQUENCE 5	elongation zone	12 h
HORVU.MOREX.r3.1HG0045510.1	0.85869774	5.275918097	5.27932849	2.46E-06	0.001532253	4.392164637	Prefoldin subunit, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0724080.1	2.194948753	2.23197157	5.18961423	3.39E-06	0.001919114	4.333751953	6,7-dimethyl-8-ribityllumazine synthase	elongation zone	12 h
HORVU.MOREX.r3.3HG0309270.1	0.459903889	8.53260482	5.34519028	1.95E-06	0.001316292	4.252144859	Proline--tRNA ligase	elongation zone	12 h
HORVU.MOREX.r3.2HG0215830.1	1.683128359	2.436514446	5.133523283	4.14E-06	0.002178793	4.129151422	CsAtPR5	elongation zone	12 h
HORVU.MOREX.r3.1HG0075440.1	-1.139139937	1.650312221	-5.189663251	3.39E-06	0.001919114	4.124086934	Protein NRT1/ PTR FAMILY 5.5	elongation zone	12 h
HORVU.MOREX.r3.1HG0068410.1	-0.489548583	4.707522572	-5.189375642	3.40E-06	0.001919114	4.045607964	E3 ubiquitin-protein ligase	elongation zone	12 h
HORVU.MOREX.r3.5HG0502990.1	5.339440458	3.237955153	5.083423799	4.95E-06	0.00247494	3.997473504	NAC domain protein,	elongation zone	12 h
HORVU.MOREX.r3.1HG0067930.1	-0.991011169	2.533288297	-5.088688699	4.85E-06	0.00247494	3.893418191	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.5HG0489790.1	2.647632598	-0.067483895	5.184079096	3.46E-06	0.001919114	3.849624559	SKP1-like protein 4	elongation zone	12 h
HORVU.MOREX.r3.1HG0050990.1	2.93628127	2.072399061	5.159396263	3.78E-06	0.002039933	3.782246362	Membrane protein insertase YidC	elongation zone	12 h
HORVU.MOREX.r3.3HG0316280.1	1.411227691	4.501603233	5.044295035	5.68E-06	0.002774234	3.757894752	Transcription initiation factor TFIID subunit 9	elongation zone	12 h
HORVU.MOREX.r3.1HG0067490.1	-3.145796854	-1.72649178	-5.376799382	1.74E-06	0.001229863	3.755370642	Retrovirus-related Pol polyprotein from transposon TNT 1-94	elongation zone	12 h
HORVU.MOREX.r3.7HG0696190.1	0.726630316	6.218032617	5.011348897	6.38E-06	0.003043527	3.391944882	Glucose-1-phosphate adenylyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0315690.1	0.659686542	5.614263673	4.971371976	7.34E-06	0.0034236	3.334600351	E3 ubiquitin-protein ligase BRE1-like 2	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.5HG0513490.1	-0.631143265	3.90283549	-4.931276729	8.45E-06	0.003650963	3.141090749	Myb transcription factor	elongation zone	12 h
HORVU.MOREX.r3.2HG0205760.1	1.24598584	5.328219399	4.859959287	1.08E-05	0.004279598	3.08080027	Glutamyl-tRNA(Gln) amidotransferase subunit A	elongation zone	12 h
HORVU.MOREX.r3.1HG0019170.1	2.293781213	4.041071012	4.790280922	1.38E-05	0.004612029	3.041330526	Replication protein A 70 kDa DNA-binding subunit	elongation zone	12 h
HORVU.MOREX.r3.7HG0717610.1	-0.830116841	4.008622047	-4.902508367	9.35E-06	0.003835781	3.030989115	Pollen-specific protein SF21	elongation zone	12 h
HORVU.MOREX.r3.4HG0337320.1	2.78145313	-0.56622922	4.955635496	7.76E-06	0.003460871	3.027816713	Ribonuclease H	elongation zone	12 h
HORVU.MOREX.r3.3HG0291580.1	0.896393635	2.805578274	4.79582302	1.36E-05	0.004612029	3.009036343	Lysosomal Pro-X carboxypeptidase	elongation zone	12 h
HORVU.MOREX.r3.2HG0120320.1	-0.999894142	1.685244219	-4.959201663	7.66E-06	0.003460871	2.983590905	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.7HG0655680.1	-2.39862148	-1.898894256	-4.786547179	1.40E-05	0.004612029	2.964654663	Serine/threonine-protein kinase	elongation zone	12 h
HORVU.MOREX.r3.6HG0550390.1	1.883693505	2.694299352	4.774444594	1.46E-05	0.004612029	2.954586941	Nitroreductase family protein, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0471070.1	-0.368137022	6.510820563	-4.928262656	8.54E-06	0.003650963	2.940632911	Oxidoreductase family, NAD-binding rossmann fold protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0513740.1	-1.89889643	-3.016736504	-4.782019719	1.42E-05	0.004612029	2.925278368	Alpha/beta-Hydrolases superfamily protein, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0628240.1	0.939462944	6.047595769	4.844780568	1.14E-05	0.004345188	2.893522627	Translation initiation factor eIF-2B subunit epsilon	elongation zone	12 h
HORVU.MOREX.r3.5HG0538060.1	3.456849261	1.093162331	4.902584859	9.34E-06	0.003835781	2.873350663	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0193110.1	2.023112426	1.962681787	4.76134155	1.53E-05	0.004612029	2.869355834	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0069030.1	-2.568152033	1.480380355	-4.729127378	1.71E-05	0.004790957	2.840166912	Calcium-transporting ATPase	elongation zone	12 h
HORVU.MOREX.r3.6HG0551980.1	2.213727095	0.689536511	4.848495075	1.13E-05	0.004345188	2.839319577	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0559690.1	1.410678913	2.590055839	4.723247988	1.74E-05	0.004790957	2.807654895	Cell division cycle 5-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0525700.1	0.515361168	7.295514432	4.879946823	1.01E-05	0.004069304	2.79062218	Leukotriene a-4 hydrolase aminopeptidase	elongation zone	12 h
HORVU.MOREX.r3.5HG0489840.1	1.327480706	2.789323341	4.679336777	2.03E-05	0.005205195	2.69344849	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0702190.1	2.268550826	3.843343484	4.671747013	2.08E-05	0.005212813	2.661083535	Fertilization independent endosperm 1 protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0166370.1	3.427632951	2.267354347	4.763054475	1.52E-05	0.004612029	2.630674368	ATP-binding ABC transporter	elongation zone	12 h
HORVU.MOREX.r3.6HG0612180.1	0.812170486	6.264662645	4.794361092	1.36E-05	0.004612029	2.621485693	NHL repeat-containing protein-like	elongation zone	12 h
HORVU.MOREX.r3.2HG0178640.1	4.143304352	2.291364412	4.811721353	1.28E-05	0.004612029	2.591941617	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.5HG0531850.1	0.979608794	4.723484706	4.695217341	1.92E-05	0.005054112	2.569814967	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0155210.1	0.875539715	6.20005446	4.747570772	1.60E-05	0.004767359	2.548862812	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0513810.1	-0.774180088	4.245645455	-4.76510475	1.51E-05	0.004612029	2.545108289	Malate dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.2HG0194450.1	0.495017707	5.50815323	4.74092719	1.64E-05	0.004790957	2.535972093	Secretory carrier-associated membrane protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0170560.1	1.300683704	3.704875465	4.626651656	2.43E-05	0.005838526	2.516684176	Ras-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0510120.1	1.524143941	5.694545128	4.675006627	2.06E-05	0.005212813	2.490020213	tRNA (guanine-N(7)-)-methyltransferase non-catalytic subunit	elongation zone	12 h
HORVU.MOREX.r3.5HG0425000.1	-3.795281094	-0.918831697	-4.766804116	1.50E-05	0.004612029	2.47751583	Transposon protein, putative, Pong sub-class	elongation zone	12 h
HORVU.MOREX.r3.5HG0453710.1	0.78968192	6.149187887	4.732048282	1.69E-05	0.004790957	2.473559635	3'(2'),5'-bisphosphate nucleotidase 1	elongation zone	12 h
HORVU.MOREX.r3.3HG0236260.1	2.482622963	3.359778756	4.624823496	2.45E-05	0.005838526	2.456733322	Protein IQ-DOMAIN 1	elongation zone	12 h
HORVU.MOREX.r3.6HG0539520.1	0.850672384	7.571274396	4.769053686	1.49E-05	0.004612029	2.439113139	tetratricopeptide repeat (TPR)-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0695920.1	1.324775331	2.660691655	4.607088889	2.60E-05	0.005931341	2.43445929	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0574510.1	1.995355805	7.321758484	4.722050834	1.75E-05	0.004790957	2.43351653	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0488640.1	2.870267469	1.861985275	4.702638806	1.87E-05	0.004990255	2.418960471	Protease 2	elongation zone	12 h
HORVU.MOREX.r3.7HG0750390.1	2.012056838	1.508596769	4.618827285	2.50E-05	0.005838526	2.357979301	F-box family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0079800.1	0.623931197	7.794068	4.782954511	1.42E-05	0.004612029	2.347123537	Farnesyl diphosphate synthase	elongation zone	12 h
HORVU.MOREX.r3.7HG0719070.1	0.964232265	5.233223615	4.632098104	2.39E-05	0.005838526	2.325052807	SUMO-activating enzyme subunit 1A	elongation zone	12 h
HORVU.MOREX.r3.4HG0372280.1	1.357728128	3.216376663	4.562042287	3.04E-05	0.006487548	2.307807428	xylulose kinase-2	elongation zone	12 h
HORVU.MOREX.r3.1HG0079040.1	1.622011088	2.231395169	4.562771861	3.03E-05	0.006487548	2.295564715	(R)-specific enoyl-CoA hydratase	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.6HG0550700.1	1.949711604	1.442253166	4.586581605	2.79E-05	0.006131428	2.295526225	F-box family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0072580.1	-0.678852299	5.490114394	-4.685482267	1.99E-05	0.005160572	2.279448692	Aminotransferase-related family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0053530.1	1.511032401	2.523226342	4.551577879	3.15E-05	0.006654271	2.26761454	Glycerol-3-phosphate acyltransferase, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.7HG0736860.1	2.706731769	3.347913234	4.541494976	3.26E-05	0.006816924	2.236455856	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B, pu	elongation zone	12 h
HORVU.MOREX.r3.5HG0441860.1	0.657645919	9.817417187	4.779827325	1.43E-05	0.004612029	2.198779	70 kDa heat shock protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0490770.1	3.350338224	1.191244216	4.730529692	1.70E-05	0.004790957	2.185818224	Inactive rhomboid 1	elongation zone	12 h
HORVU.MOREX.r3.3HG0220340.1	2.161152826	2.953247644	4.517080222	3.54E-05	0.007193905	2.185490509	Disease resistance protein RPM1	elongation zone	12 h
HORVU.MOREX.r3.7HG0701140.1	0.536748951	7.955915849	4.715403956	1.79E-05	0.004837811	2.157177058	Tyrosine--tRNA ligase	elongation zone	12 h
HORVU.MOREX.r3.3HG0289070.1	1.802384306	2.310763629	4.521803499	3.48E-05	0.007193905	2.152366504	Protein TIC 22-like, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.2HG0117010.1	1.684308619	3.380763648	4.494678551	3.82E-05	0.007270797	2.11518682	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0749460.1	0.69582768	5.222321052	4.618239152	2.50E-05	0.005838526	2.083063357	Thioredoxin	elongation zone	12 h
HORVU.MOREX.r3.7HG0705220.1	0.99333491	5.990205142	4.587108075	2.79E-05	0.006131428	2.08114599	Squamous cell carcinoma antigen recognized by T-cells 3	elongation zone	12 h
HORVU.MOREX.r3.3HG0312510.1	-1.426682866	-1.358373367	-4.50063275	3.74E-05	0.007270797	2.07306892	cDNA clone:J013058P10, full insert sequence	elongation zone	12 h
HORVU.MOREX.r3.4HG0369090.1	1.464715253	2.892329497	4.474069638	4.09E-05	0.007570079	2.05293318	30S ribosomal protein S5	elongation zone	12 h
HORVU.MOREX.r3.5HG0500650.1	1.753345297	3.978679874	4.488390967	3.90E-05	0.007343205	2.042697766	Protein MCM10-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0418640.1	0.831752212	4.260686402	4.508248921	3.65E-05	0.007193905	1.986747413	C2 domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0564590.1	0.632636227	6.449269546	4.60817632	2.59E-05	0.005931341	1.97543396	O-fucosyltransferase family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0080590.1	0.956117052	6.502287926	4.584709135	2.81E-05	0.006131428	1.959890266	60 kDa chaperonin	elongation zone	12 h
HORVU.MOREX.r3.1HG0062050.1	0.918185403	4.541885731	4.479074138	4.03E-05	0.007510284	1.940935392	Tocopherol cyclase	elongation zone	12 h
HORVU.MOREX.r3.3HG0306210.1	0.800598064	7.280706243	4.593898556	2.72E-05	0.006131428	1.898462157	RAN GTPase activating protein 2	elongation zone	12 h
HORVU.MOREX.r3.2HG0121270.1	2.391501674	1.148782547	4.50926895	3.63E-05	0.007193905	1.89441405	DNA helicase	elongation zone	12 h
HORVU.MOREX.r3.5HG0519810.1	0.559589673	7.61792539	4.625851799	2.44E-05	0.005838526	1.846523776	Diphosphomevalonate decarboxylase	elongation zone	12 h
HORVU.MOREX.r3.7HG0666340.1	0.694955925	4.728875506	4.50867853	3.64E-05	0.007193905	1.832190513	Hexosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0634460.1	1.755818124	3.57799637	4.397512789	5.30E-05	0.008749778	1.81717179	WD repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0607000.1	2.375111223	0.642043492	4.495925972	3.80E-05	0.007270797	1.723583653	Pectin acetylesterase	elongation zone	12 h
HORVU.MOREX.r3.2HG0196130.1	3.364349198	1.315960104	4.494021162	3.83E-05	0.007270797	1.72351579	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0204940.1	0.68750571	6.058216754	4.514502714	3.57E-05	0.007193905	1.717558121	Crossover junction endonuclease EME1	elongation zone	12 h
HORVU.MOREX.r3.1HG0084760.1	-1.726027674	-3.229685836	-4.391089299	5.42E-05	0.008749778	1.695446641	Myb transcription factor	elongation zone	12 h
HORVU.MOREX.r3.6HG0542140.1	3.496397909	1.647553312	4.455551439	4.36E-05	0.007988512	1.695149944	Pentatricopeptide repeat-containing family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0414710.1	2.292008753	1.532728058	4.380499213	5.62E-05	0.008749778	1.676296539	CENP-C	elongation zone	12 h
HORVU.MOREX.r3.5HG0515930.1	2.308579427	2.608899599	4.357265128	6.07E-05	0.009232427	1.641744917	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0636630.1	-1.352768357	-0.128553353	-4.426834311	4.81E-05	0.008500545	1.626304839	WAT1-related protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0098420.1	1.673601771	5.161437075	4.394942065	5.35E-05	0.008749778	1.624062378	CDT1-like protein a, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.5HG0455830.1	1.089503503	3.143860089	4.329529237	6.67E-05	0.00998459	1.587883468	Dynamin family protein, putative, expressed	elongation zone	12 h
HORVU.MOREX.r3.7HG0679060.1	-0.977683057	1.156648697	-4.405242508	5.17E-05	0.008691469	1.586169175	Nuclear transport factor 2 family protein, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0350800.1	2.735540074	1.296960322	4.382179125	5.59E-05	0.008749778	1.584573783	FBD-associated F-box protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0569480.1	3.671851508	2.886545793	4.381981337	5.59E-05	0.008749778	1.57923168	Tubby-like F-box protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0231780.1	1.215955735	5.499283637	4.408670257	5.11E-05	0.008691469	1.57665909	Charged multivesicular body protein 5	elongation zone	12 h
HORVU.MOREX.r3.2HG0212990.1	0.976137725	5.148472217	4.38699698	5.50E-05	0.008749778	1.57445818	Acyl-protein thioesterase 1	elongation zone	12 h
HORVU.MOREX.r3.1HG0091820.1	0.830782436	5.321522929	4.426813448	4.81E-05	0.008500545	1.542499669	Glutamyl-tRNA (Gln) amidotransferase subunit A	elongation zone	12 h
HORVU.MOREX.r3.4HG0354540.1	3.135429099	4.811312014	4.307915711	7.17E-05	0.010284717	1.538068974	Receptor-like kinase	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.5HG0485200.1	3.250539611	1.510380714	4.402872747	5.21E-05	0.008691469	1.5023303	ATP-dependent zinc metalloprotease FtsH	elongation zone	12 h
HORVU.MOREX.r3.2HG0116440.1	1.01636209	6.979177665	4.43937838	4.61E-05	0.008363327	1.501496415	Ubiquitin carboxyl-terminal hydrolase	elongation zone	12 h
HORVU.MOREX.r3.6HG0629160.1	1.729513557	2.999097227	4.295569853	7.47E-05	0.010284717	1.501211421	Disease resistance protein RPM1	elongation zone	12 h
HORVU.MOREX.r3.3HG0301030.1	1.267160968	6.005129777	4.379922862	5.63E-05	0.008749778	1.461744205	Nuclear pore complex protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0615710.1	0.740825625	6.427381525	4.435098138	4.67E-05	0.008410831	1.461400198	Nucleobase ascorbate transporter	elongation zone	12 h
HORVU.MOREX.r3.3HG0231940.1	1.898204353	2.008606845	4.270823453	8.11E-05	0.011021723	1.415280701	Shikimate kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0559140.1	1.986336	0.485291142	4.301642401	7.32E-05	0.010284717	1.38375808	Sn1-specific diacylglycerol lipase alpha	elongation zone	12 h
HORVU.MOREX.r3.1HG0065020.1	1.342195953	5.184531424	4.322233671	6.83E-05	0.010084309	1.380913953	BZIP transcription factor	elongation zone	12 h
HORVU.MOREX.r3.1HG0079140.1	-0.693066624	4.43581546	-4.405447208	5.16E-05	0.008691469	1.33134306	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0079810.1	0.637003405	3.696599347	4.298948608	7.38E-05	0.010284717	1.326134536	WD repeat protein-like	elongation zone	12 h
HORVU.MOREX.r3.5HG0432550.1	1.326517537	3.011061408	4.24116913	8.95E-05	0.011688702	1.312418621	Protein ROOT HAIR DEFECTIVE 3 homolog	elongation zone	12 h
HORVU.MOREX.r3.1HG0051190.1	0.921638363	5.372233168	4.334241392	6.56E-05	0.009900454	1.311833874	COP9 signalosome complex subunit 1	elongation zone	12 h
HORVU.MOREX.r3.5HG0447870.1	1.190871632	7.933348257	4.416867172	4.97E-05	0.008641942	1.311333453	Chaperone protein htpG family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0232890.1	-2.60709898	-2.364614764	-4.297104937	7.43E-05	0.010284717	1.298530058	NADP-dependent alkenal double bond reductase	elongation zone	12 h
HORVU.MOREX.r3.2HG0114290.1	0.398510779	6.856362561	4.419393446	4.93E-05	0.008641782	1.283958309	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0443920.1	0.642104899	3.840341821	4.309441591	7.13E-05	0.010284717	1.276854516	Calmodulin-binding protein, putative, expressed	elongation zone	12 h
HORVU.MOREX.r3.6HG0552860.1	1.28060679	6.655909595	4.359674838	6.03E-05	0.009226352	1.262682419	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.6HG0552800.1	1.203396933	7.010448703	4.387620576	5.48E-05	0.008749778	1.258259644	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.7HG0749150.1	2.336801621	3.418594548	4.208041678	9.99E-05	0.012270488	1.24590653	DUF241 domain protein (DUF241)	elongation zone	12 h
HORVU.MOREX.r3.2HG0178430.1	1.140746232	4.94211731	4.271828496	8.08E-05	0.011021723	1.237854657	RNA binding protein, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0052120.1	0.726326777	3.548831498	4.245585438	8.82E-05	0.011603516	1.227982636	GDP-mannose transporter	elongation zone	12 h
HORVU.MOREX.r3.4HG0342950.1	1.279335892	6.384536094	4.32381816	6.79E-05	0.010084309	1.204190614	50S ribosomal protein L25	elongation zone	12 h
HORVU.MOREX.r3.3HG0247250.1	1.52225923	3.952989106	4.220459804	9.59E-05	0.01214534	1.203620212	V-type proton ATPase subunit E	elongation zone	12 h
HORVU.MOREX.r3.3HG0238570.1	1.445357224	3.98707821	4.197357631	0.0001	0.012421033	1.166756111	Remodeling and spacing factor 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0655210.1	-2.064080552	-1.689922301	-4.214144288	9.79E-05	0.012270488	1.142463393	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.7HG0664130.1	0.53598335	5.138266164	4.298533007	7.39E-05	0.010284717	1.135134778	Dipeptidyl peptidase family member 6	elongation zone	12 h
HORVU.MOREX.r3.1HG0082770.1	0.368524786	7.702552295	4.411369363	5.06E-05	0.008691469	1.12100928	Reticulon-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0329040.1	-1.88709672	-0.454710292	-4.245575901	8.82E-05	0.011603516	1.117758658	Vacuolar-processing enzyme	elongation zone	12 h
HORVU.MOREX.r3.4HG0343760.1	2.624383724	1.366971799	4.261952425	8.35E-05	0.011233153	1.115721846	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0629830.1	1.582798338	3.458001717	4.165922894	0.00011	0.012462233	1.110068276	Riboflavin biosynthesis protein RibD	elongation zone	12 h
HORVU.MOREX.r3.2HG0122440.1	2.902775269	2.054200931	4.209939475	9.93E-05	0.012270488	1.102772372	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0406270.1	3.729681347	2.424364145	4.191873371	0.00011	0.012430307	1.093536158	RING/FYVE/PHD-type zinc finger family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0207790.1	-1.513396937	-2.594215752	-4.155398424	0.00012	0.012462233	1.090188244	Serine/threonine-protein kinase	elongation zone	12 h
HORVU.MOREX.r3.2HG0211900.1	1.687710081	2.028349871	4.156779012	0.00012	0.012462233	1.071436815	Phytol kinase 1	elongation zone	12 h
HORVU.MOREX.r3.4HG0372230.1	-1.986087807	-1.629808544	-4.164200917	0.00012	0.012462233	1.067852713	Transposon protein, putative, CACTA, En/Spm sub-class, expresse	elongation zone	12 h
HORVU.MOREX.r3.2HG0126850.1	3.148296787	2.517894712	4.195570061	0.0001	0.012422054	1.067806823	RNA-binding protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0334130.1	2.371042704	2.234967175	4.16185419	0.00012	0.012462233	1.065912588	Thymocyte nuclear protein 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0634680.1	2.623417965	5.267359917	4.156682163	0.00012	0.012462233	1.043120819	disease resistance protein (TIR-NBS-LRR class)	elongation zone	12 h
HORVU.MOREX.r3.5HG0518640.1	1.37911009	2.499571845	4.160617535	0.00012	0.012462233	1.037923113	Methionine S-methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0244140.1	1.316798238	5.689186186	4.230904961	9.26E-05	0.011878355	1.027798767	Formate-dependent phosphoribosylglycinamide formyltransfera	elongation zone	12 h
HORVU.MOREX.r3.3HG0320840.1	0.372905525	7.26652398	4.363400925	5.95E-05	0.009180086	1.027503909	Signal peptide peptidase family protein	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0274100.1	1.703767433	1.731697294	4.141845225	0.00012	0.012462233	1.020507371	50S ribosomal protein L31	elongation zone	12 h
HORVU.MOREX.r3.1HG0081540.1	2.095482321	3.160387272	4.131168898	0.00013	0.012462233	1.016515007	Acid phosphatase/vanadium-dependent haloperoxidase-related	elongation zone	12 h
HORVU.MOREX.r3.6HG0623830.1	2.642047754	4.072429437	4.128436509	0.00013	0.012462233	1.010427748	Disease resistance protein (NBS-LRR class) family	elongation zone	12 h
HORVU.MOREX.r3.7HG0709860.1	0.544776359	6.368460733	4.304578139	7.25E-05	0.010284717	1.010038994	Polyadenylate-binding protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0315050.1	1.031870078	5.388583561	4.221540467	9.55E-05	0.01214534	1.007124038	SET domain containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0463310.1	2.142007927	4.179176168	4.134572711	0.00013	0.012462233	0.999401757	Mitotic spindle checkpoint protein BUBR1	elongation zone	12 h
HORVU.MOREX.r3.5HG0515020.1	1.550591317	4.49745777	4.15507704	0.00012	0.012462233	0.994012727	Alpha N-terminal protein methyltransferase 1	elongation zone	12 h
HORVU.MOREX.r3.5HG0492650.1	1.327756263	7.121607235	4.296643677	7.44E-05	0.010284717	0.989306445	O-fucosyltransferase family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0546590.1	2.982566107	1.264052484	4.184121856	0.00011	0.012462233	0.981802876	Glutamate receptor	elongation zone	12 h
HORVU.MOREX.r3.3HG0318400.1	1.092536172	6.359365817	4.258134665	8.46E-05	0.011273388	0.970371471	S-formylglutathione hydrolase	elongation zone	12 h
HORVU.MOREX.r3.7HG0722660.1	-1.052031306	1.474969139	-4.145997163	0.00012	0.012462233	0.958541961	Diacylglycerol kinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0272430.1	0.501110097	5.817079707	4.297405009	7.42E-05	0.010284717	0.9537935	Pectin lyase-like superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0261960.1	1.031364808	4.490303333	4.168088279	0.00011	0.012462233	0.951792287	ATP-dependent Clp protease proteolytic subunit	elongation zone	12 h
HORVU.MOREX.r3.2HG0111130.1	0.99516057	3.835075352	4.153889908	0.00012	0.012462233	0.948883313	Short chain dehydrogenase/reductase	elongation zone	12 h
HORVU.MOREX.r3.5HG0431780.1	0.982307281	5.673780891	4.211620936	9.87E-05	0.012270488	0.947400092	Homocysteine s-methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0462220.1	-1.167193216	1.070356343	-4.235962576	9.11E-05	0.01175404	0.918316081	Calmodulin protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0056980.1	2.276631998	2.210568558	4.108052197	0.00014	0.013074743	0.915391732	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0719120.1	1.123157408	6.876683069	4.261166421	8.38E-05	0.011233153	0.900272017	50S ribosomal protein L1	elongation zone	12 h
HORVU.MOREX.r3.2HG0106750.1	1.452546652	0.325037267	4.088724303	0.00015	0.013386102	0.882330973	Alpha-1,4 glucan phosphorylase	elongation zone	12 h
HORVU.MOREX.r3.3HG0265690.1	1.849101387	0.540508683	4.129136259	0.00013	0.012462233	0.881294824	Oxidoreductase/transition metal ion-binding protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0394830.1	-1.038348436	0.997429304	-4.166999038	0.00011	0.012462233	0.868168821	Lecithin-cholesterol acyltransferase-like 1	elongation zone	12 h
HORVU.MOREX.r3.3HG0268350.1	1.076230438	2.559660591	4.088081906	0.00015	0.013386102	0.867824838	Exocyst complex component SEC3A	elongation zone	12 h
HORVU.MOREX.r3.4HG0354140.1	-1.578908935	-2.197267006	-4.076833751	0.00015	0.013607526	0.858620091	CheY-like two-component responsive regulator family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0173190.1	1.780538455	7.090068817	4.203897447	0.0001	0.012270488	0.844842343	ABC transporter ATP-binding protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0526320.1	1.595123908	5.285699775	4.125247608	0.00013	0.012462233	0.828624845	Condensin-2 complex subunit D3	elongation zone	12 h
HORVU.MOREX.r3.6HG0540200.1	0.90587335	7.189746969	4.239540632	9.00E-05	0.011688702	0.805401952	60 kDa chaperonin	elongation zone	12 h
HORVU.MOREX.r3.1HG0024230.1	0.705352839	5.422255112	4.179025214	0.00011	0.012462233	0.770717216	Tubulin beta chain	elongation zone	12 h
HORVU.MOREX.r3.5HG0437710.1	1.153255721	2.135740553	4.044943812	0.00017	0.014133454	0.761631519	Protein FAR1-RELATED SEQUENCE 5	elongation zone	12 h
HORVU.MOREX.r3.3HG0302860.1	2.415955213	4.061597972	4.053418044	0.00017	0.014078728	0.76129776	Pathogenesis-related thaumatin-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0093950.1	3.30445539	-0.165782629	4.206236198	0.0001	0.012270488	0.752630371	Ubiquitin carboxyl-terminal hydrolase 2	elongation zone	12 h
HORVU.MOREX.r3.3HG0221000.1	3.505444984	0.305296124	4.193394521	0.0001	0.012430307	0.736729495	Xyloglucan galactosyltransferase KATAMARI1-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0647290.1	1.606308967	4.111332047	4.050948207	0.00017	0.014078728	0.729759632	ATP-dependent Clp protease proteolytic subunit	elongation zone	12 h
HORVU.MOREX.r3.3HG0290660.1	0.896981389	5.959969367	4.174054036	0.00011	0.012462233	0.712759967	Ribosomal protein S24/S35, mitochondrial	elongation zone	12 h
HORVU.MOREX.r3.6HG0546330.1	1.946105904	7.259910966	4.158473198	0.00012	0.012462233	0.708735779	GMP synthase [glutamine-hydrolyzing]	elongation zone	12 h
HORVU.MOREX.r3.6HG0610960.1	1.066482718	3.725371239	4.055208355	0.00017	0.014078728	0.702630692	DNA-directed RNA polymerase II subunit rpb4	elongation zone	12 h
HORVU.MOREX.r3.3HG0280960.1	-0.892882973	1.80535629	-4.139160324	0.00013	0.012462233	0.697293869	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.1HG0007570.1	-2.737520062	-2.580123327	-4.202815134	0.0001	0.012270488	0.694215041	Werner Syndrome-like exonuclease	elongation zone	12 h
HORVU.MOREX.r3.5HG0487790.1	3.180964661	2.300592707	4.073039122	0.00016	0.013659522	0.692832291	Cyclin family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0105650.1	1.309918635	6.31756936	4.1597246	0.00012	0.012462233	0.691950364	Cleavage and polyadenylation specificity factor subunit 1	elongation zone	12 h
HORVU.MOREX.r3.3HG0264580.1	1.162985702	5.433253416	4.12809563	0.00013	0.012462233	0.691495684	Protein HASTY 1	elongation zone	12 h
HORVU.MOREX.r3.1HG0090300.1	1.263832133	5.866767988	4.150485178	0.00012	0.012462233	0.689963652	Topoisomerase 1-associated factor 1	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.5HG0440410.1	2.757532816	1.14377569	4.095472538	0.00014	0.013319392	0.685255675	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0057040.1	1.75610823	4.042158307	4.035403024	0.00018	0.014282864	0.683309861	10 kDa chaperonin	elongation zone	12 h
HORVU.MOREX.r3.2HG0106870.1	3.573121745	1.977348744	4.124076005	0.00013	0.012462233	0.682440269	Amine oxidase	elongation zone	12 h
HORVU.MOREX.r3.5HG0514360.1	2.245961786	2.884542848	4.015446853	0.00019	0.014546646	0.681118001	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B, pu	elongation zone	12 h
HORVU.MOREX.r3.7HG0665250.1	2.990950353	2.254845156	4.030864102	0.00018	0.014382161	0.663372564	B3 domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0049620.1	2.851045367	0.745244638	4.10512282	0.00014	0.01314062	0.661390691	CRS1 / YhbY (CRM) domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0064740.1	-0.757267995	3.101051154	-4.143530675	0.00012	0.012462233	0.661258042	Phospholipase A1	elongation zone	12 h
HORVU.MOREX.r3.3HG0301400.1	2.297555535	2.640514127	4.012030201	0.00019	0.014582974	0.65166826	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0173350.1	1.179167308	5.060871752	4.08213258	0.00015	0.013490162	0.642868065	ATPase ASNA1	elongation zone	12 h
HORVU.MOREX.r3.6HG0586570.1	1.175433995	0.923323863	4.000259029	0.0002	0.014672221	0.636955991	Transposon Ty3-G Gag-Pol polyprotein	elongation zone	12 h
HORVU.MOREX.r3.7HG0664400.1	1.619263438	1.704982407	4.002341161	0.0002	0.014672221	0.633690907	Protein curvature thylakoid chloroplastic-like	elongation zone	12 h
HORVU.MOREX.r3.6HG0566530.1	1.566984487	5.563778173	4.083161556	0.00015	0.013490162	0.626026746	DNA-directed RNA polymerase subunit	elongation zone	12 h
HORVU.MOREX.r3.3HG0256040.1	3.021985858	4.80598677	3.999939009	0.0002	0.014672221	0.622883431	DNA gyrase subunit B	elongation zone	12 h
HORVU.MOREX.r3.2HG0204340.1	2.629191461	-0.821479425	4.173860679	0.00011	0.012462233	0.611673865	ERD (early-responsive to dehydration stress) family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0681830.1	1.801603165	2.778247346	3.991976434	0.0002	0.014738733	0.610161163	DUF1666 family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0397510.1	2.838349777	-0.24383738	4.163917185	0.00012	0.012462233	0.607051609	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0280910.1	1.886481541	6.11959171	4.089693269	0.00015	0.013386102	0.604251116	Microtubule-associated protein-like	elongation zone	12 h
HORVU.MOREX.r3.5HG0453030.1	-0.568462346	4.568693004	-4.140433561	0.00012	0.012462233	0.604202656	P-loop containing nucleoside triphosphate hydrolases superfamil	elongation zone	12 h
HORVU.MOREX.r3.2HG0196960.1	2.899581685	1.756153365	4.035947122	0.00018	0.014282864	0.600427549	Y' element ATP-dependent helicase YEL077C	elongation zone	12 h
HORVU.MOREX.r3.2HG0121570.1	0.59748518	4.65733005	4.134215372	0.00013	0.012462233	0.598716397	Protein LTV1	elongation zone	12 h
HORVU.MOREX.r3.1HG0070730.1	-1.689617293	-0.4130893	-3.990848613	0.0002	0.014738733	0.596657584	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0725060.1	2.066410813	3.350962126	3.985113179	0.00021	0.014738733	0.594174154	Microtubule associated family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0396370.1	1.025997318	7.480547656	4.186674514	0.00011	0.012462233	0.59388767	Methionine--tRNA ligase	elongation zone	12 h
HORVU.MOREX.r3.2HG0190240.1	1.57266757	2.851074202	3.982592424	0.00021	0.014789061	0.586773693	Smr domain-containing protein, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0056230.1	0.893528829	6.035858906	4.128785131	0.00013	0.012462233	0.577113195	3-hydroxyisobutyryl-CoA hydrolase-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0738300.1	1.652097342	4.034657467	4.017353991	0.00019	0.014546646	0.561787932	Allantoate amidohydrolase	elongation zone	12 h
HORVU.MOREX.r3.1HG0074730.1	0.880902142	4.444359724	4.030852125	0.00018	0.014382161	0.561211183	Cell division protein ftsZ	elongation zone	12 h
HORVU.MOREX.r3.7HG0685520.1	2.273718823	0.843971763	4.000851375	0.0002	0.014672221	0.556365546	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0730510.1	-1.130110195	-1.831161525	-4.046416528	0.00017	0.014133454	0.552971552	Germin-like protein 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0720650.1	1.214033194	6.481386112	4.125907375	0.00013	0.012462233	0.551876098	Elongation factor like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0287790.1	3.401051345	1.995670245	4.043381228	0.00017	0.014140313	0.532623689	rRNA methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0528930.1	1.930300707	4.365037424	3.975204645	0.00021	0.014889852	0.520006393	GPI-anchored adhesin-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0663730.1	2.607266074	2.179590294	3.959292465	0.00023	0.014924834	0.51970011	Galactoside 2-alpha-L-fucosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.6HG0555600.1	2.485035762	-0.223969439	4.010128121	0.00019	0.014582974	0.516379838	MADS-box transcription factor	elongation zone	12 h
HORVU.MOREX.r3.4HG0345000.1	1.053739417	3.705245563	4.019985102	0.00019	0.014546646	0.515746414	Kinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0281860.1	0.788939478	3.606297573	4.011062184	0.00019	0.014582974	0.514231466	Peptidyl-tRNA hydrolase	elongation zone	12 h
HORVU.MOREX.r3.7HG0702450.1	3.27209467	1.274342504	4.053398052	0.00017	0.014078728	0.513769047	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0342640.1	2.124148368	4.773274899	3.989876945	0.0002	0.014738733	0.497099001	Cyclin	elongation zone	12 h
HORVU.MOREX.r3.6HG0585670.1	1.094434762	4.325989876	4.014352627	0.00019	0.014546646	0.494373871	E2F transcription factor	elongation zone	12 h
HORVU.MOREX.r3.2HG0214090.1	1.1209979	7.152074623	4.134832121	0.00013	0.012462233	0.493385686	C2 calcium/lipid-binding and GRAM domain protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0141000.1	1.36045243	5.662430793	4.048562308	0.00017	0.014130693	0.49106694	ATP-dependent RNA helicase DeaD	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.7HG0662210.1	0.638567643	8.387753705	4.21168385	9.87E-05	0.012270488	0.489415571	T-complex protein 1 subunit delta	elongation zone	12 h
HORVU.MOREX.r3.2HG0211010.1	2.854219095	1.796615013	3.984713952	0.00021	0.014738733	0.4838759	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0724610.1	1.215371359	3.83877381	3.965832278	0.00022	0.014924834	0.477252974	Ribose-phosphate pyrophosphokinase	elongation zone	12 h
HORVU.MOREX.r3.2HG0197180.2	1.331193706	1.736102374	3.944402677	0.00024	0.015309918	0.477057857	Exocyst complex component SEC15A	elongation zone	12 h
HORVU.MOREX.r3.2HG0141200.1	1.36562103	5.885442827	4.056797663	0.00016	0.014078728	0.458410769	Endoribonuclease L-PSP family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0283730.1	1.002996977	8.227085107	4.17471352	0.00011	0.012462233	0.453158063	60S ribosomal protein l28	elongation zone	12 h
HORVU.MOREX.r3.5HG0527050.1	1.761539039	2.801057467	3.933837846	0.00024	0.015587775	0.44747613	Mitochondrial carrier protein, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0038800.1	-0.694589742	2.879103431	-4.066640726	0.00016	0.013829713	0.443357093	Protein kinase	elongation zone	12 h
HORVU.MOREX.r3.5HG0509060.1	-0.621564372	4.702327944	-4.141901922	0.00012	0.012462233	0.433591767	Non-specific serine/threonine protein kinase	elongation zone	12 h
HORVU.MOREX.r3.1HG0036930.1	1.216360965	6.161597548	4.079416764	0.00015	0.013551547	0.427634346	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.4HG0354980.1	-0.769667545	2.412831318	-4.035410208	0.00018	0.014282864	0.422315108	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0113740.1	2.339588086	1.01695296	3.994167326	0.0002	0.014738733	0.418320764	Metallothiol transferase FosB	elongation zone	12 h
HORVU.MOREX.r3.7HG0728280.1	2.235417335	1.355492103	3.955944486	0.00023	0.014924834	0.416262186	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0485840.1	2.110059694	1.087632654	3.964021133	0.00022	0.014924834	0.415429099	DUF1644 family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0069870.1	-0.876101801	2.55224648	-4.066663361	0.00016	0.013829713	0.415316576	#N/A	elongation zone	12 h
HORVU.MOREX.r3.4HG0402070.1	-0.601716247	3.388938852	-4.127388282	0.00013	0.012462233	0.404636846	IQ domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0660840.1	1.851344092	2.942614733	3.917741598	0.00026	0.015692177	0.39592039	Pectinesterase	elongation zone	12 h
HORVU.MOREX.r3.3HG0224260.1	1.287856406	3.431079477	3.923531615	0.00025	0.015692177	0.378660523	ABC transporter G family member	elongation zone	12 h
HORVU.MOREX.r3.6HG0569490.1	0.603495331	6.255599873	4.095496917	0.00014	0.013319392	0.373953699	Rad23 UV excision repair protein family	elongation zone	12 h
HORVU.MOREX.r3.5HG0529630.1	5.015427678	8.94083134	4.003432086	0.0002	0.014672221	0.37067545	Lipoxygenase	elongation zone	12 h
HORVU.MOREX.r3.7HG0728120.1	1.723432037	1.131059546	3.913186113	0.00026	0.015692177	0.368207032	Macrophage migration inhibitory factor	elongation zone	12 h
HORVU.MOREX.r3.1HG0085960.1	0.654406567	5.291265231	4.028253021	0.00018	0.014447555	0.355361994	ARM repeat superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0526940.1	0.467894156	7.556680019	4.157312039	0.00012	0.012462233	0.3552297	Alpha-mannosidase	elongation zone	12 h
HORVU.MOREX.r3.3HG0231730.1	2.263734712	2.401658147	3.908868536	0.00027	0.015692177	0.345585742	Receptor-like protein kinase	elongation zone	12 h
HORVU.MOREX.r3.2HG0183320.1	2.064327138	2.199260923	3.900691152	0.00027	0.015692177	0.34290641	mRNA cap guanine-N7 methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.1HG0086360.1	1.732565978	4.548392115	3.919366556	0.00026	0.015692177	0.299628965	Ribonuclease PH	elongation zone	12 h
HORVU.MOREX.r3.2HG0111790.1	2.186526824	4.937039867	3.887145418	0.00028	0.015800471	0.292911719	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.2HG0191230.1	1.845140313	3.939439112	3.890390937	0.00028	0.015756066	0.292486212	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0061220.1	1.485404067	4.835260837	3.944287818	0.00024	0.015309918	0.292015443	DNA primase	elongation zone	12 h
HORVU.MOREX.r3.1HG0085840.1	2.885479614	1.255424894	3.960029088	0.00022	0.014924834	0.291688295	Maturase-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0665640.1	1.65993869	4.705582024	3.908548103	0.00027	0.015692177	0.286678838	electron protein, putative (Protein of unknown function, DUF547	elongation zone	12 h
HORVU.MOREX.r3.2HG0167500.2	1.993793502	4.031521806	3.898746046	0.00027	0.015692177	0.281536426	Repetitive proline-rich cell wall protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0033310.1	1.031709046	5.652380892	4.003540798	0.0002	0.014672221	0.27431727	DNA mismatch repair protein mutS	elongation zone	12 h
HORVU.MOREX.r3.3HG0322660.1	1.497013775	5.027667147	3.961619121	0.00022	0.014924834	0.271695603	Receptor protein kinase, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0184630.1	2.226495219	2.780348233	3.874868521	0.0003	0.016177895	0.268543102	Elongation factor G	elongation zone	12 h
HORVU.MOREX.r3.6HG0560290.1	2.278392923	-0.187239249	3.927949231	0.00025	0.015638414	0.259546777	Cyclin	elongation zone	12 h
HORVU.MOREX.r3.5HG0460720.1	0.588358277	6.55235057	4.073672635	0.00016	0.013659522	0.250596267	L-galactono-1,4-lactone dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.2HG0165840.1	0.712182054	6.204491334	4.044765985	0.00017	0.014133454	0.2454484	Protein kinase	elongation zone	12 h
HORVU.MOREX.r3.4HG0354780.1	1.406092835	5.895136905	3.976681278	0.00021	0.014881142	0.244867087	Proline-, glutamic acid-and leucine-rich protein 1	elongation zone	12 h
HORVU.MOREX.r3.4HG0405600.1	0.63958473	7.101161055	4.087170778	0.00015	0.013386102	0.238037687	Eukaryotic translation initiation factor 3 subunit K	elongation zone	12 h
HORVU.MOREX.r3.1HG0020820.1	2.113618289	3.048519021	3.858988051	0.00031	0.016585421	0.235307214	Serine protease	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0304280.1	2.564599159	2.903876701	3.866085627	0.0003	0.016454463	0.230102946	Exocyst complex component, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0716100.1	2.550954856	0.460823771	3.907599331	0.00027	0.015692177	0.218408403	magnesium-protoporphyrin IX methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0648600.1	0.804735658	5.91516897	4.019189025	0.00019	0.014546646	0.213149344	Elongation factor 4	elongation zone	12 h
HORVU.MOREX.r3.5HG0486060.1	3.712550108	1.638161843	3.936173228	0.00024	0.015535305	0.21181594	Protease 2	elongation zone	12 h
HORVU.MOREX.r3.4HG0416290.1	1.760615777	3.543238154	3.852268775	0.00032	0.016710658	0.204801419	Sphingomyelin phosphodiesterase 4	elongation zone	12 h
HORVU.MOREX.r3.2HG0173340.1	3.30603414	1.078294475	3.980028468	0.00021	0.014824212	0.196086443	Pentatricopeptide repeat-containing protein, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0073670.1	2.981109236	-0.381423856	3.879796169	0.00029	0.016089033	0.193654181	Aldo-keto reductase	elongation zone	12 h
HORVU.MOREX.r3.1HG0060080.1	2.28538379	1.496119533	3.853469367	0.00032	0.016689644	0.189903092	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0704310.1	2.545096699	3.178531848	3.842902668	0.00033	0.016953892	0.18934172	Receptor-like protein kinase	elongation zone	12 h
HORVU.MOREX.r3.4HG0381360.1	1.349447717	6.018407731	3.97075027	0.00022	0.014924834	0.188206109	Adenylosuccinate lyase	elongation zone	12 h
HORVU.MOREX.r3.2HG0185190.1	1.031435224	3.839589672	3.891062602	0.00028	0.015756066	0.187209911	Yellow stripe-like 9 transporter	elongation zone	12 h
HORVU.MOREX.r3.6HG0583670.1	0.644399157	4.442077678	3.95938608	0.00023	0.014924834	0.185310934	WD repeat protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0263410.1	1.21577542	4.597647088	3.899610073	0.00027	0.015692177	0.162172134	Bromo-adjacent-like (BAH) domain protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0678230.1	0.646995834	6.137580535	4.022528808	0.00018	0.014546646	0.158155308	Eukaryotic translation initiation factor 3 subunit F	elongation zone	12 h
HORVU.MOREX.r3.6HG0616960.1	0.751845658	4.492256721	3.937999013	0.00024	0.015525106	0.157449453	Polyadenylate-binding protein family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0514790.1	0.538341919	9.909631182	4.175373618	0.00011	0.012462233	0.15732349	Elongation factor 1-alpha	elongation zone	12 h
HORVU.MOREX.r3.3HG0329300.1	1.620498345	4.353107466	3.861336588	0.00031	0.016574489	0.156678179	Dual-specificity RNA methyltransferase RlmN	elongation zone	12 h
HORVU.MOREX.r3.3HG0303970.1	0.739326708	5.516060256	3.999208334	0.0002	0.014672221	0.150266923	Internal alternative NAD(P)H-ubiquinone oxidoreductase A1, mit	elongation zone	12 h
HORVU.MOREX.r3.5HG0448120.1	1.587689475	1.313003386	3.8280143	0.00034	0.017220216	0.14618403	Polyol transporter	elongation zone	12 h
HORVU.MOREX.r3.2HG0195640.1	0.73376492	4.790343179	3.9407358	0.00024	0.015437333	0.14442023	Imidazoleglycerol-phosphate dehydratase	elongation zone	12 h
HORVU.MOREX.r3.3HG0228790.1	1.323301162	7.11644995	4.014715227	0.00019	0.014546646	0.142473385	Mitochondrial glycoprotein	elongation zone	12 h
HORVU.MOREX.r3.5HG0420980.1	-0.846719469	2.046048282	-3.92111939	0.00025	0.015692177	0.141177259	ERD (Early-responsive to dehydration stress) family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0644560.1	1.303103331	3.358673269	3.841832776	0.00033	0.016953892	0.140921191	Cell cycle regulated microtubule associated protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0039730.1	0.832354754	5.716966668	3.953311465	0.00023	0.014965579	0.128273391	Glutamine synthetase	elongation zone	12 h
HORVU.MOREX.r3.4HG0404740.1	-0.805475298	2.889075204	-4.041634671	0.00017	0.014164068	0.127797275	Hydrolase, alpha/beta fold family protein, expressed	elongation zone	12 h
HORVU.MOREX.r3.1HG0012330.1	1.034950725	6.207327614	3.98762397	0.00021	0.014738733	0.126686707	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0218560.1	-1.177863642	0.309747036	-3.922919815	0.00025	0.015692177	0.126065287	Receptor-like protein kinase	elongation zone	12 h
HORVU.MOREX.r3.6HG0548350.1	-1.271959689	1.250846794	-3.827107967	0.00034	0.017220216	0.122929005	Jacalin-related lectin	elongation zone	12 h
HORVU.MOREX.r3.5HG0439710.1	2.52221901	-0.510687428	3.907245313	0.00027	0.015692177	0.122368224	Zinc finger protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0366210.2	2.950360036	1.77805932	3.858676987	0.00031	0.016585421	0.118805445	Agenet domain containing protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0305500.1	1.221664499	2.378582061	3.825237191	0.00035	0.01726164	0.116050851	50S ribosomal protein-related, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0508890.1	3.176031881	0.546502989	3.926140707	0.00025	0.015638414	0.115290497	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0727460.1	0.953900379	8.013727164	4.056161393	0.00016	0.014078728	0.099655865	60S acidic ribosomal protein P3	elongation zone	12 h
HORVU.MOREX.r3.5HG0487850.1	1.657061676	4.243040388	3.835553602	0.00033	0.017055324	0.096485334	Phosphoribosylaminoimidazole-succinocarboxamide synthase	elongation zone	12 h
HORVU.MOREX.r3.6HG0628050.1	2.321577804	7.370628441	3.955284516	0.00023	0.014924834	0.096189441	Cytosine-specific methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.1HG0008380.1	2.127712065	2.770842782	3.810393631	0.00036	0.017580172	0.094616763	methyl-coenzyme M reductase II subunit gamma, putative (DUF3	elongation zone	12 h
HORVU.MOREX.r3.2HG0122060.1	0.691827666	5.958624172	3.987741712	0.00021	0.014738733	0.09001685	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0477040.1	0.464050238	5.558139817	3.990802462	0.0002	0.014738733	0.08118903	MND1-interacting protein 1	elongation zone	12 h
HORVU.MOREX.r3.6HG0590190.1	0.732725588	4.321131534	3.88217705	0.00029	0.016010182	0.074687373	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0307120.1	0.586916242	8.36463409	4.10050642	0.00014	0.013220171	0.073661056	S-adenosyl-L-methionine-dependent methyltransferases superfa	elongation zone	12 h
HORVU.MOREX.r3.3HG0256300.1	0.629949286	7.085102404	4.023383297	0.00018	0.014546646	0.073448068	Glutamate--tRNA ligase	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.5HG0534640.1	0.693334145	8.816317071	4.089169467	0.00015	0.013386102	0.063185292	Elongation factor Tu	elongation zone	12 h
HORVU.MOREX.r3.6HG0540620.1	1.909573227	4.022997546	3.815005313	0.00036	0.017468576	0.057654537	Malignant brain tumor repeat protein 1	elongation zone	12 h
HORVU.MOREX.r3.5HG0527750.1	0.643499104	5.066219563	3.926153742	0.00025	0.015638414	0.05756769	Kinetochore protein NDC80	elongation zone	12 h
HORVU.MOREX.r3.4HG0407860.1	-3.4950011	-1.046602776	-3.794006546	0.00038	0.017696476	0.054127743	Cytochrome P450, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0541240.1	1.935447584	3.029974348	3.794454298	0.00038	0.017696476	0.053139255	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0199560.1	1.752865944	5.029113972	3.910702542	0.00026	0.015692177	0.048198084	Organic cation transporter-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0687220.1	-1.437481623	-1.361787113	-3.834512678	0.00034	0.017059301	0.04626063	Cytochrome P450	elongation zone	12 h
HORVU.MOREX.r3.6HG0578170.1	0.908877578	6.59140041	3.979733215	0.00021	0.014824212	0.044541824	Histone deacetylase	elongation zone	12 h
HORVU.MOREX.r3.5HG0528100.1	2.000493752	1.953644846	3.795614441	0.00038	0.017696476	0.044112405	50S ribosomal protein L18	elongation zone	12 h
HORVU.MOREX.r3.3HG0328480.1	1.861367417	1.933391674	3.79067411	0.00039	0.017696476	0.040876071	Rotundifolia-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0121290.1	1.522528007	2.766171938	3.792687356	0.00038	0.017696476	0.037697827	DNA/RNA helicase protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0514980.1	1.767692517	7.445624912	3.961651264	0.00022	0.014924834	0.036857073	Inosine-5'-monophosphate dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.4HG0345400.1	1.449205441	6.016920639	3.900559522	0.00027	0.015692177	0.026885518	DAG protein, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.5HG0528920.1	1.497277525	6.19180472	3.908618796	0.00027	0.015692177	0.018279211	Phosphoribosylformylglycinamidine cyclo-ligase	elongation zone	12 h
HORVU.MOREX.r3.2HG0198550.1	3.043469204	0.396712397	3.888873026	0.00028	0.015756066	0.015855512	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0674720.1	-1.721705558	-1.463275625	-3.818964056	0.00035	0.017458382	0.014867266	Epoxide hydrolase 2	elongation zone	12 h
HORVU.MOREX.r3.1HG0064610.1	1.057723138	5.770306439	3.918724558	0.00026	0.015692177	0.008106542	membrane-associated kinase regulator	elongation zone	12 h
HORVU.MOREX.r3.4HG0369200.1	0.790980446	4.224154659	3.858934594	0.00031	0.016585421	0.000952895	RNA-binding protein Nova	elongation zone	12 h
HORVU.MOREX.r3.1HG0015760.1	1.936266237	4.576039572	3.797523707	0.00038	0.017696476	-0.00814129	Regulator of chromosome condensation (RCC1) family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0386280.1	0.683923146	6.657437418	3.986663577	0.00021	0.014738733	-0.01154922	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0490180.1	0.699261414	11.07313729	4.143585582	0.00012	0.012462233	-0.0121694	Heat shock protein 90	elongation zone	12 h
HORVU.MOREX.r3.1HG0058260.1	1.846807755	2.383540747	3.770802674	0.00041	0.017914792	-0.01487359	50S ribosomal protein L18	elongation zone	12 h
HORVU.MOREX.r3.6HG0555830.1	1.090011624	5.364563421	3.893068357	0.00028	0.015751512	-0.0148904	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B	elongation zone	12 h
HORVU.MOREX.r3.4HG0357750.1	0.412432361	9.218441158	4.100637669	0.00014	0.013220171	-0.01660595	Alanine--tRNA ligase	elongation zone	12 h
HORVU.MOREX.r3.6HG0540280.1	0.979932544	5.482684853	3.898767998	0.00027	0.015692177	-0.01661585	F-box family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0011880.1	-0.939593396	0.780281969	-3.959492059	0.00023	0.014924834	-0.01693149	Voltage-dependent T-type calcium channel subunit alpha-1G	elongation zone	12 h
HORVU.MOREX.r3.5HG0522760.1	3.213034747	0.069285095	3.870176349	0.0003	0.016327144	-0.01886347	imidazolonepropionase (Protein of unknown function, DUF642)	elongation zone	12 h
HORVU.MOREX.r3.7HG0669580.1	-0.707492592	1.55116404	-3.993062076	0.0002	0.014738733	-0.022011	Caleosin	elongation zone	12 h
HORVU.MOREX.r3.3HG0310680.1	0.757497523	7.418942266	4.005623884	0.00019	0.014672221	-0.02580974	Mitochondrial import receptor subunit TOM20	elongation zone	12 h
HORVU.MOREX.r3.4HG0342160.1	0.472826079	5.308472026	3.957640712	0.00023	0.014924834	-0.02924309	Presenilin	elongation zone	12 h
HORVU.MOREX.r3.4HG0346720.1	0.553394526	10.60860825	4.151088987	0.00012	0.012462233	-0.03028004	Protein disulfide-isomerase	elongation zone	12 h
HORVU.MOREX.r3.4HG0413690.1	0.579686778	4.40336351	3.905640063	0.00027	0.015692177	-0.03428482	26S proteasome non-ATPase regulatory subunit-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0494740.1	1.43924588	7.598359813	3.956615456	0.00023	0.014924834	-0.03488462	DAG protein, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.1HG0067410.1	0.436932936	5.64638285	3.962454563	0.00022	0.014924834	-0.03500155	1-acyl-sn-glycerol-3-phosphate acyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0298120.1	1.338941445	3.348184436	3.771819366	0.00041	0.017914792	-0.04138534	BTB/POZ domain containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0077880.1	1.055812612	3.552074142	3.805976685	0.00037	0.017598677	-0.04263445	BAG family molecular chaperone regulator 7	elongation zone	12 h
HORVU.MOREX.r3.4HG0338340.1	1.827924217	3.481593478	3.768939688	0.00041	0.017948348	-0.04736242	GRAS transcription factor	elongation zone	12 h
HORVU.MOREX.r3.5HG0439640.1	1.002119824	3.420116187	3.800622124	0.00037	0.017696476	-0.05034008	Expansin protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0543100.1	3.124336468	1.312256801	3.824819411	0.00035	0.01726164	-0.05258822	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0517490.1	-0.858383105	1.614894636	-3.897186614	0.00028	0.015726837	-0.05618385	Protein kinase	elongation zone	12 h
HORVU.MOREX.r3.6HG0632320.1	0.458402212	5.523777089	3.962546686	0.00022	0.014924834	-0.06492276	Leucine-rich repeat protein	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0050880.1	1.48303653	5.389192002	3.838027078	0.00033	0.017006082	-0.06657299	Methyltransferase-like protein 17, mitochondrial	elongation zone	12 h
HORVU.MOREX.r3.5HG0493850.1	0.558372719	7.419096029	4.025347836	0.00018	0.014527878	-0.06780218	Acyl-[acyl-carrier-protein] hydrolase	elongation zone	12 h
HORVU.MOREX.r3.5HG0427080.1	1.524451711	5.258314535	3.849603062	0.00032	0.016767189	-0.06795918	Kinesin-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0124910.1	0.886909253	9.424538243	4.054701509	0.00017	0.014078728	-0.06884262	40S ribosomal protein SA	elongation zone	12 h
HORVU.MOREX.r3.2HG0141900.1	0.668246315	5.9402647	3.976436261	0.00021	0.014881142	-0.07121645	L-ascorbate oxidase-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0142760.1	1.530216188	5.505958362	3.839235726	0.00033	0.016983175	-0.07470097	#N/A	elongation zone	12 h
HORVU.MOREX.r3.4HG0386830.1	1.11565737	3.806923626	3.803685478	0.00037	0.017603779	-0.07637784	UDP-glucuronate decarboxylase protein 1	elongation zone	12 h
HORVU.MOREX.r3.3HG0288420.1	0.969784624	7.285552254	3.96225572	0.00022	0.014924834	-0.07729412	Mannan endo-1,4-beta-mannosidase-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0462450.1	-1.399345648	-0.846663356	-3.752410566	0.00044	0.018288218	-0.08802032	S-acyltransferase	elongation zone	12 h
HORVU.MOREX.r3.4HG0375550.1	2.704694656	0.494963378	3.807832092	0.00037	0.017580172	-0.08927401	Rapid ALkalinization Factor family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0656360.1	1.76887709	7.497142351	3.935852718	0.00024	0.015535305	-0.09078711	Ribonucleoside-diphosphate reductase	elongation zone	12 h
HORVU.MOREX.r3.5HG0510940.1	1.392537918	5.282693497	3.848005824	0.00032	0.01680982	-0.09545177	HMG-Y-related protein A	elongation zone	12 h
HORVU.MOREX.r3.3HG0230090.1	-0.896099977	1.525121802	-4.014886429	0.00019	0.014546646	-0.09557855	Cysteine protease, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0240450.1	0.82868465	4.298635098	3.841353568	0.00033	0.016953892	-0.09620189	Protein gamma response 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0182750.1	0.914582292	5.83880247	3.914227872	0.00026	0.015692177	-0.09730277	Protein RETICULATA, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.5HG0424440.1	1.696287723	2.104628459	3.739677556	0.00045	0.018562843	-0.09809411	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0639380.1	1.178003064	7.629623995	3.958914122	0.00023	0.014924834	-0.09918018	60 kDa chaperonin	elongation zone	12 h
HORVU.MOREX.r3.6HG0541490.1	2.005880897	2.862577415	3.737877706	0.00046	0.018607144	-0.10144701	Mitochondrial transcription termination factor-like	elongation zone	12 h
HORVU.MOREX.r3.7HG0689040.1	2.001654105	2.151352586	3.745522922	0.00045	0.018421721	-0.10278845	RNA-binding protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0090820.1	0.58786292	4.907388768	3.89421745	0.00028	0.015751512	-0.10397451	Protein CHUP1, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.7HG0659030.1	0.789550842	7.54316044	3.964215859	0.00022	0.014924834	-0.10948842	Ubiquitin carboxyl-terminal hydrolase, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0634320.1	0.475201555	4.501085155	3.898891273	0.00027	0.015692177	-0.10980924	NAC domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0450100.1	0.604748966	5.024744254	3.889522479	0.00028	0.015756066	-0.11062129	Quinolinate synthase A	elongation zone	12 h
HORVU.MOREX.r3.2HG0096760.1	1.066723121	4.203419621	3.80389811	0.00037	0.017603779	-0.11541609	TOM1-like protein 2	elongation zone	12 h
HORVU.MOREX.r3.7HG0663790.1	1.898648736	4.045385183	3.753995234	0.00043	0.018288218	-0.12581478	Galactoside 2-alpha-L-fucosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0119160.1	0.562141433	6.243872664	3.929229704	0.00025	0.015626386	-0.12629021	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0257850.1	1.86381901	2.089146786	3.733073283	0.00046	0.018667357	-0.12677276	Magnesium-protoporphyrin IX monomethyl ester [oxidative] cycl	elongation zone	12 h
HORVU.MOREX.r3.5HG0491230.1	1.19002053	2.284227707	3.752975009	0.00043	0.018288218	-0.12737294	Dihydroflavonol-4-reductase	elongation zone	12 h
HORVU.MOREX.r3.1HG0054000.1	1.172877099	4.221868706	3.778182727	0.0004	0.017833387	-0.12813916	ATP-dependent Clp protease proteolytic subunit	elongation zone	12 h
HORVU.MOREX.r3.4HG0385300.1	0.593895166	9.307024474	4.051588368	0.00017	0.014078728	-0.13494948	Elongation factor 1-alpha	elongation zone	12 h
HORVU.MOREX.r3.4HG0418530.1	1.226654501	4.704048819	3.794315962	0.00038	0.017696476	-0.13775081	ATP-dependent chaperone ClpB	elongation zone	12 h
HORVU.MOREX.r3.1HG0086010.1	0.560533979	5.131586677	3.90033892	0.00027	0.015692177	-0.14386209	TSA: Wollemia nobilis Ref_Wollemi_Transcript_14910_3291 tran	elongation zone	12 h
HORVU.MOREX.r3.2HG0205680.1	2.359673438	1.160765307	3.77305137	0.00041	0.017914792	-0.14665082	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0573900.1	1.042973827	4.176459117	3.772368707	0.00041	0.017914792	-0.14744881	SWI/SNF complex subunit SWI3B	elongation zone	12 h
HORVU.MOREX.r3.2HG0095970.1	1.56109742	3.317154222	3.733378805	0.00046	0.018667357	-0.16905724	NBS-LRR disease resistance protein-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0242880.1	-0.928528605	-0.890008185	-3.789830288	0.00039	0.017696476	-0.17344614	Phloem protein 2-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0606040.1	1.730174942	3.594810934	3.718386509	0.00048	0.019097198	-0.17638392	Survival motor neuron	elongation zone	12 h
HORVU.MOREX.r3.6HG0549930.1	1.893574699	3.393056211	3.714759561	0.00049	0.019131832	-0.17678405	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0640560.1	2.450937624	0.442208837	3.751660882	0.00044	0.018290689	-0.17977253	NBS-LRR disease resistance protein-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0508680.1	1.740392098	2.582186545	3.749329245	0.00044	0.018313253	-0.18012033	Eukaryotic aspartyl protease family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0725700.1	-2.273909445	-1.181670666	-3.721765866	0.00048	0.019002693	-0.1816591	Receptor-like protein kinase	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0304490.1	-1.029896928	-1.400694178	-3.786732496	0.00039	0.017712844	-0.19029298	Myosin IC heavy chain	elongation zone	12 h
HORVU.MOREX.r3.1HG0092430.1	1.177273546	4.997512913	3.790293047	0.00039	0.017696476	-0.19457707	Asparagine synthetase	elongation zone	12 h
HORVU.MOREX.r3.4HG0416070.1	2.257225879	7.030233778	3.893243038	0.00028	0.015751512	-0.19466809	GATA transcription factor	elongation zone	12 h
HORVU.MOREX.r3.5HG0460170.1	1.961910199	2.2284743	3.70138203	0.00051	0.019449812	-0.21040802	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0095390.1	1.399258203	8.175356882	3.929632038	0.00025	0.015626386	-0.21122047	Histone deacetylase, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0347310.1	1.665646513	5.304851749	3.775917177	0.0004	0.017855434	-0.21578795	DNA polymerase	elongation zone	12 h
HORVU.MOREX.r3.1HG0094480.1	1.348983487	4.237351174	3.746610293	0.00044	0.018395923	-0.21816165	ATP-dependent Clp protease proteolytic subunit	elongation zone	12 h
HORVU.MOREX.r3.7HG0677580.1	1.377613874	5.782252606	3.853974711	0.00032	0.016689644	-0.2182241	Protein O-linked-mannose beta-1,4-N-acetylglucosaminyltransfe	elongation zone	12 h
HORVU.MOREX.r3.5HG0468930.1	2.64618113	3.393289477	3.695109452	0.00052	0.019449812	-0.21900988	Argonaute	elongation zone	12 h
HORVU.MOREX.r3.1HG0005840.1	1.465162812	1.736344477	3.691891215	0.00053	0.019449812	-0.22802844	Embryo defective 2735	elongation zone	12 h
HORVU.MOREX.r3.4HG0387040.1	1.285401259	5.073389367	3.786857757	0.00039	0.017712844	-0.22873255	RNA-binding protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0497180.1	2.540756619	0.857668817	3.740014119	0.00045	0.018562843	-0.23505186	Pentatricopeptide repeat-containing protein, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0114930.1	2.325672271	8.18750701	3.877999598	0.00029	0.016094925	-0.24873057	Nucleolar protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0303110.1	0.981411394	7.531826753	3.91444678	0.00026	0.015692177	-0.25280806	30S ribosomal protein S8, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0336830.1	0.529865777	6.56218357	3.901668516	0.00027	0.015692177	-0.25822231	ATP-dependent RNA helicase	elongation zone	12 h
HORVU.MOREX.r3.4HG0342440.1	2.425563027	3.291704004	3.680189758	0.00055	0.019711469	-0.25911867	myosin-2 heavy chain-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0057990.1	0.639221577	4.4289102	3.809259891	0.00036	0.017580172	-0.26720386	O-fucosyltransferase family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0516720.1	1.967991277	6.439287689	3.776146284	0.0004	0.017855434	-0.26861529	Glutathione-S-transferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0163290.1	1.627642012	1.166577297	3.679501944	0.00055	0.019711469	-0.27748172	RecQ-mediated genome instability protein 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0749600.1	1.238952692	3.788333413	3.715171331	0.00049	0.019131832	-0.27812263	Gamma-tubulin complex component	elongation zone	12 h
HORVU.MOREX.r3.1HG0048070.1	2.094624759	2.001188019	3.67270249	0.00056	0.019889362	-0.29265493	Folylpolyglutamate synthase	elongation zone	12 h
HORVU.MOREX.r3.4HG0331260.1	1.231570587	3.068963796	3.673199341	0.00056	0.019889362	-0.29553709	ABC transporter ATP-binding protein ARB1	elongation zone	12 h
HORVU.MOREX.r3.6HG0554800.1	1.080418235	4.238669575	3.742204212	0.00045	0.018540177	-0.29684055	Transmembrane protein 53	elongation zone	12 h
HORVU.MOREX.r3.3HG0300870.1	1.787806976	5.149023989	3.736258396	0.00046	0.018625563	-0.30234637	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0611290.1	1.079786181	7.158294058	3.871002518	0.0003	0.016327144	-0.30334899	Acetolactate synthase	elongation zone	12 h
HORVU.MOREX.r3.2HG0215550.1	1.076161527	7.917137824	3.919469534	0.00026	0.015692177	-0.31860406	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.2HG0200640.1	0.440489098	7.509809216	3.929752623	0.00025	0.015626386	-0.32453776	Carboxypeptidase	elongation zone	12 h
HORVU.MOREX.r3.1HG0027380.1	2.623071012	1.136430417	3.7098177	0.0005	0.019247224	-0.32668582	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0295680.1	-0.585662433	4.416665159	-3.892494031	0.00028	0.015751512	-0.32957069	Dihydropyrimidinase	elongation zone	12 h
HORVU.MOREX.r3.7HG0652830.1	1.930400883	0.863490792	3.674539948	0.00056	0.019889362	-0.33204205	Disease resistance protein RPP13	elongation zone	12 h
HORVU.MOREX.r3.6HG0558800.1	0.608218993	5.008690522	3.808543161	0.00036	0.017580172	-0.33352505	DNA-binding protein BIN4	elongation zone	12 h
HORVU.MOREX.r3.3HG0329870.1	-1.188891159	-1.903215009	-3.767460619	0.00042	0.017977071	-0.33877421	Pectin acetylesterase	elongation zone	12 h
HORVU.MOREX.r3.2HG0213240.1	1.297868338	2.83023571	3.664953315	0.00057	0.020165373	-0.33927185	Actin-related protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0200450.1	1.043475115	0.466638302	3.723058016	0.00048	0.019002693	-0.3394893	Beta-fructofuranosidase, insoluble isoenzyme 1	elongation zone	12 h
HORVU.MOREX.r3.1HG0070640.1	1.080389264	5.376818556	3.762943092	0.00042	0.01805759	-0.33949757	KH domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0299990.1	-0.712534083	6.228942935	-3.93016709	0.00025	0.015626386	-0.33959842	Glutathione-S-transferase	elongation zone	12 h
HORVU.MOREX.r3.6HG0633420.1	0.974342945	7.127371427	3.874716956	0.0003	0.016177895	-0.34587705	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0662670.1	0.695345569	4.911988083	3.815819148	0.00036	0.017465122	-0.34994719	aminoalcoholphosphotransferase 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0676040.1	-0.792488955	-0.533828415	-3.739711873	0.00045	0.018562843	-0.3551845	Decaprenyl-phosphate N-acetylglucosaminephosphotransferase	elongation zone	12 h
HORVU.MOREX.r3.1HG0051020.1	0.660151682	5.895903782	3.84206365	0.00033	0.016953892	-0.35596042	Membrane protein insertase YidC	elongation zone	12 h
HORVU.MOREX.r3.3HG0221460.1	0.622848705	7.255590658	3.909916342	0.00026	0.015692177	-0.35694119	Glycosyltransferase	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.7HG0732610.1	1.500245523	4.827784988	3.711734336	0.0005	0.019227921	-0.35943804	DNA polymerase alpha subunit B	elongation zone	12 h
HORVU.MOREX.r3.2HG0175590.1	2.94068047	3.241311809	3.644971384	0.00061	0.020507565	-0.36176498	ATP-dependent zinc metalloprotease FtsH 2	elongation zone	12 h
HORVU.MOREX.r3.1HG0093710.1	0.266430777	6.865906621	3.916464361	0.00026	0.015692177	-0.36629462	dihydroflavonol 4-reductase/flavanone protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0174030.1	2.561601845	1.901242042	3.672923982	0.00056	0.019889362	-0.36991449	RNA-dependent RNA polymerase	elongation zone	12 h
HORVU.MOREX.r3.7HG0643280.1	0.98822067	7.144031345	3.862066649	0.00031	0.016574489	-0.37095603	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0671880.1	0.886956638	3.67043834	3.702082327	0.00051	0.019449812	-0.37753819	RING/U-box protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0442360.1	1.081916712	6.472159574	3.827397511	0.00034	0.017220216	-0.38222113	Diaminopimelate epimerase	elongation zone	12 h
HORVU.MOREX.r3.5HG0498530.1	3.055988022	3.096808835	3.633380806	0.00063	0.020646627	-0.38549414	Subtilisin-like protease	elongation zone	12 h
HORVU.MOREX.r3.7HG0708820.1	0.838151521	5.143802841	3.761765209	0.00042	0.018086982	-0.38566705	PHD finger family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0256580.1	0.483826913	6.795309482	3.878374605	0.00029	0.016094925	-0.3896554	NEDD8-activating enzyme E1 catalytic subunit	elongation zone	12 h
HORVU.MOREX.r3.5HG0489810.1	1.088823816	3.755916949	3.697314584	0.00052	0.019449812	-0.39051409	Caffeoyl-CoA O-methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.6HG0577760.2	3.221193491	1.21790513	3.700850403	0.00051	0.019449812	-0.39273698	Ran-binding zinc finger protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0312290.1	1.828693254	2.160544907	3.63480839	0.00063	0.020623325	-0.39454269	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.4HG0387850.1	1.434073074	4.670908916	3.692599869	0.00053	0.019449812	-0.3983981	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0581570.1	0.397031917	4.929735327	3.81736707	0.00035	0.017465122	-0.39878496	Leucine-rich repeat-containing protein 1	elongation zone	12 h
HORVU.MOREX.r3.4HG0345330.1	1.597331619	3.738426759	3.658871306	0.00058	0.020375761	-0.40246251	DNA-directed RNA polymerase	elongation zone	12 h
HORVU.MOREX.r3.7HG0640430.1	0.890259147	3.689469005	3.68166363	0.00054	0.019711469	-0.40381677	Disease resistance protein (TIR-NBS-LRR class)	elongation zone	12 h
HORVU.MOREX.r3.1HG0084850.1	1.402388705	4.250961882	3.689079015	0.00053	0.019449812	-0.40397038	Histone chaperone	elongation zone	12 h
HORVU.MOREX.r3.4HG0370380.1	0.472861239	5.905711064	3.855983905	0.00031	0.016685099	-0.40456454	Erlin-2	elongation zone	12 h
HORVU.MOREX.r3.1HG0071050.1	-1.15528135	-0.746820209	-3.715672568	0.00049	0.019131832	-0.40479133	Expansin	elongation zone	12 h
HORVU.MOREX.r3.6HG0551300.1	1.885463903	0.944462851	3.639449283	0.00062	0.020516782	-0.40483502	F-box family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0487010.1	1.878015489	2.469699433	3.625507145	0.00065	0.020713759	-0.40595576	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0703580.1	0.716774355	4.485598753	3.794504145	0.00038	0.017696476	-0.40706487	Glyceraldehyde-3-phosphate dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.1HG0046180.1	-0.496732635	5.918664759	-3.910461387	0.00026	0.015692177	-0.40909638	Ser/Thr protein phosphatase family protein, expressed	elongation zone	12 h
HORVU.MOREX.r3.5HG0478010.1	0.790400761	3.664153717	3.696398391	0.00052	0.019449812	-0.41128551	Chaperone protein DnaJ	elongation zone	12 h
HORVU.MOREX.r3.2HG0194120.1	1.035455542	4.519929846	3.706266591	0.0005	0.019342524	-0.41198606	Phospholipid scramblase	elongation zone	12 h
HORVU.MOREX.r3.6HG0605940.1	-0.811550697	3.17964847	-3.792933316	0.00038	0.017696476	-0.41325016	Xyloglucan endotransglucosylase/hydrolase	elongation zone	12 h
HORVU.MOREX.r3.2HG0170840.1	0.441757548	6.055499187	3.842260554	0.00033	0.016953892	-0.41690148	26S proteasome non-ATPase regulatory subunit-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0248280.1	0.416878457	8.506150471	3.95514316	0.00023	0.014924834	-0.41869663	Reticulon-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0335990.1	2.896453733	2.777740737	3.628032557	0.00064	0.020713759	-0.41999475	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0079750.1	-1.279614574	-1.155378593	-3.680163317	0.00055	0.019711469	-0.42028166	MYB transcription factor	elongation zone	12 h
HORVU.MOREX.r3.2HG0197560.1	0.747212548	5.10495621	3.763249268	0.00042	0.01805759	-0.42354107	RNA-binding protein 39	elongation zone	12 h
HORVU.MOREX.r3.5HG0478390.1	0.588109754	5.551366827	3.807547332	0.00037	0.017580172	-0.42416109	PCI domain-containing protein 2	elongation zone	12 h
HORVU.MOREX.r3.5HG0501270.1	1.777626755	6.40008053	3.767020967	0.00042	0.017977071	-0.42464445	Chromatin assembly factor-1	elongation zone	12 h
HORVU.MOREX.r3.4HG0396660.1	1.968604424	6.770443008	3.778517059	0.0004	0.017833387	-0.42705547	Replication protein A 70 kDa DNA-binding subunit	elongation zone	12 h
HORVU.MOREX.r3.1HG0086120.1	1.964556698	4.055301306	3.651439682	0.0006	0.020507565	-0.43030629	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.1HG0050860.1	1.656957356	2.488742376	3.615029906	0.00067	0.020839563	-0.43401747	HIT zinc finger family protein, expressed	elongation zone	12 h
HORVU.MOREX.r3.5HG0461170.1	0.678107149	4.201237205	3.725532012	0.00047	0.018928454	-0.44293964	Protein FAR1-RELATED SEQUENCE 5	elongation zone	12 h
HORVU.MOREX.r3.1HG0003930.1	0.962297706	6.637383562	3.814120626	0.00036	0.017476052	-0.45274573	50S ribosomal protein L22	elongation zone	12 h
HORVU.MOREX.r3.2HG0100770.1	0.543533917	4.593259975	3.781860548	0.0004	0.017833387	-0.45479275	Glutamyl-tRNA(Gln) amidotransferase subunit A	elongation zone	12 h
HORVU.MOREX.r3.1HG0072540.1	1.086136261	5.751312553	3.788414291	0.00039	0.017712844	-0.45659796	Histone H4	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0017310.1	1.300190628	6.737539169	3.790038435	0.00039	0.017696476	-0.45710296	Auxin influx transporter	elongation zone	12 h
HORVU.MOREX.r3.5HG0526170.1	-1.105496647	-1.761923852	-3.659614159	0.00058	0.02036338	-0.45786442	Actin depolymerizing factor	elongation zone	12 h
HORVU.MOREX.r3.3HG0288320.1	1.061262251	6.036276973	3.773713739	0.00041	0.017914792	-0.46570255	Nuclear pore complex protein NUP85	elongation zone	12 h
HORVU.MOREX.r3.6HG0564510.1	1.00389942	4.576465099	3.698714608	0.00052	0.019449812	-0.46609928	Arabinose 5-phosphate isomerase, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0542170.1	2.675167317	-0.57519434	3.719074923	0.00048	0.019092689	-0.46848266	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0466010.1	0.600223118	3.637083856	3.688886776	0.00053	0.019449812	-0.47359046	Glutaredoxin	elongation zone	12 h
HORVU.MOREX.r3.7HG0656370.1	3.700888403	3.059766906	3.605225397	0.00069	0.021013719	-0.4789416	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albu	elongation zone	12 h
HORVU.MOREX.r3.7HG0667510.1	0.999018287	1.198678787	3.608937762	0.00068	0.020937187	-0.48220901	ADP-ribosylation factor family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0307240.1	-2.293989484	-3.376882233	-3.603978199	0.00069	0.021039776	-0.48249504	Amino acid permease	elongation zone	12 h
HORVU.MOREX.r3.4HG0405960.1	1.28664455	4.60369269	3.668070952	0.00057	0.020073937	-0.48495636	Origin recognition complex subunit 2	elongation zone	12 h
HORVU.MOREX.r3.6HG0631400.1	-0.920202146	2.336066158	-3.787352023	0.00039	0.017712844	-0.48766214	Disease resistance protein RPM1	elongation zone	12 h
HORVU.MOREX.r3.2HG0181010.1	1.410523911	4.533256071	3.651280628	0.0006	0.020507565	-0.49513039	RNA binding protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0297180.1	1.537818976	2.307651608	3.594693845	0.00071	0.021178576	-0.49674734	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0195110.2	1.838439388	0.674913375	3.596566636	0.00071	0.021178576	-0.50014782	Remorin family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0403200.1	2.533786693	0.946991273	3.627980753	0.00064	0.020713759	-0.50037778	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0277200.1	1.200202633	6.184721678	3.796644156	0.00038	0.017696476	-0.50205984	Pyruvate kinase	elongation zone	12 h
HORVU.MOREX.r3.2HG0113870.1	1.548708327	2.572538505	3.593993109	0.00071	0.021178576	-0.50346811	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0416570.1	1.975996615	1.341219886	3.591318713	0.00072	0.021247809	-0.50419438	Major facilitator superfamily domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0685290.1	0.875490369	7.739023195	3.850005913	0.00032	0.016767189	-0.5045831	Glycine--tRNA ligase	elongation zone	12 h
HORVU.MOREX.r3.2HG0173270.1	1.70675105	4.153097441	3.614840613	0.00067	0.020839563	-0.50646911	ATP-dependent RNA helicase	elongation zone	12 h
HORVU.MOREX.r3.7HG0736160.2	2.379610321	1.391443228	3.616830888	0.00067	0.020839563	-0.50946837	DNA primase/helicase	elongation zone	12 h
HORVU.MOREX.r3.5HG0514790.3	0.568863209	10.92395731	3.995506629	0.0002	0.014738733	-0.51168087	Elongation factor 1-alpha	elongation zone	12 h
HORVU.MOREX.r3.2HG0100900.1	-0.379504376	4.579241165	-3.799164817	0.00038	0.017696476	-0.5122824	Phosphoglycerate mutase-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0183640.1	1.585572849	4.446959637	3.641817687	0.00062	0.020516782	-0.51919242	P-loop containing nucleoside triphosphate hydrolases superfami	elongation zone	12 h
HORVU.MOREX.r3.2HG0188760.1	1.860179119	0.265515101	3.625507807	0.00065	0.020713759	-0.51960045	Glycosyltransferases	elongation zone	12 h
HORVU.MOREX.r3.3HG0329590.1	1.265359979	1.948546577	3.587410104	0.00073	0.021412735	-0.52013584	30S ribosomal protein S17	elongation zone	12 h
HORVU.MOREX.r3.3HG0219410.1	-0.869457323	3.869903081	-3.780708403	0.0004	0.017833387	-0.52674691	Hydroxyproline-rich glycoprotein family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0467960.1	1.455384419	2.390386799	3.576156653	0.00075	0.021691049	-0.53886412	DNA-directed RNA polymerase subunit	elongation zone	12 h
HORVU.MOREX.r3.4HG0334890.1	1.096206981	7.019132846	3.791184535	0.00039	0.017696476	-0.53998225	Glycine-rich family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0611730.1	1.935721726	6.381854124	3.699304715	0.00051	0.019449812	-0.54512436	H/ACA ribonucleoprotein complex subunit 2-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0243420.1	1.232380764	4.335089839	3.640045562	0.00062	0.020516782	-0.55572377	DNA polymerase delta subunit 3	elongation zone	12 h
HORVU.MOREX.r3.3HG0283990.1	0.522128773	7.009142279	3.840389447	0.00033	0.01696336	-0.55578352	Glycylpeptide N-tetradecanoyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0294270.1	2.959702511	-0.244504286	3.65244831	0.0006	0.020507565	-0.55646035	Protein BIG GRAIN 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0118800.1	0.856877637	4.917895689	3.71074039	0.0005	0.019227921	-0.56245996	Mitochondrial inner membrane translocase subunit Tim44	elongation zone	12 h
HORVU.MOREX.r3.3HG0268790.1	2.653313743	1.412428125	3.611058505	0.00068	0.020915275	-0.56880837	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0199600.1	2.118480391	2.139351569	3.566133052	0.00078	0.021941854	-0.57051048	Organic cation transporter protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0186650.1	0.969578529	7.283329417	3.804676665	0.00037	0.017603779	-0.57060133	Non-specific serine/threonine protein kinase	elongation zone	12 h
HORVU.MOREX.r3.1HG0039000.1	1.168896713	5.928790739	3.725835651	0.00047	0.018928454	-0.5720679	Translin family protein, expressed	elongation zone	12 h
HORVU.MOREX.r3.3HG0259970.1	0.590626069	6.103470349	3.781597633	0.0004	0.017833387	-0.57430802	Bromo-adjacent-like (BAH) domain protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0388320.1	0.718737277	3.811059557	3.647024897	0.00061	0.020507565	-0.57487862	ubiquitin carboxyl-terminal hydrolase	elongation zone	12 h
HORVU.MOREX.r3.5HG0486780.1	0.770020347	2.89699251	3.61226515	0.00067	0.020885636	-0.5877369	Zinc-binding dehydrogenase family protein	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.2HG0152530.1	-0.452677668	4.851529635	-3.792132056	0.00038	0.017696476	-0.58778282	Fasciclin-like arabinogalactan protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0117880.1	-3.132515163	-0.66122785	-3.561528127	0.00079	0.022039057	-0.58784169	GDSL esterase/lipase	elongation zone	12 h
HORVU.MOREX.r3.3HG0306870.1	2.819877444	0.992463659	3.597778949	0.00071	0.021178576	-0.5885416	nuclear pore anchor	elongation zone	12 h
HORVU.MOREX.r3.3HG0309820.1	0.80884575	5.758874854	3.757695938	0.00043	0.018168927	-0.58958121	Small ubiquitin-related modifier	elongation zone	12 h
HORVU.MOREX.r3.1HG0024910.1	0.893573348	9.026974973	3.869037902	0.0003	0.016343249	-0.5916618	Ubiquitin	elongation zone	12 h
HORVU.MOREX.r3.7HG0731780.1	1.083508591	5.146448477	3.662368559	0.00058	0.020275771	-0.59251743	Gag polyprotein	elongation zone	12 h
HORVU.MOREX.r3.6HG0624580.1	1.362308894	4.00677816	3.612167884	0.00067	0.020885636	-0.59385685	Translation initiation factor IF-2, putative isoform 2	elongation zone	12 h
HORVU.MOREX.r3.4HG0416450.1	0.693097767	6.139964885	3.763879698	0.00042	0.01805759	-0.59623987	Protein ARABIDILLO 1	elongation zone	12 h
HORVU.MOREX.r3.5HG0520260.1	2.544275733	1.284181653	3.593278217	0.00072	0.021178576	-0.59800101	GTPase obg	elongation zone	12 h
HORVU.MOREX.r3.5HG0471960.1	1.307390422	3.222285397	3.594784106	0.00071	0.021178576	-0.59897355	Chromosome transmission fidelity protein 8	elongation zone	12 h
HORVU.MOREX.r3.6HG0548670.1	0.980441257	5.252080241	3.727247317	0.00047	0.018928454	-0.59923073	Histone H4	elongation zone	12 h
HORVU.MOREX.r3.3HG0284120.1	0.835427551	7.524666369	3.808600202	0.00036	0.017580172	-0.60135103	WD-40 repeat protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0015270.1	2.158625882	5.354810827	3.610247774	0.00068	0.020915275	-0.60288145	RRP15-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0377830.1	0.479953561	7.17360811	3.827974997	0.00034	0.017220216	-0.60381843	Nuclear cap-binding protein subunit 1	elongation zone	12 h
HORVU.MOREX.r3.4HG0380360.1	-0.783196742	-1.11903663	-3.641297931	0.00062	0.020516782	-0.60777248	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.7HG0650300.1	-0.643332762	3.514135404	-3.739269814	0.00045	0.018562843	-0.60842153	Protein kinase	elongation zone	12 h
HORVU.MOREX.r3.4HG0335750.1	1.871155301	7.585427625	3.735669592	0.00046	0.018625563	-0.61113628	Pescadillo homolog	elongation zone	12 h
HORVU.MOREX.r3.1HG0059770.1	0.693039334	8.691483921	3.864931839	0.00031	0.016471701	-0.61133086	Nascent polypeptide-associated complex subunit alpha-like prot	elongation zone	12 h
HORVU.MOREX.r3.2HG0109970.1	0.664064513	7.705771322	3.830469881	0.00034	0.017205109	-0.61423782	Lon protease homolog	elongation zone	12 h
HORVU.MOREX.r3.5HG0507820.1	0.623243424	8.522605219	3.854439286	0.00032	0.016689644	-0.61716243	Methyl-CpG binding domain containing protein, expressed	elongation zone	12 h
HORVU.MOREX.r3.7HG0638400.1	0.999912254	3.0032628	3.586061436	0.00073	0.021412967	-0.62005256	30S ribosomal protein S13	elongation zone	12 h
HORVU.MOREX.r3.1HG0071300.1	1.71242917	7.640000377	3.760547537	0.00042	0.018118761	-0.62304888	DNA helicase	elongation zone	12 h
HORVU.MOREX.r3.5HG0465060.1	2.386785555	0.671256507	3.593242466	0.00072	0.021178576	-0.62318215	Pentatricopeptide repeat-containing family protein	elongation zone	12 h
HORVU.MOREX.r3.UnG0753320.1	1.228288324	4.78278288	3.631976929	0.00063	0.020646627	-0.62429652	Nucleoporin protein Ndc1-Nup	elongation zone	12 h
HORVU.MOREX.r3.7HG0642890.1	2.046639053	5.571712758	3.655557198	0.00059	0.020437054	-0.63054682	Acid phosphatase 1	elongation zone	12 h
HORVU.MOREX.r3.5HG0489530.1	2.793480429	0.386435685	3.623741246	0.00065	0.020713759	-0.63238918	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0585150.1	0.314629888	5.680949913	3.778460211	0.0004	0.017833387	-0.63449807	NHL repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0116790.1	1.280270779	3.25502819	3.5612267	0.00079	0.022039057	-0.63704295	E3 ubiquitin-protein ligase	elongation zone	12 h
HORVU.MOREX.r3.2HG0215310.1	1.689559112	7.090699835	3.749375438	0.00044	0.018313253	-0.63805518	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.4HG0395060.1	2.586894382	0.480504378	3.62599001	0.00065	0.020713759	-0.63888005	#N/A	elongation zone	12 h
HORVU.MOREX.r3.4HG0332620.1	2.538542806	-0.394695086	3.595267176	0.00071	0.021178576	-0.64038205	DUF868 family protein (DUF868)	elongation zone	12 h
HORVU.MOREX.r3.3HG0231880.1	1.03549124	2.985187022	3.574196831	0.00076	0.021740481	-0.64143974	Leucine-rich repeat (LRR) family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0396240.1	1.898892028	0.669237595	3.551247416	0.00081	0.022303809	-0.64234881	Ferredoxin--NAD(P)(+) reductase (naphthalene dioxygenase/sali	elongation zone	12 h
HORVU.MOREX.r3.6HG0589360.1	1.246358777	7.208700986	3.75904465	0.00043	0.018129366	-0.64365421	Nucleosome assembly protein 1-like 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0703750.1	0.886785189	6.844981761	3.759800942	0.00043	0.018123749	-0.65017147	Programmed cell death protein 4	elongation zone	12 h
HORVU.MOREX.r3.3HG0288020.1	1.124944208	3.529030436	3.584633173	0.00073	0.021473531	-0.65068389	Tryptophan--tRNA ligase	elongation zone	12 h
HORVU.MOREX.r3.3HG0323600.1	-0.58841575	4.35559343	-3.76886603	0.00041	0.017948348	-0.6510716	Phosphatidylserine decarboxylase proenzyme 2	elongation zone	12 h
HORVU.MOREX.r3.1HG0032230.1	1.067916356	4.67002403	3.636560013	0.00063	0.020577395	-0.65476163	Rad3-related DNA helicase family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0573870.1	0.705197149	4.150119935	3.649157157	0.0006	0.020507565	-0.65535517	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.3HG0237870.1	1.990211986	5.343811141	3.627558375	0.00064	0.020713759	-0.65617286	Histone-lysine N-methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0260150.1	1.175350512	-0.115050093	3.530873509	0.00087	0.022907481	-0.66031948	Acylamino-acid-releasing enzyme	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0286530.1	-1.381196215	-2.561378469	-3.534879354	0.00086	0.022899718	-0.66307293	Transposon protein, putative, mutator sub-class	elongation zone	12 h
HORVU.MOREX.r3.3HG0278540.1	-0.434545725	6.253662754	-3.815891163	0.00036	0.017465122	-0.66566399	Hydroxyacylglutathione hydrolase	elongation zone	12 h
HORVU.MOREX.r3.4HG0401040.1	2.549656401	6.811727505	3.640146058	0.00062	0.020516782	-0.66900757	Expansin	elongation zone	12 h
HORVU.MOREX.r3.3HG0308530.1	0.896321964	4.112501755	3.596985871	0.00071	0.021178576	-0.66944322	Histone deacetylase, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0316000.1	0.836221039	6.5484869	3.752352936	0.00044	0.018288218	-0.67065001	Salicylate O-methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.6HG0552190.1	1.343656741	4.860782531	3.605572036	0.00069	0.021013719	-0.67108719	Ribose-phosphate pyrophosphokinase family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0551860.1	0.58560237	7.532070736	3.807045214	0.00037	0.017580172	-0.67120079	Eukaryotic translation initiation factor 3 subunit F	elongation zone	12 h
HORVU.MOREX.r3.2HG0214200.1	-0.735289243	1.301757812	-3.777673881	0.0004	0.017833387	-0.67155456	Dihydroflavonol 4-reductase	elongation zone	12 h
HORVU.MOREX.r3.6HG0634260.1	0.846884139	4.589475239	3.639723874	0.00062	0.020516782	-0.67745659	TSA: Wollemia nobilis Ref_Wollemi_Transcript_29242_1275 tran	elongation zone	12 h
HORVU.MOREX.r3.5HG0500680.1	0.740789255	6.785876601	3.782640615	0.0004	0.017833387	-0.6792495	Acyl carrier protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0684300.1	1.344741376	5.071242343	3.630431686	0.00064	0.020706437	-0.68072537	Bifunctional uridylyltransferase/uridylyl-removing enzyme	elongation zone	12 h
HORVU.MOREX.r3.2HG0207380.1	1.765994394	4.363598916	3.562883522	0.00079	0.022017161	-0.68744243	Double-strand break repair protein MRE11	elongation zone	12 h
HORVU.MOREX.r3.1HG0065100.1	1.664313313	7.852856437	3.75046428	0.00044	0.018313253	-0.68778342	DNA helicase	elongation zone	12 h
HORVU.MOREX.r3.6HG0552180.1	1.143322381	5.108310854	3.63923938	0.00062	0.020516782	-0.69065943	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0564520.1	1.297245436	5.49826859	3.635741221	0.00063	0.020596683	-0.6966649	Single-stranded DNA-binding protein WHY3	elongation zone	12 h
HORVU.MOREX.r3.7HG0676160.1	1.306034251	6.283730528	3.694505564	0.00052	0.019449812	-0.70549152	Mitochondrial glycoprotein-like	elongation zone	12 h
HORVU.MOREX.r3.3HG0295530.1	1.92527103	3.813404323	3.516147947	0.00091	0.023235104	-0.70607561	UDP-glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0296610.1	1.325569062	2.287341464	3.51379045	0.00091	0.023235104	-0.70704702	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0496170.1	0.968711547	5.175044795	3.654214434	0.00059	0.020437054	-0.71618303	RNA polymerase II transcriptional coactivator	elongation zone	12 h
HORVU.MOREX.r3.1HG0013020.1	2.655846757	0.328708637	3.576280844	0.00075	0.021691049	-0.71685901	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0650970.1	1.096035255	7.468679104	3.766050822	0.00042	0.017994261	-0.71826672	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.5HG0467500.1	1.873668171	3.330218247	3.516319512	0.00091	0.023235104	-0.71908279	Pseudouridine synthase family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0304420.1	1.219362598	5.851634764	3.693286143	0.00052	0.019449812	-0.72045741	#N/A	elongation zone	12 h
HORVU.MOREX.r3.1HG0053940.1	1.447428463	5.672823401	3.629890158	0.00064	0.020708432	-0.72065532	stress response protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0077010.1	0.917491844	4.063866452	3.594361948	0.00071	0.021178576	-0.72167211	Transcriptional regulatory plant protein, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0023610.1	1.209616487	5.36944383	3.675654945	0.00055	0.019889362	-0.72272311	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0121130.1	2.737765063	2.407479747	3.51595798	0.00091	0.023235104	-0.72320185	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0737460.1	1.244885953	4.569245525	3.576174427	0.00075	0.021691049	-0.72332934	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.1HG0075430.1	2.095082013	4.723898757	3.542456467	0.00084	0.022605629	-0.72495976	Amidophosphoribosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0703170.1	1.389539465	4.025119613	3.543648012	0.00083	0.022553062	-0.72533215	BTB/POZ and MATH domain-containing protein 2	elongation zone	12 h
HORVU.MOREX.r3.7HG0704180.1	0.67134139	6.317889073	3.725966277	0.00047	0.018928454	-0.72596677	COP9 signalosome complex subunit 3	elongation zone	12 h
HORVU.MOREX.r3.3HG0316210.1	1.848147722	7.250167183	3.691100706	0.00053	0.019449812	-0.7266567	Basic 7S globulin 2	elongation zone	12 h
HORVU.MOREX.r3.5HG0513920.1	1.353469816	4.916144619	3.594546702	0.00071	0.021178576	-0.72706557	NADPH--cytochrome P450 reductase	elongation zone	12 h
HORVU.MOREX.r3.2HG0211230.1	1.884151653	1.198269179	3.515718181	0.00091	0.023235104	-0.72724164	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0005590.1	0.725566297	3.576430878	3.596957576	0.00071	0.021178576	-0.72842318	Mitochondrial import inner membrane translocase subunit tim2	elongation zone	12 h
HORVU.MOREX.r3.2HG0170060.1	1.237013122	5.035774752	3.617125895	0.00066	0.020839563	-0.72851056	Protein TIC 40, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.4HG0417410.1	1.397608728	0.91597262	3.508273205	0.00093	0.023255319	-0.73079491	Cold regulated protein 27	elongation zone	12 h
HORVU.MOREX.r3.2HG0204590.1	1.106220574	4.606565659	3.610247555	0.00068	0.020915275	-0.73091601	Receptor protein kinase, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0616490.1	1.378969231	4.602188135	3.580669907	0.00074	0.021613876	-0.73314051	Peptidyl-prolyl cis-trans isomerase	elongation zone	12 h
HORVU.MOREX.r3.4HG0343330.1	4.629059127	-0.333480115	3.529919452	0.00087	0.022944774	-0.73355675	Endonuclease III homolog	elongation zone	12 h
HORVU.MOREX.r3.5HG0526830.1	0.416496166	5.623951381	3.72128394	0.00048	0.019002693	-0.73431601	Hsp70 nucleotide exchange factor fes1	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.7HG0749870.1	-0.633155909	4.569999785	-3.782156275	0.0004	0.017833387	-0.73521981	Glucuronoxylan 4-O-methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0267680.1	2.728600722	4.551509802	3.51458863	0.00091	0.023235104	-0.74340314	UBP1-associated proteins 1C	elongation zone	12 h
HORVU.MOREX.r3.1HG0063560.1	2.214197615	-0.256820188	3.532154967	0.00086	0.022899718	-0.74636583	Sulfotransferase	elongation zone	12 h
HORVU.MOREX.r3.4HG0338270.1	2.127970295	7.140700386	3.654563815	0.00059	0.020437054	-0.74660103	ATP-dependent DNA helicase DDM1	elongation zone	12 h
HORVU.MOREX.r3.2HG0173240.1	0.905322125	4.646167723	3.605135315	0.00069	0.021013719	-0.75021337	Nucleosome assembly protein 1-like 1	elongation zone	12 h
HORVU.MOREX.r3.1HG0039710.1	0.980529664	3.112736137	3.53192345	0.00086	0.022899718	-0.75102951	Protein fluG	elongation zone	12 h
HORVU.MOREX.r3.2HG0161020.1	0.899356595	7.262436364	3.770969004	0.00041	0.017914792	-0.75125719	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0627970.1	0.70359547	6.26071971	3.734035243	0.00046	0.018667357	-0.75414021	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0180580.1	1.801057555	7.018787121	3.680355735	0.00055	0.019711469	-0.75475998	Proliferating cell nuclear antigen	elongation zone	12 h
HORVU.MOREX.r3.6HG0624620.1	1.571442515	7.088282878	3.693291944	0.00052	0.019449812	-0.75677566	DNA helicase	elongation zone	12 h
HORVU.MOREX.r3.2HG0108490.1	1.344716739	3.170050036	3.548906472	0.00082	0.022369939	-0.75877838	Xyloglucan endotransglucosylase/hydrolase	elongation zone	12 h
HORVU.MOREX.r3.5HG0529140.1	0.413909922	10.35930424	3.906179673	0.00027	0.015692177	-0.76045175	Elongation factor	elongation zone	12 h
HORVU.MOREX.r3.7HG0665990.1	-0.666005138	6.15668184	-3.833923275	0.00034	0.017059301	-0.76399587	Shikimate kinase	elongation zone	12 h
HORVU.MOREX.r3.5HG0460900.1	0.967734088	6.775177122	3.721196446	0.00048	0.019002693	-0.76430828	2-isopropylmalate synthase	elongation zone	12 h
HORVU.MOREX.r3.5HG0534510.1	0.962585172	7.454533079	3.744172722	0.00045	0.018462873	-0.76544312	Nascent polypeptide-associated complex subunit beta	elongation zone	12 h
HORVU.MOREX.r3.4HG0401740.1	2.406224252	1.996606862	3.49947913	0.00095	0.023511243	-0.76827912	Eukaryotic translation initiation factor 3 subunit H	elongation zone	12 h
HORVU.MOREX.r3.2HG0172050.1	0.450273143	8.585873782	3.822945782	0.00035	0.017322598	-0.77184881	RNA-binding protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0306420.1	0.922603897	3.782406003	3.575847243	0.00075	0.021691049	-0.77640611	TPR repeat-containing protein ZIP4	elongation zone	12 h
HORVU.MOREX.r3.6HG0556980.1	1.789584424	5.184914753	3.557528695	0.0008	0.022169819	-0.78264814	RNA binding protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0086110.1	1.163300713	5.469120462	3.62493285	0.00065	0.020713759	-0.78545373	50S ribosomal protein L21	elongation zone	12 h
HORVU.MOREX.r3.2HG0130960.1	-0.751241114	1.762022677	-3.558003947	0.0008	0.022167528	-0.78716425	Benzene 1,2-dioxygenase subunit alpha	elongation zone	12 h
HORVU.MOREX.r3.4HG0334580.1	1.904393791	3.64777309	3.50394945	0.00094	0.023362135	-0.78733196	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0690370.1	0.844051772	2.109174244	3.501530999	0.00095	0.023426471	-0.78937633	Malate dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.2HG0106340.1	2.716736448	1.552213778	3.512392812	0.00092	0.023235104	-0.78978037	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0505140.1	-0.547640677	6.833596665	-3.81654762	0.00036	0.017465122	-0.78989101	Phosphatase 2C family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0735200.1	0.449670967	10.46904646	3.892377852	0.00028	0.015751512	-0.7901656	Elongation factor	elongation zone	12 h
HORVU.MOREX.r3.2HG0152140.1	0.688200135	5.200813775	3.645652475	0.00061	0.020507565	-0.79127253	D-amino acid dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.1HG0067720.1	-1.057154991	-2.106023761	-3.569687492	0.00077	0.021876787	-0.79211567	#N/A	elongation zone	12 h
HORVU.MOREX.r3.1HG0020280.1	0.839107842	7.185819282	3.736351811	0.00046	0.018625563	-0.79417599	Pentatricopeptide repeat superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0281850.1	0.971727967	5.846586489	3.645411502	0.00061	0.020507565	-0.79487605	Threonine synthase	elongation zone	12 h
HORVU.MOREX.r3.7HG0684630.1	1.250228158	6.041630602	3.645869628	0.00061	0.020507565	-0.79719195	DAG protein, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.1HG0069800.1	2.350056869	0.744516388	3.532762613	0.00086	0.022899718	-0.7982619	Histone-lysine N-methyltransferase, H3 lysine-9 specific	elongation zone	12 h
HORVU.MOREX.r3.7HG0680060.1	2.095002975	2.004315332	3.482070341	0.00101	0.024008795	-0.7983037	Mitochondrial transcription termination factor family protein, pu	elongation zone	12 h
HORVU.MOREX.r3.5HG0532630.1	1.471979904	4.235353088	3.551177825	0.00081	0.022303809	-0.80051171	Sister chromatid cohesion protein DCC1	elongation zone	12 h
HORVU.MOREX.r3.2HG0155140.1	1.432451139	3.347249234	3.490547967	0.00098	0.023786521	-0.80056725	tRNA dimethylallyltransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0127160.1	1.895807616	2.05404778	3.47598243	0.00102	0.024166531	-0.80077995	WD40 repeat-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0163090.1	1.019459254	7.015883321	3.71114994	0.0005	0.019227921	-0.80488218	Heavy metal-associated protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0541690.1	2.219268074	-0.276490972	3.518910329	0.0009	0.023235104	-0.80778142	Mitochondrial transcription termination factor-like	elongation zone	12 h
HORVU.MOREX.r3.4HG0406380.1	0.475265826	5.163918803	3.672727036	0.00056	0.019889362	-0.81255923	GEM-like protein 1	elongation zone	12 h
HORVU.MOREX.r3.5HG0468290.1	0.973879791	9.889642173	3.819167586	0.00035	0.017458382	-0.81476109	Polyadenylate-binding protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0119360.1	1.93374086	-1.10964552	3.472776936	0.00103	0.024215578	-0.81795375	Gibberellin receptor GID1A	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.4HG0342990.1	1.626563212	4.752270826	3.555318129	0.0008	0.022260348	-0.82011429	Condensin-2 complex subunit G2	elongation zone	12 h
HORVU.MOREX.r3.1HG0022460.1	0.484459438	7.308294084	3.74672678	0.00044	0.018395923	-0.82114811	Transport inhibitor response 1	elongation zone	12 h
HORVU.MOREX.r3.4HG0402600.2	1.120008014	2.451455995	3.482830803	0.001	0.023981387	-0.82215209	5-dehydro-2-deoxygluconokinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0323490.1	1.214523625	4.264274151	3.533212071	0.00086	0.022899718	-0.8245389	DNA mismatch repair protein MutL	elongation zone	12 h
HORVU.MOREX.r3.6HG0588300.1	1.627355075	2.046655197	3.466147534	0.00105	0.024538512	-0.8262988	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0291380.1	2.328969179	4.361758282	3.488805179	0.00098	0.023815524	-0.82670011	Peptidoglycan-recognition protein SB2	elongation zone	12 h
HORVU.MOREX.r3.2HG0125870.1	0.679690857	9.837842611	3.836127739	0.00033	0.017055324	-0.82718556	50S ribosomal protein L15	elongation zone	12 h
HORVU.MOREX.r3.2HG0173960.1	-0.72336846	2.814914619	-3.571208587	0.00077	0.021819151	-0.82732264	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.2HG0177450.1	1.270710518	4.715585642	3.565784884	0.00078	0.021941854	-0.82895407	Ribosome-recycling factor	elongation zone	12 h
HORVU.MOREX.r3.7HG0750000.1	-1.153031864	-2.120414367	-3.5522524	0.00081	0.022303809	-0.83386982	Disease resistance protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0502580.1	1.764688339	4.788366911	3.520741339	0.00089	0.023235104	-0.83724914	Regulator of Vps4 activity in the MVB pathway protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0119970.1	3.117197447	3.337857733	3.458811692	0.00108	0.024669554	-0.84539319	Heat shock transcription factor	elongation zone	12 h
HORVU.MOREX.r3.3HG0313070.1	1.975475577	6.095175499	3.604997811	0.00069	0.021013719	-0.8476503	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0467900.1	3.109191459	1.256467408	3.511574702	0.00092	0.023235104	-0.84933997	Cyclin	elongation zone	12 h
HORVU.MOREX.r3.1HG0032910.1	0.658230142	5.350158872	3.666206083	0.00057	0.020121419	-0.8569504	Lysine-specific demethylase	elongation zone	12 h
HORVU.MOREX.r3.2HG0204440.1	0.886612016	4.696803122	3.572602382	0.00076	0.021766161	-0.85755461	4-hydroxy-tetrahydrodipicolinate synthase	elongation zone	12 h
HORVU.MOREX.r3.3HG0236000.1	0.434116877	6.001989313	3.692931383	0.00053	0.019449812	-0.85866516	Ectonucleotide pyrophosphatase/phosphodiesterase, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0478280.1	1.775642454	3.919076773	3.48416512	0.001	0.023938404	-0.85916159	ATP-dependent RNA helicase	elongation zone	12 h
HORVU.MOREX.r3.2HG0113180.1	0.789913887	4.229499943	3.566324392	0.00078	0.021941854	-0.86158599	DNA-directed RNA polymerases I, II, and III subunit rpabc3	elongation zone	12 h
HORVU.MOREX.r3.2HG0186750.1	2.547989855	1.34331984	3.490151936	0.00098	0.023786999	-0.86344391	Growth-regulating factor	elongation zone	12 h
HORVU.MOREX.r3.UnG0765280.1	1.289981496	2.589811572	3.478150622	0.00102	0.024127373	-0.86546819	F-box family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0752350.1	2.502256874	3.186534982	3.450523484	0.00111	0.025099251	-0.86689727	AT hook motif DNA-binding family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0741780.1	0.952452873	6.389609859	3.674522214	0.00056	0.019889362	-0.86792621	40S ribosomal protein S27	elongation zone	12 h
HORVU.MOREX.r3.5HG0522140.1	0.863971331	5.949304073	3.645755854	0.00061	0.020507565	-0.86893197	Cleavage and polyadenylation specificity factor subunit 2	elongation zone	12 h
HORVU.MOREX.r3.6HG0572260.1	2.26777119	-0.289254551	3.489084156	0.00098	0.023815524	-0.87631201	Exocyst complex component SEC3A	elongation zone	12 h
HORVU.MOREX.r3.7HG0672900.1	1.995551471	0.425915719	3.466538142	0.00105	0.02453734	-0.8770273	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0113530.1	1.440138181	3.744005308	3.475714253	0.00102	0.024166531	-0.8772812	THUMP domain-containing protein 1 like	elongation zone	12 h
HORVU.MOREX.r3.6HG0567330.1	1.262892859	5.748868839	3.615181719	0.00067	0.020839563	-0.88212548	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit	elongation zone	12 h
HORVU.MOREX.r3.2HG0194130.1	0.993908903	5.878463741	3.613339417	0.00067	0.020873129	-0.88452115	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0724060.1	-1.225376035	0.588187119	-3.624484261	0.00065	0.020713759	-0.88507511	U-box domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0438300.1	3.028000787	-0.03895989	3.483806422	0.001	0.023938404	-0.88717202	Protein FAR1-RELATED SEQUENCE 5	elongation zone	12 h
HORVU.MOREX.r3.2HG0172190.1	2.096060395	1.141861715	3.454723216	0.00109	0.024865394	-0.88989135	Meiosis-specific with OB domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0493060.1	0.811596358	7.550677769	3.716429376	0.00049	0.019131832	-0.89159709	60S ribosomal protein L32	elongation zone	12 h
HORVU.MOREX.r3.1HG0031730.1	1.232462337	7.573338482	3.696258422	0.00052	0.019449812	-0.89174928	DNA helicase	elongation zone	12 h
HORVU.MOREX.r3.1HG0073600.1	1.287806815	3.523923593	3.474247022	0.00103	0.024201764	-0.89187327	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0204920.1	1.186495269	3.638603207	3.485849927	0.00099	0.023901967	-0.89241444	Crossover junction endonuclease EME1B	elongation zone	12 h
HORVU.MOREX.r3.3HG0232070.1	2.076589318	5.516136915	3.533270699	0.00086	0.022899718	-0.89945128	Protein O-linked-mannose beta-1,4-N-acetylglucosaminyltransfe	elongation zone	12 h
HORVU.MOREX.r3.3HG0325830.1	2.963445661	1.73334501	3.457962177	0.00108	0.024705447	-0.90468215	Uridylate kinase	elongation zone	12 h
HORVU.MOREX.r3.7HG0740180.1	1.357187766	5.365923975	3.562414063	0.00079	0.022018823	-0.90631132	MMS19 nucleotide excision repair protein-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0118530.1	1.81166156	5.0118675	3.504236396	0.00094	0.023362135	-0.907091	ATP-dependent RNA helicase	elongation zone	12 h
HORVU.MOREX.r3.3HG0303330.1	0.887815573	6.555668972	3.68280774	0.00054	0.019711469	-0.90821332	#N/A	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.2HG0125550.1	0.647263091	8.919649801	3.779174832	0.0004	0.017833387	-0.90863472	Elongation factor 1-beta	elongation zone	12 h
HORVU.MOREX.r3.2HG0179940.1	1.006834788	5.507339313	3.600532801	0.0007	0.021178576	-0.90958903	#N/A	elongation zone	12 h
HORVU.MOREX.r3.1HG0066530.1	1.129152114	4.906097437	3.541231878	0.00084	0.022660635	-0.91056253	DUF630 family protein, putative (DUF630 and DUF632)	elongation zone	12 h
HORVU.MOREX.r3.5HG0514490.1	0.599303615	5.559766109	3.64757304	0.0006	0.020507565	-0.91689691	Hexosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0514100.1	0.651308964	4.963873023	3.604860016	0.00069	0.021013719	-0.91986501	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0659670.1	1.28852847	5.414107691	3.554459596	0.00081	0.022275873	-0.92097586	Nucleoporin NUP188	elongation zone	12 h
HORVU.MOREX.r3.7HG0674840.1	2.741855128	0.633419814	3.478848895	0.00101	0.024104211	-0.92220056	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0622440.1	0.572347423	6.187280102	3.659992255	0.00058	0.02036338	-0.92327465	Protein FLX-like 1	elongation zone	12 h
HORVU.MOREX.r3.6HG0591270.1	-0.345735511	5.135492747	-3.689968114	0.00053	0.019449812	-0.92521127	Vacuolar protein sorting-associated protein 20	elongation zone	12 h
HORVU.MOREX.r3.2HG0183740.1	1.046224556	5.211569422	3.56448663	0.00078	0.021955355	-0.92911056	Sugar transporter, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0088350.1	2.567967827	-0.24071049	3.497833905	0.00096	0.02354153	-0.93566289	F-box protein (DUF295)	elongation zone	12 h
HORVU.MOREX.r3.5HG0428840.1	0.759195213	5.358223693	3.60139784	0.0007	0.021176603	-0.93606715	BTB/POZ domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0616300.1	-0.557978062	5.182691489	-3.721608299	0.00048	0.019002693	-0.93796601	Histidine kinase	elongation zone	12 h
HORVU.MOREX.r3.1HG0080320.1	1.738536443	1.65312479	3.426508229	0.00119	0.025731015	-0.9383112	IQ domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0626050.1	1.084176504	4.114338477	3.533583557	0.00086	0.022899718	-0.94528891	RNA binding	elongation zone	12 h
HORVU.MOREX.r3.5HG0471400.1	2.303806854	3.16323989	3.42165568	0.00121	0.025782931	-0.94659532	QWRF motif protein (DUF566)	elongation zone	12 h
HORVU.MOREX.r3.6HG0540980.1	1.756296565	4.62525369	3.46570845	0.00106	0.024543314	-0.94956655	Trihelix transcription factor GT-2	elongation zone	12 h
HORVU.MOREX.r3.5HG0529120.1	0.785666683	7.801286727	3.705841279	0.0005	0.019342524	-0.95118095	Elongation factor	elongation zone	12 h
HORVU.MOREX.r3.2HG0158900.1	1.629803963	1.613344832	3.41725039	0.00122	0.02596429	-0.9526706	Ribonuclease P/MRP protein subunit POP5	elongation zone	12 h
HORVU.MOREX.r3.1HG0077170.1	0.702719956	4.830924904	3.569120098	0.00077	0.021876787	-0.95579365	Protein EMBRYONIC FLOWER 1	elongation zone	12 h
HORVU.MOREX.r3.6HG0616480.1	0.590987208	5.832985524	3.655962644	0.00059	0.020437054	-0.95655354	#N/A	elongation zone	12 h
HORVU.MOREX.r3.4HG0401320.1	-0.741179368	0.708055432	-3.520151491	0.0009	0.023235104	-0.96039096	Tetraspanin	elongation zone	12 h
HORVU.MOREX.r3.1HG0044670.1	1.500055821	5.661428894	3.552384268	0.00081	0.022303809	-0.96638823	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0714570.1	1.188959822	4.671992391	3.513028138	0.00091	0.023235104	-0.96716648	50S ribosomal protein L19, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0404110.1	0.956882915	7.328767239	3.666978988	0.00057	0.020107621	-0.96720693	Adenylosuccinate synthetase	elongation zone	12 h
HORVU.MOREX.r3.6HG0552550.1	1.714292627	4.44139878	3.459234121	0.00108	0.024665565	-0.96894145	Upstream activation factor subunit spp27	elongation zone	12 h
HORVU.MOREX.r3.3HG0298200.1	2.006165546	3.96464743	3.428566098	0.00118	0.025704276	-0.97682762	Cobalt ion binding	elongation zone	12 h
HORVU.MOREX.r3.3HG0236810.1	2.740145429	3.500823851	3.414553898	0.00123	0.026021602	-0.9776118	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0523860.1	-0.610291748	4.167580678	-3.637505378	0.00062	0.020550106	-0.97803048	Calcium-dependent protein kinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0322190.1	1.081504368	4.857803386	3.531083939	0.00087	0.022907481	-0.97807547	30S ribosomal protein S11	elongation zone	12 h
HORVU.MOREX.r3.6HG0543780.1	0.808781272	7.397821422	3.707600353	0.0005	0.019342524	-0.97852186	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.6HG0606460.1	1.645821798	7.91527308	3.65409772	0.00059	0.020437054	-0.98121405	DNA topoisomerase 2	elongation zone	12 h
HORVU.MOREX.r3.2HG0206380.1	0.911940865	5.584402928	3.564244859	0.00078	0.021955355	-0.98466227	DNA-directed RNA polymerase subunit beta	elongation zone	12 h
HORVU.MOREX.r3.5HG0466780.1	0.915659588	7.10069964	3.648197127	0.0006	0.020507565	-0.99139738	Carbamoyl-phosphate synthase small chain	elongation zone	12 h
HORVU.MOREX.r3.7HG0719410.1	1.02288595	6.134815643	3.583676864	0.00074	0.021475647	-0.99235335	Trichome birefringence-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0470640.1	0.68030928	4.647151278	3.57342482	0.00076	0.021761735	-0.99515527	WD40 repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0330120.1	-2.266911887	-3.009670865	-3.41122508	0.00124	0.026060689	-0.99757556	O-methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.4HG0390380.1	0.917972135	6.629358353	3.62123954	0.00066	0.020810194	-1.0007143	Importin-4	elongation zone	12 h
HORVU.MOREX.r3.7HG0643190.1	1.123931854	4.36385392	3.499893979	0.00095	0.023509855	-1.00436266	Ribosomal protein L29 family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0624450.1	2.008515761	3.649637416	3.407890101	0.00126	0.026083278	-1.0055563	Zinc finger protein VAR3, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.4HG0417850.1	0.644846445	4.694211226	3.564307902	0.00078	0.021955355	-1.00606073	Cyclin delta-3, putative	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.7HG0700320.1	2.966417693	0.851795789	3.433958153	0.00116	0.025647345	-1.00742906	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0196800.1	-1.670335251	-0.209944285	-3.408917045	0.00125	0.026083278	-1.00789161	Multidrug resistance protein ABC transporter family	elongation zone	12 h
HORVU.MOREX.r3.6HG0578070.1	1.072244483	7.144692186	3.638216799	0.00062	0.020537791	-1.01040076	Nuclear pore complex protein NUP205	elongation zone	12 h
HORVU.MOREX.r3.5HG0504520.1	-1.109472727	0.68442194	-3.522433208	0.00089	0.023206422	-1.01083909	Phytoene synthase	elongation zone	12 h
HORVU.MOREX.r3.4HG0343850.1	0.44044438	6.579849823	3.662097786	0.00058	0.020275771	-1.01416639	La	elongation zone	12 h
HORVU.MOREX.r3.2HG0125940.1	1.40781657	2.626858817	3.402881118	0.00128	0.026178272	-1.01446012	Methyltransferase-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0507770.1	2.050249052	2.818084292	3.393559257	0.00131	0.026348744	-1.01720196	Cytosolic 5-nucleotidase	elongation zone	12 h
HORVU.MOREX.r3.5HG0519930.1	1.386614023	8.04952968	3.656951234	0.00059	0.020428272	-1.0218576	30S ribosomal protein S19	elongation zone	12 h
HORVU.MOREX.r3.6HG0617940.1	1.634656725	4.532901735	3.447627087	0.00112	0.025172156	-1.02476215	Replication factor C subunit	elongation zone	12 h
HORVU.MOREX.r3.3HG0277330.1	0.625401879	4.294396239	3.547829376	0.00082	0.022414047	-1.02654741	CASP-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0553310.1	0.905923064	4.173624101	3.476918578	0.00102	0.024161792	-1.02685913	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0493430.1	1.975598498	1.099113261	3.394806784	0.00131	0.026348744	-1.02917053	tRNA-splicing endonuclease subunit SEN54	elongation zone	12 h
HORVU.MOREX.r3.4HG0370520.1	0.678991664	3.910657525	3.514589464	0.00091	0.023235104	-1.03259812	inactive purple acid phosphatase-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0344470.1	1.51268705	6.296849234	3.538707266	0.00085	0.022755386	-1.0338962	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0543480.1	1.200963145	3.781413567	3.448021002	0.00111	0.025172156	-1.03486582	Disease resistance protein (NBS-LRR class) family	elongation zone	12 h
HORVU.MOREX.r3.5HG0486070.1	0.665887224	6.53847179	3.639862118	0.00062	0.020516782	-1.03734953	Aminotransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0302510.1	1.599628644	2.670886155	3.386757167	0.00134	0.026498466	-1.03767675	ATP-dependent zinc metalloprotease FtsH	elongation zone	12 h
HORVU.MOREX.r3.1HG0081090.1	1.897166645	1.704255649	3.384991504	0.00135	0.026498466	-1.03811704	30S ribosomal protein S1	elongation zone	12 h
HORVU.MOREX.r3.2HG0157610.1	1.29444426	5.355379445	3.514436111	0.00091	0.023235104	-1.04019947	Aspartate carbamoyltransferase	elongation zone	12 h
HORVU.MOREX.r3.6HG0607150.1	-0.361471359	5.329149771	-3.671839727	0.00056	0.019908381	-1.04104397	Syntaxin family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0061390.1	-0.695262848	1.721091073	-3.706815462	0.0005	0.019342524	-1.04408875	Trichome birefringence-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0573930.1	-0.431494247	3.609831823	-3.551744913	0.00081	0.022303809	-1.0449799	Mediator of RNA polymerase II transcription subunit 18	elongation zone	12 h
HORVU.MOREX.r3.2HG0124470.1	2.708125132	0.969557895	3.404593523	0.00127	0.026178272	-1.04875238	Transposon protein, putative, Mutator sub-class	elongation zone	12 h
HORVU.MOREX.r3.4HG0399210.1	0.841593427	6.281577577	3.609143046	0.00068	0.020937187	-1.05152409	Serine--tRNA ligase	elongation zone	12 h
HORVU.MOREX.r3.3HG0320580.1	1.214034251	2.137390256	3.391730891	0.00132	0.026441594	-1.05260963	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0278440.1	0.807832441	8.62320918	3.696898407	0.00052	0.019449812	-1.05422291	60S ribosomal protein L18a	elongation zone	12 h
HORVU.MOREX.r3.7HG0636580.1	0.818019731	9.366307276	3.732414477	0.00046	0.018669328	-1.05576776	50S ribosomal protein L6	elongation zone	12 h
HORVU.MOREX.r3.3HG0269960.1	-0.45547752	4.098981318	-3.625547518	0.00065	0.020713759	-1.05894867	Protein kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0469740.1	0.83750342	6.005540796	3.593382958	0.00072	0.021178576	-1.05910802	WD repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0659760.1	1.18125835	6.289693825	3.586013691	0.00073	0.021412967	-1.06012315	Origin recognition complex subunit 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0680880.1	1.910552467	2.289472989	3.374208039	0.00139	0.026563254	-1.06250401	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0459530.1	2.247849206	2.402607807	3.379710803	0.00137	0.026563254	-1.06299172	AT hook motif DNA-binding family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0341080.1	2.112717987	4.721757022	3.436681862	0.00115	0.025575256	-1.06333057	interferon-activable protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0494890.1	-0.664869431	5.12004239	-3.618801508	0.00066	0.020839563	-1.06457378	Esterase/lipase/thioesterase family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0096440.1	1.6064863	6.317526302	3.526937323	0.00088	0.023065637	-1.0656414	tRNA-dihydrouridine(47) synthase [NAD(P)(+)]	elongation zone	12 h
HORVU.MOREX.r3.5HG0519510.1	1.664279744	2.934455383	3.37763276	0.00138	0.026563254	-1.06973596	Pseudouridine synthase	elongation zone	12 h
HORVU.MOREX.r3.5HG0447720.1	0.539129137	7.798320353	3.700000381	0.00051	0.019449812	-1.07020796	Dicarboxylate transporter 2.1, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.5HG0499910.1	1.230508401	2.676451276	3.390220856	0.00133	0.026498466	-1.07408954	BTB/POZ domain containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0021330.1	0.650527053	7.729068078	3.669535672	0.00056	0.020017114	-1.07476353	Asparagine--tRNA ligase	elongation zone	12 h
HORVU.MOREX.r3.6HG0627090.1	-0.81166539	1.382859959	-3.449523932	0.00111	0.025121413	-1.07483575	Alcohol dehydrogenase 3	elongation zone	12 h
HORVU.MOREX.r3.3HG0277760.1	2.36500543	1.654351235	3.38954525	0.00133	0.026498466	-1.07556134	Mannan endo-1,4-beta-mannosidase 1	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.7HG0704790.1	1.911314694	5.362516783	3.428223621	0.00118	0.025704276	-1.07764814	IQ domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0664110.1	2.218394835	-1.073195206	3.462913738	0.00107	0.024644437	-1.07849664	Polynucleotidyl transferase, ribonuclease H-like superfamily prot	elongation zone	12 h
HORVU.MOREX.r3.4HG0416730.1	0.85423567	6.869698753	3.62411018	0.00065	0.020713759	-1.07973951	Kinesin-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0173210.1	1.111091884	5.578205888	3.539961957	0.00084	0.02271895	-1.0819638	Kinesin-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0588750.2	1.26222121	2.298912834	3.376592968	0.00138	0.026563254	-1.08249707	Basic-leucine zipper (bZIP) transcription factor family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0109620.1	-1.446558504	0.349033917	-3.37695475	0.00138	0.026563254	-1.08546241	Retrotransposon protein, putative, Ty3-gypsy subclass	elongation zone	12 h
HORVU.MOREX.r3.6HG0634100.1	2.066987701	5.582248586	3.45722133	0.00108	0.02473329	-1.08627858	O-linked-mannose beta-1,4-N-acetylglucosaminyltransferase-like	elongation zone	12 h
HORVU.MOREX.r3.6HG0627010.1	1.58409629	5.519545424	3.498313891	0.00096	0.023538121	-1.08843018	Proliferating cell nuclear antigen	elongation zone	12 h
HORVU.MOREX.r3.2HG0217550.1	-0.475797058	5.544284998	-3.695275224	0.00052	0.019449812	-1.09064051	rRNA N-glycosidase	elongation zone	12 h
HORVU.MOREX.r3.5HG0482220.1	0.689982232	8.482975852	3.689193429	0.00053	0.019449812	-1.09139437	Eukaryotic translation initiation factor 3 subunit C	elongation zone	12 h
HORVU.MOREX.r3.2HG0116210.1	0.718196638	8.951948174	3.714038705	0.00049	0.019138691	-1.09208365	Elongation factor 1-beta	elongation zone	12 h
HORVU.MOREX.r3.2HG0116870.1	1.018721167	6.95000519	3.619639122	0.00066	0.020839563	-1.09220361	Condensin complex subunit 1	elongation zone	12 h
HORVU.MOREX.r3.3HG0249410.1	2.578480722	4.478527107	3.384632382	0.00135	0.026498466	-1.09540557	Cyclin family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0731860.1	0.712410723	4.962633306	3.505565961	0.00094	0.023303902	-1.0960883	Ran-binding protein 1 domain-containing	elongation zone	12 h
HORVU.MOREX.r3.2HG0182150.1	0.781089015	4.062913174	3.501457914	0.00095	0.023426471	-1.0975967	Charged multivesicular body protein 7	elongation zone	12 h
HORVU.MOREX.r3.6HG0572280.1	-0.572635585	3.513127043	-3.628906255	0.00064	0.020713759	-1.09809626	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0122720.1	1.091868594	3.012374132	3.411816032	0.00124	0.026060689	-1.09864406	Serine hydroxymethyltransferase	elongation zone	12 h
HORVU.MOREX.r3.4HG0334360.1	-0.833176487	4.121321037	-3.645756693	0.00061	0.020507565	-1.10034344	Homeobox protein BEL1 like	elongation zone	12 h
HORVU.MOREX.r3.3HG0289860.1	0.611581705	6.345885753	3.598668328	0.0007	0.021178576	-1.1011817	choice-of-anchor C domain protein, putative (Protein of unknow	elongation zone	12 h
HORVU.MOREX.r3.5HG0524250.1	0.788521005	3.283171645	3.41189489	0.00124	0.026060689	-1.10300581	Mg-protoporphyrin IX chelatase	elongation zone	12 h
HORVU.MOREX.r3.1HG0029840.1	-0.713231069	1.808873342	-3.420571613	0.00121	0.025813316	-1.10975042	WEB family protein, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.2HG0193460.1	0.800175958	3.83689201	3.449133809	0.00111	0.025121413	-1.10975584	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0549050.1	2.379044016	0.900308474	3.369921822	0.00141	0.026719424	-1.11058562	Pentatricopeptide repeat-containing protein, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0530810.1	0.993019373	5.275506896	3.519787048	0.0009	0.023235104	-1.11178591	Ammonium transporter	elongation zone	12 h
HORVU.MOREX.r3.4HG0395410.1	1.44187097	6.47047948	3.547071901	0.00082	0.022436302	-1.11401768	Nuclear pore complex protein Nup155	elongation zone	12 h
HORVU.MOREX.r3.1HG0059190.1	2.709941602	-1.006758538	3.432341862	0.00117	0.025668159	-1.11889279	Cytochrome P450	elongation zone	12 h
HORVU.MOREX.r3.7HG0727510.1	0.460193597	9.85060615	3.753609002	0.00043	0.018288218	-1.12174761	ATP-dependent RNA helicase	elongation zone	12 h
HORVU.MOREX.r3.4HG0408030.1	1.033347969	5.109700092	3.488201388	0.00099	0.023815524	-1.12184322	Methyltransferase-like protein 1	elongation zone	12 h
HORVU.MOREX.r3.5HG0505990.1	1.40584563	3.985167002	3.430342907	0.00118	0.025679564	-1.12378004	Molybdenum cofactor sulfurase protein-like	elongation zone	12 h
HORVU.MOREX.r3.5HG0478260.1	1.331750045	5.335995353	3.507386557	0.00093	0.023256457	-1.12410464	Protein kinase	elongation zone	12 h
HORVU.MOREX.r3.2HG0160800.1	0.621035745	8.570133613	3.692194023	0.00053	0.019449812	-1.12555701	Nuclear transport factor 2 family protein with RNA binding doma	elongation zone	12 h
HORVU.MOREX.r3.3HG0221630.1	1.475227092	6.479981921	3.521625634	0.00089	0.023234115	-1.12870372	Ethylene-responsive transcription factor	elongation zone	12 h
HORVU.MOREX.r3.3HG0277810.1	0.698695993	5.684125322	3.568380858	0.00077	0.021876787	-1.13249872	Kinase-related protein DUF1296	elongation zone	12 h
HORVU.MOREX.r3.1HG0078160.1	1.172223493	5.033832594	3.469209021	0.00104	0.024422909	-1.13433519	S-adenosyl-L-methionine-dependent methyltransferases superfa	elongation zone	12 h
HORVU.MOREX.r3.1HG0081960.1	2.114628418	1.77002833	3.352377834	0.00148	0.027239638	-1.13606143	Mitochondrial carrier protein, expressed	elongation zone	12 h
HORVU.MOREX.r3.2HG0166740.1	2.418362485	1.177029533	3.366856917	0.00142	0.026855068	-1.13726922	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0567530.1	1.568641845	4.356508323	3.41042699	0.00125	0.026062006	-1.13783391	Ribonuclease H2 subunit C	elongation zone	12 h
HORVU.MOREX.r3.7HG0662160.1	0.502710996	5.721315271	3.577400145	0.00075	0.021691049	-1.13886547	Phosphopantothenoylcysteine decarboxylase	elongation zone	12 h
HORVU.MOREX.r3.5HG0462370.1	0.546230719	4.87439825	3.524888297	0.00088	0.023172964	-1.13907195	F-box protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0335740.1	2.079892843	3.576868841	3.360765569	0.00145	0.027076709	-1.14036767	WD-repeat protein, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0579370.1	0.565234994	8.57000807	3.6868512	0.00054	0.019538954	-1.14413714	Aminopeptidase	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.5HG0501970.1	3.18254406	-0.116227004	3.410189894	0.00125	0.026062006	-1.14592347	DUF674 family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0107850.2	0.554666623	6.853519311	3.632072836	0.00063	0.020646627	-1.14929405	Elongation factor 1-alpha	elongation zone	12 h
HORVU.MOREX.r3.1HG0031890.1	0.885965694	7.824402431	3.63187664	0.00063	0.020646627	-1.15078973	40S ribosomal protein S7	elongation zone	12 h
HORVU.MOREX.r3.1HG0083980.1	1.084638627	4.41183861	3.428046199	0.00118	0.025704276	-1.15316499	Thymidine kinase	elongation zone	12 h
HORVU.MOREX.r3.6HG0617390.1	1.914060433	2.152837321	3.33831123	0.00155	0.027506911	-1.15408272	50S ribosomal protein L29	elongation zone	12 h
HORVU.MOREX.r3.4HG0343750.1	2.0083277	3.214895301	3.345904674	0.00151	0.027239638	-1.15595341	Protein FAM136A	elongation zone	12 h
HORVU.MOREX.r3.5HG0483980.1	-1.353018539	-1.844541926	-3.361908844	0.00144	0.02703001	-1.15679418	Cinnamoyl CoA reductase	elongation zone	12 h
HORVU.MOREX.r3.5HG0529130.1	0.618811142	9.571785293	3.715966585	0.00049	0.019131832	-1.15928889	Elongation factor	elongation zone	12 h
HORVU.MOREX.r3.6HG0619920.1	-2.584684009	-1.999158359	-3.35051079	0.00149	0.027239638	-1.16230954	Tetratricopeptide repeat protein 38	elongation zone	12 h
HORVU.MOREX.r3.3HG0254910.1	1.495185032	1.641129906	3.336462679	0.00156	0.027532387	-1.163242	Replication protein A 14 kDa subunit B	elongation zone	12 h
HORVU.MOREX.r3.2HG0128190.1	0.690217678	6.703219641	3.588870382	0.00073	0.021347237	-1.16541663	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0556580.1	1.842655323	2.247275253	3.333519781	0.00157	0.02762467	-1.16666953	Ribosomal RNA small subunit methyltransferase H	elongation zone	12 h
HORVU.MOREX.r3.5HG0505730.1	2.384222949	4.302003717	3.355512878	0.00147	0.027209299	-1.16713608	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0473860.1	1.926104239	0.945240803	3.339200371	0.00154	0.027475011	-1.1683866	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0705960.1	0.951065763	7.124115161	3.577985613	0.00075	0.021691049	-1.16854197	Far upstream element-binding protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0294930.1	2.318261919	4.769733248	3.377735652	0.00138	0.026563254	-1.16975761	Serine/Threonine-kinase WNK (WNK)-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0390010.1	0.442855906	6.991406485	3.61818404	0.00066	0.020839563	-1.17038033	Splicing factor 3A subunit 2	elongation zone	12 h
HORVU.MOREX.r3.4HG0341160.1	1.703517194	5.238782121	3.423052395	0.0012	0.025763058	-1.17162608	WD40 repeat-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0045360.1	0.843088485	4.090890615	3.426832198	0.00119	0.025731015	-1.1741422	Nijmegen breakage syndrome 1 protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0626100.1	0.903852548	7.271720005	3.592845182	0.00072	0.021178576	-1.17549345	30S ribosomal protein S15	elongation zone	12 h
HORVU.MOREX.r3.4HG0407610.1	1.265532049	3.868431006	3.408225257	0.00126	0.026083278	-1.17607345	Cyclin-dependent kinases regulatory subunit	elongation zone	12 h
HORVU.MOREX.r3.3HG0280990.1	0.847072406	9.328992522	3.686068748	0.00054	0.019551933	-1.17804698	Guanine nucleotide-binding protein beta subunit-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0097190.1	2.048954594	0.265000574	3.374715825	0.00139	0.026563254	-1.17840335	Fructokinase-2	elongation zone	12 h
HORVU.MOREX.r3.6HG0587460.1	-1.080911799	-2.657116661	-3.344182717	0.00152	0.027297085	-1.17874159	D-alanine--D-alanine ligase	elongation zone	12 h
HORVU.MOREX.r3.5HG0510150.1	2.637673921	3.882701354	3.339344509	0.00154	0.027475011	-1.18222132	Sigma non-opioid intracellular receptor 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0142740.1	-0.330259531	6.623244558	-3.679788536	0.00055	0.019711469	-1.18229607	Protein phosphatase 2c	elongation zone	12 h
HORVU.MOREX.r3.1HG0073350.1	1.659865315	2.87898944	3.349200204	0.0015	0.027239638	-1.18397802	70 kDa heat shock protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0086370.1	-1.627311857	-3.209110522	-3.326156628	0.0016	0.027832573	-1.18455705	Glyoxal oxidase	elongation zone	12 h
HORVU.MOREX.r3.5HG0534960.1	0.799757165	5.864296719	3.534208371	0.00086	0.022899718	-1.18617365	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0218330.1	1.65411808	8.028797595	3.589521004	0.00072	0.02133511	-1.18625284	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0659390.1	3.146265022	5.47393541	3.380028249	0.00137	0.026563254	-1.18667922	Hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyltrar	elongation zone	12 h
HORVU.MOREX.r3.3HG0231630.1	1.504429394	3.593294948	3.355757536	0.00147	0.027209299	-1.18981068	Zinc-finger domain of monoamine-oxidase A repressor R1 protei	elongation zone	12 h
HORVU.MOREX.r3.7HG0750100.1	2.369542258	0.414991589	3.331696127	0.00158	0.02769762	-1.1922457	Basic-leucine zipper (BZIP) transcription factor family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0384390.1	-0.88994331	1.57490258	-3.492814661	0.00097	0.023707462	-1.19622145	Protein kinase family protein, putative, expressed	elongation zone	12 h
HORVU.MOREX.r3.3HG0270450.1	2.180534089	1.889574407	3.325701724	0.00161	0.027832573	-1.19721121	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albu	elongation zone	12 h
HORVU.MOREX.r3.7HG0643620.1	2.222015504	3.330782685	3.329055955	0.00159	0.027806246	-1.19735813	B3 domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0004300.1	1.954975263	1.490538886	3.322919173	0.00162	0.027925695	-1.19753941	Disease resistance protein (TIR-NBS-LRR class) family	elongation zone	12 h
HORVU.MOREX.r3.2HG0133400.1	1.727526417	2.606200127	3.32427213	0.00161	0.027860864	-1.20417087	Methyltransferase family protein, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0358890.1	0.635070137	6.541550372	3.574210034	0.00076	0.021740481	-1.20551821	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0598360.1	2.777783718	0.051977317	3.362566619	0.00144	0.02703001	-1.20670779	Nucleoporin autopeptidase	elongation zone	12 h
HORVU.MOREX.r3.7HG0679050.1	-0.576508162	4.002867978	-3.506988586	0.00093	0.023256457	-1.20798971	Upstream activation factor subunit spp27	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0054500.1	0.891881558	5.920468629	3.56018618	0.00079	0.022079483	-1.21005105	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0474550.1	1.228456363	5.604885166	3.477517405	0.00102	0.024145821	-1.21014307	Histone acetyltransferase type B catalytic subunit	elongation zone	12 h
HORVU.MOREX.r3.2HG0122750.1	-2.712376774	-2.143475904	-3.348151152	0.0015	0.027239638	-1.21440398	Regulator of chromosome condensation (RCC1) family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0485610.1	-1.205983685	0.794719635	-3.444646667	0.00113	0.025241276	-1.21441974	Cytochrome P450, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0056420.1	0.845240947	8.535003487	3.691500598	0.00053	0.019449812	-1.2150864	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albu	elongation zone	12 h
HORVU.MOREX.r3.2HG0105270.1	1.53147355	3.902906721	3.353496853	0.00148	0.027239638	-1.21691731	UPF0307 protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0700220.1	1.223983362	2.018022978	3.324822227	0.00161	0.027838944	-1.21708689	Carboxypeptidase Y homolog A	elongation zone	12 h
HORVU.MOREX.r3.2HG0167620.1	1.427622797	2.679480768	3.327623116	0.0016	0.027806246	-1.22282317	Plastid-lipid associated protein PAP / fibrillin family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0725470.1	1.179637565	2.027520928	3.32768951	0.0016	0.027806246	-1.22303341	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0078040.1	-0.55511889	5.57940583	-3.639065738	0.00062	0.020516782	-1.22384796	Absent in melanoma 1 protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0055550.1	2.566910767	2.424299381	3.309632205	0.00168	0.028265516	-1.22473441	histone acetyltransferase of the CBP family 12	elongation zone	12 h
HORVU.MOREX.r3.3HG0302080.1	0.848266177	4.735593914	3.455602183	0.00109	0.024826998	-1.22502572	Aldo-keto reductase	elongation zone	12 h
HORVU.MOREX.r3.3HG0323440.1	2.587780903	0.455380393	3.345266198	0.00152	0.027239638	-1.22612532	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0270270.1	1.333470411	5.100425589	3.461185756	0.00107	0.024644437	-1.2284944	Kinesin-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0512510.1	0.711116537	7.202032188	3.632512279	0.00063	0.020646627	-1.23015064	Subtilisin-like protease	elongation zone	12 h
HORVU.MOREX.r3.3HG0234670.1	1.924714108	5.483714808	3.413998681	0.00123	0.026021602	-1.23208638	Mini-chromosome maintenance complex-binding protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0625200.1	2.678486856	0.649401402	3.364810783	0.00143	0.026979742	-1.23219403	defensin-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0519170.1	0.694592572	8.3989122	3.639693017	0.00062	0.020516782	-1.23401591	60S ribosomal protein L4	elongation zone	12 h
HORVU.MOREX.r3.5HG0450470.1	0.602233179	3.631343249	3.431085236	0.00117	0.025676928	-1.23486055	Basic-leucine zipper (bZIP) transcription factor family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0296590.1	1.71475109	4.817113451	3.384112008	0.00135	0.026498466	-1.2353634	Zinc finger protein VAR3, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.4HG0343180.1	1.735315704	1.398218777	3.304191768	0.00171	0.028348165	-1.23802048	Diphthamide biosynthesis protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0702560.1	0.793080412	10.1678559	3.701958447	0.00051	0.019449812	-1.24254761	60S acidic ribosomal protein P0	elongation zone	12 h
HORVU.MOREX.r3.2HG0164770.1	2.0566667	2.242803081	3.301592542	0.00172	0.028397697	-1.24526155	DNA cross-link repair protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0306150.1	-1.239948703	0.587040762	-3.34682628	0.00151	0.027239638	-1.24658326	RING/FYVE/PHD zinc finger superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0601210.1	1.287582464	-0.829190823	3.310097621	0.00168	0.028265516	-1.24674841	En/Spm transposon protein-like	elongation zone	12 h
HORVU.MOREX.r3.1HG0053640.1	1.83911017	1.981161553	3.300334093	0.00173	0.028397697	-1.24730053	Pentatricopeptide repeat-containing protein, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0317800.1	0.778179081	3.512446305	3.383571044	0.00135	0.026499651	-1.24818296	Protein kinase superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0540020.1	-1.878886981	-2.701095093	-3.325536257	0.00161	0.027832573	-1.24970787	Ubiquitin carboxyl-terminal hydrolase 2	elongation zone	12 h
HORVU.MOREX.r3.1HG0069480.1	1.509475144	3.796517346	3.358145485	0.00146	0.027115369	-1.25040432	Cyclin	elongation zone	12 h
HORVU.MOREX.r3.1HG0095030.1	1.250789137	2.631178482	3.315322627	0.00166	0.028097383	-1.25146634	Tudor/PWWP/MBT superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0512380.1	1.28692172	6.515264522	3.511783212	0.00092	0.023235104	-1.25169521	Aspartate-semialdehyde dehydrogenase, N-acetyl-gamma-glutar	elongation zone	12 h
HORVU.MOREX.r3.5HG0504000.1	2.080494257	-0.714764534	3.330959331	0.00158	0.027734466	-1.2540319	DEP domain-containing protein 5	elongation zone	12 h
HORVU.MOREX.r3.1HG0073480.1	1.701909389	3.492165186	3.325461683	0.00161	0.027832573	-1.2571554	Myb-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0502760.1	0.818558062	7.161461629	3.595078462	0.00071	0.021178576	-1.26053522	Histone H4	elongation zone	12 h
HORVU.MOREX.r3.2HG0205550.1	0.981826331	5.792379962	3.47982564	0.00101	0.024088685	-1.26233207	Thymidylate synthase	elongation zone	12 h
HORVU.MOREX.r3.6HG0560180.1	1.233905824	7.215113646	3.544832135	0.00083	0.022530917	-1.2629593	Diaminopimelate decarboxylase	elongation zone	12 h
HORVU.MOREX.r3.4HG0403380.1	2.295288904	0.78477187	3.311114027	0.00168	0.028253315	-1.26323494	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0420330.1	2.574031917	4.123826071	3.303108096	0.00172	0.028392091	-1.26602652	Receptor-like protein kinase	elongation zone	12 h
HORVU.MOREX.r3.1HG0078760.1	2.135829127	4.578212279	3.340404335	0.00154	0.02745794	-1.26643268	tRNA pseudouridine synthase d, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0122110.1	2.012891559	3.790294672	3.313340541	0.00167	0.028155399	-1.26816631	Exosome complex component	elongation zone	12 h
HORVU.MOREX.r3.4HG0399930.1	0.954229737	4.063960499	3.393628686	0.00131	0.026348744	-1.2687485	Ribosome biogenesis protein TSR3-like protein	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.6HG0594410.1	0.900513879	4.144620416	3.402998274	0.00128	0.026178272	-1.26934675	Protein TIC 20, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.2HG0140980.1	1.736325207	4.118667294	3.33906157	0.00154	0.027475011	-1.2699497	RNA-binding family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0702770.1	2.656959315	0.424380843	3.347785083	0.0015	0.027239638	-1.27124054	Tetratricopeptide repeat (TPR)-like superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0039230.1	0.740005367	5.567693484	3.49189848	0.00098	0.023723522	-1.27188511	AT-rich interactive domain-containing protein 2	elongation zone	12 h
HORVU.MOREX.r3.3HG0310510.1	1.165415981	5.599216728	3.460526911	0.00107	0.024651876	-1.27234322	RNA-binding protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0255530.1	0.92403902	3.072891497	3.32747384	0.0016	0.027806246	-1.27617131	Phenazine biosynthesis PhzC/PhzF family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0648100.1	1.499895174	0.956664255	3.29126948	0.00178	0.028617771	-1.27633699	CsAtPR5	elongation zone	12 h
HORVU.MOREX.r3.4HG0347760.1	-0.787430845	2.347769018	-3.394918139	0.00131	0.026348744	-1.27668966	MYB transcription factor	elongation zone	12 h
HORVU.MOREX.r3.2HG0151710.1	1.379481714	7.682528676	3.550259249	0.00082	0.022336842	-1.27794238	Cytosine-specific methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0123800.1	0.883290569	4.716102679	3.430482835	0.00117	0.025679564	-1.27938011	Multifunctional methyltransferase subunit TRM112-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0310280.1	-0.349579612	5.67062812	-3.61945494	0.00066	0.020839563	-1.28167284	CBS domain containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0700930.1	1.584575673	4.508976778	3.348902645	0.0015	0.027239638	-1.28436417	RING/U-box superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0264800.1	1.648470552	4.015971181	3.349796386	0.0015	0.027239638	-1.28521671	DNA helicase	elongation zone	12 h
HORVU.MOREX.r3.3HG0230190.1	1.016060523	2.957930782	3.320998563	0.00163	0.02796111	-1.28562121	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0149820.1	1.155499115	6.513488761	3.510950278	0.00092	0.023235104	-1.2858033	Small nuclear ribonucleoprotein-associated protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0380430.1	-0.384317714	3.638981565	-3.461152769	0.00107	0.024644437	-1.28627434	Membrane steroid-binding protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0717720.1	0.684651634	9.161719424	3.657250653	0.00059	0.020428272	-1.2895325	T-complex protein 1 subunit epsilon	elongation zone	12 h
HORVU.MOREX.r3.4HG0415180.1	3.14881883	3.10939606	3.283566644	0.00182	0.028793645	-1.29052386	Jasmonate-zim-domain protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0367550.1	0.66593969	6.581101357	3.531829126	0.00086	0.022899718	-1.29066392	Apoptotic chromatin condensation inducer in the nucleus	elongation zone	12 h
HORVU.MOREX.r3.3HG0258440.1	1.912620465	2.205284764	3.283377309	0.00182	0.028793645	-1.29107945	CRS2-associated factor 1, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.1HG0079060.1	1.846404669	2.517249753	3.283399914	0.00182	0.028793645	-1.2941246	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0069940.1	0.911205604	7.781675396	3.583853866	0.00074	0.021475647	-1.29521547	60S ribosomal protein L30	elongation zone	12 h
HORVU.MOREX.r3.1HG0051960.1	1.175623672	1.90386557	3.285958682	0.00181	0.028744755	-1.29538381	DNA topoisomerase 2	elongation zone	12 h
HORVU.MOREX.r3.7HG0650090.1	1.287463902	3.089010373	3.309581521	0.00168	0.028265516	-1.29683625	Single-stranded DNA-binding protein WHY1, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.3HG0314030.1	2.546285916	-0.769398738	3.355552209	0.00147	0.027209299	-1.29693158	F-box domain containing protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0410210.1	1.412892596	6.140943336	3.451140337	0.0011	0.025080286	-1.30046353	Protein O-linked-mannose beta-1,4-N-acetylglucosaminyltransfe	elongation zone	12 h
HORVU.MOREX.r3.3HG0243130.1	0.817868586	2.631713432	3.418546487	0.00122	0.025897833	-1.30504598	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.7HG0692650.1	3.325650074	3.60398256	3.276754088	0.00186	0.028861865	-1.30592496	Ribonuclease E/G family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0349950.1	0.808773249	5.968153859	3.487816709	0.00099	0.023815524	-1.30595037	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0633020.1	1.965152676	1.254863943	3.277272349	0.00185	0.028861865	-1.30903558	Disease resistance protein RPM1	elongation zone	12 h
HORVU.MOREX.r3.1HG0029280.1	0.466737879	7.393407536	3.581823905	0.00074	0.02156782	-1.30934303	FACT complex subunit SSRP1	elongation zone	12 h
HORVU.MOREX.r3.7HG0647980.1	0.97944166	3.018864795	3.316338859	0.00165	0.028050531	-1.30935248	Coiled-coil domain-containing protein 97	elongation zone	12 h
HORVU.MOREX.r3.7HG0720810.1	-0.377117687	4.98512073	-3.535131178	0.00086	0.022899718	-1.31070591	Alpha/beta-Hydrolases superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0099780.1	-1.093983314	-0.017792574	-3.352075201	0.00149	0.027239638	-1.31100805	Maternal effect embryo arrest protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0685920.1	-0.509432712	4.571683277	-3.568115053	0.00077	0.021876787	-1.31143453	Solute carrier family 35 protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0323810.1	0.575497566	6.634620504	3.549008731	0.00082	0.022369939	-1.31160054	SWAP (Suppressor-of-White-APricot)/surp domain-containing pr	elongation zone	12 h
HORVU.MOREX.r3.7HG0675050.1	1.351939474	5.035182354	3.398595662	0.00129	0.026336616	-1.31194822	Histone deacetylase, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0555240.1	1.182276985	4.912990377	3.398773056	0.00129	0.026336616	-1.31261179	Kinase-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0718150.1	0.744538449	8.476808649	3.615519222	0.00067	0.020839563	-1.31346587	40S ribosomal protein S24	elongation zone	12 h
HORVU.MOREX.r3.3HG0232420.1	0.758925227	9.487579567	3.65020675	0.0006	0.020507565	-1.3164565	30S ribosomal protein S7	elongation zone	12 h
HORVU.MOREX.r3.5HG0421470.1	0.957935006	6.457449928	3.50827182	0.00093	0.023255319	-1.31766769	Pyridine nucleotide-disulfide oxidoreductase domain-containing	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0041030.1	1.826212576	0.101262697	3.300589142	0.00173	0.028397697	-1.31781036	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0599760.1	0.901687226	4.051408872	3.372552572	0.0014	0.026598639	-1.3210378	U6 snRNA phosphodiesterase	elongation zone	12 h
HORVU.MOREX.r3.3HG0228020.1	-1.268718884	-1.433568275	-3.299017652	0.00174	0.02840648	-1.32150655	Glycogen synthase	elongation zone	12 h
HORVU.MOREX.r3.6HG0556190.1	1.958129273	1.897109288	3.270023435	0.00189	0.029006839	-1.32313964	50S ribosomal protein L3	elongation zone	12 h
HORVU.MOREX.r3.2HG0168730.1	0.497700447	7.047952151	3.558353828	0.0008	0.022167528	-1.32322967	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0078370.1	1.926874695	4.28064148	3.310546193	0.00168	0.028265516	-1.32365481	breast cancer associated RING 1	elongation zone	12 h
HORVU.MOREX.r3.6HG0632980.1	1.810827275	5.615727708	3.414439127	0.00123	0.026021602	-1.32385076	Replication protein A 32 kDa subunit	elongation zone	12 h
HORVU.MOREX.r3.6HG0545630.1	1.397239824	3.709729912	3.352400299	0.00148	0.027239638	-1.32408339	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.3HG0255500.2	1.442309649	2.726992	3.282698345	0.00182	0.028808148	-1.32524777	La related protein-like	elongation zone	12 h
HORVU.MOREX.r3.6HG0595190.1	-1.508815449	-2.072106303	-3.298361759	0.00174	0.02840648	-1.32614332	GDSL esterase/lipase	elongation zone	12 h
HORVU.MOREX.r3.7HG0656260.1	0.550169552	5.217076705	3.484134534	0.001	0.023938404	-1.3289912	Metaxin-related	elongation zone	12 h
HORVU.MOREX.r3.2HG0109850.1	0.970283881	5.983148067	3.495518511	0.00096	0.023625697	-1.3302296	Protein kinase	elongation zone	12 h
HORVU.MOREX.r3.4HG0364440.1	0.901708156	6.096424332	3.496374452	0.00096	0.02359246	-1.33111211	translation initiation factor	elongation zone	12 h
HORVU.MOREX.r3.7HG0652110.1	0.49536997	5.273679743	3.508824066	0.00093	0.023255319	-1.33122155	Ubiquinone biosynthesis O-methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0181680.1	-1.439485141	-1.908817715	-3.418448011	0.00122	0.025897833	-1.33131411	CASP-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0194580.1	2.852123438	5.284996064	3.320894229	0.00163	0.02796111	-1.33221704	High mobility group family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0392970.1	2.003431615	6.133609232	3.405040054	0.00127	0.026178272	-1.33282091	Ribosomal protein l7ae	elongation zone	12 h
HORVU.MOREX.r3.3HG0318700.1	-0.49615998	6.088388292	-3.614987456	0.00067	0.020839563	-1.3343867	Phosphotransferase	elongation zone	12 h
HORVU.MOREX.r3.6HG0630920.1	2.885365412	-2.009589986	3.330289659	0.00158	0.027765848	-1.33624466	NBS-LRR disease resistance protein-like	elongation zone	12 h
HORVU.MOREX.r3.5HG0432030.1	0.684027373	7.313410269	3.557060736	0.0008	0.022171653	-1.33723249	Tesmin/TSO1-like CXC domain containing protein, expressed	elongation zone	12 h
HORVU.MOREX.r3.6HG0591340.1	1.471461505	5.612016666	3.40333054	0.00127	0.026178272	-1.33816969	Ribosomal RNA small subunit methyltransferase NEP1	elongation zone	12 h
HORVU.MOREX.r3.6HG0629990.1	1.642455445	2.855652822	3.273130062	0.00188	0.028923495	-1.33865952	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0720670.1	0.658099568	2.879624117	3.352980574	0.00148	0.027239638	-1.34095122	Nucleoside diphosphate kinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0311510.1	1.259732943	6.871599224	3.498525186	0.00096	0.023538121	-1.34211503	Dek protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0309580.1	1.209304949	8.340368599	3.568096873	0.00077	0.021876787	-1.34265266	RNA binding protein-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0426480.1	1.319211091	2.819296038	3.297898876	0.00174	0.02840648	-1.34318211	1-deoxy-D-xylulose 5-phosphate synthase 1	elongation zone	12 h
HORVU.MOREX.r3.3HG0327630.1	1.325185715	4.246104341	3.345186396	0.00152	0.027239638	-1.34621219	Cyclin family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0270750.1	-0.399886973	6.689944506	-3.645656779	0.00061	0.020507565	-1.34719258	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0266920.1	0.926810316	7.650919912	3.538579927	0.00085	0.022755386	-1.34763488	Carbamoyl-phosphate synthase large chain	elongation zone	12 h
HORVU.MOREX.r3.4HG0416120.1	1.791294944	5.199636546	3.367049947	0.00142	0.026855068	-1.34802173	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0176040.1	-0.814884789	2.922347917	-3.514181162	0.00091	0.023235104	-1.34816536	Transducin/WD40 repeat protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0187470.1	2.030335101	4.280507622	3.298369252	0.00174	0.02840648	-1.3484807	Replication factor C subunit	elongation zone	12 h
HORVU.MOREX.r3.1HG0058500.1	1.992898173	1.953197262	3.260432619	0.00195	0.029482217	-1.34868233	Carbon catabolite repressor protein 4	elongation zone	12 h
HORVU.MOREX.r3.6HG0566930.1	0.865248955	4.26253915	3.387153869	0.00134	0.026498466	-1.349377	Biotin holocarboxylase synthetase 1-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0114200.1	2.465974992	0.611042475	3.297693387	0.00174	0.02840648	-1.34955267	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0143770.1	1.469078755	2.829580346	3.267579241	0.00191	0.029085354	-1.3500481	Phosphate-responsive 1 family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0136010.1	0.690939171	2.50549698	3.318835793	0.00164	0.028033028	-1.35028584	DNA repair family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0386590.1	0.721570799	6.15515178	3.508020028	0.00093	0.023255319	-1.35211512	Ribosomal protein S10	elongation zone	12 h
HORVU.MOREX.r3.7HG0686470.1	1.369501361	6.33041116	3.441476994	0.00114	0.025400464	-1.354557	60S ribosomal protein L7	elongation zone	12 h
HORVU.MOREX.r3.7HG0650590.1	2.10462261	-0.768965688	3.272532822	0.00188	0.028923495	-1.35469993	RNA-directed DNA polymerase (reverse transcriptase)-related fa	elongation zone	12 h
HORVU.MOREX.r3.6HG0612340.1	-1.304867094	-2.225003498	-3.277046998	0.00185	0.028861865	-1.35593485	AWPM-19-like membrane family protein	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0080170.1	0.797193624	7.403972972	3.544949043	0.00083	0.022530917	-1.35683686	60S ribosomal protein l28	elongation zone	12 h
HORVU.MOREX.r3.7HG0708120.1	1.516365587	6.60602094	3.473584155	0.00103	0.024207459	-1.36059132	High mobility group family	elongation zone	12 h
HORVU.MOREX.r3.5HG0504790.1	1.156457223	7.009436866	3.51320682	0.00091	0.023235104	-1.36183717	Zinc finger protein hangover	elongation zone	12 h
HORVU.MOREX.r3.3HG0275910.1	2.820172993	-0.86003395	3.303210787	0.00172	0.028392091	-1.36444646	Transcription factor GTE4-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0291490.1	0.692292499	7.190585134	3.59368278	0.00071	0.021178576	-1.37034066	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0111570.1	-0.733658094	1.289253696	-3.369429238	0.00141	0.026723686	-1.37151979	Polynucleotidyl transferase, ribonuclease H-like superfamily prot	elongation zone	12 h
HORVU.MOREX.r3.4HG0392160.1	1.068172747	6.711088276	3.508505981	0.00093	0.023255319	-1.37210916	Glucan endo-1,3-beta-glucosidase, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0502740.1	2.508017898	5.228316694	3.292333949	0.00177	0.028575945	-1.37386288	LysM domain GPI-anchored protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0177000.1	1.349283287	4.493234445	3.326957691	0.0016	0.027806246	-1.37564305	DNA-directed RNA polymerase II	elongation zone	12 h
HORVU.MOREX.r3.5HG0441980.1	3.418686043	5.375222678	3.275294034	0.00186	0.028906691	-1.37612299	Glutamate-1-semialdehyde 2,1-aminomutase	elongation zone	12 h
HORVU.MOREX.r3.1HG0025870.1	-0.564845069	4.903163827	-3.513316951	0.00091	0.023235104	-1.37748925	6,7-dimethyl-8-ribityllumazine synthase	elongation zone	12 h
HORVU.MOREX.r3.6HG0629700.1	-0.691106023	3.612143683	-3.524577786	0.00088	0.023172964	-1.37749925	Protein PLASTID MOVEMENT IMPAIRED 1	elongation zone	12 h
HORVU.MOREX.r3.6HG0605130.1	-0.961971866	-2.052059751	-3.299676412	0.00173	0.02840648	-1.38052313	Invertase inhibitor	elongation zone	12 h
HORVU.MOREX.r3.2HG0216050.1	0.922092235	3.582358028	3.345978798	0.00151	0.027239638	-1.38054997	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase-like protei	elongation zone	12 h
HORVU.MOREX.r3.5HG0477490.1	1.979070139	2.081852442	3.24455422	0.00204	0.030344376	-1.38497826	CST complex subunit CTC1	elongation zone	12 h
HORVU.MOREX.r3.3HG0263400.1	0.489316639	6.016519655	3.49472968	0.00097	0.023626021	-1.38587833	evolutionarily conserved C-terminal region 2	elongation zone	12 h
HORVU.MOREX.r3.5HG0531560.1	2.441650516	-0.689139632	3.299986509	0.00173	0.028404126	-1.38643798	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0066050.1	1.332033621	5.419215562	3.391904154	0.00132	0.026441594	-1.3880472	Serine protease	elongation zone	12 h
HORVU.MOREX.r3.4HG0371500.1	1.411647236	7.969743783	3.52346949	0.00089	0.02319596	-1.38807042	H/ACA ribonucleoprotein complex subunit 1-like protein 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0670020.1	1.757151711	7.089520342	3.468633163	0.00105	0.024437696	-1.3884825	Ribonucleoside-diphosphate reductase small chain	elongation zone	12 h
HORVU.MOREX.r3.2HG0105120.1	0.478786289	6.067458615	3.51651975	0.00091	0.023235104	-1.3893308	Prostaglandin E synthase 2	elongation zone	12 h
HORVU.MOREX.r3.4HG0353450.1	2.059580251	2.283432519	3.242811082	0.00205	0.030414208	-1.39030356	Cell division control protein 45-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0631210.1	0.419192357	7.433011137	3.572452248	0.00076	0.021766161	-1.39051373	RNA-binding protein Nova	elongation zone	12 h
HORVU.MOREX.r3.6HG0593330.2	1.629471518	3.765007283	3.292937012	0.00177	0.028575945	-1.39185577	Acetolactate synthase small subunit	elongation zone	12 h
HORVU.MOREX.r3.5HG0486180.1	1.703277632	5.053805616	3.325184058	0.00161	0.027832573	-1.39381087	F-box protein-like	elongation zone	12 h
HORVU.MOREX.r3.5HG0500740.1	1.302758204	5.554889337	3.402656453	0.00128	0.026178272	-1.39600238	WD-repeat protein, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0462850.1	2.626048181	2.419844835	3.240400439	0.00206	0.03054087	-1.40223032	Peroxisomal membrane MPV17/PMP22-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0251470.1	2.90132338	2.189387907	3.243085527	0.00205	0.030411811	-1.40261172	Kinesin-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0210950.1	1.870397621	0.661852208	3.236836159	0.00209	0.030699736	-1.40492934	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0725580.1	-1.288733552	-0.151355091	-3.236401072	0.00209	0.030700472	-1.40937935	Protein TRANSPARENT TESTA 1	elongation zone	12 h
HORVU.MOREX.r3.1HG0057870.1	0.709880123	6.695838064	3.494731337	0.00097	0.023626021	-1.40958534	Serine hydroxymethyltransferase	elongation zone	12 h
HORVU.MOREX.r3.1HG0069550.1	1.954977375	5.304263931	3.338086743	0.00155	0.027506911	-1.41032047	Cyclin	elongation zone	12 h
HORVU.MOREX.r3.5HG0477290.1	1.212023439	0.968509278	3.245330706	0.00203	0.030322567	-1.41034035	cDNA clone:J013058P10, full insert sequence	elongation zone	12 h
HORVU.MOREX.r3.7HG0667340.1	3.325714743	1.732788988	3.287356566	0.0018	0.028691351	-1.41349359	Trichome birefringence-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0647520.1	0.584244134	6.632237001	3.508259546	0.00093	0.023255319	-1.41534347	GDP-mannose 4,6 dehydratase-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0342000.1	-0.736962917	0.190754791	-3.37323121	0.00139	0.026569474	-1.41751269	4-coumarate:CoA ligase-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0689590.1	1.806974217	6.156729257	3.385419958	0.00134	0.026498466	-1.41866563	Dihydroxy-acid dehydratase	elongation zone	12 h
HORVU.MOREX.r3.5HG0524730.1	0.866683327	8.875281474	3.586838383	0.00073	0.021412967	-1.42310351	40S ribosomal protein S26	elongation zone	12 h
HORVU.MOREX.r3.4HG0374570.1	1.351811777	3.614922227	3.276594686	0.00186	0.028861865	-1.42452837	glycine-rich RNA-binding-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0218930.1	3.264383974	2.999856259	3.229174387	0.00213	0.030911827	-1.42584332	telomeric DNA binding protein 1	elongation zone	12 h
HORVU.MOREX.r3.5HG0507950.2	-2.477107944	-2.471541906	-3.280765679	0.00183	0.028819302	-1.4262269	Protein IQ-DOMAIN 1	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.7HG0653210.1	0.81790727	3.132795054	3.279183686	0.00184	0.028839684	-1.42918644	F-box family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0399920.1	1.788665191	6.69753872	3.415810959	0.00123	0.026021602	-1.43027286	RNA cytidine acetyltransferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0440860.1	-0.36216103	4.818593256	-3.49747852	0.00096	0.02354153	-1.43181803	Foldase protein prsA 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0181310.1	1.784088474	4.106143284	3.281311466	0.00183	0.028819302	-1.4330203	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B, pu	elongation zone	12 h
HORVU.MOREX.r3.1HG0080230.1	1.1587159	6.650953832	3.486491605	0.00099	0.023883457	-1.43605039	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0592230.1	2.23646925	0.020065053	3.248261139	0.00202	0.030129448	-1.43835115	Mitochondrial transcription termination factor family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0188300.1	0.474727034	4.693991942	3.428748469	0.00118	0.025704276	-1.44011474	CsAtPR5	elongation zone	12 h
HORVU.MOREX.r3.1HG0001510.1	0.930978676	3.140126593	3.308722834	0.00169	0.028279404	-1.44330839	NBS-LRR-like resistance protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0430710.1	1.74109837	1.861597982	3.220349988	0.00219	0.031406458	-1.44410335	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0040570.1	2.760688027	1.96316218	3.229528786	0.00213	0.030911827	-1.44678023	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0229650.1	0.587474431	8.40993175	3.580201082	0.00074	0.021614457	-1.44820399	Threonine--tRNA ligase	elongation zone	12 h
HORVU.MOREX.r3.3HG0314250.1	1.345933616	4.306407266	3.297800542	0.00174	0.02840648	-1.44956938	Spermatogenesis-associated protein 20	elongation zone	12 h
HORVU.MOREX.r3.2HG0174250.1	1.09335977	4.093580531	3.306551478	0.0017	0.028288147	-1.45143152	Poly(A)-specific ribonuclease PARN	elongation zone	12 h
HORVU.MOREX.r3.1HG0056950.1	1.846283004	2.268962637	3.217474825	0.00221	0.031443869	-1.45163011	Maturase	elongation zone	12 h
HORVU.MOREX.r3.5HG0463350.1	1.6574046	5.140919247	3.360623372	0.00145	0.027076709	-1.45256085	Cell division control 45-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0549010.1	0.647661085	4.591957387	3.391146083	0.00132	0.02646207	-1.45642336	Protein DETOXIFICATION	elongation zone	12 h
HORVU.MOREX.r3.4HG0410520.1	1.35289199	2.028956772	3.223741233	0.00217	0.031206894	-1.45893953	Cytochrome c-type biogenesis CcmH	elongation zone	12 h
HORVU.MOREX.r3.7HG0701760.1	2.153092672	3.061025791	3.213518869	0.00223	0.031515925	-1.460761	NAD(P)H dehydrogenase (Quinone)	elongation zone	12 h
HORVU.MOREX.r3.6HG0578020.1	1.693959855	6.079593404	3.374394766	0.00139	0.026563254	-1.46182316	Alba DNA/RNA-binding protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0021110.1	2.122004324	-1.06471218	3.288678224	0.00179	0.028679559	-1.46318219	Disease resistance protein (NBS-LRR class) family	elongation zone	12 h
HORVU.MOREX.r3.3HG0235960.1	0.781497577	5.136869032	3.384272	0.00135	0.026498466	-1.4632093	ATP-dependent RNA helicase p62	elongation zone	12 h
HORVU.MOREX.r3.2HG0105680.1	2.009935424	1.363898856	3.21261123	0.00224	0.031520621	-1.46325292	Pyridoxamine 5-phosphate oxidase family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0669710.1	1.6226739	5.508591997	3.348426047	0.0015	0.027239638	-1.46556975	Condensin complex subunit 3	elongation zone	12 h
HORVU.MOREX.r3.1HG0062650.1	0.823249391	3.036967678	3.279759883	0.00184	0.028819302	-1.46745343	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0478780.1	3.107922423	1.412999456	3.241183104	0.00206	0.030515114	-1.47070845	Myb family transcription factor-like	elongation zone	12 h
HORVU.MOREX.r3.2HG0210320.1	1.485105044	2.321433783	3.218602089	0.0022	0.031443869	-1.4708572	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0169540.1	1.796493985	1.072754222	3.217121069	0.00221	0.031443869	-1.47330539	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0196720.1	2.285326565	-0.225277908	3.226782745	0.00215	0.031018589	-1.47478417	XH/XS domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0489440.1	2.416177932	2.658027414	3.20728373	0.00227	0.031692167	-1.47582247	Subtilisin-like protease	elongation zone	12 h
HORVU.MOREX.r3.1HG0014350.1	1.71320114	4.738056098	3.313273922	0.00167	0.028155399	-1.47701096	P-loop containing nucleoside triphosphate hydrolases superfamil	elongation zone	12 h
HORVU.MOREX.r3.6HG0593990.1	1.078794311	4.654306111	3.350011581	0.00149	0.027239638	-1.47761841	30S ribosomal protein S17	elongation zone	12 h
HORVU.MOREX.r3.5HG0455760.1	1.430929068	6.696936172	3.425349789	0.00119	0.025739392	-1.4778073	RNA helicase	elongation zone	12 h
HORVU.MOREX.r3.5HG0447150.1	3.468525469	2.535633305	3.219615963	0.00219	0.031443869	-1.48113701	DNA binding protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0337010.1	2.820212361	1.286313481	3.249187633	0.00201	0.030069779	-1.4835474	Homologous-pairing protein 2-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0081780.1	1.302033728	4.770668925	3.323709868	0.00162	0.027883821	-1.48562947	Cleavage and polyadenylation specificity factor subunit 5	elongation zone	12 h
HORVU.MOREX.r3.7HG0712100.1	1.41484454	1.596116844	3.205337124	0.00229	0.031785508	-1.48663635	Aminotransferase-related family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0657930.1	0.727475558	4.769359272	3.379356875	0.00137	0.026563254	-1.49104013	Aberrant root formation protein 4	elongation zone	12 h
HORVU.MOREX.r3.1HG0070100.1	-0.403123107	4.109158355	-3.432154654	0.00117	0.025668159	-1.49116313	Prolyl 4-hydroxylase alpha subunit, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0689320.1	0.998810283	7.120907428	3.488532796	0.00099	0.023815524	-1.49208519	Kinesin-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0256890.1	0.929127756	6.520171866	3.42382213	0.0012	0.025763058	-1.49453214	Argonaute	elongation zone	12 h
HORVU.MOREX.r3.6HG0609520.1	0.489028146	8.96663263	3.605140168	0.00069	0.021013719	-1.49517216	Fatty acid desaturase	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0059000.1	1.081616838	2.194539462	3.217375102	0.00221	0.031443869	-1.49672425	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.1HG0040400.1	3.004563624	4.472815111	3.233965552	0.0021	0.030821023	-1.49690313	Xyloglucan galactosyltransferase KATAMARI1-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0200330.1	1.3747188	4.462805147	3.274453146	0.00187	0.028923495	-1.49704159	Cell division protein ftsZ	elongation zone	12 h
HORVU.MOREX.r3.5HG0527890.1	-0.331735724	6.194702471	-3.527789888	0.00087	0.0230352	-1.49709478	Anthranilate synthase	elongation zone	12 h
HORVU.MOREX.r3.2HG0204960.1	0.396247647	4.354857362	3.404489483	0.00127	0.026178272	-1.50004266	RING/U-box superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0443620.1	1.456175913	2.064194108	3.203372188	0.0023	0.031887924	-1.50047568	Pentatricopeptide repeat-containing protein, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0050700.1	-1.105818947	2.994863261	-3.460997221	0.00107	0.024644437	-1.501271	ATP-dependent zinc metalloprotease FtsH	elongation zone	12 h
HORVU.MOREX.r3.6HG0551230.1	3.200642751	2.012376965	3.21695496	0.00221	0.031443869	-1.50301339	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.3HG0275170.1	1.718419022	4.459730287	3.257908646	0.00196	0.029613672	-1.50479547	Single-stranded DNA-binding protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0516840.1	1.748235842	2.497565851	3.199676787	0.00232	0.031903923	-1.50503335	DNA topoisomerase	elongation zone	12 h
HORVU.MOREX.r3.2HG0181590.1	0.810437736	7.96866194	3.5226954	0.00089	0.023206422	-1.50653453	60S ribosomal protein L14, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0555690.1	0.832504036	4.095938839	3.312448829	0.00167	0.028188358	-1.50705797	F-box family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0008200.1	2.040115576	1.354368368	3.287723384	0.0018	0.028691351	-1.50764395	Cytochrome P450	elongation zone	12 h
HORVU.MOREX.r3.1HG0062130.1	1.488851614	6.63509952	3.397884294	0.0013	0.026344787	-1.51067691	Importin subunit beta-1	elongation zone	12 h
HORVU.MOREX.r3.7HG0685970.1	-0.694211882	4.801919798	-3.577570512	0.00075	0.021691049	-1.51079553	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0102500.1	2.412016545	-0.677166593	3.259173537	0.00195	0.029569389	-1.51247587	60 kDa chaperonin	elongation zone	12 h
HORVU.MOREX.r3.6HG0570960.1	1.140601422	6.423530915	3.439066276	0.00114	0.025432695	-1.51247849	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.4HG0385270.1	0.569214878	9.972411854	3.621485849	0.00066	0.020810194	-1.51700703	Elongation factor 1-alpha	elongation zone	12 h
HORVU.MOREX.r3.7HG0650920.1	1.5399166	7.40240725	3.434552357	0.00116	0.02562904	-1.51755779	Nucleosome assembly protein 1-1	elongation zone	12 h
HORVU.MOREX.r3.6HG0629800.1	0.903217131	6.18269492	3.427555677	0.00119	0.025704276	-1.51762799	50S ribosomal protein L13	elongation zone	12 h
HORVU.MOREX.r3.2HG0174140.1	0.60914574	4.885352835	3.414258818	0.00123	0.026021602	-1.51788141	Agmatine deiminase	elongation zone	12 h
HORVU.MOREX.r3.2HG0131630.1	-2.018281512	-3.028166822	-3.19470538	0.00236	0.032009236	-1.51940428	vacuolar sorting-associated protein (DUF946)	elongation zone	12 h
HORVU.MOREX.r3.2HG0212900.1	0.610083511	6.207724717	3.449278009	0.00111	0.025121413	-1.52060411	Methylthioribose kinase	elongation zone	12 h
HORVU.MOREX.r3.7HG0637330.1	1.05958791	3.159355737	3.238943823	0.00207	0.03060905	-1.52094846	ATP-dependent RNA helicase	elongation zone	12 h
HORVU.MOREX.r3.4HG0338450.1	2.140081472	0.677849295	3.212570923	0.00224	0.031520621	-1.52194805	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0396270.1	-1.929387802	-0.551483003	-3.186601695	0.00241	0.032503127	-1.52605448	RNA-directed DNA polymerase (reverse transcriptase)-related fa	elongation zone	12 h
HORVU.MOREX.r3.4HG0362830.1	1.191014308	6.738047017	3.434881048	0.00116	0.02562904	-1.52625622	TRAF-like superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0499490.1	0.309273954	6.586701245	3.502714709	0.00094	0.023393436	-1.52845569	Transcription initiation factor IIB	elongation zone	12 h
HORVU.MOREX.r3.6HG0631040.1	-0.766829263	2.526682694	-3.362239601	0.00144	0.02703001	-1.52973654	Mesoderm induction early response protein 1, putative isoform	elongation zone	12 h
HORVU.MOREX.r3.4HG0342880.1	1.292016604	0.599719418	3.184700396	0.00243	0.032575632	-1.53058729	Oxidoreductase, aldo/keto reductase family protein, expressed	elongation zone	12 h
HORVU.MOREX.r3.2HG0176650.1	0.993957609	4.874812167	3.340569543	0.00154	0.02745794	-1.53168115	Anaphase-promoting complex subunit 2	elongation zone	12 h
HORVU.MOREX.r3.6HG0573240.1	1.535164211	5.752755014	3.348069463	0.0015	0.027239638	-1.53178478	Chaperone protein dnaJ, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0368770.2	1.250433891	2.047876559	3.197848831	0.00234	0.03195973	-1.53195499	ATP-dependent Clp protease proteolytic subunit	elongation zone	12 h
HORVU.MOREX.r3.6HG0581990.1	-1.058423062	0.470811621	-3.212438893	0.00224	0.031520621	-1.53228992	Mitochondrial carrier protein-like	elongation zone	12 h
HORVU.MOREX.r3.3HG0294470.1	1.546152475	2.140692119	3.187998302	0.0024	0.032414492	-1.53326301	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0674340.1	0.924617841	5.899987322	3.413178011	0.00124	0.026041204	-1.53798666	Ribosomal protein L46	elongation zone	12 h
HORVU.MOREX.r3.2HG0203060.1	0.814666089	6.067213545	3.420679972	0.00121	0.025813316	-1.53806742	COP9 signalosome complex subunit 5	elongation zone	12 h
HORVU.MOREX.r3.5HG0526750.1	2.129235516	1.870786541	3.180904227	0.00245	0.032706849	-1.54067913	Ribosomal RNA large subunit methyltransferase E	elongation zone	12 h
HORVU.MOREX.r3.4HG0389790.1	-0.491829151	3.234107873	-3.385183946	0.00135	0.026498466	-1.54071197	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.1HG0079250.1	0.889095276	7.964832516	3.51249491	0.00092	0.023235104	-1.54172393	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.7HG0726810.1	2.811028686	-1.043010381	3.203435191	0.0023	0.031887924	-1.54200714	HAT transposon superfamily protein, putative	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.4HG0366460.1	0.71957863	6.79957525	3.462360239	0.00107	0.024644437	-1.54358873	Embryo defective 2765	elongation zone	12 h
HORVU.MOREX.r3.3HG0254850.1	0.350760332	4.808158728	3.412564775	0.00124	0.026060689	-1.54368608	sucrose synthase 1	elongation zone	12 h
HORVU.MOREX.r3.3HG0268950.1	0.760510843	5.053714073	3.379031103	0.00137	0.026563254	-1.54533237	Helicase-related family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0293310.1	-1.093013618	-2.571332228	-3.217296831	0.00221	0.031443869	-1.54559388	Protein upstream of flc	elongation zone	12 h
HORVU.MOREX.r3.3HG0248130.1	1.314345608	4.234048933	3.258585474	0.00196	0.029576765	-1.54710066	3-methyl-2-oxobutanoate hydroxymethyltransferase	elongation zone	12 h
HORVU.MOREX.r3.4HG0333550.2	-0.781069804	1.181426652	-3.306139442	0.0017	0.028288147	-1.54719699	senescence-associated family protein, putative (DUF581)	elongation zone	12 h
HORVU.MOREX.r3.2HG0141420.1	1.048923897	5.442729657	3.355421845	0.00147	0.027209299	-1.54767197	tRNA wybutosine-synthesizing protein 2/3/4	elongation zone	12 h
HORVU.MOREX.r3.7HG0722350.1	0.708974997	5.076598366	3.353518273	0.00148	0.027239638	-1.54771781	UBX domain-containing protein, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0625100.1	0.592122328	2.539221075	3.278574652	0.00185	0.028847361	-1.55089264	E3 ubiquitin-protein ligase	elongation zone	12 h
HORVU.MOREX.r3.2HG0194250.1	0.752651335	7.844284678	3.506634333	0.00093	0.023256457	-1.55119514	Ribosomal protein L11	elongation zone	12 h
HORVU.MOREX.r3.4HG0401710.1	1.388840025	4.660057465	3.282682399	0.00182	0.028808148	-1.55328038	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.1HG0071940.1	0.568570628	6.762417038	3.471695115	0.00104	0.024267361	-1.55533705	Sorting and assembly machinery component 50 like	elongation zone	12 h
HORVU.MOREX.r3.2HG0167500.1	1.554086969	3.557899401	3.2308992	0.00212	0.030866089	-1.55659075	Repetitive proline-rich cell wall protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0104890.1	2.455617258	3.602032019	3.183739084	0.00243	0.032618994	-1.55755373	Rho GTPase-activating protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0183440.1	1.24000503	2.73877678	3.206450111	0.00228	0.031725905	-1.56026995	Mitochondrial intermembrane space import and assembly protei	elongation zone	12 h
HORVU.MOREX.r3.4HG0405590.1	0.82005499	9.149514262	3.552524553	0.00081	0.022303809	-1.56053541	40S ribosomal protein SA	elongation zone	12 h
HORVU.MOREX.r3.4HG0336000.1	-0.713337329	2.469297952	-3.382291565	0.00136	0.026553975	-1.56160741	Transcription activator of gluconeogenesis ERT1	elongation zone	12 h
HORVU.MOREX.r3.4HG0396550.1	0.736924067	5.452542851	3.394055434	0.00131	0.026348744	-1.56182599	Mitotic checkpoint protein bub3.1	elongation zone	12 h
HORVU.MOREX.r3.7HG0667510.2	0.67946036	2.422869832	3.267732199	0.00191	0.029085354	-1.56266974	ADP-ribosylation factor family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0746770.1	0.482956335	10.27031467	3.640535763	0.00062	0.020516782	-1.56337738	Chaperone protein htpG family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0718540.1	-0.700790426	3.33578157	-3.334336088	0.00157	0.027599669	-1.56365483	Heat shock transcription factor	elongation zone	12 h
HORVU.MOREX.r3.6HG0556470.1	0.982873866	6.2652176	3.406412969	0.00126	0.026146241	-1.56491585	Splicing factor 3B subunit-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0391330.1	0.399991626	6.457455724	3.491810853	0.00098	0.023723522	-1.5656444	Phosphomevalonate kinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0291320.1	1.916177767	0.885868778	3.183563413	0.00244	0.032618994	-1.56729787	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0669620.1	-0.926534689	0.714004188	-3.201821922	0.00231	0.031894634	-1.56733662	Receptor-like protein kinase	elongation zone	12 h
HORVU.MOREX.r3.1HG0044850.1	1.063034834	2.603766468	3.207390591	0.00227	0.031692167	-1.56765083	Metal-dependent phosphohydrolase, HD subdomain	elongation zone	12 h
HORVU.MOREX.r3.5HG0509880.1	0.583624351	6.303653309	3.443639017	0.00113	0.025290479	-1.57160938	Kinase	elongation zone	12 h
HORVU.MOREX.r3.5HG0532090.1	0.64678767	8.117226923	3.518211665	0.0009	0.023235104	-1.57164729	Prohibitin	elongation zone	12 h
HORVU.MOREX.r3.5HG0443530.1	1.646144069	6.796564929	3.384234475	0.00135	0.026498466	-1.5748829	DNA helicase	elongation zone	12 h
HORVU.MOREX.r3.3HG0328320.1	2.281814822	1.36086251	3.169854728	0.00253	0.033099534	-1.57531773	Heavy metal transport/detoxification superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0444350.1	-0.812737967	2.597522561	-3.310333897	0.00168	0.028265516	-1.57535509	Sn1-specific diacylglycerol lipase alpha	elongation zone	12 h
HORVU.MOREX.r3.1HG0081380.1	-0.653245533	2.215537802	-3.413770537	0.00124	0.026021602	-1.57609489	transcription factor BIG PETAL P (BPE)	elongation zone	12 h
HORVU.MOREX.r3.3HG0295540.1	1.733907399	6.067104647	3.346177784	0.00151	0.027239638	-1.5771653	Cyclin	elongation zone	12 h
HORVU.MOREX.r3.2HG0196830.1	2.182084546	0.59388019	3.186957915	0.00241	0.032490942	-1.5779072	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0308420.1	0.689894839	3.844691287	3.302575195	0.00172	0.028392091	-1.58000238	Integrator complex subunit	elongation zone	12 h
HORVU.MOREX.r3.5HG0490320.1	0.665321716	7.95248412	3.50784982	0.00093	0.023255319	-1.58092324	Eukaryotic translation initiation factor 3 subunit E	elongation zone	12 h
HORVU.MOREX.r3.7HG0729940.1	2.104260395	1.804584133	3.163650052	0.00258	0.033395092	-1.58139886	Leucine-rich repeat receptor-like protein kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0389210.1	2.135309706	3.54018037	3.176487468	0.00249	0.032843155	-1.58281059	Mitochondrial carrier protein, expressed	elongation zone	12 h
HORVU.MOREX.r3.1HG0041060.1	0.821521649	7.230752246	3.45966094	0.00108	0.024665565	-1.58301035	WD40 repeat-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0458010.1	-0.332189141	5.942045141	-3.473264642	0.00103	0.024207459	-1.58341349	Protein kinase, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0648460.1	-0.51023731	2.500172303	-3.386335039	0.00134	0.026498466	-1.58439952	Glycosyltransferase	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.2HG0124120.1	2.626675424	1.689838316	3.170938164	0.00253	0.033099534	-1.5846469	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0659440.1	3.610178308	3.492381947	3.166057706	0.00256	0.033247885	-1.58565333	Anthocyanin 5-aromatic acyltransferase-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0416620.1	0.537579496	5.629102912	3.409584512	0.00125	0.026082866	-1.58780087	Post-GPI attachment to proteins factor 3	elongation zone	12 h
HORVU.MOREX.r3.5HG0431350.1	1.79605298	0.368564414	3.165117214	0.00257	0.033296092	-1.58825586	5'-3' exoribonuclease 4	elongation zone	12 h
HORVU.MOREX.r3.6HG0606410.1	0.921813121	8.824885632	3.523415893	0.00089	0.02319596	-1.58828314	50S ribosomal protein L11	elongation zone	12 h
HORVU.MOREX.r3.5HG0450950.1	0.498013774	4.96403423	3.363693066	0.00143	0.027010031	-1.5889725	GDP-L-galactose phosphorylase 1	elongation zone	12 h
HORVU.MOREX.r3.1HG0061740.1	0.851517377	6.215496352	3.394486805	0.00131	0.026348744	-1.589863	Ran-binding protein 1 domain-containing	elongation zone	12 h
HORVU.MOREX.r3.7HG0708050.1	2.474527973	-1.430799155	3.205598874	0.00228	0.031782886	-1.59165324	Cytochrome b561	elongation zone	12 h
HORVU.MOREX.r3.3HG0220360.1	0.884069747	4.616464522	3.318652135	0.00164	0.028033028	-1.59277186	Disease resistance protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0659410.1	2.834496914	7.290126011	3.347791098	0.0015	0.027239638	-1.59321334	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0479950.1	1.800870716	1.83204156	3.158843941	0.00262	0.033669786	-1.59498454	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0211800.1	1.697089691	2.154731344	3.173650102	0.00251	0.03299418	-1.5965961	Serine/threonine-protein kinase	elongation zone	12 h
HORVU.MOREX.r3.7HG0666710.1	2.828660165	0.417146587	3.211669609	0.00224	0.031545502	-1.59706212	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0569700.1	1.198830649	6.267855445	3.381150053	0.00136	0.026563254	-1.60114835	Protein CYPRO4	elongation zone	12 h
HORVU.MOREX.r3.2HG0113700.1	1.156906256	4.987099523	3.388340131	0.00133	0.026498466	-1.6018124	Rubber elongation factor family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0661290.1	-0.612448358	0.704847423	-3.385140433	0.00135	0.026498466	-1.60240633	Inositol-tetrakisphosphate 1-kinase	elongation zone	12 h
HORVU.MOREX.r3.5HG0508190.1	0.536178871	8.082339826	3.54381911	0.00083	0.022553062	-1.60258159	1-deoxy-D-xylulose 5-phosphate synthase 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0100670.1	0.590353213	8.076646951	3.513382299	0.00091	0.023235104	-1.603626	Eukaryotic translation initiation factor 3 subunit M	elongation zone	12 h
HORVU.MOREX.r3.1HG0063870.1	0.632869755	6.880931169	3.46278757	0.00107	0.024644437	-1.60377565	Kinesin-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0546810.1	2.348725546	-0.232723193	3.201478974	0.00231	0.031894634	-1.60500495	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0108540.1	0.938404779	6.78478822	3.424250521	0.0012	0.025763058	-1.60509689	Eukaryotic translation initiation factor 2 subunit alpha	elongation zone	12 h
HORVU.MOREX.r3.5HG0441010.1	1.331248543	3.529366075	3.19002748	0.00239	0.032288187	-1.60709864	Asparagine synthetase, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0099120.1	1.258845032	3.152513512	3.201635118	0.00231	0.031894634	-1.60757698	Disease resistance protein (NBS-LRR class) family	elongation zone	12 h
HORVU.MOREX.r3.2HG0181550.1	1.06870708	3.831201973	3.28553055	0.00181	0.028744755	-1.61160417	Imidazole glycerol phosphate synthase subunit HisF	elongation zone	12 h
HORVU.MOREX.r3.1HG0062390.3	0.953275202	1.005907134	3.17677448	0.00248	0.032837066	-1.61233657	Dehydration responsive element-binding factor protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0298810.1	2.492829581	-2.743442253	3.210376636	0.00225	0.031580217	-1.61314169	Protein NRT1/ PTR FAMILY 5.5	elongation zone	12 h
HORVU.MOREX.r3.6HG0544400.1	1.066368588	6.141473387	3.359244913	0.00145	0.027115369	-1.61503026	RNA-binding NOB1	elongation zone	12 h
HORVU.MOREX.r3.2HG0209030.1	1.66268062	0.629763314	3.157392791	0.00263	0.033716726	-1.61661081	RING finger protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0073440.1	1.348767502	4.629259021	3.271253183	0.00189	0.028966331	-1.61779147	Kinesin-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0466020.1	0.770205985	7.677986698	3.502833419	0.00094	0.023393436	-1.61798729	Omega-3 fatty acid desaturase	elongation zone	12 h
HORVU.MOREX.r3.6HG0632020.2	-1.168745607	-2.239832204	-3.207822851	0.00227	0.031692167	-1.61802624	Photosystem II 22 kDa, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.5HG0524930.1	0.601179016	4.635265951	3.345725462	0.00151	0.027239638	-1.61866359	Myosin heavy chain-like protein, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0328740.1	2.27274107	4.710593389	3.21529146	0.00222	0.031454344	-1.62145896	WD-repeat protein, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0344990.1	1.115807489	2.816049021	3.196329741	0.00235	0.032009236	-1.62180695	NBS-LRR disease resistance protein family-1	elongation zone	12 h
HORVU.MOREX.r3.2HG0172320.3	0.498810237	5.240874315	3.402139569	0.00128	0.0261927	-1.62435763	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.5HG0455140.1	2.713511499	-2.159476557	3.200880619	0.00232	0.031894634	-1.62448195	tRNA (guanine(37)-N1)-methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0517790.1	1.504194555	5.254951629	3.269169611	0.0019	0.029041385	-1.62546594	Evolutionarily conserved C-terminal region 2	elongation zone	12 h
HORVU.MOREX.r3.4HG0365450.1	0.626849291	4.01791179	3.293279333	0.00177	0.028575945	-1.62636105	Thiol:disulfide interchange protein txlA	elongation zone	12 h
HORVU.MOREX.r3.6HG0631760.1	0.381575359	5.489051319	3.422258782	0.0012	0.025763058	-1.62662171	Signal peptide peptidase-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0397300.1	1.403854057	3.644537391	3.191882368	0.00238	0.032199922	-1.62811129	Tyrosine-specific transport protein, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0397850.1	1.373476022	3.722866272	3.199720094	0.00232	0.031903923	-1.62916563	Methionine--tRNA ligase	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0011440.1	-1.416850113	-1.581106574	-3.149303357	0.00269	0.033864708	-1.63042014	Glucan endo-1,3-beta-glucosidase, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0303920.1	1.5828651	2.04413203	3.145843236	0.00272	0.033883993	-1.63154271	HIT zinc finger family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0715150.1	1.702654321	4.93366821	3.230165768	0.00213	0.030888027	-1.63199886	WD-repeat protein, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0067160.1	-1.140144512	0.452737078	-3.322422841	0.00162	0.02794328	-1.63245935	Wound-induced protease inhibitor	elongation zone	12 h
HORVU.MOREX.r3.3HG0310210.1	0.548042606	7.031206457	3.466586196	0.00105	0.02453734	-1.63275224	Acyl-[acyl-carrier-protein] desaturase	elongation zone	12 h
HORVU.MOREX.r3.2HG0188620.1	-0.513568777	4.015975413	-3.369116667	0.00141	0.026723934	-1.6332952	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0156390.1	0.301545598	6.734888733	3.474097558	0.00103	0.024201764	-1.6347325	Protein kinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0250640.1	0.782772682	5.868281794	3.388248548	0.00133	0.026498466	-1.63726367	Leucine--tRNA ligase	elongation zone	12 h
HORVU.MOREX.r3.7HG0677860.1	2.460081871	2.903040617	3.146319209	0.00271	0.033864708	-1.63829257	RNA polymerase II elongation factor	elongation zone	12 h
HORVU.MOREX.r3.3HG0269890.1	1.935473054	5.144673374	3.224484588	0.00216	0.031161246	-1.63927829	Activating transcription factor 7-interacting 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0659310.1	0.806402105	3.341339311	3.215705797	0.00222	0.031454344	-1.6395403	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0294550.1	1.283227749	5.803277229	3.317902035	0.00164	0.028035058	-1.63974538	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0219810.1	0.939116149	3.950557979	3.228613477	0.00214	0.030940575	-1.64071029	Agenet domain containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0659400.1	2.182969104	7.513960163	3.377107178	0.00138	0.026563254	-1.64142362	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0096600.1	0.520400134	8.083914516	3.529406006	0.00087	0.022951249	-1.64197878	Pyruvate dehydrogenase E1 component subunit alpha	elongation zone	12 h
HORVU.MOREX.r3.5HG0537150.1	-0.793424641	-2.246878812	-3.226821963	0.00215	0.031018589	-1.64221185	Protein DETOXIFICATION	elongation zone	12 h
HORVU.MOREX.r3.4HG0412630.1	2.655384143	3.079994324	3.138467986	0.00277	0.03425211	-1.64291345	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.6HG0605290.1	0.623397675	4.144725964	3.278627161	0.00185	0.028847361	-1.64427736	Protein phosphatase 2C	elongation zone	12 h
HORVU.MOREX.r3.1HG0046280.1	0.532859514	7.208401788	3.454335524	0.00109	0.024866938	-1.64428801	Chloroplast inner envelope protein, putative, expressed	elongation zone	12 h
HORVU.MOREX.r3.5HG0421570.1	2.401053783	5.345365617	3.226843255	0.00215	0.031018589	-1.64484266	Deoxyuridine 5'-triphosphate nucleotidohydrolase	elongation zone	12 h
HORVU.MOREX.r3.7HG0636750.1	0.875519168	7.072570729	3.463413884	0.00106	0.024644437	-1.64491188	carbohydrate esterase, putative (DUF303)	elongation zone	12 h
HORVU.MOREX.r3.2HG0200630.1	0.81646507	9.635164688	3.554211376	0.00081	0.022275873	-1.64583121	Adenosylhomocysteinase	elongation zone	12 h
HORVU.MOREX.r3.4HG0337770.1	-0.69669679	5.839765801	-3.511272801	0.00092	0.023235104	-1.6464253	Histidine kinase	elongation zone	12 h
HORVU.MOREX.r3.7HG0659510.1	2.162882906	0.823748924	3.146760675	0.00271	0.033864708	-1.65159108	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0363330.1	0.867156344	2.648390841	3.25539201	0.00198	0.029636522	-1.65329341	F-box/RNI-like superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0410710.1	2.484405258	1.150606136	3.150091823	0.00268	0.033864708	-1.65408219	DNA polymerase delta small subunit	elongation zone	12 h
HORVU.MOREX.r3.3HG0231840.1	1.551122172	1.492682319	3.139362944	0.00277	0.03425211	-1.65450751	Disease resistance protein (NBS-LRR class) family	elongation zone	12 h
HORVU.MOREX.r3.2HG0108460.1	0.759543968	5.625884288	3.336465077	0.00156	0.027532387	-1.65474486	Ubiquitin activating enzyme E1	elongation zone	12 h
HORVU.MOREX.r3.7HG0662090.1	1.116703086	1.086674019	3.141796864	0.00275	0.034124913	-1.65632729	F-box protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0641550.1	0.758881155	5.040372267	3.307658324	0.00169	0.02828778	-1.6581353	Chaperone protein dnaJ	elongation zone	12 h
HORVU.MOREX.r3.4HG0385160.1	1.580699868	4.698386898	3.230335505	0.00213	0.030888027	-1.65818749	Transmembrane protein 209	elongation zone	12 h
HORVU.MOREX.r3.5HG0533330.1	0.619518397	3.431932283	3.255568626	0.00197	0.029636522	-1.65832024	Long-chain-fatty-acid CoA ligase, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0383590.1	0.927599408	7.128541216	3.422794432	0.0012	0.025763058	-1.65854878	Aminotransferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0507540.1	0.799592838	3.379116795	3.232105343	0.00211	0.030866089	-1.65892083	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase,C subunit	elongation zone	12 h
HORVU.MOREX.r3.2HG0212570.1	0.392966711	10.53927453	3.618065703	0.00066	0.020839563	-1.66275482	Calreticulin	elongation zone	12 h
HORVU.MOREX.r3.2HG0117150.1	1.6051674	1.019556079	3.130811118	0.00283	0.034668194	-1.66294188	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0110060.1	0.520632972	6.526409036	3.442912292	0.00113	0.025318336	-1.66620033	Aldehyde dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.5HG0503530.1	-0.539750374	0.239465893	-3.336118252	0.00156	0.027532387	-1.6662299	transmembrane protein, putative (DUF594)	elongation zone	12 h
HORVU.MOREX.r3.5HG0504820.1	2.074411625	4.749265507	3.217303673	0.00221	0.031443869	-1.66657383	Uveal autoantigen with coiled-coil domains and ankyrin repeats i	elongation zone	12 h
HORVU.MOREX.r3.2HG0097390.1	0.522564444	4.644505302	3.379711989	0.00137	0.026563254	-1.66933783	Inosine-5'-monophosphate dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.1HG0073890.1	1.986788952	3.385036735	3.146447218	0.00271	0.033864708	-1.66969166	Microtubule binding protein	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.4HG0407540.1	0.798812629	6.028730279	3.375269388	0.00139	0.026563254	-1.67239178	Ankyrin repeat domain protein, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0543770.1	0.787434127	7.792354173	3.480776787	0.00101	0.024060672	-1.68199249	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.2HG0171930.1	1.328774792	3.812478286	3.160945312	0.0026	0.033587945	-1.68383277	Phosphate carrier protein, mitochondrial	elongation zone	12 h
HORVU.MOREX.r3.3HG0256600.1	1.150024475	3.275742589	3.178076067	0.00247	0.032834207	-1.68457035	ATP-dependent Clp protease proteolytic subunit	elongation zone	12 h
HORVU.MOREX.r3.2HG0169030.1	1.469232821	5.125078024	3.257004702	0.00197	0.029636522	-1.68643862	ATP-dependent RNA helicase DeaD	elongation zone	12 h
HORVU.MOREX.r3.2HG0201770.1	1.104991427	4.924549228	3.263237962	0.00193	0.029341049	-1.68829885	Ribosomal protein S4	elongation zone	12 h
HORVU.MOREX.r3.2HG0115290.1	2.386481221	3.505789531	3.142473224	0.00274	0.034095864	-1.68860019	Kinase interacting (KIP1-like) family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0161340.1	0.905476128	6.240076424	3.358101635	0.00146	0.027115369	-1.6905995	Methyltransferase-like protein 13	elongation zone	12 h
HORVU.MOREX.r3.7HG0745430.1	5.182605326	4.479660325	3.118761011	0.00293	0.035349763	-1.6917984	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albu	elongation zone	12 h
HORVU.MOREX.r3.2HG0207860.1	-1.162842427	-2.164021772	-3.19103761	0.00238	0.032236279	-1.69202811	Serine/threonine-protein kinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0321260.1	1.120790738	7.27024282	3.395014349	0.00131	0.026348744	-1.69375507	Orotate phosphoribosyltransferase, Orotidine-5'-phosphate deca	elongation zone	12 h
HORVU.MOREX.r3.6HG0542360.1	0.671027945	7.686684687	3.446643878	0.00112	0.025172156	-1.69419755	U5 small nuclear ribonucleoprotein helicase	elongation zone	12 h
HORVU.MOREX.r3.6HG0624720.1	0.435425905	7.91443531	3.480592051	0.00101	0.024060672	-1.6948411	ABC transporter ATP-binding protein ARB1	elongation zone	12 h
HORVU.MOREX.r3.6HG0547570.1	-0.48105541	5.07323181	-3.440238539	0.00114	0.025432695	-1.69504986	LURP-one-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0283250.1	-0.615820559	3.003628567	-3.419515599	0.00121	0.02586849	-1.69572504	MYB transcription factor	elongation zone	12 h
HORVU.MOREX.r3.7HG0648740.1	1.179625464	2.892311845	3.14745735	0.0027	0.033864708	-1.69618456	Pentatricopeptide repeat-containing family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0122420.1	1.606556212	3.865411996	3.175556613	0.00249	0.032910434	-1.697613	Origin recognition complex subunit 6	elongation zone	12 h
HORVU.MOREX.r3.6HG0591300.1	1.544720939	6.018441169	3.283803547	0.00182	0.028793645	-1.69794499	CCAAT/enhancer-binding protein zeta	elongation zone	12 h
HORVU.MOREX.r3.3HG0319570.1	1.260387179	3.275640979	3.151247282	0.00267	0.033864708	-1.69865468	Crossover junction endonuclease mus81	elongation zone	12 h
HORVU.MOREX.r3.4HG0401720.1	1.035943904	7.267357119	3.42546233	0.00119	0.025739392	-1.69885216	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.5HG0488290.1	1.100009367	6.25888895	3.337239404	0.00155	0.027528501	-1.69956432	Ribosomal RNA small subunit methyltransferase F	elongation zone	12 h
HORVU.MOREX.r3.4HG0354970.1	0.593744529	6.732308281	3.445026429	0.00112	0.025239957	-1.70472186	Omega-3 fatty acid desaturase	elongation zone	12 h
HORVU.MOREX.r3.4HG0381070.1	-0.485400896	3.312494191	-3.296198222	0.00175	0.028450551	-1.70606863	helicase domain-containing protein / IBR domain-containing prot	elongation zone	12 h
HORVU.MOREX.r3.1HG0068380.1	0.409960461	5.314485157	3.38944548	0.00133	0.026498466	-1.70748111	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0530750.1	0.404234396	5.706473606	3.399064024	0.00129	0.026336616	-1.70813704	Post-GPI attachment to proteins factor 3	elongation zone	12 h
HORVU.MOREX.r3.2HG0160160.1	1.228122433	6.43005085	3.350577717	0.00149	0.027239638	-1.70831627	Kinesin-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0516650.1	0.318338905	6.060187193	3.416241656	0.00123	0.026016162	-1.70845172	Nuclear-interacting partner of ALK	elongation zone	12 h
HORVU.MOREX.r3.5HG0507230.1	1.46258788	4.207892853	3.1722202	0.00252	0.033037836	-1.71074148	RNA-binding protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0252850.1	0.864332523	7.821717991	3.43175649	0.00117	0.025668159	-1.71330107	Importin subunit alpha	elongation zone	12 h
HORVU.MOREX.r3.2HG0176570.1	1.117925721	5.576785683	3.288391179	0.00179	0.028681437	-1.71415539	Kelch domain-containing 4	elongation zone	12 h
HORVU.MOREX.r3.5HG0497370.1	0.956888463	9.177672535	3.475171192	0.00103	0.024178546	-1.71509921	ATP-dependent RNA helicase	elongation zone	12 h
HORVU.MOREX.r3.6HG0545970.1	0.411901732	5.654969195	3.408640039	0.00125	0.026083278	-1.71555455	Short-chain dehydrogenase/reductase family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0714720.1	2.59689246	4.54757859	3.169736415	0.00253	0.033099534	-1.71597355	3'-N-debenzoyl-2'-deoxytaxol N-benzoyltransferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0523140.1	1.685796788	5.884927616	3.289811729	0.00179	0.028628646	-1.71969631	DNA ligase-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0311730.1	-0.296824223	5.970093793	-3.447336669	0.00112	0.025172156	-1.72038392	S-acyltransferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0509260.1	-0.532830892	4.152888421	-3.434657733	0.00116	0.02562904	-1.72283174	BTB/POZ domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0104510.1	0.360638277	7.315942183	3.440708681	0.00114	0.025431673	-1.72321344	FACT complex subunit SPT16	elongation zone	12 h
HORVU.MOREX.r3.3HG0238730.1	2.14467479	4.16441507	3.139930261	0.00276	0.034221402	-1.72373985	DNA mismatch repair protein mutS	elongation zone	12 h
HORVU.MOREX.r3.1HG0053990.1	0.520060747	5.229624499	3.335250368	0.00156	0.027548584	-1.72487506	Ankyrin repeat family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0669190.2	1.903734334	0.693680419	3.108321973	0.00302	0.035840683	-1.72586921	Adenylyltransferase and sulfurtransferase MOCS3	elongation zone	12 h
HORVU.MOREX.r3.5HG0470890.1	1.097784667	6.799446968	3.396426623	0.0013	0.026348744	-1.72749001	#N/A	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.7HG0655530.1	0.844974947	5.262456683	3.280937823	0.00183	0.028819302	-1.73081839	Serine/threonine-protein phosphatase	elongation zone	12 h
HORVU.MOREX.r3.3HG0243180.1	0.808237474	8.802526067	3.476378339	0.00102	0.024166531	-1.73093636	50S ribosomal protein L5	elongation zone	12 h
HORVU.MOREX.r3.5HG0458890.1	-0.450872992	3.514885037	-3.342887311	0.00153	0.027378374	-1.73285406	senescence regulator (Protein of unknown function, DUF584)	elongation zone	12 h
HORVU.MOREX.r3.7HG0634400.1	1.436626187	6.04833754	3.305096009	0.00171	0.028318301	-1.73383656	Kinesin-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0506300.1	-0.359045766	5.425044791	-3.439072733	0.00114	0.025432695	-1.73566219	Potassium transporter	elongation zone	12 h
HORVU.MOREX.r3.4HG0353200.1	-0.553168164	2.886286462	-3.382247329	0.00136	0.026553975	-1.73626245	heat-inducible transcription repressor	elongation zone	12 h
HORVU.MOREX.r3.7HG0642830.1	2.150902026	5.18214762	3.200753578	0.00232	0.031894634	-1.73644378	Scarecrow transcription factor family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0507460.1	1.702438321	6.376315971	3.293072384	0.00177	0.028575945	-1.73727844	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0322720.1	1.69978198	4.211989362	3.1598411	0.00261	0.033615353	-1.73830582	Protein RETICULATA, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.3HG0315280.1	2.501590913	6.440086434	3.19637771	0.00235	0.032009236	-1.74195774	Eukaryotic aspartyl protease family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0470230.1	0.823376227	9.108223054	3.48454413	0.001	0.023938404	-1.74294624	40S ribosomal protein S19	elongation zone	12 h
HORVU.MOREX.r3.4HG0383340.1	1.700056526	0.2957173	3.100228114	0.00309	0.036259291	-1.7434892	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0333190.1	2.660670593	0.389975525	3.145698041	0.00272	0.033883993	-1.74397172	N utilization substance protein B-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0252460.1	0.730766996	6.678630411	3.383905679	0.00135	0.026498466	-1.74503895	50S ribosomal protein L3, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0248810.1	0.471633611	8.679714325	3.493746947	0.00097	0.023668509	-1.74572243	Eukaryotic translation initiation factor 3 subunit L	elongation zone	12 h
HORVU.MOREX.r3.4HG0383870.1	0.686038888	7.088831513	3.425884594	0.00119	0.025739392	-1.74589167	Malonyl CoA-acyl carrier protein transacylase containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0739930.1	0.837618542	6.017002486	3.346584208	0.00151	0.027239638	-1.74605986	60S ribosomal protein L30	elongation zone	12 h
HORVU.MOREX.r3.3HG0320600.1	1.00039752	4.369351337	3.198904771	0.00233	0.031930285	-1.74606258	RNA-dependent RNA polymerase	elongation zone	12 h
HORVU.MOREX.r3.5HG0439450.1	2.027562996	3.124129671	3.11118636	0.003	0.035630935	-1.74628745	Chromosome alignment-maintaining phosphoprotein 1	elongation zone	12 h
HORVU.MOREX.r3.1HG0019240.1	-0.547581682	2.336885411	-3.292478453	0.00177	0.028575945	-1.74739787	N-acetyltransferase, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0191650.1	2.203705514	-0.087996826	3.121183815	0.00291	0.035234858	-1.74895762	Methionine aminopeptidase	elongation zone	12 h
HORVU.MOREX.r3.4HG0379470.1	1.106455011	2.488131719	3.120810505	0.00292	0.035234858	-1.75162005	Endoglucanase	elongation zone	12 h
HORVU.MOREX.r3.7HG0725660.1	1.063667199	1.229915497	3.113199408	0.00298	0.035529393	-1.75197097	FBD-associated F-box protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0067200.1	1.54096817	4.612988993	3.215302564	0.00222	0.031454344	-1.75322618	ATP-dependent DNA helicase Hel308	elongation zone	12 h
HORVU.MOREX.r3.1HG0088590.1	0.679097962	5.072719668	3.306126653	0.0017	0.028288147	-1.7541448	Urease accessory protein ureG	elongation zone	12 h
HORVU.MOREX.r3.3HG0236710.1	2.732706935	3.114508496	3.090117929	0.00318	0.036772996	-1.7574599	IQ domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0197700.1	1.084066192	3.163704659	3.153997796	0.00265	0.033864708	-1.75836111	Rho GTPase-activating protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0069490.1	1.92790817	2.67154507	3.102514514	0.00307	0.036128346	-1.75881105	Cyclin	elongation zone	12 h
HORVU.MOREX.r3.5HG0498890.1	1.557417299	1.232074563	3.088148273	0.0032	0.036875974	-1.76031478	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0183630.1	2.273522283	0.168588997	3.114862768	0.00297	0.035453096	-1.76090859	Hus1-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0221030.1	2.501449767	3.659641944	3.091559505	0.00317	0.036725711	-1.76227166	Xyloglucan galactosyltransferase KATAMARI1-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0204270.1	2.217588978	3.872721928	3.112768079	0.00299	0.035540654	-1.76289292	Small RNA degrading nuclease	elongation zone	12 h
HORVU.MOREX.r3.2HG0183080.1	0.978634145	4.793681433	3.271008543	0.00189	0.028966331	-1.76289298	Carboxypeptidase	elongation zone	12 h
HORVU.MOREX.r3.1HG0064320.1	0.557267225	6.073377779	3.384981324	0.00135	0.026498466	-1.76361504	Argininosuccinate synthase	elongation zone	12 h
HORVU.MOREX.r3.6HG0545620.1	0.361655666	11.02319041	3.613496652	0.00067	0.020873129	-1.76398976	Heat shock 70 kDa protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0398400.1	0.923046348	7.165881715	3.380757994	0.00136	0.026563254	-1.7661431	BTB/POZ domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0187800.1	0.459672722	5.669988682	3.358478021	0.00146	0.027115369	-1.76637582	DNA/RNA helicase protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0535890.1	1.464014798	4.676851416	3.180977273	0.00245	0.032706849	-1.76778893	Protein BCCIP homolog	elongation zone	12 h
HORVU.MOREX.r3.2HG0123850.1	1.430508719	2.154095266	3.099275686	0.0031	0.036288602	-1.76964121	Pentatricopeptide repeat-containing protein, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0540060.1	1.912387354	3.856993307	3.120878159	0.00292	0.035234858	-1.769743	DAG, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.5HG0420970.1	-0.767277527	2.17073124	-3.291425337	0.00178	0.028617771	-1.77124361	ERD (Early-responsive to dehydration stress) family protein	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.5HG0524260.1	1.645563045	3.901736522	3.139120938	0.00277	0.03425211	-1.77309688	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0628810.1	0.881553059	9.237220048	3.478914295	0.00101	0.024104211	-1.77341385	50S ribosomal protein L14	elongation zone	12 h
HORVU.MOREX.r3.4HG0413030.1	0.852856504	3.465134839	3.192158578	0.00238	0.03219541	-1.77394521	Plant/F12P19-7 protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0601810.1	2.113645424	0.425545697	3.092741384	0.00316	0.036685118	-1.77474032	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0711300.1	-1.37202072	-2.949290087	-3.082217962	0.00326	0.036983216	-1.77619775	DNA topoisomerase	elongation zone	12 h
HORVU.MOREX.r3.2HG0196740.1	1.738788674	4.447891765	3.171885266	0.00252	0.033048664	-1.7772245	DNA replication helicase dna2, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0120930.1	1.926190855	9.035111364	3.401144803	0.00128	0.026244722	-1.77789505	Glycine rich protein 3	elongation zone	12 h
HORVU.MOREX.r3.4HG0333740.1	1.304451093	6.115426012	3.292869328	0.00177	0.028575945	-1.77888022	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0291030.1	-0.625522459	1.945137651	-3.429530272	0.00118	0.025704276	-1.78119528	Glucan endo-1,3-beta-glucosidase 1	elongation zone	12 h
HORVU.MOREX.r3.5HG0502130.1	0.743880485	6.543409785	3.35973054	0.00145	0.027106935	-1.7818264	T-complex protein 1 subunit beta	elongation zone	12 h
HORVU.MOREX.r3.1HG0089390.1	0.817704058	7.416473196	3.398318825	0.00129	0.026336616	-1.78211477	Kinase-related protein DUF1296	elongation zone	12 h
HORVU.MOREX.r3.1HG0031980.1	1.337742465	3.013898901	3.115000484	0.00297	0.035453096	-1.78270687	Trichome birefringence-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0496660.1	1.793506321	2.466297521	3.086539571	0.00322	0.036928455	-1.78419333	Sister chromatid cohesion 1 protein 3	elongation zone	12 h
HORVU.MOREX.r3.2HG0171550.1	0.693456337	4.111529363	3.253109234	0.00199	0.029748302	-1.78590454	Major facilitator superfamily transporter	elongation zone	12 h
HORVU.MOREX.r3.7HG0706330.1	0.379726576	4.543866555	3.314757925	0.00166	0.028112171	-1.78715163	TOM1-like protein 2	elongation zone	12 h
HORVU.MOREX.r3.6HG0609730.1	0.861109311	8.141507493	3.427768638	0.00118	0.025704276	-1.78816942	60S ribosomal protein L31	elongation zone	12 h
HORVU.MOREX.r3.5HG0468500.1	0.6853649	5.407656046	3.316524759	0.00165	0.028050531	-1.78835407	Diphthine synthase, putative, expressed	elongation zone	12 h
HORVU.MOREX.r3.7HG0702400.1	0.373907307	6.100976213	3.396253652	0.0013	0.026348744	-1.78837942	Nucleotide/sugar transporter family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0378580.1	0.444561012	5.353083837	3.373642335	0.00139	0.026563254	-1.78959456	Transcription factor	elongation zone	12 h
HORVU.MOREX.r3.2HG0134290.1	2.21027021	-1.166968614	3.098648576	0.00311	0.036312806	-1.78960322	SKP1-like protein 4	elongation zone	12 h
HORVU.MOREX.r3.3HG0307400.1	-1.278950751	1.770342762	-3.195657377	0.00235	0.032009236	-1.79020936	GRAS family transcription factor	elongation zone	12 h
HORVU.MOREX.r3.2HG0111990.1	2.053261086	1.973815438	3.075191061	0.00332	0.037190743	-1.79039361	tRNA (Guanine(26)-N(2))-dimethyltransferase	elongation zone	12 h
HORVU.MOREX.r3.4HG0400520.1	-1.138277317	-0.785996541	-3.275627218	0.00186	0.028906691	-1.79169687	Lipid transfer protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0751620.1	2.010350862	5.432363147	3.206757343	0.00228	0.031719121	-1.79289888	Cyclin	elongation zone	12 h
HORVU.MOREX.r3.7HG0641230.1	-1.088674119	-1.229188244	-3.305744865	0.0017	0.028288147	-1.79462854	Retrovirus-related Pol polyprotein from transposon TNT 1-94	elongation zone	12 h
HORVU.MOREX.r3.2HG0105350.1	2.500687248	3.890755994	3.098311702	0.00311	0.036312806	-1.79557473	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0384120.1	0.843507092	2.064852893	3.147997473	0.0027	0.033864708	-1.7991017	serine/arginine repetitive matrix-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0026830.1	-0.547525637	3.566935325	-3.371672239	0.0014	0.026619212	-1.80133095	Leucine-rich repeat receptor-like protein kinase family	elongation zone	12 h
HORVU.MOREX.r3.2HG0205050.1	-1.768321951	-2.492233883	-3.084494752	0.00324	0.036928455	-1.80143107	Receptor-like protein kinase	elongation zone	12 h
HORVU.MOREX.r3.4HG0397020.1	2.230720084	3.896750304	3.10249891	0.00307	0.036128346	-1.80160474	TPX2 (Targeting protein for Xklp2) family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0383330.1	0.732586125	3.253673369	3.168173687	0.00255	0.033171389	-1.8021846	DNA polymerase III polC-type	elongation zone	12 h
HORVU.MOREX.r3.6HG0621750.1	1.189750639	3.464859945	3.137972556	0.00278	0.034261617	-1.80310887	Mitochondrial transcription termination factor	elongation zone	12 h
HORVU.MOREX.r3.2HG0196310.1	-2.198046866	-1.066921445	-3.090995839	0.00318	0.036736339	-1.80562193	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.6HG0557770.1	2.724783425	-1.181003261	3.115088967	0.00297	0.035453096	-1.80589102	FBD-associated F-box protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0111630.1	-1.533920536	-2.706877531	-3.079563747	0.00328	0.036983216	-1.80703395	carboxyl-terminal peptidase (DUF239)	elongation zone	12 h
HORVU.MOREX.r3.1HG0003150.1	0.693728718	4.554905765	3.231751194	0.00212	0.030866089	-1.80782537	Chaperone protein DnaJ	elongation zone	12 h
HORVU.MOREX.r3.5HG0503930.1	1.64538256	4.348826856	3.154903175	0.00265	0.033831284	-1.80821625	Helicase-related family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0090940.1	0.62038187	8.802081872	3.463629194	0.00106	0.024644437	-1.81142345	GTP-binding nuclear protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0166530.1	0.687476585	8.752681538	3.459326535	0.00108	0.024665565	-1.81219179	30S ribosomal protein S11	elongation zone	12 h
HORVU.MOREX.r3.3HG0243990.1	0.758546317	9.014711028	3.461380317	0.00107	0.024644437	-1.81289896	50S ribosomal protein L24	elongation zone	12 h
HORVU.MOREX.r3.4HG0357230.1	0.991021518	5.25636344	3.265834409	0.00192	0.029184417	-1.81370058	Pyridoxal 5'-phosphate synthase subunit PdxS	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.6HG0567060.1	2.809092855	1.964019752	3.067834992	0.00339	0.03736784	-1.8152174	Tyrosyl-DNA phosphodiesterase 2	elongation zone	12 h
HORVU.MOREX.r3.5HG0497930.1	1.877324252	2.406259764	3.069695464	0.00337	0.037331432	-1.8169582	Protein ROOT PRIMORDIUM DEFECTIVE 1	elongation zone	12 h
HORVU.MOREX.r3.6HG0616800.1	3.025961981	0.815040624	3.093507209	0.00315	0.036644453	-1.81707179	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0404070.1	0.884289898	10.53082143	3.513698537	0.00091	0.023235104	-1.81888186	60S ribosomal protein L4	elongation zone	12 h
HORVU.MOREX.r3.5HG0536490.1	1.070401832	4.431143848	3.283687208	0.00182	0.028793645	-1.819588	Acyl carrier protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0581690.1	1.02504988	5.816798645	3.273573221	0.00187	0.028923495	-1.82039895	60S ribosomal protein L6	elongation zone	12 h
HORVU.MOREX.r3.2HG0112910.1	0.899254479	4.17912055	3.23089499	0.00212	0.030866089	-1.82091539	Pectinesterase	elongation zone	12 h
HORVU.MOREX.r3.6HG0559400.1	0.813045807	3.632007207	3.191149046	0.00238	0.032236279	-1.82154537	Exocyst complex component EXO70A1	elongation zone	12 h
HORVU.MOREX.r3.3HG0286160.1	1.508599307	6.290215457	3.29428897	0.00176	0.028575945	-1.82232817	Pollen Ole e 1 allergen/extensin	elongation zone	12 h
HORVU.MOREX.r3.7HG0674860.1	-2.292838694	-0.715552338	-3.061975207	0.00345	0.037649994	-1.82349515	Acyl-coenzyme A oxidase	elongation zone	12 h
HORVU.MOREX.r3.7HG0662830.1	1.021418636	4.730197892	3.198187364	0.00233	0.031954117	-1.82462655	Mechanosensitive ion channel family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0535750.1	0.804652482	6.040528497	3.296827544	0.00175	0.028442815	-1.82552626	Cleavage and polyadenylation specificity factor subunit 3	elongation zone	12 h
HORVU.MOREX.r3.4HG0380110.1	0.791828939	7.38894714	3.394110764	0.00131	0.026348744	-1.82563306	Mitochondrial import receptor subunit TOM40-1-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0675950.1	2.040727342	2.306247473	3.059931195	0.00347	0.037761197	-1.82584263	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0723410.1	2.073124644	2.947363407	3.067331719	0.0034	0.037381068	-1.82597601	A/G-specific adenine DNA glycosylase	elongation zone	12 h
HORVU.MOREX.r3.7HG0697940.1	1.417248786	0.148475214	3.060127518	0.00347	0.037761197	-1.82647507	UvrABC system protein C	elongation zone	12 h
HORVU.MOREX.r3.2HG0165190.1	0.864639839	5.986651179	3.308076501	0.00169	0.028279404	-1.82650526	Mitochondrial import inner membrane translocase subunit TIM2	elongation zone	12 h
HORVU.MOREX.r3.1HG0058800.1	0.588892113	3.603852967	3.211525537	0.00225	0.031545502	-1.82767393	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0698550.1	0.587840312	4.953445471	3.272580165	0.00188	0.028923495	-1.82816091	Zinc finger CCCH domain protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0395010.1	1.350537666	5.440099558	3.223048404	0.00217	0.031226117	-1.82909353	Nuclear pore complex protein NUP133	elongation zone	12 h
HORVU.MOREX.r3.5HG0465080.1	1.468895996	2.12956565	3.069126451	0.00338	0.037331432	-1.82910296	Pentatricopeptide repeat-containing family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0647930.1	1.266580186	1.498899177	3.070651779	0.00337	0.037331001	-1.82971555	S-adenosyl-L-methionine-dependent methyltransferases superfa	elongation zone	12 h
HORVU.MOREX.r3.7HG0695930.1	1.258162734	0.297229831	3.059281915	0.00348	0.037764638	-1.83067289	Succinate--CoA ligase [ADP-forming] subunit beta	elongation zone	12 h
HORVU.MOREX.r3.2HG0147770.1	0.439116515	5.593653187	3.346892527	0.00151	0.027239638	-1.8333241	Growth-regulating factor	elongation zone	12 h
HORVU.MOREX.r3.5HG0438160.1	0.407802487	5.336636433	3.32095254	0.00163	0.02796111	-1.83590477	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0744860.1	0.876076148	8.187638293	3.408179291	0.00126	0.026083278	-1.83705061	Isoleucine--tRNA ligase	elongation zone	12 h
HORVU.MOREX.r3.5HG0479210.1	1.084684885	7.833408605	3.387710523	0.00134	0.026498466	-1.83705065	HMG-Y-related protein A	elongation zone	12 h
HORVU.MOREX.r3.1HG0023800.1	0.837157363	8.954713759	3.439059142	0.00114	0.025432695	-1.8386441	60S ribosomal protein L18-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0728000.1	-0.575742542	5.007313233	-3.407020394	0.00126	0.026125006	-1.83880177	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.4HG0349500.1	2.071397304	3.603219849	3.068669491	0.00338	0.037339648	-1.84003626	Meiosis arrest female protein 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0104690.1	2.190110422	4.777741937	3.130485093	0.00284	0.034669947	-1.84042329	Coiled-coil domain-containing protein 6	elongation zone	12 h
HORVU.MOREX.r3.2HG0099010.1	-0.870444269	-2.649782075	-3.099362912	0.0031	0.036288602	-1.84053881	Glutamyl-tRNA (Gln) amidotransferase subunit A	elongation zone	12 h
HORVU.MOREX.r3.5HG0524340.1	1.815526167	0.089050807	3.079912317	0.00328	0.036983216	-1.84081671	Mitochondrial transcription termination factor-like	elongation zone	12 h
HORVU.MOREX.r3.4HG0338400.1	0.840377395	8.453676741	3.434692882	0.00116	0.02562904	-1.84105547	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.2HG0146690.1	2.438126631	1.304324057	3.072122551	0.00335	0.037256101	-1.84159382	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0186490.1	0.978130843	3.316357094	3.110670309	0.003	0.035642237	-1.84275119	Transmembrane protein 14C	elongation zone	12 h
HORVU.MOREX.r3.4HG0343350.1	1.050046888	5.871663592	3.290820002	0.00178	0.02862189	-1.84403034	40S ribosomal protein S27	elongation zone	12 h
HORVU.MOREX.r3.6HG0590420.1	1.708161893	3.163300203	3.075969356	0.00332	0.037190743	-1.84437015	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0178110.1	2.648682964	5.730948227	3.132775704	0.00282	0.034576444	-1.84443921	transmembrane protein, putative (Protein of unknown function,	elongation zone	12 h
HORVU.MOREX.r3.4HG0352920.1	0.687636454	4.352513751	3.23889739	0.00207	0.03060905	-1.84543875	Cysteine desulfurase, putative, expressed	elongation zone	12 h
HORVU.MOREX.r3.5HG0511960.1	2.364742463	-0.602478814	3.053008861	0.00354	0.037872249	-1.84671564	Disease resistance protein RPM1	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.7HG0735580.1	2.670958571	5.931976842	3.186112138	0.00242	0.032527883	-1.84691578	Xyloglucan endotransglucosylase/hydrolase	elongation zone	12 h
HORVU.MOREX.r3.7HG0692820.1	0.406934392	7.244663118	3.414953754	0.00123	0.026021602	-1.84729198	2-oxoglutarate/malate translocator, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.1HG0025320.1	-1.144218237	0.572544846	-3.124106943	0.00289	0.035131319	-1.84748228	Receptor-like kinase, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0120940.1	2.16753448	6.482268735	3.221331993	0.00218	0.031338693	-1.84751152	P-loop containing nucleoside triphosphate hydrolases superfami	elongation zone	12 h
HORVU.MOREX.r3.1HG0049180.1	0.576448547	5.507193954	3.299001942	0.00174	0.02840648	-1.84809582	Chaperone protein dnaJ, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0230970.1	0.806004081	7.763065022	3.411280489	0.00124	0.026060689	-1.84848072	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.2HG0215250.1	1.119017439	6.918385048	3.374409361	0.00139	0.026563254	-1.84967117	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.6HG0631790.1	1.844833356	0.262211449	3.052534457	0.00354	0.037882054	-1.85040865	50S ribosomal protein L9	elongation zone	12 h
HORVU.MOREX.r3.4HG0414860.1	2.127947158	-0.918019416	3.075038886	0.00332	0.037190743	-1.85083972	Cysteine proteinase	elongation zone	12 h
HORVU.MOREX.r3.5HG0420010.1	-0.27669041	6.947534958	-3.446709504	0.00112	0.025172156	-1.85172151	Sucrose-phosphatase	elongation zone	12 h
HORVU.MOREX.r3.7HG0697480.1	0.683947457	4.08465238	3.223338387	0.00217	0.03122163	-1.85300726	LETM1-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0054200.1	0.373278625	5.861579496	3.356975909	0.00146	0.027181772	-1.85334886	E2 ubiquitin-conjugating-like enzyme	elongation zone	12 h
HORVU.MOREX.r3.6HG0601260.1	-0.943026534	3.05036359	-3.381105698	0.00136	0.026563254	-1.85448583	Sulfotransferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0424560.1	-0.555903246	7.021103992	-3.446023956	0.00112	0.025191667	-1.85510447	Glutathione S-transferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0169670.1	2.468836937	0.536677325	3.068755366	0.00338	0.037339648	-1.85570653	Ribosome maturation factor RimP	elongation zone	12 h
HORVU.MOREX.r3.7HG0635160.1	0.414987003	6.815127135	3.373620924	0.00139	0.026563254	-1.85646438	Monocopper oxidase-like protein SKU5	elongation zone	12 h
HORVU.MOREX.r3.7HG0725050.1	-0.456077258	4.544757744	-3.385193648	0.00135	0.026498466	-1.8581384	Protein IQ-DOMAIN 1	elongation zone	12 h
HORVU.MOREX.r3.1HG0085420.1	0.630699934	3.718026856	3.199585868	0.00232	0.031903923	-1.85975936	DNA replication complex GINS protein PSF2	elongation zone	12 h
HORVU.MOREX.r3.5HG0441110.1	1.585913436	5.425609299	3.195371638	0.00235	0.032009236	-1.86059082	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0242030.1	1.339096872	2.331267829	3.072598264	0.00335	0.037256101	-1.86116627	Alpha/beta-Hydrolases superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0738670.1	0.826153265	6.751476612	3.332791001	0.00157	0.027655159	-1.86141763	Hydroxyproline-rich glycoprotein-like	elongation zone	12 h
HORVU.MOREX.r3.7HG0691910.1	0.72962165	6.395808606	3.333452009	0.00157	0.02762467	-1.86248752	Regulator of chromosome condensation (RCC1) family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0674590.1	-0.974602162	1.003958233	-3.127676362	0.00286	0.034856493	-1.86273271	Retrovirus-related Pol polyprotein from transposon TNT 1-94	elongation zone	12 h
HORVU.MOREX.r3.5HG0495520.1	0.946042616	4.992603158	3.229196468	0.00213	0.030911827	-1.86283415	Hsp70 nucleotide exchange factor fes1	elongation zone	12 h
HORVU.MOREX.r3.3HG0290890.1	0.895259763	5.267096293	3.237037575	0.00208	0.030699736	-1.86331283	TSA: Wollemia nobilis Ref_Wollemi_Transcript_16418_819 trans	elongation zone	12 h
HORVU.MOREX.r3.2HG0096710.1	-1.20833013	-1.753677392	-3.156147874	0.00264	0.033771061	-1.86459458	Cytochrome P450	elongation zone	12 h
HORVU.MOREX.r3.2HG0157500.1	1.647382548	3.758991925	3.087487085	0.00321	0.036913075	-1.86667059	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.2HG0113710.1	0.940133773	6.360748126	3.302778984	0.00172	0.028392091	-1.86887888	Protein arginine methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0664240.1	-0.560753126	2.462412603	-3.292298787	0.00177	0.028575945	-1.86902753	12-oxophytodienoate reductase-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0299220.1	-0.478757376	5.799007839	-3.438895511	0.00115	0.025432695	-1.87001234	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0593640.1	0.802997426	6.680974514	3.341030922	0.00153	0.02745794	-1.87046502	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0021320.1	1.46535533	5.526590149	3.208667092	0.00226	0.031672617	-1.87101665	4-hydroxy-tetrahydrodipicolinate reductase	elongation zone	12 h
HORVU.MOREX.r3.7HG0749060.1	1.552546345	0.00150025	3.043946753	0.00363	0.038433444	-1.87373036	Transducin/WD40 repeat-like superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0081810.1	1.610575161	3.256327076	3.083283097	0.00325	0.036948704	-1.87508155	tRNA-2-methylthio-N(6)-dimethylallyladenosine synthase	elongation zone	12 h
HORVU.MOREX.r3.6HG0540370.1	1.357108844	3.67357023	3.081788786	0.00326	0.036983216	-1.87518589	Myb family transcription factor-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0749430.1	1.173471481	3.338386635	3.088426746	0.0032	0.03686745	-1.87810903	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0541700.1	0.824878651	2.333953765	3.083827295	0.00324	0.036928455	-1.87871996	Mitochondrial transcription termination factor-like	elongation zone	12 h
HORVU.MOREX.r3.2HG0178050.1	-0.54577067	4.22962604	-3.326929695	0.0016	0.027806246	-1.87903004	F-box protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0256960.1	0.936205818	6.374900604	3.293715109	0.00177	0.028575945	-1.88047984	60S ribosomal protein L30	elongation zone	12 h
HORVU.MOREX.r3.2HG0107900.1	0.385160643	7.940344995	3.431553344	0.00117	0.025668159	-1.88055009	Elongation factor 1-alpha	elongation zone	12 h
HORVU.MOREX.r3.4HG0333810.1	0.827244061	10.90713435	3.532199699	0.00086	0.022899718	-1.88065551	RNA-binding protein	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.2HG0128940.1	2.546350025	-1.078037265	3.069432375	0.00338	0.037331432	-1.88099552	GTP cyclohydrolase 1	elongation zone	12 h
HORVU.MOREX.r3.5HG0516590.1	2.053432233	0.441151426	3.044809165	0.00362	0.038379585	-1.88321796	Exostosin family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0723530.1	-0.765526903	3.176738798	-3.36437759	0.00143	0.026979742	-1.8837425	Cinnamoyl-CoA reductase family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0427780.1	1.959838613	6.100942308	3.218590008	0.0022	0.031443869	-1.88390927	Kinesin-related protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0710130.1	0.869820404	7.526331028	3.371678477	0.0014	0.026619212	-1.88440168	60S ribosomal protein L22, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0254240.1	1.962307527	0.725794066	3.038295124	0.00369	0.038671495	-1.88567436	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0604930.1	1.256208466	6.186846553	3.261629238	0.00194	0.029444171	-1.88575495	UPF0160 protein MYG1, mitochondrial	elongation zone	12 h
HORVU.MOREX.r3.2HG0162920.1	1.057308764	3.457721936	3.11534192	0.00296	0.035453096	-1.8864712	Mediator of RNA polymerase II transcription subunit 30, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0153800.1	2.614697409	0.271349874	3.057419577	0.00349	0.037796967	-1.88728278	Aldo/keto reductase family-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0014320.1	1.732487335	2.690834854	3.039725556	0.00367	0.038641262	-1.88786294	Importin subunit beta-1	elongation zone	12 h
HORVU.MOREX.r3.2HG0150450.1	0.598216908	7.245663801	3.396372869	0.0013	0.026348744	-1.88799092	Pyruvate kinase	elongation zone	12 h
HORVU.MOREX.r3.4HG0400700.1	1.428305391	3.339687411	3.07376144	0.00334	0.037244624	-1.88888607	DNA polymerase III PolC-type	elongation zone	12 h
HORVU.MOREX.r3.3HG0307000.1	2.377338765	1.0320042	3.039125529	0.00368	0.038641262	-1.88967331	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0575770.1	-0.34335707	5.020687417	-3.335926473	0.00156	0.027532387	-1.88971289	Protein FAR1-RELATED SEQUENCE 5	elongation zone	12 h
HORVU.MOREX.r3.3HG0273010.1	0.914653021	4.355122207	3.173568518	0.00251	0.03299418	-1.89165217	Protein transport protein SEC13	elongation zone	12 h
HORVU.MOREX.r3.5HG0427050.1	1.197723312	5.45206071	3.195367689	0.00235	0.032009236	-1.89184424	60S ribosomal protein L24	elongation zone	12 h
HORVU.MOREX.r3.7HG0735360.1	0.770471401	5.209545448	3.234534246	0.0021	0.030802035	-1.89406901	Zinc finger CCCH domain-containing protein 45	elongation zone	12 h
HORVU.MOREX.r3.6HG0543730.1	0.765746152	7.651801236	3.395290729	0.00131	0.026348744	-1.89510777	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.2HG0192900.1	1.113319702	6.268762483	3.279741684	0.00184	0.028819302	-1.89597683	Xyloglucan endotransglucosylase/hydrolase	elongation zone	12 h
HORVU.MOREX.r3.4HG0391960.1	1.059660853	4.485614922	3.165400748	0.00257	0.0332899	-1.89607429	ATP-dependent Clp protease ATP-binding subunit	elongation zone	12 h
HORVU.MOREX.r3.2HG0119710.1	1.758257811	3.695173693	3.065542727	0.00341	0.037489533	-1.89671183	DNA/RNA helicase protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0014190.1	-1.199302143	0.720317016	-3.035814158	0.00371	0.038729899	-1.89778136	Transducin/WD-like repeat-protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0731600.1	1.192350592	1.21065695	3.029431482	0.00378	0.039090877	-1.89794303	NBS-LRR disease resistance protein, putative, expressed	elongation zone	12 h
HORVU.MOREX.r3.3HG0223950.1	0.633337466	4.288990681	3.202027304	0.00231	0.031894634	-1.89932249	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0160590.1	2.333429814	1.119229386	3.035777573	0.00371	0.038729899	-1.89938373	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0040910.1	0.812327561	8.88503314	3.422270767	0.0012	0.025763058	-1.89982219	60S ribosomal protein L21	elongation zone	12 h
HORVU.MOREX.r3.1HG0073160.1	-0.475802396	5.054880201	-3.373968094	0.00139	0.026563254	-1.90147676	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.3HG0316960.1	0.708721785	5.757042157	3.268583337	0.0019	0.029064599	-1.90210309	Nascent polypeptide-associated complex subunit alpha-like prot	elongation zone	12 h
HORVU.MOREX.r3.3HG0285840.1	-0.863360921	-0.694836738	-3.221436316	0.00218	0.031338693	-1.90427459	Senescence/dehydration-associated protein-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0535780.1	0.786219099	6.219128882	3.306284686	0.0017	0.028288147	-1.90464601	Transmembrane protein 70, mitochondrial	elongation zone	12 h
HORVU.MOREX.r3.2HG0135650.1	-2.205372175	-3.487652168	-3.027293151	0.0038	0.039110161	-1.90518101	Laccase	elongation zone	12 h
HORVU.MOREX.r3.6HG0616160.1	1.235466699	2.633093791	3.046900652	0.0036	0.038272175	-1.90842012	ATP-dependent RNA helicase family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0163860.1	2.196353102	5.202440706	3.105064335	0.00305	0.0360299	-1.9091126	Histone H2A.Z-specific chaperone CHZ1	elongation zone	12 h
HORVU.MOREX.r3.6HG0579510.1	-1.599692123	-0.908498026	-3.023406093	0.00385	0.039284359	-1.91006765	LINE-1 reverse transcriptase like	elongation zone	12 h
HORVU.MOREX.r3.4HG0371790.1	0.951756361	1.111486812	3.084027791	0.00324	0.036928455	-1.91043658	ROP binding protein kinases 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0209340.1	0.981093056	5.833737893	3.244084009	0.00204	0.030345139	-1.91204768	Clathrin light chain	elongation zone	12 h
HORVU.MOREX.r3.4HG0406290.1	1.755855789	4.255608694	3.079480867	0.00328	0.036983216	-1.912638	DNA-directed RNA polymerase subunit	elongation zone	12 h
HORVU.MOREX.r3.3HG0222390.1	3.573051669	3.41727625	3.024371245	0.00384	0.03925602	-1.91357755	Trypsin inhibitor	elongation zone	12 h
HORVU.MOREX.r3.3HG0314070.1	-1.202460791	-1.612808778	-3.120020302	0.00292	0.035293865	-1.9147704	Protein kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0228860.1	3.492194609	2.735909792	3.025125864	0.00383	0.03925602	-1.91621741	Mitochondrial glycoprotein	elongation zone	12 h
HORVU.MOREX.r3.3HG0302410.1	0.910267216	8.959776352	3.405849364	0.00126	0.026164076	-1.91647051	30S ribosomal protein S5	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.5HG0498810.1	0.69698823	6.020060381	3.296377117	0.00175	0.028450551	-1.91972868	60S ribosomal protein L44	elongation zone	12 h
HORVU.MOREX.r3.3HG0270170.1	1.016309305	2.933164716	3.085400975	0.00323	0.036928455	-1.92012612	Anthranilate phosphoribosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0239160.1	1.507870861	3.929564631	3.10133095	0.00308	0.036191331	-1.92096572	DNA polymerase epsilon subunit	elongation zone	12 h
HORVU.MOREX.r3.6HG0582230.1	0.548537175	3.581325437	3.209292196	0.00226	0.031636696	-1.92224216	GDSL esterase/lipase	elongation zone	12 h
HORVU.MOREX.r3.3HG0228120.1	-0.594905974	2.921074778	-3.211031712	0.00225	0.031545502	-1.92277267	MYB-related transcription factor	elongation zone	12 h
HORVU.MOREX.r3.4HG0340710.1	1.471725754	3.663251486	3.079821337	0.00328	0.036983216	-1.92300507	WD40 repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0206470.1	-0.466690454	6.277699834	-3.422636789	0.0012	0.025763058	-1.92517253	Loricrin-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0446090.1	1.599034996	3.10746457	3.051692243	0.00355	0.037906495	-1.92581835	rRNA-processing protein FYV7	elongation zone	12 h
HORVU.MOREX.r3.3HG0327680.1	1.861832812	2.040746476	3.019839113	0.00388	0.039444701	-1.92601678	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0205020.1	1.780853014	1.613831825	3.020852772	0.00387	0.039407591	-1.92620632	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.6HG0627910.1	0.891987141	6.146155843	3.278004741	0.00185	0.028860537	-1.92640855	Kinesin like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0465780.1	1.282633811	6.661609217	3.247666372	0.00202	0.030159961	-1.92705209	60S acidic ribosomal protein P0	elongation zone	12 h
HORVU.MOREX.r3.1HG0076540.1	0.418591389	7.761395839	3.403238302	0.00127	0.026178272	-1.9292884	Mitochondrial-processing peptidase subunit alpha	elongation zone	12 h
HORVU.MOREX.r3.5HG0527230.1	1.022326258	3.048538089	3.069393582	0.00338	0.037331432	-1.92933284	DCD (Development and cell death) domain protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0093330.1	1.743233156	1.327218247	3.014958332	0.00394	0.039714168	-1.93055096	Protein N-methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.4HG0412190.1	1.406649064	2.746246921	3.045296464	0.00362	0.038346619	-1.93101342	50S ribosomal protein L5	elongation zone	12 h
HORVU.MOREX.r3.2HG0099920.1	0.840652582	2.370731385	3.093527985	0.00315	0.036644453	-1.93242924	Glyoxylate reductase/hydroxypyruvate reductase	elongation zone	12 h
HORVU.MOREX.r3.7HG0684880.1	-0.649635025	3.761266823	-3.269109531	0.0019	0.029041385	-1.93358931	meiosis chromosome segregation family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0646210.1	0.709898698	4.882966115	3.215857825	0.00222	0.031454344	-1.93399297	tRNA-modifying protein YgfZ	elongation zone	12 h
HORVU.MOREX.r3.3HG0324310.1	1.852990761	-0.544565087	3.023076304	0.00385	0.039301249	-1.93421854	Disease resistance protein RPP13	elongation zone	12 h
HORVU.MOREX.r3.3HG0305200.1	1.634880304	3.248140536	3.044596326	0.00362	0.038382831	-1.9356399	Monooxygenase	elongation zone	12 h
HORVU.MOREX.r3.6HG0577950.1	-1.425750963	-1.781795644	-3.047402306	0.00359	0.038237792	-1.93585958	F-box/kelch-repeat protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0409600.1	-0.536529812	4.470888926	-3.375088533	0.00139	0.026563254	-1.9362235	Protein kinase family protein, putative, expressed	elongation zone	12 h
HORVU.MOREX.r3.2HG0139810.1	-0.839989314	0.636540026	-3.340339499	0.00154	0.02745794	-1.93622675	Heavy metal transport/detoxification superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0124930.1	0.623321904	6.004755837	3.28117205	0.00183	0.028819302	-1.93671942	DNA-directed RNA polymerase II family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0400870.1	2.983484565	0.562362935	3.048267519	0.00359	0.03818403	-1.93802044	Ribosomal large subunit pseudouridine synthase B	elongation zone	12 h
HORVU.MOREX.r3.1HG0065030.2	0.316154394	5.236932218	3.287205741	0.0018	0.028691351	-1.93802664	Nucleic acid binding protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0117180.1	0.838449881	7.219922766	3.335738548	0.00156	0.027532387	-1.93986486	30S ribosomal protein S9	elongation zone	12 h
HORVU.MOREX.r3.7HG0683960.1	1.19900695	5.237797772	3.178988735	0.00247	0.032817853	-1.94087579	#N/A	elongation zone	12 h
HORVU.MOREX.r3.4HG0388470.1	1.962704821	0.659213336	3.015535082	0.00393	0.039669391	-1.94144872	Rotundifolia-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0359890.1	0.671120889	3.726697938	3.126025365	0.00287	0.035000997	-1.94168221	tRNA-2-methylthio-N(6)-dimethylallyladenosine synthase	elongation zone	12 h
HORVU.MOREX.r3.5HG0462720.1	0.860241772	4.47715704	3.151101263	0.00267	0.033864708	-1.94273687	WD-repeat protein, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0658660.1	-0.809424112	2.135277695	-3.157826583	0.00262	0.033716726	-1.94405439	Ethylene-responsive transcription factor	elongation zone	12 h
HORVU.MOREX.r3.2HG0116060.1	0.740923569	4.617910192	3.181165681	0.00245	0.032706849	-1.9441837	Pre-rRNA-processing protein ESF2	elongation zone	12 h
HORVU.MOREX.r3.6HG0557980.1	1.040467687	6.414210139	3.268303239	0.0019	0.029066843	-1.94520601	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0114280.1	2.39465624	0.876588196	3.027293626	0.0038	0.039110161	-1.94676949	GTPase obg	elongation zone	12 h
HORVU.MOREX.r3.1HG0050920.1	-0.840532016	2.478719451	-3.348718584	0.0015	0.027239638	-1.94892274	Trehalase	elongation zone	12 h
HORVU.MOREX.r3.3HG0291600.1	0.879756792	6.498873317	3.279871126	0.00184	0.028819302	-1.95075239	ATP-dependent RNA helicase, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0442460.1	-0.516510715	3.36756339	-3.369792428	0.00141	0.026719424	-1.95144848	Protein kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0173660.1	2.260590702	1.241411952	3.018537658	0.0039	0.03951103	-1.95202785	Pentatricopeptide repeat-containing family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0095070.2	0.772874098	5.248934381	3.233499258	0.00211	0.030829102	-1.95355988	ATP-dependent RNA helicase	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.4HG0331540.1	1.368698864	1.537888525	3.014185878	0.00395	0.039746874	-1.95381613	ACT domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0715110.1	3.035833241	-1.38874377	3.0391258	0.00368	0.038641262	-1.95533259	Double-strand break repair protein MRE11	elongation zone	12 h
HORVU.MOREX.r3.1HG0054820.1	1.821744079	1.976629801	3.008976096	0.00401	0.040012973	-1.95737717	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0402030.1	0.390885137	5.321937852	3.290484751	0.00178	0.02862189	-1.96074654	Basic helix-loop-helix (BHLH) family transcription factor	elongation zone	12 h
HORVU.MOREX.r3.4HG0406710.1	-0.536291124	2.527858084	-3.29036666	0.00178	0.02862189	-1.96127138	Homeobox protein, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0669190.1	1.680398279	2.070139492	3.009840933	0.004	0.039974405	-1.96226298	Adenylyltransferase and sulfurtransferase MOCS3	elongation zone	12 h
HORVU.MOREX.r3.5HG0426820.1	2.193150953	-0.173769083	3.026645546	0.00381	0.039161886	-1.96286972	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0722300.1	2.361106359	-0.952880022	3.032897019	0.00374	0.038936762	-1.9629701	Lipase	elongation zone	12 h
HORVU.MOREX.r3.5HG0432300.1	0.776798545	6.175259496	3.280545405	0.00184	0.028819302	-1.96508784	Tetratricopeptide repeat-containing family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0539850.1	1.832443221	4.423652728	3.076687214	0.00331	0.037174732	-1.96566272	Kinesin-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0666080.1	2.439192345	1.746087834	2.99961963	0.00411	0.040307075	-1.96686959	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0478950.1	1.610976482	3.390125726	3.031137565	0.00376	0.03899655	-1.96883031	Centromere protein V	elongation zone	12 h
HORVU.MOREX.r3.4HG0349170.1	1.092584494	4.64522884	3.255451972	0.00198	0.029636522	-1.97288724	Long-Chain Acyl-CoA Synthetase	elongation zone	12 h
HORVU.MOREX.r3.6HG0613230.1	0.351954535	6.00935735	3.360410818	0.00145	0.027076709	-1.97352793	Allergen, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0384570.1	0.787788514	4.311382607	3.139942695	0.00276	0.034221402	-1.97540936	Transcription factor bHLH140	elongation zone	12 h
HORVU.MOREX.r3.4HG0402670.1	1.588832253	4.040868248	3.057467253	0.00349	0.037796967	-1.9759917	DNA topoisomerase	elongation zone	12 h
HORVU.MOREX.r3.2HG0113160.1	0.749053454	8.454057913	3.380620149	0.00136	0.026563254	-1.9766184	60S ribosomal protein L22, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0405370.1	2.181412764	0.021144763	3.012204696	0.00397	0.039849721	-1.97669429	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0377890.1	0.936541272	8.002111855	3.32791172	0.0016	0.027806246	-1.97676155	Nucleolar GTP-binding protein 2	elongation zone	12 h
HORVU.MOREX.r3.3HG0272120.1	1.457174544	4.043401107	3.058353692	0.00348	0.037779464	-1.97684592	DVA-1 polyprotein	elongation zone	12 h
HORVU.MOREX.r3.7HG0661600.1	1.314929305	7.721715927	3.285659619	0.00181	0.028744755	-1.97761955	Nucleolar GTP-binding protein 1	elongation zone	12 h
HORVU.MOREX.r3.4HG0393980.1	2.254339775	1.396411503	2.997710006	0.00413	0.040391635	-1.97876604	DNA-directed RNA polymerase subunit beta	elongation zone	12 h
HORVU.MOREX.r3.1HG0044230.1	0.774774547	8.794273122	3.394478445	0.00131	0.026348744	-1.98058872	40S ribosomal protein S17, putative, expressed	elongation zone	12 h
HORVU.MOREX.r3.5HG0528890.1	1.137532095	5.084336588	3.155498856	0.00264	0.033804921	-1.98195742	GATA transcription factor, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0082060.1	-0.662969886	2.494333616	-3.114791948	0.00297	0.035453096	-1.98245689	epstein-barr nuclear antigen	elongation zone	12 h
HORVU.MOREX.r3.4HG0374180.1	1.239260768	0.480598598	2.99893698	0.00412	0.040329959	-1.98272281	TSC22 domain family protein 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0641750.1	-1.784449415	-2.739012037	-3.054734652	0.00352	0.037808566	-1.98526921	Aspartic proteinase nepenthesin-2	elongation zone	12 h
HORVU.MOREX.r3.5HG0527180.1	1.152590365	3.570770348	3.065184531	0.00342	0.037489533	-1.98528999	HAT transposon superfamily, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0664470.1	1.976558575	2.932550253	3.00307849	0.00407	0.040229538	-1.9863202	KAT8 regulatory NSL complex subunit 3	elongation zone	12 h
HORVU.MOREX.r3.5HG0514110.1	0.559242217	6.244309832	3.304545409	0.00171	0.02834146	-1.98703621	#N/A	elongation zone	12 h
HORVU.MOREX.r3.4HG0407520.1	1.088490314	2.035180635	3.001467573	0.00409	0.040265883	-1.98744656	Mitochondrial import inner membrane translocase subunit TIM2	elongation zone	12 h
HORVU.MOREX.r3.3HG0308640.1	-0.335025446	7.154318973	-3.432491967	0.00117	0.025668159	-1.98876882	lysine ketoglutarate reductase trans-splicing protein (DUF707)	elongation zone	12 h
HORVU.MOREX.r3.5HG0419590.1	-0.474850288	6.133126066	-3.404065661	0.00127	0.026178272	-1.99018642	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0452940.1	2.13309728	1.671260459	2.989021152	0.00424	0.040956128	-1.99109355	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0255400.1	1.167708274	5.346293272	3.173114539	0.00251	0.032994826	-1.99180251	Translin family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0069950.1	1.131950512	4.849761786	3.137107914	0.00278	0.034272194	-1.99193763	Protein KRI1	elongation zone	12 h
HORVU.MOREX.r3.1HG0028320.1	0.388656968	6.850868413	3.35390038	0.00148	0.027239638	-1.99354767	70 kDa heat shock protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0082500.1	0.918974402	4.721829471	3.159597962	0.00261	0.033617799	-1.99376074	DNA replication complex GINS protein PSF3	elongation zone	12 h
HORVU.MOREX.r3.5HG0511950.1	1.749451765	4.233239305	3.057996806	0.00349	0.037779464	-1.99492776	Kinesin-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0512440.1	1.397386263	5.921251417	3.189414974	0.00239	0.032324245	-1.99496849	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0303380.1	-0.758451374	-0.867377041	-3.177082926	0.00248	0.032834207	-1.99528868	Zinc finger protein CONSTANS	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.4HG0379050.1	-0.349419688	5.079597644	-3.277785047	0.00185	0.028860537	-1.99694732	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.4HG0345810.1	1.296974257	1.299714382	2.994563035	0.00417	0.040632794	-1.99894516	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0684940.1	-0.556588218	4.72025707	-3.27968366	0.00184	0.028819302	-2.00001161	Zinc finger constans-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0516470.1	1.478568679	4.720536401	3.077446986	0.0033	0.037119446	-2.00103448	GDSL esterase/lipase	elongation zone	12 h
HORVU.MOREX.r3.3HG0266740.1	0.602464238	4.583959119	3.197667162	0.00234	0.03195973	-2.00181721	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0617080.1	-0.509498602	4.452280294	-3.317262259	0.00165	0.028043664	-2.00497971	Lipid transfer protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0337200.1	1.258608172	4.676780151	3.095126944	0.00314	0.036539994	-2.00856472	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.6HG0631440.1	1.290996814	2.780766611	3.036311371	0.00371	0.038729899	-2.00994738	Janus kinase and microtubule-interacting protein 3	elongation zone	12 h
HORVU.MOREX.r3.5HG0508640.1	2.689467447	1.961761663	2.982020516	0.00432	0.04129762	-2.01023655	Protein recA	elongation zone	12 h
HORVU.MOREX.r3.1HG0047710.1	1.09909545	1.697525089	2.99927559	0.00412	0.040310975	-2.01071857	Ribosomal RNA small subunit methyltransferase H	elongation zone	12 h
HORVU.MOREX.r3.6HG0614700.1	0.935297452	2.36393809	3.055497352	0.00351	0.037808566	-2.01090611	ATP synthase delta-subunit protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0319710.1	3.585050404	1.482728189	3.005869954	0.00404	0.040178373	-2.0111656	Glutathione S-transferase	elongation zone	12 h
HORVU.MOREX.r3.1HG0080610.1	1.640693674	4.932591417	3.094795761	0.00314	0.036553757	-2.01214036	Flap endonuclease 1	elongation zone	12 h
HORVU.MOREX.r3.1HG0005370.1	0.593479208	4.817106872	3.194615452	0.00236	0.032009236	-2.01328079	Replication protein A 70 kDa DNA-binding subunit	elongation zone	12 h
HORVU.MOREX.r3.1HG0006610.1	0.908887879	8.693329567	3.378025123	0.00137	0.026563254	-2.01344622	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.5HG0537290.1	0.714790323	7.867863715	3.340148531	0.00154	0.02745794	-2.01395241	60 kDa chaperonin	elongation zone	12 h
HORVU.MOREX.r3.3HG0325290.1	0.758564558	7.787813279	3.337378813	0.00155	0.027528501	-2.01418639	Ribosomal protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0149130.1	0.373987121	5.403092628	3.275419855	0.00186	0.028906691	-2.0144363	Ubiquitin-conjugating enzyme (E2)	elongation zone	12 h
HORVU.MOREX.r3.6HG0604200.1	0.925619712	0.7623065	3.081636822	0.00326	0.036983216	-2.01472793	transcription repressor	elongation zone	12 h
HORVU.MOREX.r3.2HG0117160.1	2.052973629	5.56954998	3.118646001	0.00294	0.035349763	-2.01605537	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0290180.1	1.170073441	3.615357964	3.0411389	0.00366	0.038619667	-2.01645666	Non-specific serine/threonine protein kinase	elongation zone	12 h
HORVU.MOREX.r3.7HG0649260.1	1.377077601	6.056376679	3.181807724	0.00245	0.032706849	-2.01661306	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0151050.1	0.562562452	6.080741385	3.271558388	0.00188	0.028962927	-2.01894622	AT-rich interactive domain protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0522390.1	2.480903918	-0.232655981	3.004364547	0.00406	0.040229538	-2.01942697	Pheophorbide a oxygenase, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.6HG0552540.1	0.80561097	3.876707041	3.090863795	0.00318	0.036736339	-2.01951769	Pyridoxal 5'-phosphate synthase subunit PdxT	elongation zone	12 h
HORVU.MOREX.r3.3HG0286150.1	-1.851403181	-0.866760921	-2.977273365	0.00438	0.041519226	-2.02142077	PHD finger protein 3	elongation zone	12 h
HORVU.MOREX.r3.2HG0172350.1	1.990114237	5.213074774	3.072944245	0.00334	0.037254747	-2.0214784	WEB family protein, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.7HG0637270.2	1.271661389	2.556416211	3.004559437	0.00406	0.040229538	-2.02222424	Ribonuclease H	elongation zone	12 h
HORVU.MOREX.r3.6HG0611880.1	-0.306103832	7.734249847	-3.410772282	0.00125	0.026062006	-2.02236237	Homeobox-leucine zipper protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0221390.1	0.978317211	2.076992594	2.999908263	0.00411	0.040307075	-2.02603324	LisH and RanBPM domains containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0054010.1	-0.546819176	5.84165697	-3.374103962	0.00139	0.026563254	-2.026295	zinc finger B-box protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0728630.1	0.978589621	1.895271753	3.017722096	0.00391	0.039547618	-2.02906501	Receptor-like protein kinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0330150.1	-1.578195	-0.302066567	-3.033797758	0.00374	0.03886761	-2.0298084	MYB transcription factor	elongation zone	12 h
HORVU.MOREX.r3.5HG0512410.1	1.275319316	5.302905234	3.146374751	0.00271	0.033864708	-2.03038299	Upstream activation factor subunit spp27	elongation zone	12 h
HORVU.MOREX.r3.6HG0634090.1	3.03988742	2.903382382	2.971967203	0.00444	0.041943839	-2.03059916	Protein O-linked-mannose beta-1,4-N-acetylglucosaminyltransfe	elongation zone	12 h
HORVU.MOREX.r3.6HG0588350.1	0.504168184	4.125370776	3.170403179	0.00253	0.033099534	-2.03358646	RING finger family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0716900.1	0.339952165	8.192568258	3.399172031	0.00129	0.026336616	-2.03370085	Transmembrane 9 superfamily member	elongation zone	12 h
HORVU.MOREX.r3.4HG0357930.1	-0.668610941	2.087250112	-3.112239928	0.00299	0.035565004	-2.03453356	Scarecrow transcription factor family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0501840.1	0.900721552	5.034273177	3.149345809	0.00269	0.033864708	-2.03718885	DNA repair protein-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0099880.2	1.839223161	1.089601057	2.974813334	0.00441	0.041702155	-2.03726711	caspase-6 protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0471060.1	0.793411069	5.409891759	3.211406304	0.00225	0.031545502	-2.03739805	topoisomerase 6 subunit B	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.7HG0652090.1	1.562525304	2.809206881	2.990464023	0.00422	0.040887644	-2.03785072	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0723540.1	-0.954100183	3.755359913	-3.317646652	0.00164	0.028035058	-2.03846759	Cinnamoyl-CoA reductase family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0217620.1	0.871340955	4.501749172	3.10731828	0.00303	0.03590208	-2.03973234	Pentatricopeptide repeat-containing family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0381080.1	0.838831122	2.763058409	3.059808538	0.00347	0.037761197	-2.03977168	Fe/S biogenesis protein nfuA	elongation zone	12 h
HORVU.MOREX.r3.6HG0620520.1	-0.627597106	3.094519972	-3.307047388	0.0017	0.028288147	-2.04004377	Aminotransferase-related family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0397940.1	0.673610665	3.598811101	3.157172736	0.00263	0.033716726	-2.0405278	Alpha-L-fucosidase 2	elongation zone	12 h
HORVU.MOREX.r3.7HG0724090.1	2.030323108	0.704867316	2.974702572	0.00441	0.041702155	-2.04112952	RING/U-box superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0607360.1	0.564019848	4.502873455	3.177520544	0.00248	0.032834207	-2.0417192	WAT1-related protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0479520.1	3.250399284	3.438825405	2.965396346	0.00452	0.042347835	-2.04400335	DNA mismatch repair protein MutS	elongation zone	12 h
HORVU.MOREX.r3.2HG0182220.1	1.989149063	1.158860243	2.963958354	0.00454	0.04241279	-2.04538683	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0626980.1	2.115976167	-1.590959919	2.996306248	0.00415	0.040512048	-2.04604321	DNA topoisomerase 2	elongation zone	12 h
HORVU.MOREX.r3.6HG0555700.1	0.367696615	8.875975145	3.432800022	0.00117	0.025668159	-2.04613132	Calreticulin/calnexin	elongation zone	12 h
HORVU.MOREX.r3.7HG0701910.1	0.963597551	5.137401888	3.167832282	0.00255	0.03318302	-2.04634802	RNA binding protein, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0407060.1	0.39061983	7.117015257	3.329968533	0.00159	0.027768577	-2.04748106	Cysteine--tRNA ligase	elongation zone	12 h
HORVU.MOREX.r3.1HG0057980.1	1.864758059	0.759657688	2.963543166	0.00455	0.04241279	-2.04878264	Sugar transporter, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0719480.1	1.002874789	4.687776647	3.140483133	0.00276	0.034208419	-2.04951961	Ribosomal RNA small subunit methyltransferase B	elongation zone	12 h
HORVU.MOREX.r3.7HG0709230.1	2.604818496	0.345142249	2.971716099	0.00444	0.041953879	-2.05088937	50S ribosomal protein L10	elongation zone	12 h
HORVU.MOREX.r3.7HG0735450.1	0.907225051	2.173354891	3.003222927	0.00407	0.040229538	-2.05130169	Small nuclear ribonucleoprotein	elongation zone	12 h
HORVU.MOREX.r3.1HG0065530.1	1.110268532	8.837409506	3.342393579	0.00153	0.027394605	-2.05141552	Cold shock protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0242830.1	2.027614179	-0.152434766	2.978246181	0.00436	0.041506896	-2.05190612	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0244010.1	0.555740157	4.561972282	3.158088038	0.00262	0.033716726	-2.05253456	Kinase superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0239970.1	1.897354341	4.731301793	3.062943224	0.00344	0.03764455	-2.05335821	Zinc-finger domain of monoamine-oxidase A repressor R1, putati	elongation zone	12 h
HORVU.MOREX.r3.1HG0092480.1	2.220149559	4.164362454	2.986655001	0.00426	0.041089957	-2.05346677	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0146330.1	0.958610886	8.982026161	3.354889066	0.00147	0.027227922	-2.05447387	Ribosomal protein L15	elongation zone	12 h
HORVU.MOREX.r3.6HG0542950.1	1.173904894	6.71326239	3.23543799	0.00209	0.030742864	-2.05755568	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0277390.1	1.722381585	3.530687581	3.001043335	0.0041	0.040265883	-2.05774532	Exosome complex component rrp4	elongation zone	12 h
HORVU.MOREX.r3.7HG0640730.1	2.058626598	-0.0905309	2.968851265	0.00448	0.042098534	-2.05883045	Methionine S-methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0635000.1	1.2210249	3.997366286	3.038322977	0.00369	0.038671495	-2.05984442	Kelch repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0320550.1	0.996701232	0.545189534	2.999711778	0.00411	0.040307075	-2.06005288	DUF241 domain protein, putative (DUF241)	elongation zone	12 h
HORVU.MOREX.r3.5HG0498150.1	1.005250588	5.564120273	3.198362435	0.00233	0.031954117	-2.06005942	2-keto-3-deoxy-L-rhamnonate aldolase	elongation zone	12 h
HORVU.MOREX.r3.1HG0022820.1	1.104556243	6.444771319	3.218943817	0.0022	0.031443869	-2.06147565	Translocase of chloroplast 159, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.5HG0505220.1	0.797887831	2.286205005	3.035335582	0.00372	0.038738812	-2.06150297	#N/A	elongation zone	12 h
HORVU.MOREX.r3.1HG0057620.1	0.681794992	6.017315999	3.255507952	0.00198	0.029636522	-2.06252929	Kinase like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0224450.1	0.516114757	8.858079699	3.377349028	0.00138	0.026563254	-2.06263232	Eukaryotic translation initiation factor 3 subunit A	elongation zone	12 h
HORVU.MOREX.r3.3HG0238180.1	0.406473549	4.144586965	3.197027161	0.00234	0.031997794	-2.0627373	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0183430.1	0.601949455	5.136892041	3.200193466	0.00232	0.031903923	-2.06347843	Mitochondrial carrier protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0288660.1	1.852839739	4.962352093	3.084104735	0.00324	0.036928455	-2.06365135	Dynamin-like	elongation zone	12 h
HORVU.MOREX.r3.1HG0087580.1	1.575732398	0.956329379	2.95804543	0.00462	0.042747009	-2.06436736	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0137600.1	1.409294069	0.781391696	2.955155396	0.00465	0.042962871	-2.06526581	Peptide chain release factor, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0219180.1	-0.647179777	2.142648299	-3.204412616	0.00229	0.031849386	-2.06554984	Adenine nucleotide alpha hydrolases-like superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0335300.1	-0.379727831	5.365809149	-3.300525854	0.00173	0.028397697	-2.06631493	Protein ENHANCED DISEASE RESISTANCE 2	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.5HG0530720.1	0.743843522	3.050857477	3.066468749	0.00341	0.037432489	-2.0680446	DNA ligase-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0616790.1	0.540627176	7.277734621	3.320349328	0.00163	0.027974391	-2.07083917	Transport inhibitor response 1-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0195910.1	-0.66128342	2.102421817	-3.301259451	0.00173	0.028397697	-2.07299822	Protease inhibitor/seed storage/lipid transfer family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0000630.1	1.2833122	7.118166762	3.232972296	0.00211	0.030854536	-2.07435669	RING-finger E3 ubiquitin ligase, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0564630.1	0.572634907	3.887737518	3.154484644	0.00265	0.033840457	-2.07437337	5'-nucleotidase SurE	elongation zone	12 h
HORVU.MOREX.r3.2HG0209800.1	0.571004237	3.215079802	3.086028031	0.00322	0.036928455	-2.07441065	Elongation factor 1-alpha	elongation zone	12 h
HORVU.MOREX.r3.6HG0621690.1	0.518847361	4.664752545	3.182433388	0.00244	0.032683152	-2.07445566	E3 ubiquitin-protein ligase	elongation zone	12 h
HORVU.MOREX.r3.5HG0427090.1	2.4155895	1.115796108	2.957942211	0.00462	0.042747009	-2.07498995	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0173120.1	-0.560595997	5.602428159	-3.384147896	0.00135	0.026498466	-2.07512168	Aldose 1-epimerase	elongation zone	12 h
HORVU.MOREX.r3.5HG0503070.1	1.088876191	2.533422681	2.993929089	0.00418	0.040647009	-2.07566176	RNA binding protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0335110.1	0.871642321	5.132212442	3.173984458	0.0025	0.03299418	-2.07575256	BHLH family protein, putative, expressed	elongation zone	12 h
HORVU.MOREX.r3.5HG0488160.1	1.549190382	2.826332785	3.012978426	0.00396	0.039818139	-2.07608849	Dicarboxylate transporter 2.1, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.2HG0126050.1	0.761745574	6.555399703	3.236654723	0.00209	0.030699736	-2.07614722	30S ribosomal protein S3	elongation zone	12 h
HORVU.MOREX.r3.3HG0242050.1	1.956369722	3.962990486	2.988085154	0.00425	0.04102313	-2.07824499	Alpha/beta-Hydrolases superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0510770.1	1.40538738	4.300400413	3.039894598	0.00367	0.038641262	-2.0785931	Protein-lysine N-methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0125780.1	1.266764621	0.405475347	2.953621498	0.00467	0.043107427	-2.07953629	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0173230.1	1.680893866	1.507460003	2.949005019	0.00473	0.043487212	-2.08047537	RAN guanine nucleotide release factor	elongation zone	12 h
HORVU.MOREX.r3.7HG0678440.1	2.354237576	0.782612295	2.96795077	0.00449	0.042132428	-2.08296386	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0067140.1	-3.375826458	1.103422222	-2.992828985	0.00419	0.040685115	-2.08577278	Wound-induced protease inhibitor	elongation zone	12 h
HORVU.MOREX.r3.2HG0187970.1	1.400917779	4.77957446	3.079855984	0.00328	0.036983216	-2.08589262	Cyclin	elongation zone	12 h
HORVU.MOREX.r3.4HG0392430.1	1.345804522	2.568155848	2.968191393	0.00449	0.042132428	-2.08595037	4-hydroxy-tetrahydrodipicolinate reductase	elongation zone	12 h
HORVU.MOREX.r3.5HG0515030.1	0.561430394	4.511137793	3.172446241	0.00251	0.033037412	-2.0861361	Obg-like ATPase 1	elongation zone	12 h
HORVU.MOREX.r3.3HG0284290.1	1.146344329	6.057281649	3.170711377	0.00253	0.033099534	-2.08670206	Mitochondrial processing peptidase	elongation zone	12 h
HORVU.MOREX.r3.7HG0649950.1	-0.517679198	3.836694774	-3.233833586	0.0021	0.030821023	-2.08692029	Nudix hydrolase	elongation zone	12 h
HORVU.MOREX.r3.6HG0605640.1	1.39160131	4.881506983	3.095158303	0.00314	0.036539994	-2.08710103	Ubiquitin carboxyl-terminal hydrolase-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0302570.1	-2.098302178	-3.210356093	-2.962910586	0.00456	0.04244798	-2.08839219	Laccase	elongation zone	12 h
HORVU.MOREX.r3.5HG0493400.1	1.619602529	1.705240672	2.948369398	0.00474	0.043524966	-2.08848882	tRNA-splicing endonuclease subunit SEN54	elongation zone	12 h
HORVU.MOREX.r3.2HG0183750.1	2.013013363	1.148914994	2.94545981	0.00478	0.043696105	-2.08984219	Transcription factor tfiiic, tau55-like protein, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0173550.1	0.777051278	7.816521867	3.308571186	0.00169	0.028279404	-2.0911123	Prohibitin	elongation zone	12 h
HORVU.MOREX.r3.5HG0535060.1	2.125065002	1.687849838	2.943098328	0.00481	0.043773947	-2.09214979	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0711890.1	-0.915948832	2.553034049	-3.246096645	0.00203	0.030276719	-2.09314464	O-methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0507920.1	0.728159155	10.41613396	3.424777187	0.00119	0.02575668	-2.09400804	60S ribosomal protein L5	elongation zone	12 h
HORVU.MOREX.r3.3HG0234950.1	1.901205322	2.174772641	2.946066662	0.00477	0.043696105	-2.0963198	Multidrug resistance 3	elongation zone	12 h
HORVU.MOREX.r3.6HG0614110.1	-0.444665409	4.183035474	-3.308034169	0.00169	0.028279404	-2.09692052	nucleolar GTP-binding protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0528860.1	1.957230528	5.888709477	3.101021285	0.00309	0.036198029	-2.09838193	Pumilio	elongation zone	12 h
HORVU.MOREX.r3.2HG0193700.1	2.87064665	-2.231369651	2.972134807	0.00444	0.041943564	-2.09862599	Glucan endo-1,3-beta-glucosidase	elongation zone	12 h
HORVU.MOREX.r3.3HG0291310.1	1.873599411	-0.134112607	2.951674515	0.0047	0.043263203	-2.09891881	Acetamidase/formamidase, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0280080.1	0.783587557	5.980620424	3.217566551	0.00221	0.031443869	-2.099079	50S ribosomal protein L15, putative, expressed	elongation zone	12 h
HORVU.MOREX.r3.5HG0476620.1	1.019012431	3.286126116	3.024890891	0.00383	0.03925602	-2.10042626	Protein SCO1, mitochondrial-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0061750.1	0.825644694	5.583468809	3.18491801	0.00243	0.032575632	-2.10136907	Chlorophyll synthase	elongation zone	12 h
HORVU.MOREX.r3.7HG0745340.1	1.081972822	7.247395442	3.256816628	0.00197	0.029636522	-2.10171384	30S ribosomal protein S5	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.4HG0370780.1	0.50022066	8.874988886	3.375716301	0.00138	0.026563254	-2.10365734	T-complex protein 1 subunit theta	elongation zone	12 h
HORVU.MOREX.r3.5HG0536240.1	-0.786361529	0.742329041	-3.092112109	0.00317	0.036688668	-2.10376384	Beta-fructofuranosidase, insoluble protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0066370.1	2.367068988	5.852246704	3.08537556	0.00323	0.036928455	-2.10380544	Glutathione S-transferase	elongation zone	12 h
HORVU.MOREX.r3.1HG0006230.1	0.417570967	5.574000008	3.254262705	0.00198	0.029691287	-2.10436104	Disease resistance protein RPM1	elongation zone	12 h
HORVU.MOREX.r3.1HG0065370.1	0.670128057	5.483156066	3.21683202	0.00221	0.031443869	-2.10553307	TPX2 (Targeting protein for Xklp2) family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0109530.1	-0.285313523	6.710852914	-3.364647523	0.00143	0.026979742	-2.10644992	Protein phosphatase 2C-like	elongation zone	12 h
HORVU.MOREX.r3.7HG0751130.1	2.277606029	-0.911602578	2.964584255	0.00453	0.042404918	-2.10692377	Ubiquitin carboxyl-terminal hydrolase 38	elongation zone	12 h
HORVU.MOREX.r3.2HG0160550.1	2.144311073	2.252307779	2.937849142	0.00488	0.044199271	-2.10793266	At4g33800-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0196710.1	1.27981585	4.927717077	3.080615516	0.00327	0.036983216	-2.10906448	Ribosome biogenesis protein BRX1-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0557080.1	1.573002231	6.140814891	3.134809894	0.0028	0.034437001	-2.10921426	Protein arginine N-methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.1HG0058530.1	1.055116627	2.661369894	3.024525409	0.00383	0.03925602	-2.10939542	Small nuclear ribonucleoprotein family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0667140.1	1.026603044	6.545087438	3.208016318	0.00227	0.031692167	-2.11027334	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0573070.1	1.397165107	3.004821099	2.96469277	0.00453	0.042404918	-2.11053751	MLO-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0619410.1	-0.769958523	1.820333919	-3.180839126	0.00245	0.032706849	-2.11075791	Flavonol synthase	elongation zone	12 h
HORVU.MOREX.r3.1HG0080750.1	1.792758606	5.902530715	3.104485558	0.00306	0.036052722	-2.1108203	Phosphoribosylformylglycinamidine synthase family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0706580.1	0.873462395	4.99575294	3.148099671	0.0027	0.033864708	-2.11234568	WD40 repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0711410.1	1.143605932	5.613777061	3.168368652	0.00254	0.033171389	-2.11240771	60S ribosomal protein L37a	elongation zone	12 h
HORVU.MOREX.r3.6HG0609720.1	0.618286162	3.853973881	3.123278535	0.0029	0.035162818	-2.11280976	Glucosamine 6-phosphate N-acetyltransferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0466320.1	-0.310574002	6.324949057	-3.313122906	0.00167	0.028155399	-2.11289487	Phosphoinositide phospholipase C	elongation zone	12 h
HORVU.MOREX.r3.2HG0123890.1	1.0627663	8.179504177	3.287260006	0.0018	0.028691351	-2.11293394	40S ribosomal protein S6	elongation zone	12 h
HORVU.MOREX.r3.1HG0086390.1	-0.807705644	-0.260888993	-3.156063515	0.00264	0.033771061	-2.11316877	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0596310.1	0.817704169	8.298151592	3.318695482	0.00164	0.028033028	-2.11565295	60S ribosomal protein L14, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0412170.1	0.8059807	9.2702411	3.362113754	0.00144	0.02703001	-2.11584083	60S ribosomal protein L21	elongation zone	12 h
HORVU.MOREX.r3.7HG0731150.1	1.859218618	4.133250031	2.981254578	0.00433	0.041308987	-2.11632466	F-box and JmjC domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0597130.1	0.916440949	4.149561941	3.069446369	0.00338	0.037331432	-2.11634002	Replication protein A subunit	elongation zone	12 h
HORVU.MOREX.r3.1HG0084680.1	1.940615311	6.696342312	3.150358559	0.00268	0.033864708	-2.11638309	Nucleolar family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0312220.1	1.024509771	4.580442378	3.073559231	0.00334	0.037245743	-2.11818743	Histone-lysine N-methyltransferase, H3 lysine-9 specific	elongation zone	12 h
HORVU.MOREX.r3.5HG0427060.1	0.966933541	5.128578703	3.153766925	0.00265	0.033864708	-2.11880283	50S ribosomal protein L14	elongation zone	12 h
HORVU.MOREX.r3.3HG0298340.1	0.777507118	4.243388819	3.102972293	0.00307	0.036128346	-2.11885751	Beta-galactosidase	elongation zone	12 h
HORVU.MOREX.r3.3HG0237590.1	1.447131086	4.756362292	3.052364293	0.00354	0.037882054	-2.11898042	ATP-dependent RNA helicase	elongation zone	12 h
HORVU.MOREX.r3.2HG0178630.1	2.350094012	3.452461861	2.945548447	0.00478	0.043696105	-2.11921848	DNA mismatch repair protein mutS	elongation zone	12 h
HORVU.MOREX.r3.7HG0704390.1	0.594795308	7.743233053	3.308158105	0.00169	0.028279404	-2.1199122	40S ribosomal protein S13	elongation zone	12 h
HORVU.MOREX.r3.7HG0682130.1	0.797678299	5.527659552	3.170004569	0.00253	0.033099534	-2.12005611	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0542970.1	0.827944026	4.467056131	3.147006181	0.00271	0.033864708	-2.12159214	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.6HG0569630.1	1.535856622	4.808423924	3.062603759	0.00344	0.03764455	-2.12233335	DNA-directed RNA polymerase subunit beta	elongation zone	12 h
HORVU.MOREX.r3.6HG0625860.1	0.679208124	4.74429219	3.123739798	0.00289	0.035147457	-2.12243374	CobW-domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0315120.1	2.282648031	0.551320449	2.945046229	0.00479	0.043697279	-2.12329952	Ribonuclease P/MRP protein subunit POP5	elongation zone	12 h
HORVU.MOREX.r3.1HG0090330.1	1.183159684	3.818381072	3.014154662	0.00395	0.039746874	-2.12553915	Aldose 1-epimerase-like	elongation zone	12 h
HORVU.MOREX.r3.3HG0305790.1	0.867390699	6.433470179	3.224747085	0.00216	0.031159303	-2.12622072	Pentatricopeptide repeat protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0461830.1	1.051449648	1.937434209	2.956342005	0.00464	0.042860101	-2.12629019	F-box/kelch-repeat protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0273130.1	0.682430886	5.87661788	3.200673833	0.00232	0.031894634	-2.13005362	Extra-large G-protein-like	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.4HG0344830.1	0.442692961	4.535567699	3.203118567	0.0023	0.031887924	-2.13064922	NBS-LRR disease resistance protein, putative, expressed	elongation zone	12 h
HORVU.MOREX.r3.7HG0726360.1	-0.295771045	5.450154375	-3.273026022	0.00188	0.028923495	-2.13239046	12-oxophytodienoate reductase	elongation zone	12 h
HORVU.MOREX.r3.6HG0619290.1	1.329604511	3.250452134	3.028668412	0.00379	0.039108923	-2.13348769	Glutaredoxin-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0600220.1	0.904161051	5.927792261	3.173343165	0.00251	0.03299418	-2.13378324	3-isopropylmalate dehydratase small subunit	elongation zone	12 h
HORVU.MOREX.r3.3HG0236160.1	0.612581313	4.863001087	3.147396792	0.0027	0.033864708	-2.13476289	Transcription factor, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0246560.1	0.609718985	5.025368236	3.143253799	0.00274	0.034060761	-2.1348304	Multiprotein-bridging factor, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0527340.1	2.016785111	-0.841855617	2.946576962	0.00477	0.04368319	-2.13538302	DNA-directed RNA polymerase subunit	elongation zone	12 h
HORVU.MOREX.r3.3HG0297400.1	2.575622397	0.76599868	2.928531968	0.00501	0.044779816	-2.13634401	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0082750.1	1.673796478	0.305019362	2.923020941	0.00509	0.045226145	-2.13693549	Ring finger protein, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0517610.1	1.469173376	4.899893762	3.054411711	0.00352	0.037808566	-2.13706699	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0646060.1	1.63321774	4.424298678	2.987723049	0.00425	0.04102761	-2.1394188	Receptor-like protein kinase	elongation zone	12 h
HORVU.MOREX.r3.2HG0119870.1	0.912473858	2.245991143	2.960905522	0.00458	0.042615343	-2.13970226	Methyltransferase family protein, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0661890.1	0.497848527	7.9160487	3.350392863	0.00149	0.027239638	-2.14103121	3-oxoacyl-[acyl-carrier-protein] synthase	elongation zone	12 h
HORVU.MOREX.r3.5HG0424490.1	2.367041664	-0.073596929	2.957066606	0.00463	0.042812485	-2.14380923	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0196140.1	0.356427435	5.377901779	3.235664006	0.00209	0.030742864	-2.14556568	Ras-related protein Rab-8B	elongation zone	12 h
HORVU.MOREX.r3.6HG0608180.1	-0.891621293	0.307405102	-3.062609238	0.00344	0.03764455	-2.14778296	Protein MIZU-KUSSEI 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0194310.1	1.612816839	7.045455879	3.188111663	0.0024	0.032414492	-2.14837676	Midasin	elongation zone	12 h
HORVU.MOREX.r3.7HG0714910.1	0.584632921	7.216849728	3.305730749	0.0017	0.028288147	-2.15082905	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0305290.1	1.807124267	1.243753956	2.916972146	0.00517	0.045490951	-2.15083308	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0380980.1	1.021205617	4.039743688	3.04193472	0.00365	0.0386017	-2.1522853	30S ribosomal protein S1	elongation zone	12 h
HORVU.MOREX.r3.7HG0720790.1	0.900041605	3.444490231	3.018714453	0.0039	0.039510918	-2.15407406	Myb family transcription factor family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0310640.1	-0.626855199	2.038725307	-3.258902654	0.00196	0.029571063	-2.15513528	Sulfotransferase	elongation zone	12 h
HORVU.MOREX.r3.6HG0615360.1	1.519973951	2.604486893	2.966860685	0.00451	0.042233448	-2.15550124	Geranylgeranyl reductase	elongation zone	12 h
HORVU.MOREX.r3.5HG0434210.1	1.674218279	2.431638709	2.923173144	0.00509	0.045226145	-2.15561596	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0513380.1	1.512039694	2.861847727	2.936288963	0.0049	0.044321273	-2.15569425	RNA-binding protein-like	elongation zone	12 h
HORVU.MOREX.r3.6HG0618690.1	1.526832417	4.702412058	3.011743659	0.00397	0.03986915	-2.15718028	DNA-binding storekeeper protein-related transcriptional regulat	elongation zone	12 h
HORVU.MOREX.r3.3HG0246190.1	1.057414556	1.250282278	3.039299085	0.00368	0.038641262	-2.15838347	Cationic amino acid transporter	elongation zone	12 h
HORVU.MOREX.r3.5HG0536500.1	0.745089958	5.276862926	3.114654074	0.00297	0.035453096	-2.15852348	ATP-dependent DNA helicase 2 subunit KU80	elongation zone	12 h
HORVU.MOREX.r3.6HG0564690.1	-0.405320666	5.759195311	-3.315215224	0.00166	0.028097383	-2.15886757	Regulator of Vps4 activity in the MVB pathway protein, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0638370.3	-0.451616422	6.33021084	-3.348790009	0.0015	0.027239638	-2.16348578	Membrane protein of er body-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0335680.1	-0.634198095	1.198730266	-3.041486154	0.00366	0.0386017	-2.16349677	Protein yippee-like	elongation zone	12 h
HORVU.MOREX.r3.5HG0507610.1	1.205052735	4.190859194	3.006622855	0.00403	0.040178373	-2.16372452	Elongation factor G	elongation zone	12 h
HORVU.MOREX.r3.6HG0556130.1	1.580081363	0.544616443	2.913382245	0.00522	0.045731286	-2.16450088	cytomegalovirus UL139 protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0430050.1	-0.560300028	4.495639375	-3.200782633	0.00232	0.031894634	-2.16451603	Stomatal closure-related actin-binding protein 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0745890.1	0.904661915	4.093881544	3.049316907	0.00358	0.038090743	-2.1647783	Elongator complex protein 4	elongation zone	12 h
HORVU.MOREX.r3.3HG0315210.1	2.199490287	-0.621766802	2.922466226	0.0051	0.045240439	-2.16628563	F-box family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0388770.1	0.83802273	6.564233193	3.200775947	0.00232	0.031894634	-2.16639778	Protein TOC75-3, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.4HG0411400.1	1.440583033	4.951130643	3.071592668	0.00336	0.037271777	-2.16691807	eisosome protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0105680.3	0.972635593	4.721414669	3.102221595	0.00308	0.036136245	-2.16778046	Translation initiation factor IF-2	elongation zone	12 h
HORVU.MOREX.r3.2HG0165110.1	-0.821019484	3.128473967	-3.159909515	0.00261	0.033615353	-2.16827757	Acetyl-coenzyme A synthetase	elongation zone	12 h
HORVU.MOREX.r3.1HG0064870.1	2.02698732	0.288676864	2.91378545	0.00522	0.045722475	-2.16865214	Pentatricopeptide repeat-containing protein	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0249790.1	0.683757417	6.336137063	3.216880531	0.00221	0.031443869	-2.16937246	Exportin-2	elongation zone	12 h
HORVU.MOREX.r3.3HG0309340.1	2.721059844	0.362849458	2.91610103	0.00519	0.045568238	-2.17161152	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0018810.1	0.740788894	5.360038976	3.14686191	0.00271	0.033864708	-2.17246015	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0292680.1	-0.696467591	2.459132616	-3.214251791	0.00223	0.031484433	-2.17248382	Replicase polyprotein 1a	elongation zone	12 h
HORVU.MOREX.r3.4HG0345340.1	-0.33029701	5.038124181	-3.263321909	0.00193	0.029341049	-2.17273643	Basic-leucine zipper (bZIP) transcription factor family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0502360.1	1.329209779	1.108342302	2.919788063	0.00513	0.045371176	-2.17322014	DNA-directed RNA polymerase subunit alpha	elongation zone	12 h
HORVU.MOREX.r3.6HG0551750.1	0.83374449	4.011205702	3.054342511	0.00352	0.037808566	-2.17359503	General transcription factor IIH subunit, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0210420.1	0.445677043	7.910636809	3.32748501	0.0016	0.027806246	-2.17488265	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase s	elongation zone	12 h
HORVU.MOREX.r3.4HG0333450.1	-0.515700817	3.618972788	-3.150232673	0.00268	0.033864708	-2.17807599	Type I inositol-1,4,5-trisphosphate 5-phosphatase CVP2	elongation zone	12 h
HORVU.MOREX.r3.3HG0299370.1	1.398384676	6.44411695	3.166804894	0.00256	0.033218309	-2.1795015	DNA polymerase	elongation zone	12 h
HORVU.MOREX.r3.5HG0435800.1	1.830471823	0.267695951	2.904601238	0.00535	0.046230732	-2.17979449	Leucine-rich repeat protein kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0512540.1	-0.269491756	5.508031516	-3.274282224	0.00187	0.028923495	-2.18196739	Prolyl 4-hydroxylase alpha subunit, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0207000.1	0.811976897	5.903816857	3.147614848	0.0027	0.033864708	-2.18249579	RNA binding protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0003620.1	-0.619013368	2.573512603	-3.133236654	0.00282	0.034551409	-2.18289139	Protein ZINC INDUCED FACILITATOR-LIKE 1	elongation zone	12 h
HORVU.MOREX.r3.1HG0061850.1	0.69606166	8.584058175	3.311638496	0.00167	0.028232736	-2.18299239	Methionine aminopeptidase 2	elongation zone	12 h
HORVU.MOREX.r3.6HG0597360.1	0.492954474	5.075212238	3.162518401	0.00259	0.033483118	-2.18305298	SET domain-containing protein 9	elongation zone	12 h
HORVU.MOREX.r3.1HG0063790.1	1.427912575	3.096652959	2.94182019	0.00483	0.043890279	-2.18338372	Sister chromatid cohesion 1 protein 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0174320.1	2.885712424	4.916755342	2.96299401	0.00455	0.04244798	-2.18548216	Kinesin-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0280610.1	0.546198489	6.601541701	3.231693631	0.00212	0.030866089	-2.1855176	Splicing factor 3A subunit 3	elongation zone	12 h
HORVU.MOREX.r3.7HG0744540.1	2.112785902	-0.407648584	2.905691325	0.00534	0.04618095	-2.18782606	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.1HG0093060.1	-0.535815937	4.965521065	-3.297529886	0.00175	0.02840648	-2.19034364	Extra-large G-protein-like	elongation zone	12 h
HORVU.MOREX.r3.5HG0454920.1	0.645586991	3.842449	3.068444669	0.00339	0.037343384	-2.19077419	RNA polymerase II subunit A C-terminal domain phosphatase SSU	elongation zone	12 h
HORVU.MOREX.r3.6HG0618170.1	0.27450393	6.062292159	3.242440988	0.00205	0.030425122	-2.19158352	1-aminocyclopropane-1-carboxylate deaminase/D-cysteine desu	elongation zone	12 h
HORVU.MOREX.r3.5HG0444920.1	0.656449317	5.104322172	3.132321445	0.00282	0.034584718	-2.19227377	Uveal autoantigen with coiled-coil domains and ankyrin repeats i	elongation zone	12 h
HORVU.MOREX.r3.4HG0341950.1	1.449947115	5.083003475	3.037215193	0.0037	0.038671495	-2.19238128	Exosome complex component	elongation zone	12 h
HORVU.MOREX.r3.2HG0150290.1	0.637520356	8.717704517	3.320792146	0.00163	0.02796111	-2.19280283	30S ribosomal protein S19	elongation zone	12 h
HORVU.MOREX.r3.7HG0725460.1	1.715981507	1.80349634	2.905818448	0.00533	0.04618095	-2.19300455	RNA-binding (RRM/RBD/RNP motifs) family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0025500.2	0.750009134	5.09562282	3.148429067	0.0027	0.033864708	-2.19433092	Arginine--tRNA ligase	elongation zone	12 h
HORVU.MOREX.r3.3HG0223960.1	1.198448361	2.937552338	2.927182672	0.00503	0.044862884	-2.19467382	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0628790.1	-0.708927991	2.686977072	-3.069454898	0.00338	0.037331432	-2.19496869	Myb-like transcription factor family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0290220.1	2.781249547	4.744100239	2.960516311	0.00459	0.042615343	-2.19561629	Nucleobase-ascorbate transporter-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0572880.1	0.677216355	6.302994109	3.183336355	0.00244	0.03261914	-2.1975852	Alpha/beta-Hydrolases superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0309000.1	0.783842918	3.431372321	3.000264042	0.0041	0.040307075	-2.1983204	snRNA-activating protein complex subunit	elongation zone	12 h
HORVU.MOREX.r3.3HG0310880.1	1.973317232	0.788604478	2.895173314	0.00549	0.046765582	-2.19897793	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0295850.1	1.609314137	4.42296407	2.993154332	0.00419	0.040685115	-2.19986333	U3 small nucleolar RNA-associated protein 11	elongation zone	12 h
HORVU.MOREX.r3.3HG0226750.1	-0.53703631	2.949436288	-3.300442799	0.00173	0.028397697	-2.200668	GDSL esterase/lipase	elongation zone	12 h
HORVU.MOREX.r3.1HG0051810.1	2.25608808	3.342547612	2.911151714	0.00526	0.045859795	-2.20185807	Glutathione S-transferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0265190.1	0.540318501	6.392012157	3.21343482	0.00223	0.031515925	-2.20253125	Exonuclease 3'-5' domain-containing protein 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0712610.1	0.565503236	8.251441205	3.313554426	0.00166	0.028155399	-2.20359163	Elongation factor G	elongation zone	12 h
HORVU.MOREX.r3.3HG0252240.1	0.861572603	7.225249207	3.244340405	0.00204	0.030344376	-2.20516122	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.2HG0145780.1	2.087711078	-0.995256061	2.904670482	0.00535	0.046230732	-2.20531261	Cinnamoyl-CoA reductase family protein	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0246500.1	-0.768614772	3.040521827	-3.289217346	0.00179	0.028656416	-2.20657319	Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A	elongation zone	12 h
HORVU.MOREX.r3.2HG0180060.1	1.229438208	1.155123868	2.896355057	0.00547	0.046711054	-2.20764981	Receptor-kinase, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0594100.1	2.520825687	2.846373641	2.894101319	0.00551	0.046806243	-2.20830044	H/ACA ribonucleoprotein complex non-core subunit NAF1	elongation zone	12 h
HORVU.MOREX.r3.7HG0648190.1	1.439825943	4.830917175	3.001725185	0.00409	0.040265883	-2.20849887	F-box family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0083320.1	1.485998598	6.710998818	3.145380041	0.00272	0.033887701	-2.20854348	Threonine synthase	elongation zone	12 h
HORVU.MOREX.r3.2HG0178560.2	1.749762628	3.749491986	2.957957347	0.00462	0.042747009	-2.2090637	LA RNA-binding protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0312020.1	-0.394709051	6.244935241	-3.348312616	0.0015	0.027239638	-2.21090975	glycosyltransferase family exostosin protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0286070.1	1.844419595	0.985153469	2.889141253	0.00558	0.047136585	-2.2118841	Pleiotropic drug resistance ABC transporter	elongation zone	12 h
HORVU.MOREX.r3.3HG0316860.1	1.660544183	0.949417462	2.889128983	0.00558	0.047136585	-2.21215991	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0339290.1	1.574426636	5.458049088	3.055686077	0.00351	0.037808566	-2.21248968	ATP dependent RNA helicase	elongation zone	12 h
HORVU.MOREX.r3.1HG0043060.1	1.800835406	1.58085499	2.888225006	0.0056	0.047175894	-2.21426803	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0058050.1	0.572747785	5.246817852	3.168404492	0.00254	0.033171389	-2.21459844	8-amino-7-oxononanoate synthase	elongation zone	12 h
HORVU.MOREX.r3.6HG0590960.1	1.94980183	0.923831685	2.887815887	0.0056	0.047190057	-2.21605617	NAC domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0258630.1	1.5076939	6.575402356	3.130372957	0.00284	0.034669947	-2.21710878	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0134300.1	1.900723637	1.307766187	2.886663147	0.00562	0.04722308	-2.21724321	Skp1, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0729090.1	1.149909236	1.917852249	2.898000902	0.00545	0.046636203	-2.21777534	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0015750.1	-1.44040578	-2.912149854	-2.933371328	0.00494	0.044514543	-2.21848572	transcription factor, putative (Protein of unknown function, DUF	elongation zone	12 h
HORVU.MOREX.r3.5HG0522770.1	0.824701905	9.471285898	3.331713308	0.00158	0.02769762	-2.21911844	30S ribosomal protein S5	elongation zone	12 h
HORVU.MOREX.r3.2HG0193220.1	0.660836492	4.020109938	3.056042948	0.00351	0.037808566	-2.21985127	Putrescine-binding periplasmic protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0383780.1	-1.735090175	-0.062687302	-3.08900952	0.00319	0.036827029	-2.22040415	Laccase	elongation zone	12 h
HORVU.MOREX.r3.3HG0302050.1	2.189760715	0.747970046	2.887942114	0.0056	0.047190057	-2.22124049	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0084890.1	-0.635883785	1.342406063	-3.107115368	0.00303	0.035902171	-2.22213536	Protein DETOXIFICATION	elongation zone	12 h
HORVU.MOREX.r3.3HG0243220.1	2.36333043	1.638276816	2.883411648	0.00567	0.047427345	-2.22648321	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0525230.1	0.872093551	2.592012409	2.926758719	0.00504	0.044862884	-2.22656172	Glucose-1-phosphate adenylyltransferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0504160.1	1.073974377	6.884631382	3.209923508	0.00226	0.031600255	-2.22695957	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0550430.1	0.853436989	5.615355597	3.132092647	0.00282	0.034584718	-2.22714949	50S ribosomal protein L4	elongation zone	12 h
HORVU.MOREX.r3.3HG0224510.1	-3.116507893	-2.729166608	-2.905391556	0.00534	0.046199549	-2.22791688	O-methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.4HG0401530.2	0.897375312	3.547060924	3.021714551	0.00386	0.039354132	-2.22815709	evolutionarily conserved C-terminal region 2	elongation zone	12 h
HORVU.MOREX.r3.5HG0472880.1	0.488383975	4.87983831	3.151759747	0.00267	0.033864708	-2.2292235	GDP-mannose transporter, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0333040.1	-0.583305297	3.140672069	-3.196041873	0.00235	0.032009236	-2.23012051	Ankyrin repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0075590.1	0.255489545	8.23086424	3.348470826	0.0015	0.027239638	-2.23112837	Coiled-coil domain-containing protein 47	elongation zone	12 h
HORVU.MOREX.r3.7HG0689220.1	0.809500216	8.338861275	3.272135425	0.00188	0.028935564	-2.23284249	Ribosomal protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0640980.1	2.178049671	5.107500163	2.986244585	0.00427	0.041090601	-2.23357612	Histone-lysine N-methyltransferase, H3 lysine-36 specific	elongation zone	12 h
HORVU.MOREX.r3.2HG0135860.1	0.424564003	5.818016201	3.18526106	0.00242	0.032575632	-2.23422506	Transcription factor jumonji domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0393080.1	1.069969998	5.199963551	3.084169461	0.00324	0.036928455	-2.23656191	Translocase of chloroplast	elongation zone	12 h
HORVU.MOREX.r3.5HG0513020.1	0.312561365	6.516881897	3.263078166	0.00193	0.029341049	-2.23760849	Transmembrane protein 147	elongation zone	12 h
HORVU.MOREX.r3.4HG0382670.1	-0.731048261	0.489338732	-3.160778558	0.0026	0.033587945	-2.23820591	Xyloglucan 6-xylosyltransferase 1	elongation zone	12 h
HORVU.MOREX.r3.6HG0576550.1	0.410575492	4.943295042	3.190240218	0.00239	0.032288187	-2.23954932	F-box protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0680610.1	1.521163888	6.192253708	3.114619258	0.00297	0.035453096	-2.2396383	Protein kinase	elongation zone	12 h
HORVU.MOREX.r3.2HG0203500.1	0.77350863	6.139707515	3.201893331	0.00231	0.031894634	-2.24065692	UPF0136 membrane protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0483020.1	0.861524531	5.236287099	3.119461137	0.00293	0.035308848	-2.24108811	Kinesin-like protein	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0038960.1	0.83681179	2.949856776	2.981650134	0.00432	0.041301836	-2.24192919	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0474720.1	2.007273662	-0.474518298	2.901738922	0.00539	0.046372512	-2.24200804	Short-chain dehydrogenase/reductase family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0045520.1	2.041508145	1.200266662	2.875502219	0.0058	0.047903389	-2.24283798	zinc finger MYM-type-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0524520.1	1.144436756	6.419522117	3.149838878	0.00268	0.033864708	-2.24301433	60S ribosomal protein L24	elongation zone	12 h
HORVU.MOREX.r3.6HG0614660.1	2.251970492	-0.348204795	2.909283439	0.00528	0.045978938	-2.24302295	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0593480.1	0.766220052	6.095309536	3.166544461	0.00256	0.033222239	-2.24390502	Arginine/serine-rich splicing factor, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0486260.1	3.324378483	3.929099308	2.893510421	0.00552	0.046829376	-2.2445433	Heat shock transcription factor	elongation zone	12 h
HORVU.MOREX.r3.5HG0493030.1	0.802374771	7.858922883	3.25318045	0.00199	0.029748302	-2.24579727	60S ribosomal protein L32	elongation zone	12 h
HORVU.MOREX.r3.6HG0600870.1	-0.40472359	4.403104904	-3.215339751	0.00222	0.031454344	-2.24657073	Acetylglutamate kinase-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0715500.1	2.269196132	0.698143251	2.883000704	0.00568	0.047427345	-2.2472865	nuclear pore anchor	elongation zone	12 h
HORVU.MOREX.r3.2HG0215220.1	0.715792721	4.050855349	3.075708123	0.00332	0.037190743	-2.24739646	Tubby-like F-box protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0713670.1	0.710373737	5.990306123	3.149616976	0.00269	0.033864708	-2.24793616	Alba DNA/RNA-binding protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0553290.1	0.618537389	5.490398459	3.149262752	0.00269	0.033864708	-2.24915035	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.6HG0544580.1	1.062300143	0.367989846	2.943273257	0.00481	0.043773947	-2.24924052	Werner Syndrome-like exonuclease	elongation zone	12 h
HORVU.MOREX.r3.7HG0726240.1	-0.82271414	-0.068180582	-3.089240941	0.00319	0.036823467	-2.24985318	Retrotransposon protein SINE subclass	elongation zone	12 h
HORVU.MOREX.r3.1HG0022710.1	0.825038705	10.37598935	3.358676936	0.00146	0.027115369	-2.25180384	40S ribosomal protein S4	elongation zone	12 h
HORVU.MOREX.r3.7HG0696340.1	0.441696898	6.08013092	3.194723399	0.00236	0.032009236	-2.25182091	RNA-binding family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0060410.1	1.15778268	3.806642977	2.961979897	0.00457	0.042538646	-2.25375157	F21O3.15 protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0420370.1	2.577187288	2.703090315	2.878905463	0.00574	0.04776728	-2.25421221	receptor kinase 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0172550.1	1.198592076	2.80726014	2.930155384	0.00499	0.044637748	-2.25429582	Synaptonemal complex protein 1	elongation zone	12 h
HORVU.MOREX.r3.4HG0415590.1	1.417263094	-0.042390657	2.973709916	0.00442	0.041779146	-2.25645446	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albu	elongation zone	12 h
HORVU.MOREX.r3.4HG0358390.1	1.559887161	4.871920016	3.001041531	0.0041	0.040265883	-2.25662626	Selenoprotein H	elongation zone	12 h
HORVU.MOREX.r3.7HG0733600.1	0.838951582	8.484163878	3.270749002	0.00189	0.028966748	-2.25666936	30S ribosomal protein S11	elongation zone	12 h
HORVU.MOREX.r3.5HG0519760.1	0.65610332	8.912276545	3.301331907	0.00173	0.028397697	-2.25686681	Eukaryotic translation initiation factor 3 subunit B	elongation zone	12 h
HORVU.MOREX.r3.6HG0565380.1	0.502605971	5.049690937	3.146972377	0.00271	0.033864708	-2.25699495	Zinc finger CCCH domain-containing protein 13	elongation zone	12 h
HORVU.MOREX.r3.3HG0250080.1	0.692220495	5.216335383	3.121158307	0.00291	0.035234858	-2.2578827	30S ribosomal protein S8, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0249590.1	0.703218326	3.607050289	3.005700607	0.00404	0.040178373	-2.25847241	Vesicle transport protein-like	elongation zone	12 h
HORVU.MOREX.r3.1HG0031520.1	0.737716091	4.885472537	3.092226371	0.00317	0.036688668	-2.25928732	Myb	elongation zone	12 h
HORVU.MOREX.r3.1HG0054150.1	0.911144648	5.965194148	3.128004293	0.00286	0.034844441	-2.25945818	N-alpha-acetyltransferase 25, NatB auxiliary subunit	elongation zone	12 h
HORVU.MOREX.r3.7HG0751140.1	0.99393265	2.824962476	2.924351019	0.00507	0.045122895	-2.26120163	F-box family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0191100.1	0.760830552	8.580211615	3.280121765	0.00184	0.028819302	-2.2614823	30S ribosomal protein S17	elongation zone	12 h
HORVU.MOREX.r3.7HG0712850.1	0.359882432	4.698390518	3.151417845	0.00267	0.033864708	-2.26157925	Fiber protein Fb34	elongation zone	12 h
HORVU.MOREX.r3.2HG0113380.1	0.525816602	7.165397632	3.227236414	0.00215	0.031018589	-2.26333793	splicing factor-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0185640.1	2.385259077	1.439291744	2.86596624	0.00595	0.048522465	-2.26334968	Protein ROOT PRIMORDIUM DEFECTIVE 1	elongation zone	12 h
HORVU.MOREX.r3.6HG0566480.1	2.309414619	-1.265754862	2.887174491	0.00561	0.047204707	-2.26421565	Retrotransposon protein, putative, unclassified	elongation zone	12 h
HORVU.MOREX.r3.6HG0568390.1	-0.439704749	4.337128784	-3.214604915	0.00223	0.031473786	-2.26608131	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0724270.1	-0.494398676	2.618489122	-3.034735887	0.00373	0.038784658	-2.2674011	F-box/kelch-repeat protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0136670.1	1.414639516	4.71390114	3.265661057	0.00192	0.029184417	-2.26748348	Cellulose synthase-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0158080.1	2.186685325	0.623463989	2.865329728	0.00596	0.048546205	-2.26759889	Pentatricopeptide repeat-containing family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0707410.1	1.84466427	-0.496688719	2.863895549	0.00598	0.048636131	-2.26819657	GRF zinc finger / Zinc knuckle protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0455490.1	0.879649417	1.390809013	2.896703289	0.00547	0.046711054	-2.27167605	Aspartic proteinase Asp1	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.4HG0411600.1	0.563670925	7.727342404	3.244552117	0.00204	0.030344376	-2.27182674	50S ribosomal protein L14	elongation zone	12 h
HORVU.MOREX.r3.7HG0697550.1	0.354853515	9.219800437	3.32868405	0.00159	0.027806246	-2.27282758	ABC transporter ATP-binding protein ARB1	elongation zone	12 h
HORVU.MOREX.r3.3HG0270190.1	0.313518027	5.543138586	3.203064696	0.0023	0.031887924	-2.27310215	dihydroflavonol 4-reductase/flavanone protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0325650.1	1.276170392	2.127342509	2.8778587	0.00576	0.04776728	-2.27479877	Cupredoxin superfamily protein, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0327830.1	2.137846479	4.138764232	2.913633033	0.00522	0.045722475	-2.27527267	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0685410.1	0.962560261	5.553236747	3.098437234	0.00311	0.036312806	-2.27537999	Retinoblastoma-related protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0085140.1	0.383226484	6.163123216	3.216500631	0.00221	0.031452409	-2.27631572	Serine/threonine protein phosphatase 2A regulatory subunit B	elongation zone	12 h
HORVU.MOREX.r3.6HG0552890.1	1.993175621	0.455902627	2.860005763	0.00605	0.048928619	-2.27657729	transmembrane protein, putative (DUF594)	elongation zone	12 h
HORVU.MOREX.r3.7HG0713340.1	1.151722849	3.465224865	2.984477492	0.00429	0.041182464	-2.27710077	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.4HG0415160.1	0.407774584	4.127593268	3.089248152	0.00319	0.036823467	-2.27938096	DUF3527 domain protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0079930.1	-2.638199949	-2.565871354	-2.884401993	0.00566	0.047404516	-2.28155431	Pectin lyase-like superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0721450.1	-0.699863446	1.569350469	-3.277642928	0.00185	0.028860537	-2.28164004	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.6HG0623920.1	0.208032036	9.176211122	3.362615964	0.00144	0.02703001	-2.28197464	Leucine aminopeptidase, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0508060.1	1.026380894	6.113062349	3.122597821	0.0029	0.035200058	-2.28307525	GTP binding protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0278550.1	0.982292361	2.026307923	2.979918031	0.00434	0.041386317	-2.28368761	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.6HG0549900.1	2.443521097	1.036021217	2.868035948	0.00592	0.048306767	-2.28798672	Hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyltrar	elongation zone	12 h
HORVU.MOREX.r3.1HG0065540.1	1.130671554	10.14930621	3.321352924	0.00163	0.02796111	-2.28977454	NA	elongation zone	12 h
HORVU.MOREX.r3.6HG0600630.1	1.496651395	-0.318534445	2.852649739	0.00617	0.049512065	-2.29213933	cotton fiber-like protein (DUF761)	elongation zone	12 h
HORVU.MOREX.r3.2HG0122450.1	0.880003501	8.533148489	3.255005892	0.00198	0.029648381	-2.29228777	30S ribosomal protein S4	elongation zone	12 h
HORVU.MOREX.r3.1HG0056560.1	0.318483658	5.466996869	3.19506386	0.00236	0.032009236	-2.29469223	AP-3 complex subunit delta	elongation zone	12 h
HORVU.MOREX.r3.2HG0107960.1	-0.486438392	3.123366617	-3.084192572	0.00324	0.036928455	-2.29497315	Phosphoinositide phospholipase C	elongation zone	12 h
HORVU.MOREX.r3.7HG0671800.1	1.312801338	5.765569408	3.071059255	0.00336	0.037308039	-2.29575993	DNA topoisomerase family	elongation zone	12 h
HORVU.MOREX.r3.4HG0417170.1	1.902631521	5.34885237	2.993954226	0.00418	0.040647009	-2.29648126	WD repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0513980.1	-1.03971357	-0.364729073	-3.020526241	0.00388	0.039407591	-2.29776697	Auxin-responsive protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0201910.1	0.760158569	6.429805807	3.177066458	0.00248	0.032834207	-2.29931708	Myosin-H heavy chain	elongation zone	12 h
HORVU.MOREX.r3.2HG0132450.1	-0.462628978	4.0992375	-3.180280669	0.00246	0.032737911	-2.30120387	L-rhamnose isomerase	elongation zone	12 h
HORVU.MOREX.r3.5HG0501430.1	1.539580101	1.709795684	2.984358844	0.00429	0.041182464	-2.30169855	Agmatine coumaroyltransferase-2	elongation zone	12 h
HORVU.MOREX.r3.3HG0255500.1	1.210363698	3.245772951	2.91687243	0.00517	0.045490951	-2.30188893	La related protein-like	elongation zone	12 h
HORVU.MOREX.r3.7HG0650810.1	1.482593165	1.931516835	2.863548354	0.00599	0.048636131	-2.30503837	Acyl-CoA synthetase family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0079280.1	0.932577532	8.411998552	3.255880596	0.00197	0.029636522	-2.30782291	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.3HG0315620.1	1.288139403	1.678500581	2.851381963	0.00619	0.049563437	-2.30803657	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0751330.1	2.61572078	4.028668411	2.876953057	0.00577	0.047810689	-2.30919417	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase far	elongation zone	12 h
HORVU.MOREX.r3.5HG0463700.1	0.553087549	4.020835168	3.039490544	0.00368	0.038641262	-2.30962491	Scarecrow transcription factor family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0487070.1	-0.452303843	4.654929378	-3.170361001	0.00253	0.033099534	-2.31148453	Alpha/beta-Hydrolases superfamily protein, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0611090.1	1.921649698	4.272440344	2.913065656	0.00523	0.04573542	-2.31160216	tRNA (Guanine(9)-N1)-methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0427370.1	0.882588634	1.30418145	3.011424483	0.00398	0.03986915	-2.31208128	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0111240.1	1.381362073	5.668492978	3.058677097	0.00348	0.037779464	-2.31228711	Nuclear pore complex protein, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0364050.1	-0.642243266	2.580176455	-3.03970572	0.00367	0.038641262	-2.3126369	Sodium/hydrogen exchanger	elongation zone	12 h
HORVU.MOREX.r3.7HG0663940.1	-0.779305635	0.764913385	-3.157056281	0.00263	0.033716726	-2.31366258	Alpha/beta-Hydrolases superfamily protein, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0525290.1	-0.689189282	5.237284387	-3.231487593	0.00212	0.030866089	-2.31525468	Amino acid transporter, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0265880.1	1.173138703	2.376813197	2.891980283	0.00554	0.046904576	-2.31628249	Pentatricopeptide repeat-containing protein	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.2HG0113730.1	1.496439827	5.221019143	3.005586597	0.00404	0.040178373	-2.31761402	60S ribosome subunit biogenesis protein NIP7 homolog	elongation zone	12 h
HORVU.MOREX.r3.2HG0178240.1	0.632328958	4.274946849	3.038394129	0.00369	0.038671495	-2.31967898	Transcription factor	elongation zone	12 h
HORVU.MOREX.r3.6HG0560680.1	-1.279253164	-0.976729155	-2.853702639	0.00615	0.049405649	-2.31983088	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0154600.1	2.306870289	1.249898666	2.846052117	0.00628	0.04989211	-2.3201747	Plastid division protein PDV2	elongation zone	12 h
HORVU.MOREX.r3.2HG0107450.1	0.863007992	3.576514789	2.995386716	0.00416	0.040578362	-2.32225816	methyl-coenzyme M reductase II subunit gamma, putative (DUF3	elongation zone	12 h
HORVU.MOREX.r3.7HG0736300.1	2.221076572	3.861077284	2.879522548	0.00573	0.047754823	-2.3228241	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0187640.1	0.650240909	2.595046236	2.949509127	0.00473	0.043465368	-2.32371355	Gamma-tubulin complex component	elongation zone	12 h
HORVU.MOREX.r3.2HG0191180.1	0.414106004	4.405018466	3.097901948	0.00311	0.036334581	-2.32388382	Xanthine phosphoribosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0438550.1	1.326017211	3.407298471	2.899724969	0.00542	0.046551797	-2.32420098	Cyclin family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0140950.1	1.457654007	3.361687211	2.883123296	0.00568	0.047427345	-2.32715005	Abnormal spindle-like microcephaly-associated protein-like prote	elongation zone	12 h
HORVU.MOREX.r3.4HG0411620.1	1.445576433	6.015681025	3.055425695	0.00351	0.037808566	-2.32756499	Thyroid adenoma-associated protein-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0070000.1	0.72621818	1.808570831	2.91965	0.00513	0.045371176	-2.32816545	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.5HG0451540.1	0.702683489	7.656228475	3.215007303	0.00222	0.031458646	-2.3283289	Chaperone DnaK	elongation zone	12 h
HORVU.MOREX.r3.7HG0714510.1	0.970958513	5.004338229	3.029660251	0.00378	0.039090877	-2.32935329	Protein phosphatase 2C	elongation zone	12 h
HORVU.MOREX.r3.1HG0000380.1	1.547131122	4.008859542	2.958164085	0.00462	0.042747009	-2.3333101	Pectin lyase-like superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0425730.1	-0.500574564	4.697689499	-3.284696598	0.00181	0.028793086	-2.33730309	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0324930.1	0.611359194	9.79870902	3.316894398	0.00165	0.028050531	-2.33976477	40S ribosomal protein S10	elongation zone	12 h
HORVU.MOREX.r3.1HG0075830.1	1.204140936	3.021026521	2.883317341	0.00567	0.047427345	-2.33981085	Polypyrimidine tract-binding protein-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0094010.1	2.369618966	-1.304615689	2.857974511	0.00608	0.049103351	-2.34134709	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0687630.1	0.532710823	7.969316852	3.274007835	0.00187	0.028923495	-2.3416885	Acyl carrier protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0336310.1	0.665749298	6.502870264	3.167117048	0.00255	0.033216773	-2.3425458	Zinc finger family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0124990.1	0.621722156	6.152886279	3.177039163	0.00248	0.032834207	-2.34413468	3-oxoacyl-[acyl-carrier-protein] synthase	elongation zone	12 h
HORVU.MOREX.r3.6HG0586220.1	0.896956745	5.61880713	3.099144584	0.0031	0.036288602	-2.34543033	Prohibitin	elongation zone	12 h
HORVU.MOREX.r3.1HG0034450.1	-1.058291733	0.621391691	-2.869552888	0.00589	0.048306767	-2.34556041	Retrovirus-related Pol polyprotein from transposon TNT 1-94	elongation zone	12 h
HORVU.MOREX.r3.7HG0751790.1	1.724851416	0.792911227	2.875576883	0.0058	0.047903389	-2.34558588	DUF241 domain protein (DUF241)	elongation zone	12 h
HORVU.MOREX.r3.4HG0384230.1	0.496041279	3.949265758	3.080778888	0.00327	0.036983216	-2.34713495	RING/U-box superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0243920.1	1.076796871	3.290866018	2.9679441	0.00449	0.042132428	-2.34768507	VQ motif-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0641160.1	0.366193133	5.342895251	3.141755174	0.00275	0.034124913	-2.34833116	Guanine nucleotide-binding protein subunit alpha-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0289250.1	0.638368448	7.766476009	3.231515012	0.00212	0.030866089	-2.34858156	Elongation factor 4	elongation zone	12 h
HORVU.MOREX.r3.2HG0167030.1	0.726699799	3.461475439	2.94312599	0.00481	0.043773947	-2.35098497	Mis18-binding protein 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0128410.1	0.885062207	4.563754238	3.014140507	0.00395	0.039746874	-2.3524001	DNA/RNA helicase protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0534140.1	1.269077477	8.004889694	3.210990048	0.00225	0.031545502	-2.35255146	Glycine rich protein 3	elongation zone	12 h
HORVU.MOREX.r3.5HG0446850.1	1.931822485	6.103829376	3.010880798	0.00398	0.039893403	-2.35281947	Myosin-1	elongation zone	12 h
HORVU.MOREX.r3.1HG0020980.1	-0.505075261	7.252012736	-3.317749012	0.00164	0.028035058	-2.35345235	Endo-1,31,4-beta-D-glucanase	elongation zone	12 h
HORVU.MOREX.r3.4HG0382090.1	0.495931996	6.628026251	3.180833339	0.00245	0.032706849	-2.35365503	#N/A	elongation zone	12 h
HORVU.MOREX.r3.1HG0060370.1	2.617985893	-0.902409718	2.848505941	0.00624	0.049739166	-2.35368169	1,4-alpha-glucan branching enzyme GlgB	elongation zone	12 h
HORVU.MOREX.r3.1HG0060320.1	0.832555173	7.084889179	3.184959932	0.00243	0.032575632	-2.3561673	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.1HG0051900.1	-0.536150041	4.657334527	-3.224923282	0.00216	0.031159303	-2.35735927	Glutathione S-transferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0746570.1	0.860675161	9.010351969	3.261296092	0.00194	0.029451158	-2.35980052	60S ribosomal protein L27	elongation zone	12 h
HORVU.MOREX.r3.5HG0494480.1	0.721096419	9.280053353	3.273313194	0.00187	0.028923495	-2.36237551	60S ribosomal protein L7a	elongation zone	12 h
HORVU.MOREX.r3.4HG0396600.1	-0.637932571	1.930667574	-2.965772275	0.00452	0.042342202	-2.36364607	Digalactosyldiacylglycerol synthase (Chloroplastic)	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.3HG0246030.1	-0.906906744	0.793865926	-3.039398299	0.00368	0.038641262	-2.36590994	Blue copper protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0677270.1	0.836675182	2.721723616	2.946374994	0.00477	0.04368814	-2.36848583	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0327170.1	0.422533198	7.966567016	3.257597214	0.00196	0.02961891	-2.37120169	Bifunctional polymyxin resistance arnA protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0630680.1	0.58352657	4.625356458	3.039122022	0.00368	0.038641262	-2.37302004	F-box family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0439040.1	0.581906443	7.004585033	3.17954824	0.00246	0.032786051	-2.37417641	Elongation factor Tu	elongation zone	12 h
HORVU.MOREX.r3.3HG0271710.1	0.446505564	4.526521133	3.048046653	0.00359	0.038188048	-2.3760517	Zinc finger CCCH domain protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0189960.1	1.648420983	8.037428277	3.148288341	0.0027	0.033864708	-2.37757216	U3 small nucleolar RNA-associated protein 10	elongation zone	12 h
HORVU.MOREX.r3.5HG0518160.1	0.729845077	8.607332408	3.239329723	0.00207	0.03060905	-2.37766762	30S ribosomal protein S13	elongation zone	12 h
HORVU.MOREX.r3.6HG0549510.1	0.66828419	8.771368712	3.290157227	0.00178	0.02862189	-2.37890894	Peptidyl-prolyl cis-trans isomerase	elongation zone	12 h
HORVU.MOREX.r3.4HG0418790.1	1.385314891	5.632641367	3.008195557	0.00401	0.040081151	-2.37991148	tRNA/rRNA methyltransferase family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0037990.1	0.949840918	2.905819651	2.890150059	0.00557	0.047062906	-2.38095707	SKP1-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0078010.1	0.355055091	5.540918622	3.138599434	0.00277	0.03425211	-2.38265716	Translation initiation factor IF-2	elongation zone	12 h
HORVU.MOREX.r3.5HG0494040.1	-1.048179492	-3.000857515	-2.872306514	0.00585	0.04818291	-2.3835304	Auxin efflux carrier component	elongation zone	12 h
HORVU.MOREX.r3.2HG0196780.1	1.391479302	4.987352017	2.98917198	0.00423	0.040956128	-2.38384064	Multidrug resistance protein ABC transporter family	elongation zone	12 h
HORVU.MOREX.r3.5HG0497200.1	0.494750829	6.465584768	3.151842017	0.00267	0.033864708	-2.38386363	Cell division cycle 5-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0349380.1	0.689664029	10.03245682	3.302095643	0.00172	0.028397697	-2.38700952	Ribosomal protein L3	elongation zone	12 h
HORVU.MOREX.r3.7HG0702050.1	-1.003240082	-0.450446856	-2.963932855	0.00454	0.04241279	-2.38822628	Blue copper protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0001130.1	0.742941765	5.638908604	3.067383262	0.0034	0.037381068	-2.38825143	Ankyrin repeat family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0429360.1	0.71137268	4.758495845	3.062514099	0.00344	0.03764455	-2.38900224	Pectinesterase	elongation zone	12 h
HORVU.MOREX.r3.7HG0680960.1	-1.48703112	0.61149754	-2.909084134	0.00529	0.045984662	-2.389173	electron transporter, putative (Protein of unknown function, DU	elongation zone	12 h
HORVU.MOREX.r3.3HG0330210.1	1.850783216	4.048874756	2.872196102	0.00585	0.04818291	-2.39096341	GDSL esterase/lipase	elongation zone	12 h
HORVU.MOREX.r3.2HG0133550.1	-0.262828495	5.768893736	-3.199419762	0.00233	0.031903923	-2.39153707	Calcium-dependent protein kinase	elongation zone	12 h
HORVU.MOREX.r3.4HG0343870.1	0.987754443	3.294242033	2.906245246	0.00533	0.04618095	-2.39197122	Transducin/WD40 repeat-like superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0242160.1	0.50994665	8.436022046	3.238384831	0.00208	0.030632868	-2.39270616	Arginine/serine-rich splicing factor, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0701300.1	1.704012836	3.314094522	2.848754051	0.00624	0.049724941	-2.39372518	Exosome complex component	elongation zone	12 h
HORVU.MOREX.r3.4HG0363440.1	1.173351947	5.032921778	2.984864597	0.00428	0.041182136	-2.39417077	DNA-directed RNA polymerase I subunit rpa49	elongation zone	12 h
HORVU.MOREX.r3.2HG0157290.1	0.843304417	3.397681153	2.940264507	0.00485	0.044001805	-2.39514597	Calcineurin-like metallo-phosphoesterase superfamily	elongation zone	12 h
HORVU.MOREX.r3.5HG0421560.1	1.675078945	3.372970967	2.846280126	0.00628	0.049885976	-2.39731054	GTPase family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0418210.1	-0.762238867	-0.146163126	-3.027885888	0.0038	0.039108923	-2.39867665	Methylsterol monooxygenase 1-2	elongation zone	12 h
HORVU.MOREX.r3.1HG0069760.1	-0.647297473	1.711709527	-3.145237304	0.00272	0.033887701	-2.40166617	Calmodulin	elongation zone	12 h
HORVU.MOREX.r3.5HG0452250.1	-0.320648299	4.804561684	-3.150252277	0.00268	0.033864708	-2.40223754	AP-2 complex subunit sigma	elongation zone	12 h
HORVU.MOREX.r3.1HG0072360.1	0.827910352	2.892056241	2.901743492	0.00539	0.046372512	-2.40273107	F-box protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0104480.1	0.556317193	3.899783698	3.000410605	0.0041	0.040307075	-2.40602023	F-box protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0443560.1	0.422712504	3.753350984	3.018002116	0.0039	0.039547618	-2.40615642	antigenic heat-stable protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0308980.1	0.741012427	4.452518559	3.003694701	0.00406	0.040229538	-2.40707756	S-adenosyl-L-methionine-dependent methyltransferase, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0527400.1	0.641563614	6.40973231	3.116775644	0.00295	0.035453096	-2.40780612	Nucleobase ascorbate transporter	elongation zone	12 h
HORVU.MOREX.r3.7HG0723500.1	0.665332952	3.424822759	2.993088881	0.00419	0.040685115	-2.41065629	Cinnamoyl-CoA reductase family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0603370.1	-0.613715281	2.324583294	-3.024695189	0.00383	0.03925602	-2.41072082	P-loop containing nucleoside triphosphate hydrolases superfami	elongation zone	12 h
HORVU.MOREX.r3.2HG0204040.1	-1.163851706	1.864217479	-2.939145524	0.00487	0.044099329	-2.41136679	Benzyl alcohol O-benzoyltransferase	elongation zone	12 h
HORVU.MOREX.r3.4HG0339880.1	0.684031125	5.464296399	3.06166099	0.00345	0.037663482	-2.41165003	Zinc finger BED domain-containing protein DAYSLEEPER	elongation zone	12 h
HORVU.MOREX.r3.2HG0217790.1	0.672477859	5.897336985	3.095894034	0.00313	0.036522359	-2.41195509	DNA/RNA helicase protein	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.2HG0218010.1	0.323501157	8.228324079	3.266856378	0.00191	0.02912546	-2.41220445	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase s	elongation zone	12 h
HORVU.MOREX.r3.5HG0524440.1	2.468436538	5.517230328	2.905802843	0.00533	0.04618095	-2.41411861	DNA gyrase subunit A	elongation zone	12 h
HORVU.MOREX.r3.5HG0532380.1	0.526092009	3.73217286	3.0077102	0.00402	0.040116223	-2.41415849	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0202070.1	0.40501178	5.440379588	3.099849256	0.0031	0.03627777	-2.41537176	Chaperone protein DnaJ	elongation zone	12 h
HORVU.MOREX.r3.2HG0136790.1	-0.427063674	6.404608075	-3.286952699	0.0018	0.028691351	-2.41655915	Serine/threonine-protein kinase	elongation zone	12 h
HORVU.MOREX.r3.6HG0554610.1	0.856449733	4.967810293	3.019285598	0.00389	0.039467053	-2.41881249	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0447730.1	0.591274089	6.269812166	3.130170491	0.00284	0.034669947	-2.41925018	Phenylalanine--tRNA ligase beta subunit	elongation zone	12 h
HORVU.MOREX.r3.2HG0099270.1	0.671436002	4.423054289	2.995211978	0.00416	0.040578362	-2.42332757	Actin-related protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0218960.1	2.875912683	4.276243736	2.863299455	0.00599	0.048636131	-2.4239297	Cysteine/Histidine-rich C1 domain family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0402170.1	-1.133222673	-0.055773461	-2.931075095	0.00498	0.044603947	-2.4264232	Heat shock transcription factor	elongation zone	12 h
HORVU.MOREX.r3.5HG0427110.1	0.719314275	3.005946314	2.887195683	0.00561	0.047204707	-2.42675553	tRNA modification GTPase MnmE	elongation zone	12 h
HORVU.MOREX.r3.4HG0362850.1	0.937180675	2.700858012	2.86867784	0.00591	0.048306767	-2.42711657	Acyl-CoA-binding domain-containing protein 4	elongation zone	12 h
HORVU.MOREX.r3.2HG0196330.1	0.589706793	3.925350182	2.981749718	0.00432	0.041301836	-2.42881483	zinc finger matrin-type protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0173920.1	0.944338783	3.666148661	2.910781153	0.00526	0.045865572	-2.43000042	Chloroplastic group IIA intron splicing facilitator CRS1, chloroplas	elongation zone	12 h
HORVU.MOREX.r3.3HG0304800.1	0.872629746	6.736708067	3.13194	0.00283	0.034584718	-2.43099468	Structural maintenance of chromosomes protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0438440.1	1.606556396	6.171046967	3.031549595	0.00376	0.03899655	-2.43202681	Kinesin-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0551740.1	0.538513784	5.295694184	3.075200597	0.00332	0.037190743	-2.43446021	Early light-inducible protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0635400.1	1.439567385	5.566493882	2.982038493	0.00432	0.04129762	-2.43469085	ATP-dependent RNA helicase family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0643820.1	1.418937762	4.511304822	2.910642912	0.00526	0.045865572	-2.43604906	6,7-dimethyl-8-ribityllumazine synthase	elongation zone	12 h
HORVU.MOREX.r3.4HG0399020.1	0.7596266	10.02639982	3.281770895	0.00183	0.028819302	-2.43788318	40S ribosomal protein S3a	elongation zone	12 h
HORVU.MOREX.r3.6HG0604860.1	0.819524889	1.903057556	2.846850511	0.00627	0.049847313	-2.43834375	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.4HG0375480.1	0.933069324	5.989901741	3.09332942	0.00316	0.036644453	-2.44075118	40S ribosomal protein S21	elongation zone	12 h
HORVU.MOREX.r3.1HG0080760.1	0.796271209	7.939029897	3.193469914	0.00237	0.032094481	-2.44081765	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.4HG0385140.1	1.694291486	3.56681819	2.84594996	0.00628	0.04989211	-2.44140948	Carbamoyl-phosphate synthase large chain	elongation zone	12 h
HORVU.MOREX.r3.4HG0380540.1	-0.52880238	3.365321911	-3.072899746	0.00334	0.037254747	-2.44291172	Aquaporin-1	elongation zone	12 h
HORVU.MOREX.r3.4HG0337170.1	0.931609903	5.504147714	3.039707692	0.00367	0.038641262	-2.44382227	Zinc-finger domain of monoamine-oxidase A repressor R1, putati	elongation zone	12 h
HORVU.MOREX.r3.4HG0348470.1	0.587997936	6.0852859	3.113506963	0.00298	0.035522336	-2.44384259	ATP-dependent RNA helicase family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0181390.1	1.435243101	5.181001175	2.977607929	0.00437	0.041519226	-2.44676239	Protein BREAST CANCER SUSCEPTIBILITY 1-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0726770.1	-0.786701712	2.292249938	-3.076537295	0.00331	0.037174732	-2.4494717	Glycine-rich protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0164540.1	-1.082261358	0.757754706	-2.846681217	0.00627	0.049850932	-2.44979039	Ethylene-responsive transcription factor, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0082020.1	1.667012203	5.076015324	2.922894547	0.00509	0.045226145	-2.45317515	WD-repeat protein, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0508150.1	-0.952664491	2.451835168	-2.996726992	0.00415	0.040483637	-2.45358822	9-cis-epoxycarotenoid dioxygenase	elongation zone	12 h
HORVU.MOREX.r3.1HG0019380.1	1.139935512	6.322023156	3.052596511	0.00354	0.037882054	-2.45404855	Glioma tumor suppressor-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0616130.1	-0.486894962	6.042280496	-3.256079508	0.00197	0.029636522	-2.45499387	Hexosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.6HG0546160.1	-0.683514128	2.97610997	-3.152216613	0.00267	0.033864708	-2.45626533	Acylamino-acid-releasing enzyme	elongation zone	12 h
HORVU.MOREX.r3.7HG0747940.1	-0.362410136	7.327177402	-3.260539579	0.00195	0.029482217	-2.4576376	Polyamine oxidase	elongation zone	12 h
HORVU.MOREX.r3.5HG0467870.1	-0.775210511	2.049337326	-3.020887034	0.00387	0.039407591	-2.45813318	Kynurenine formamidase	elongation zone	12 h
HORVU.MOREX.r3.3HG0287640.1	0.522662408	5.945191223	3.102781652	0.00307	0.036128346	-2.46007369	Endoribonuclease YbeY	elongation zone	12 h
HORVU.MOREX.r3.2HG0116280.1	1.955955558	7.824467532	3.079320387	0.00328	0.036983216	-2.46196643	Nucleolar family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0472840.1	-0.521599718	2.862571295	-3.092453211	0.00316	0.036688668	-2.46272011	NBS-LRR disease resistance protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0540430.3	-0.758792887	2.730080782	-3.003769326	0.00406	0.040229538	-2.46330518	F-box and associated interaction domains-containing protein	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0059790.1	0.632238552	4.636699296	3.02896506	0.00379	0.039108923	-2.46332967	Hydroxyproline-rich glycoprotein-like	elongation zone	12 h
HORVU.MOREX.r3.2HG0155810.1	0.743493165	3.567203574	2.970936915	0.00445	0.041967805	-2.46455786	Replication protein A 70 kDa DNA-binding subunit A	elongation zone	12 h
HORVU.MOREX.r3.2HG0160930.1	0.642755589	9.218628834	3.240570734	0.00206	0.03054087	-2.46456014	50S ribosomal protein L29	elongation zone	12 h
HORVU.MOREX.r3.3HG0290900.1	0.551515443	4.951870278	3.051483994	0.00355	0.037906495	-2.46662441	Rhomboid family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0647360.1	1.430705396	5.375391659	2.951003454	0.00471	0.043324391	-2.46699921	Ribosome production factor 1	elongation zone	12 h
HORVU.MOREX.r3.6HG0610140.1	0.800890002	4.922162889	3.003377306	0.00407	0.040229538	-2.46765292	tRNA uridine 5-carboxymethylaminomethyl modification enzyme	elongation zone	12 h
HORVU.MOREX.r3.4HG0347230.1	0.847182336	2.503173448	2.883525248	0.00567	0.047427345	-2.46777527	Polygalacturonase-1 non-catalytic beta subunit	elongation zone	12 h
HORVU.MOREX.r3.1HG0064190.1	0.885868019	4.191166014	2.944289341	0.0048	0.043746094	-2.46899801	30S ribosomal protein S18	elongation zone	12 h
HORVU.MOREX.r3.7HG0728060.1	-0.451888306	5.512336647	-3.129129075	0.00285	0.034752936	-2.47173513	Aminodeoxychorismate synthase	elongation zone	12 h
HORVU.MOREX.r3.5HG0530420.1	-0.876440271	-0.668836111	-3.01708203	0.00392	0.03957523	-2.47176319	Leucine-rich repeat receptor-like protein kinase	elongation zone	12 h
HORVU.MOREX.r3.4HG0415420.1	0.554077964	6.947213857	3.17817799	0.00247	0.032834207	-2.47182963	Tubulin beta chain	elongation zone	12 h
HORVU.MOREX.r3.3HG0234340.1	0.822425084	2.809522003	2.85530491	0.00612	0.049306414	-2.47284495	Protein FRA10AC1	elongation zone	12 h
HORVU.MOREX.r3.2HG0142190.1	0.318515243	5.689012541	3.110725767	0.003	0.035642237	-2.47409286	Potassium transporter	elongation zone	12 h
HORVU.MOREX.r3.2HG0119860.2	0.75005228	6.022614408	3.095158274	0.00314	0.036539994	-2.47449001	10 kDa chaperonin	elongation zone	12 h
HORVU.MOREX.r3.7HG0656030.1	-0.601122951	3.605834777	-3.124233039	0.00289	0.035131319	-2.47627326	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0267880.1	1.381119207	6.864792855	3.061106597	0.00346	0.037702619	-2.47673924	Small subunit processome component 20-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0403800.1	0.929709129	5.863635554	3.032447644	0.00375	0.038936762	-2.47702004	Nuclear pore complex protein NUP96	elongation zone	12 h
HORVU.MOREX.r3.1HG0083020.1	-0.861629366	0.461711884	-2.884700112	0.00565	0.047400081	-2.47752707	aconitase 2	elongation zone	12 h
HORVU.MOREX.r3.2HG0166640.1	1.129147215	8.213121972	3.152913947	0.00266	0.033864708	-2.47813601	60S ribosomal protein L5	elongation zone	12 h
HORVU.MOREX.r3.7HG0674480.1	0.265081919	6.37117646	3.167040472	0.00255	0.033216773	-2.47873693	RING/U-box superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0238450.1	0.463274518	6.670539813	3.135611734	0.0028	0.03437844	-2.48093723	Protein FRIGIDA	elongation zone	12 h
HORVU.MOREX.r3.5HG0462460.1	0.807227957	3.212594193	2.913253284	0.00523	0.045731286	-2.48180584	complex 1 protein, LYR family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0558880.1	1.224520591	5.027918082	2.978774161	0.00436	0.041480063	-2.48410224	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.3HG0271870.2	1.224268008	3.842763992	2.871090281	0.00587	0.048231861	-2.48448462	CTP synthase	elongation zone	12 h
HORVU.MOREX.r3.6HG0599090.1	-0.825820153	-2.428665549	-2.849934744	0.00622	0.049681395	-2.48953778	Vacuolar iron transporter	elongation zone	12 h
HORVU.MOREX.r3.2HG0163890.1	0.693978992	3.526119037	2.892895735	0.00553	0.046871369	-2.49178048	Multifunctional CCA protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0736960.1	0.63693711	3.878659947	2.952116093	0.00469	0.043259525	-2.49185388	BTB/POZ domain containing protein, expressed	elongation zone	12 h
HORVU.MOREX.r3.7HG0695960.1	0.568643106	9.98141728	3.274791529	0.00187	0.028923495	-2.491919	30S ribosomal protein S3	elongation zone	12 h
HORVU.MOREX.r3.6HG0555630.1	1.447928109	6.693514895	3.027838801	0.0038	0.039108923	-2.49604393	DNA polymerase V	elongation zone	12 h
HORVU.MOREX.r3.3HG0231480.1	0.63377134	3.882014662	2.951866877	0.0047	0.043259525	-2.49651388	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.7HG0715570.1	0.363397787	6.466382964	3.154795117	0.00265	0.033831284	-2.49774843	Transmembrane protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0176920.1	1.216255934	3.864016179	2.877316766	0.00577	0.047801075	-2.49825069	ATP-dependent RNA helicase DeaD	elongation zone	12 h
HORVU.MOREX.r3.4HG0393640.1	0.894147341	5.209210225	3.005600432	0.00404	0.040178373	-2.49940389	Anaphase-promoting complex subunit 6-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0615820.1	-0.399539888	5.121094299	-3.120830135	0.00292	0.035234858	-2.49972963	Chaperone protein dnaJ	elongation zone	12 h
HORVU.MOREX.r3.3HG0292240.1	1.214740143	4.324488603	2.902665477	0.00538	0.046332224	-2.50109105	Mitochondrial glycoprotein	elongation zone	12 h
HORVU.MOREX.r3.2HG0203510.1	-0.516836427	5.236895283	-3.118355755	0.00294	0.035358381	-2.50238258	Jasmonate ZIM domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0554520.1	0.912284876	5.131198847	2.965424499	0.00452	0.042347835	-2.50466	BRCT domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0596980.1	0.887438626	5.451026715	3.005427438	0.00405	0.040178373	-2.50544384	B-block binding subunit of TFIIIC	elongation zone	12 h
HORVU.MOREX.r3.1HG0066210.1	0.829811916	2.989216297	2.863269315	0.00599	0.048636131	-2.50561589	NBS-LRR-like resistance protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0632380.1	0.422825523	7.961705372	3.183654531	0.00243	0.032618994	-2.50717336	Splicing factor 3B subunit 2	elongation zone	12 h
HORVU.MOREX.r3.1HG0082450.1	2.145164155	4.566459078	2.855909474	0.00611	0.049244636	-2.50858999	Early nodulin-like protein	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.5HG0430720.1	0.967473326	4.903886981	2.933263619	0.00495	0.044514543	-2.50922702	ATP-dependent DNA helicase 2 subunit KU70	elongation zone	12 h
HORVU.MOREX.r3.1HG0038170.1	1.162106729	6.453681313	3.054039253	0.00353	0.037821239	-2.51014482	DNA polymerase epsilon, catalytic subunit, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0078630.1	1.160326316	4.590043583	2.931199118	0.00497	0.044603947	-2.51067249	Single-stranded DNA-binding protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0449030.1	1.188222306	4.657038603	2.910096109	0.00527	0.045915159	-2.51084008	GRF1-interacting factor-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0577130.1	0.593831568	6.344518727	3.103852365	0.00306	0.036088436	-2.51115888	RNA-binding family protein, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0403250.1	0.926361383	4.254712987	2.934934737	0.00492	0.044439465	-2.51218378	50S ribosomal L32	elongation zone	12 h
HORVU.MOREX.r3.4HG0399600.1	0.503686721	5.665530959	3.072284202	0.00335	0.037256101	-2.51330607	COP9 signalosome complex subunit 4	elongation zone	12 h
HORVU.MOREX.r3.1HG0090780.1	0.870631822	9.407223354	3.207320208	0.00227	0.031692167	-2.51621324	Ketol-acid reductoisomerase (NADP(+))	elongation zone	12 h
HORVU.MOREX.r3.3HG0296490.1	0.560713394	6.526216847	3.138358444	0.00277	0.03425211	-2.51786541	NADH-cytochrome b5 reductase	elongation zone	12 h
HORVU.MOREX.r3.1HG0049980.1	-0.324181039	8.42398264	-3.318514373	0.00164	0.028033028	-2.52028845	Actin	elongation zone	12 h
HORVU.MOREX.r3.4HG0398610.1	2.056786602	4.947656787	2.860889807	0.00603	0.048830126	-2.52095053	Urb2/Npa2 family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0724580.2	0.737017445	3.515564828	2.894728912	0.0055	0.046792558	-2.5213583	Zinc finger CCCH domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0589920.1	0.73371016	9.535234774	3.231230094	0.00212	0.030866089	-2.5225892	60S ribosomal protein L6	elongation zone	12 h
HORVU.MOREX.r3.1HG0085240.1	1.031075396	5.724080625	2.98686426	0.00426	0.041087503	-2.52268879	RuvB-like helicase	elongation zone	12 h
HORVU.MOREX.r3.4HG0411240.1	1.795323233	4.73256603	2.850343999	0.00621	0.049645466	-2.52281442	WD-repeat protein, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0497770.1	-0.459784356	6.416725076	-3.237779903	0.00208	0.030664986	-2.5251608	BAG family molecular chaperone regulator-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0185840.1	0.883363535	7.644996465	3.148435691	0.0027	0.033864708	-2.52643229	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0474900.1	1.364429733	6.343269298	3.003434193	0.00407	0.040229538	-2.52705383	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0682750.1	0.898401815	7.225422779	3.106527387	0.00304	0.035941769	-2.5277776	60S ribosomal protein L32	elongation zone	12 h
HORVU.MOREX.r3.4HG0403070.1	0.496770997	6.742400409	3.136493561	0.00279	0.034312101	-2.53094894	Serine/threonine-protein phosphatase	elongation zone	12 h
HORVU.MOREX.r3.7HG0704060.1	0.521273442	4.974659306	2.98733573	0.00426	0.041052717	-2.53140652	AT hook motif DNA-binding family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0255580.1	-0.435316006	5.497551901	-3.173481952	0.00251	0.03299418	-2.53224662	Respiratory burst oxidase, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0128230.1	0.768068763	5.522586618	3.037743044	0.00369	0.038671495	-2.53270341	Thaumatin	elongation zone	12 h
HORVU.MOREX.r3.2HG0114570.1	0.827674359	6.160354978	3.054562535	0.00352	0.037808566	-2.53354735	Adenylyl cyclase	elongation zone	12 h
HORVU.MOREX.r3.7HG0714900.1	0.626634738	4.447401071	2.980872249	0.00433	0.041314646	-2.5347502	S-acyltransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0156960.1	0.88211348	8.772916108	3.177027596	0.00248	0.032834207	-2.53476277	50S ribosomal protein L13	elongation zone	12 h
HORVU.MOREX.r3.3HG0237990.1	-0.519217488	4.191673583	-3.087069463	0.00321	0.036927181	-2.53705966	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0510860.1	2.057230763	6.298847295	2.957942621	0.00462	0.042747009	-2.53761038	Kinesin-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0407670.1	0.594925846	5.172481666	3.017505872	0.00391	0.039547618	-2.53793188	Pentatricopeptide repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0572330.1	0.434142676	5.22316415	3.055918842	0.00351	0.037808566	-2.53859974	Actin-related family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0251830.1	0.804572214	3.41268951	2.877723091	0.00576	0.04776728	-2.53934545	Plant regulator RWP-RK	elongation zone	12 h
HORVU.MOREX.r3.3HG0321700.1	-0.527573174	3.776225864	-2.999480669	0.00411	0.040307075	-2.54073008	FMN-dependent NADPH-azoreductase	elongation zone	12 h
HORVU.MOREX.r3.3HG0293040.1	0.482822666	5.431413902	3.055367421	0.00351	0.037808566	-2.54374111	Purple acid phosphatase	elongation zone	12 h
HORVU.MOREX.r3.1HG0037800.1	1.372893762	6.016136386	2.974136407	0.00441	0.041748755	-2.5467904	3'-5' exonuclease domain-containing family protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0176660.1	0.932480964	4.897976898	2.945905833	0.00478	0.043696105	-2.5478462	Elongator complex protein 3	elongation zone	12 h
HORVU.MOREX.r3.2HG0174520.1	-0.583238854	4.527587866	-3.131859666	0.00283	0.034584718	-2.54791335	Cytochrome P450 protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0085250.1	1.38975589	4.749802186	2.876058981	0.00579	0.047903389	-2.54921963	60S ribosomal protein l35a	elongation zone	12 h
HORVU.MOREX.r3.6HG0630650.1	1.715248133	3.863030917	2.875339084	0.0058	0.047905463	-2.54948814	Protein DETOXIFICATION	elongation zone	12 h
HORVU.MOREX.r3.5HG0467880.1	0.489782479	5.367744504	3.023454512	0.00385	0.039284359	-2.55151975	DNA-directed RNA polymerase family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0595860.1	0.358663363	5.620864894	3.081007753	0.00327	0.036983216	-2.5519206	E3 ubiquitin-protein ligase	elongation zone	12 h
HORVU.MOREX.r3.7HG0739490.1	0.871371761	7.817057502	3.151161398	0.00267	0.033864708	-2.55310706	Histone H2B	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.6HG0620220.1	0.793928373	5.661795132	3.015815649	0.00393	0.039657644	-2.55384138	Isoleucine--tRNA ligase	elongation zone	12 h
HORVU.MOREX.r3.2HG0174160.1	0.934592382	5.210032118	2.959121249	0.0046	0.042722832	-2.55629235	Testis-expressed sequence 10 protein-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0333940.1	1.435094108	6.071660271	2.992582286	0.00419	0.040685115	-2.55731485	Transmembrane protein, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0039910.1	0.781508648	5.062796176	2.968882323	0.00448	0.042098534	-2.55900084	Polyadenylate-binding protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0162900.2	0.629737189	2.320158811	2.868289978	0.00591	0.048306767	-2.56257374	Aldo-keto reductase	elongation zone	12 h
HORVU.MOREX.r3.6HG0607740.1	1.295555813	5.336911121	2.931803234	0.00497	0.044592291	-2.56605856	ATPase family AAA domain-containing protein 3	elongation zone	12 h
HORVU.MOREX.r3.6HG0597640.1	-0.597444683	3.081428676	-3.005766988	0.00404	0.040178373	-2.56831141	Nitrilase	elongation zone	12 h
HORVU.MOREX.r3.7HG0636740.1	-0.809303603	0.502771414	-2.84740516	0.00626	0.049810831	-2.56870925	NBS-LRR-like resistance protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0598750.1	-0.893142952	0.858146068	-3.163780312	0.00258	0.033395092	-2.56975004	Remorin	elongation zone	12 h
HORVU.MOREX.r3.7HG0723670.1	0.82816187	3.921322603	2.879740743	0.00573	0.047754823	-2.5700048	Mitochondrial 39S ribosomal protein L53	elongation zone	12 h
HORVU.MOREX.r3.2HG0207720.1	-0.657276104	0.894336802	-3.029493704	0.00378	0.039090877	-2.57144163	Flavin-containing monooxygenase	elongation zone	12 h
HORVU.MOREX.r3.3HG0313340.1	0.491306581	4.971353448	3.012544395	0.00397	0.039847155	-2.57345802	nuclear factor Y, subunit B13	elongation zone	12 h
HORVU.MOREX.r3.2HG0139050.1	1.014867435	3.432927884	2.862648841	0.006	0.048692565	-2.57363638	Protein kinase	elongation zone	12 h
HORVU.MOREX.r3.2HG0143570.1	0.773965363	5.102737064	2.969783222	0.00447	0.042044934	-2.57412737	Asparagine-tRNA ligase	elongation zone	12 h
HORVU.MOREX.r3.5HG0528940.1	0.395096768	5.397306806	3.054655357	0.00352	0.037808566	-2.57456727	GPI-anchored adhesin-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0569990.1	-0.284743152	6.145643496	-3.1572907	0.00263	0.033716726	-2.57686103	Calmodulin binding protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0091360.1	0.440320086	6.214276876	3.104439543	0.00306	0.036052722	-2.57800134	Delta(14)-sterol reductase	elongation zone	12 h
HORVU.MOREX.r3.4HG0393260.1	0.332632262	7.041152087	3.110331701	0.00301	0.035656113	-2.57896832	Oxidoreductase, 2OG-Fe(II) oxygenase family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0280160.1	-0.40439279	4.904831015	-3.115950296	0.00296	0.035453096	-2.57981466	Evolutionarily conserved C-terminal region 2	elongation zone	12 h
HORVU.MOREX.r3.4HG0415600.1	1.370804841	5.888146948	2.992947168	0.00419	0.040685115	-2.58075247	HXXXD-type acyl-transferase family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0030670.1	0.800379012	8.049604649	3.133403642	0.00281	0.034551409	-2.582793	50S ribosomal protein L5	elongation zone	12 h
HORVU.MOREX.r3.5HG0491040.1	0.731377343	3.434830866	2.875556933	0.0058	0.047903389	-2.58593307	DNA-directed RNA polymerase	elongation zone	12 h
HORVU.MOREX.r3.3HG0309410.1	0.919093153	3.365237867	2.849223818	0.00623	0.049700096	-2.58673133	Subtilisin-like protease	elongation zone	12 h
HORVU.MOREX.r3.4HG0411040.1	0.446605954	5.23830385	3.022041123	0.00386	0.039354132	-2.58779872	Chaperone protein dnaJ	elongation zone	12 h
HORVU.MOREX.r3.7HG0744870.1	0.617379516	4.001055586	2.903288225	0.00537	0.046274876	-2.58920119	Mis12 protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0588960.1	0.93167083	4.77862855	2.930662085	0.00498	0.044603947	-2.58943701	Small nuclear ribonucleoprotein Sm D1	elongation zone	12 h
HORVU.MOREX.r3.5HG0430740.1	0.528396134	5.807467475	3.030891847	0.00377	0.03899655	-2.59176146	#N/A	elongation zone	12 h
HORVU.MOREX.r3.1HG0010370.1	0.844421371	6.023951457	3.013362326	0.00396	0.03979475	-2.59343728	Nuclear pore complex protein Nup107	elongation zone	12 h
HORVU.MOREX.r3.7HG0711940.2	0.527083598	2.784849309	2.917503675	0.00517	0.045490951	-2.59452348	Aminotransferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0437670.1	0.645420414	4.311696419	2.895541991	0.00549	0.046758121	-2.59763662	Histone deacetylase	elongation zone	12 h
HORVU.MOREX.r3.4HG0395910.1	0.766599059	6.108491299	3.030826544	0.00377	0.03899655	-2.59855587	Glucan endo-1,3-beta-glucosidase 3	elongation zone	12 h
HORVU.MOREX.r3.1HG0023650.1	0.676192423	5.863281229	3.027306938	0.0038	0.039110161	-2.59980577	Small nuclear ribonucleoprotein	elongation zone	12 h
HORVU.MOREX.r3.7HG0686530.1	0.509591542	5.623092015	3.02626003	0.00382	0.039184772	-2.6008783	La protein like	elongation zone	12 h
HORVU.MOREX.r3.1HG0013050.1	1.158848842	6.187182499	2.971042141	0.00445	0.041967805	-2.60109319	Ribosome biogenesis regulatory protein-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0444030.1	1.774767835	6.014101665	2.9450132	0.00479	0.043697279	-2.60301465	Cellulose synthase-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0219160.1	0.539703859	7.250382019	3.119673686	0.00293	0.035308123	-2.60542186	Protein decapping 5	elongation zone	12 h
HORVU.MOREX.r3.2HG0140960.1	0.814068008	4.296824079	2.910840436	0.00526	0.045865572	-2.60609167	Condensin-2 complex subunit H2	elongation zone	12 h
HORVU.MOREX.r3.6HG0543800.1	0.70438517	7.420452333	3.138457012	0.00277	0.03425211	-2.60638832	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.6HG0628850.1	0.819008686	8.487070812	3.14990647	0.00268	0.033864708	-2.60700111	Ribosomal protein L37	elongation zone	12 h
HORVU.MOREX.r3.1HG0065860.1	-0.555639358	4.236426412	-3.082397634	0.00326	0.036983216	-2.60835361	MLO-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0466770.1	0.671678036	8.962400466	3.178180437	0.00247	0.032834207	-2.60994875	Ribosomal protein L15	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.4HG0383530.3	-0.856017228	1.457398746	-3.037381313	0.0037	0.038671495	-2.6135996	Pathogenesis-related protein 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0192000.1	-0.755359295	0.357063756	-3.062402032	0.00345	0.03764455	-2.61529299	HXXXD-type acyl-transferase family protein, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0042740.1	0.29319926	6.415284526	3.11635128	0.00295	0.035453096	-2.61530071	Adaptin ear-binding coat-associated protein, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0275530.1	0.710212482	3.985890373	2.89585475	0.00548	0.046755804	-2.61602734	Sodium Bile acid symporter family	elongation zone	12 h
HORVU.MOREX.r3.3HG0304660.1	-0.456799472	3.802909764	-3.078122101	0.00329	0.037068643	-2.61692531	Ceramide glucosyltransferase, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0541810.1	1.017732188	4.305459183	2.884341613	0.00566	0.047404516	-2.61993918	28S ribosomal S34, mitochondrial	elongation zone	12 h
HORVU.MOREX.r3.5HG0428100.1	0.644473392	7.163221856	3.08198573	0.00326	0.036983216	-2.62115755	Auxin response factor	elongation zone	12 h
HORVU.MOREX.r3.4HG0398900.1	0.868716167	8.042634537	3.137842889	0.00278	0.034261617	-2.62133383	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.1HG0083440.1	-0.379636324	5.222068752	-3.115255062	0.00296	0.035453096	-2.62261466	Lactation elevated protein 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0683780.1	0.741662068	7.910611567	3.112682452	0.00299	0.035540654	-2.62457481	50S ribosomal protein L22	elongation zone	12 h
HORVU.MOREX.r3.7HG0726790.1	0.314734579	7.796481048	3.161136136	0.0026	0.033587945	-2.62464242	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.1HG0001410.1	1.361470383	3.89097838	2.86433404	0.00598	0.048603777	-2.62934798	Transmembrane protein, putative (DUF247)	elongation zone	12 h
HORVU.MOREX.r3.2HG0164150.1	0.63614831	4.261815439	2.920712838	0.00512	0.045330047	-2.63047286	Protein TSSC4	elongation zone	12 h
HORVU.MOREX.r3.5HG0437610.1	0.840850922	5.573525032	2.983436635	0.0043	0.041269326	-2.63480199	caspase-6 protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0375240.1	0.833639464	5.249290851	2.975616871	0.0044	0.041634412	-2.63482154	Acyl carrier protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0014410.1	0.607903059	5.218845032	2.998358292	0.00413	0.040356839	-2.63499285	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.1HG0032200.1	-0.546035013	3.740470542	-3.056109241	0.00351	0.037808566	-2.63514346	S-type anion channel	elongation zone	12 h
HORVU.MOREX.r3.7HG0710600.1	0.537689638	5.301457053	3.003432806	0.00407	0.040229538	-2.63571642	Protein kinase	elongation zone	12 h
HORVU.MOREX.r3.4HG0353330.1	0.891525709	5.045545148	2.944322701	0.0048	0.043746094	-2.6371162	Protein kinase	elongation zone	12 h
HORVU.MOREX.r3.5HG0430460.1	-0.505765954	1.634629182	-3.046005791	0.00361	0.03830948	-2.63775877	Proline-rich family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0413410.1	0.886347356	7.171547875	3.115850778	0.00296	0.035453096	-2.63847456	Hydroxymethylglutaryl-CoA synthase	elongation zone	12 h
HORVU.MOREX.r3.1HG0052080.1	0.364882537	6.314334235	3.073776721	0.00334	0.037244624	-2.63932527	C-terminal binding protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0041180.1	0.791541723	8.516186529	3.137318215	0.00278	0.034272194	-2.64225357	50S ribosomal protein L14	elongation zone	12 h
HORVU.MOREX.r3.3HG0259660.1	0.606329168	3.912666018	2.882188609	0.00569	0.047513562	-2.64619201	CRS2-associated factor 1, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.4HG0411740.1	1.238878192	6.110179775	2.949177637	0.00473	0.043485864	-2.64816112	ATP-dependent RNA helicase	elongation zone	12 h
HORVU.MOREX.r3.3HG0239980.1	-0.999714079	1.292153679	-2.961761134	0.00457	0.042545213	-2.64868342	Alpha/beta-Hydrolases superfamily protein, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0094520.1	0.528825462	7.217789849	3.083724899	0.00324	0.036928455	-2.64870873	DNA damage-binding protein 1	elongation zone	12 h
HORVU.MOREX.r3.5HG0455100.1	0.9100108	9.647836002	3.169585512	0.00254	0.033099534	-2.65083467	Ribosomal protein L3	elongation zone	12 h
HORVU.MOREX.r3.7HG0635550.1	1.291484076	6.336423435	3.001542256	0.00409	0.040265883	-2.65222601	Lipoxygenase domain-containing 1	elongation zone	12 h
HORVU.MOREX.r3.5HG0492480.1	0.742684496	5.7458778	3.012172661	0.00397	0.039849721	-2.65314529	30S ribosomal protein S16	elongation zone	12 h
HORVU.MOREX.r3.7HG0704330.1	0.748307947	8.747152339	3.142950533	0.00274	0.034069783	-2.65327898	40S ribosomal protein S13	elongation zone	12 h
HORVU.MOREX.r3.7HG0730720.1	0.917177613	6.181638114	2.981441822	0.00433	0.041306621	-2.65330149	RNA polymerase I-specific transcription initiation factor RRN3	elongation zone	12 h
HORVU.MOREX.r3.3HG0218440.1	0.592758563	5.530527629	2.978043685	0.00437	0.041506896	-2.65368864	Serine/threonine-protein kinase ATM	elongation zone	12 h
HORVU.MOREX.r3.5HG0533630.1	1.171668092	5.193357564	3.063566969	0.00343	0.037620683	-2.65402163	Expansin	elongation zone	12 h
HORVU.MOREX.r3.1HG0024280.1	0.620755139	7.969902425	3.147187425	0.0027	0.033864708	-2.65476049	Dihydrolipoyl dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.6HG0558580.1	1.007775594	4.169275691	2.849021981	0.00623	0.049708047	-2.65560573	Ribosomal protein L37, mitochondrial	elongation zone	12 h
HORVU.MOREX.r3.1HG0074490.1	1.172620623	4.901731214	2.904213313	0.00536	0.046251967	-2.65975686	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0099160.1	-0.955595031	-0.22735804	-2.931106774	0.00497	0.044603947	-2.66084311	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfami	elongation zone	12 h
HORVU.MOREX.r3.6HG0623070.1	-0.424527683	3.799863701	-3.016576923	0.00392	0.039611908	-2.66186463	Ankyrin repeat-containing protein, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0314820.1	-0.614023021	3.291171778	-3.072193846	0.00335	0.037256101	-2.66272343	26S proteasome regulatory subunit RPN2	elongation zone	12 h
HORVU.MOREX.r3.3HG0246810.1	0.623290955	5.554940352	2.999629571	0.00411	0.040307075	-2.66286539	30S ribosomal protein S6	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.7HG0696930.2	1.782333554	6.181980146	2.896413332	0.00547	0.046711054	-2.66386514	RNA-binding protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0400040.1	-0.48670251	1.083905502	-3.072930384	0.00334	0.037254747	-2.66399436	Cytochrome b561 and DOMON domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0173380.1	-0.415020896	4.283255367	-3.058004798	0.00349	0.037779464	-2.66463043	Amino acid transporter, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0287070.1	0.888676954	6.192472525	3.074320749	0.00333	0.037226047	-2.66572486	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0269430.1	0.534839276	6.166272467	3.011302328	0.00398	0.03986915	-2.66850694	Chaperone protein dnaJ	elongation zone	12 h
HORVU.MOREX.r3.3HG0309800.1	0.630885253	5.007429359	2.977295509	0.00438	0.041519226	-2.67027326	Small ubiquitin-related modifier	elongation zone	12 h
HORVU.MOREX.r3.1HG0068810.1	-0.347513093	4.949596997	-3.103690073	0.00306	0.036088436	-2.67212607	#N/A	elongation zone	12 h
HORVU.MOREX.r3.4HG0352780.1	-0.652795797	1.138744691	-2.963535589	0.00455	0.04241279	-2.67358106	WRKY transcription factor	elongation zone	12 h
HORVU.MOREX.r3.3HG0298790.1	0.590235249	4.931630051	2.917076475	0.00517	0.045490951	-2.67376613	Amidophosphoribosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.6HG0543740.1	0.770980734	7.842284834	3.124700493	0.00289	0.035113249	-2.67523405	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.7HG0692740.1	0.347805226	6.659164505	3.066580903	0.0034	0.037432489	-2.67614653	RNA-binding protein 25	elongation zone	12 h
HORVU.MOREX.r3.2HG0187940.1	-0.618914677	5.04269045	-3.064987882	0.00342	0.037489533	-2.67769091	Niemann-Pick C1 protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0298750.1	0.48894195	5.760333104	3.056461457	0.0035	0.037808566	-2.67838938	magnesium transporter NIPA (DUF803)	elongation zone	12 h
HORVU.MOREX.r3.1HG0015470.1	-0.867341334	2.791232652	-2.983058802	0.00431	0.041274283	-2.67941499	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfami	elongation zone	12 h
HORVU.MOREX.r3.2HG0183390.1	-0.673212153	2.00100842	-3.002381104	0.00408	0.040250079	-2.68012193	GRAM domain-containing protein / ABA-responsive	elongation zone	12 h
HORVU.MOREX.r3.2HG0196630.1	-0.938337318	-0.811111303	-2.901830233	0.00539	0.046372512	-2.68097371	Invertase/pectin methylesterase inhibitor family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0307310.1	0.278875991	5.321616586	3.059287423	0.00348	0.037764638	-2.68296916	magnesium transporter, putative (DUF803)	elongation zone	12 h
HORVU.MOREX.r3.6HG0555870.1	1.723763945	5.140784525	2.851936445	0.00618	0.049512564	-2.68350568	Kinesin-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0505300.1	1.491501307	6.157248139	2.921000553	0.00512	0.045330047	-2.68459906	Ribosome biogenesis protein BOP1 homolog	elongation zone	12 h
HORVU.MOREX.r3.4HG0398910.1	0.904080276	7.143679884	3.068027622	0.00339	0.037367493	-2.68541389	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.1HG0094770.1	0.516483447	3.670278309	2.886791844	0.00562	0.04722308	-2.6868407	Transmembrane protein, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0610110.1	0.886783337	4.84135302	2.876947955	0.00577	0.047810689	-2.68932737	FKBP-like peptidyl-prolyl cis-trans isomerase family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0529180.1	0.584180011	6.543237435	3.053010829	0.00354	0.037872249	-2.68941016	Huntingtin interacting protein K	elongation zone	12 h
HORVU.MOREX.r3.2HG0192180.1	0.195825764	9.138579	3.212890053	0.00224	0.031520621	-2.69027996	26S proteasome non-ATPase regulatory subunit 1	elongation zone	12 h
HORVU.MOREX.r3.3HG0313090.1	-0.684053204	2.944420659	-2.92156782	0.00511	0.045296428	-2.69108713	Thiamin pyrophosphokinase 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0204570.1	-0.458359572	5.322525667	-3.120902231	0.00292	0.035234858	-2.69305496	glucuronoxylan 4-O-methyltransferase-like protein (DUF579)	elongation zone	12 h
HORVU.MOREX.r3.2HG0124660.1	-0.303025569	4.762294428	-3.027855229	0.0038	0.039108923	-2.69320797	Dihydropteroate synthase, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0730070.1	1.046749275	6.723991887	3.030940021	0.00377	0.03899655	-2.69380606	Thaumatin-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0340230.1	0.651971583	6.673601725	3.032725178	0.00375	0.038936762	-2.69417171	Alba DNA/RNA-binding protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0676250.1	0.778801625	3.644955906	2.896404078	0.00547	0.046711054	-2.69442031	Protein DETOXIFICATION	elongation zone	12 h
HORVU.MOREX.r3.1HG0029460.1	-0.476249944	2.800322038	-2.893680663	0.00551	0.046829376	-2.69628304	Fatty acid oxidation complex subunit alpha	elongation zone	12 h
HORVU.MOREX.r3.1HG0091240.1	-0.463161552	4.910103678	-3.086793841	0.00321	0.036928455	-2.69966775	Mitogen-activated protein kinase	elongation zone	12 h
HORVU.MOREX.r3.6HG0630200.1	0.358235467	6.20685434	3.036734589	0.0037	0.038704216	-2.70390934	Protein FAR1-RELATED SEQUENCE 3	elongation zone	12 h
HORVU.MOREX.r3.3HG0240180.1	0.444765694	6.812791234	3.054971105	0.00352	0.037808566	-2.70448689	Ubiquitinyl hydrolase 1	elongation zone	12 h
HORVU.MOREX.r3.2HG0134400.1	-0.329250881	6.098222844	-3.078627516	0.00329	0.037035763	-2.70627825	Protein DETOXIFICATION	elongation zone	12 h
HORVU.MOREX.r3.6HG0546130.1	0.553661511	4.48574317	2.920817329	0.00512	0.045330047	-2.70753992	BTB/POZ domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0387120.1	0.964614023	6.92928788	3.0310846	0.00376	0.03899655	-2.70993498	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.7HG0654170.1	1.123031841	4.7582708	2.849462314	0.00622	0.049700096	-2.71162339	rRNA-processing protein FCF1-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0252610.1	0.329636418	7.233438842	3.09136114	0.00317	0.036725735	-2.712318	Protein kinase	elongation zone	12 h
HORVU.MOREX.r3.4HG0418290.1	-0.24042844	6.480281927	-3.107563214	0.00303	0.035897692	-2.71720742	Charged multivesicular body protein 3	elongation zone	12 h
HORVU.MOREX.r3.5HG0447330.1	1.010880355	4.611100684	2.941610925	0.00483	0.043896282	-2.71835592	Aquaporin	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.7HG0640580.1	0.765500507	6.013252126	2.945344079	0.00478	0.043696105	-2.71879948	Phosphoglucan, water dikinase	elongation zone	12 h
HORVU.MOREX.r3.5HG0471150.1	-0.514698599	3.92040144	-3.045745789	0.00361	0.038317796	-2.71914599	Cobyric acid synthase	elongation zone	12 h
HORVU.MOREX.r3.2HG0170160.1	0.28568758	8.212366788	3.160150504	0.00261	0.033615353	-2.71943818	Cleft lip and palate transmembrane 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0721930.1	0.507493414	4.955957757	2.947978032	0.00475	0.043552747	-2.71963443	B-cell receptor-associated protein 31-like containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0089160.1	0.617887456	7.967866402	3.083992217	0.00324	0.036928455	-2.72760932	Eukaryotic translation initiation factor 3 subunit D	elongation zone	12 h
HORVU.MOREX.r3.6HG0568910.1	-0.626591428	3.99891951	-3.085929937	0.00322	0.036928455	-2.73070601	L-gulonolactone oxidase	elongation zone	12 h
HORVU.MOREX.r3.2HG0178420.1	1.726238559	5.745692204	2.880314042	0.00572	0.04769973	-2.73398729	transmembrane protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0548420.1	1.193184457	4.579374657	2.852337184	0.00617	0.049512065	-2.73431295	Histone H4	elongation zone	12 h
HORVU.MOREX.r3.1HG0032650.1	-0.40982402	2.965330327	-3.019497226	0.00389	0.039463094	-2.73537803	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0743900.1	-0.498606898	5.143712272	-3.080568147	0.00327	0.036983216	-2.73708154	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0460120.1	-0.494044967	1.893832399	-2.907278603	0.00531	0.04613544	-2.74261283	Alpha/beta-Hydrolases superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0022680.1	0.844078	6.559679477	2.984866514	0.00428	0.041182136	-2.74409913	Histidine--tRNA ligase	elongation zone	12 h
HORVU.MOREX.r3.5HG0487950.1	-0.406072418	5.865567848	-3.105693336	0.00305	0.035985971	-2.74602874	Purine permease-like protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0746810.1	0.32669202	5.647823023	3.028303405	0.00379	0.039108923	-2.74657248	Transcription factor	elongation zone	12 h
HORVU.MOREX.r3.6HG0545460.1	-0.544741871	3.011798115	-3.043076424	0.00364	0.038508115	-2.74753612	Transmembrane protein 97	elongation zone	12 h
HORVU.MOREX.r3.5HG0508600.1	0.727568582	5.919054895	2.941300718	0.00484	0.043914566	-2.74904692	WD-40 repeat protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0420410.1	-0.384877321	5.049102333	-3.037237122	0.0037	0.038671495	-2.75048915	Ubiquitin-conjugating enzyme E2	elongation zone	12 h
HORVU.MOREX.r3.4HG0355430.1	1.2985144	5.48935292	2.858595008	0.00607	0.049059031	-2.75704231	ATP-dependent RNA helicase	elongation zone	12 h
HORVU.MOREX.r3.3HG0298330.1	-0.457575836	4.860908662	-3.022419993	0.00386	0.039334712	-2.75716631	Chaperone protein dnaJ	elongation zone	12 h
HORVU.MOREX.r3.7HG0707860.1	-0.464131508	3.600785372	-2.970644465	0.00446	0.041982723	-2.75828223	CASP-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0254940.1	-0.759562086	2.451212431	-3.113472109	0.00298	0.035522336	-2.7590522	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.2HG0176290.1	0.407436024	6.030618554	2.997929852	0.00413	0.040386019	-2.76005131	Mitochondrial inner membrane protease ATP23	elongation zone	12 h
HORVU.MOREX.r3.4HG0414480.1	0.728552235	4.891800711	2.903822522	0.00536	0.046274876	-2.76034111	Small nuclear ribonucleoprotein-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0379960.1	0.366579445	5.175067919	2.982184928	0.00432	0.04129762	-2.76061691	Exostosin family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0684410.1	0.759824335	9.154592415	3.117807378	0.00294	0.03539314	-2.76334386	60S ribosomal protein L7a	elongation zone	12 h
HORVU.MOREX.r3.1HG0072520.1	0.878179753	4.709600772	2.916894946	0.00517	0.045490951	-2.76760036	#N/A	elongation zone	12 h
HORVU.MOREX.r3.1HG0007670.1	-0.592060024	3.984670291	-2.929867974	0.00499	0.044653737	-2.77024224	OCS-element binding factor 5	elongation zone	12 h
HORVU.MOREX.r3.6HG0630420.1	0.342163539	4.567048698	2.93400715	0.00494	0.044514442	-2.77132896	Myosin type-2 heavy chain 2	elongation zone	12 h
HORVU.MOREX.r3.7HG0712780.1	1.181868359	6.591425476	2.945384629	0.00478	0.043696105	-2.77132952	Pre-rRNA-processing protein TSR1-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0159500.1	0.749873777	5.303207265	2.907324958	0.00531	0.04613544	-2.77365647	tRNA (Adenine-N(1)-)-methyltransferase catalytic subunit trmt61	elongation zone	12 h
HORVU.MOREX.r3.1HG0044060.2	0.744066386	4.318494758	2.868390034	0.00591	0.048306767	-2.7755288	28S ribosomal protein S29, mitochondrial	elongation zone	12 h
HORVU.MOREX.r3.6HG0608110.1	0.577701005	6.16140251	2.979385367	0.00435	0.041428624	-2.77619538	Histidinol-phosphate aminotransferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0485990.1	0.944825522	5.054014433	2.865059261	0.00596	0.048546205	-2.77665588	Nuclear pore complex protein NUP58	elongation zone	12 h
HORVU.MOREX.r3.3HG0299820.1	0.872151401	7.690345431	3.053832854	0.00353	0.037823562	-2.77795237	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.3HG0310540.1	0.490138688	5.76487875	3.00248009	0.00408	0.040250079	-2.77919365	Mannosyl-oligosaccharide glucosidase	elongation zone	12 h
HORVU.MOREX.r3.2HG0203840.1	0.923463679	7.328278373	3.003886563	0.00406	0.040229538	-2.77943118	Nuclease S1	elongation zone	12 h
HORVU.MOREX.r3.3HG0303520.1	0.742021506	8.112661201	3.06919691	0.00338	0.037331432	-2.77966762	30S ribosomal protein S12	elongation zone	12 h
HORVU.MOREX.r3.3HG0244240.1	-0.894845174	3.630904343	-2.94211804	0.00483	0.043873519	-2.78046385	Alpha/beta-Hydrolases superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0006650.1	0.739642108	8.905369094	3.114561294	0.00297	0.035453096	-2.78327632	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.7HG0674750.1	0.341449749	5.335659117	2.9953152	0.00416	0.040578362	-2.78710085	Dual specificity protein phosphatase, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0463410.1	0.837641248	7.370416612	3.024667286	0.00383	0.03925602	-2.79141806	30S ribosomal protein S9	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.7HG0667730.1	-0.376986414	5.42923688	-3.046584842	0.0036	0.038286492	-2.79196385	Chaperone protein dnaJ	elongation zone	12 h
HORVU.MOREX.r3.6HG0619320.1	0.524889287	6.069339622	2.976901156	0.00438	0.04154313	-2.79246115	Prolyl-tRNA synthetase associated domain-containing protein 1	elongation zone	12 h
HORVU.MOREX.r3.5HG0467810.1	0.478186104	7.61265314	3.056216133	0.00351	0.037808566	-2.79372706	Aspartate--tRNA ligase	elongation zone	12 h
HORVU.MOREX.r3.6HG0550670.1	1.788517458	7.005257995	2.944036869	0.0048	0.043752599	-2.79405762	Glycine-rich cell wall structural protein 2	elongation zone	12 h
HORVU.MOREX.r3.5HG0521570.1	0.641181619	5.72311113	2.93178869	0.00497	0.044592291	-2.79623829	Cell division cycle 5-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0581010.1	0.544923574	4.497989908	2.891438705	0.00555	0.046935568	-2.79626834	Poly(A) polymerase	elongation zone	12 h
HORVU.MOREX.r3.7HG0709680.1	0.616348841	8.315627784	3.084704192	0.00323	0.036928455	-2.79657734	T-complex protein 1 subunit gamma	elongation zone	12 h
HORVU.MOREX.r3.2HG0104980.1	0.816566773	8.609674328	3.074720838	0.00333	0.037204054	-2.79803673	40S ribosomal protein S6	elongation zone	12 h
HORVU.MOREX.r3.5HG0420210.1	0.361202649	6.548287697	3.035422698	0.00372	0.038738812	-2.79922739	Plasma membrane ATPase	elongation zone	12 h
HORVU.MOREX.r3.5HG0534180.1	0.562587711	5.30730743	2.915247784	0.0052	0.045616889	-2.80082444	KH domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0112970.1	0.808747478	8.618139404	3.079324071	0.00328	0.036983216	-2.80254688	60S ribosomal protein L18	elongation zone	12 h
HORVU.MOREX.r3.4HG0340180.1	0.921748292	7.057162416	2.976277005	0.00439	0.041577055	-2.80307387	Transducin/WD-like repeat-protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0610500.1	-0.769965883	1.298618032	-3.080565787	0.00327	0.036983216	-2.80341927	Eukaryotic aspartyl protease family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0233150.1	0.719573793	5.953619348	2.971518462	0.00445	0.04195768	-2.8085982	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.7HG0719170.1	-0.655002581	5.542866148	-3.083141987	0.00325	0.036948704	-2.80895407	O-fucosyltransferase-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0081790.1	0.58634546	5.419367045	2.918117634	0.00516	0.045451924	-2.80995113	Phosphotransferase	elongation zone	12 h
HORVU.MOREX.r3.4HG0389240.1	0.460233016	4.623069502	2.9332577	0.00495	0.044514543	-2.81073176	DUF3527 domain protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0288140.1	0.26824346	6.173911395	3.046146136	0.00361	0.03830948	-2.81075513	Golgin candidate 1	elongation zone	12 h
HORVU.MOREX.r3.4HG0331980.1	0.843644191	8.08863791	3.051468417	0.00355	0.037906495	-2.81200432	40S ribosomal protein S25, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0382500.1	0.371141106	5.221396135	2.96788538	0.00449	0.042132428	-2.81358977	Seed maturation protein PM36, putative, expressed	elongation zone	12 h
HORVU.MOREX.r3.5HG0455740.1	0.710395368	6.88962885	2.986164928	0.00427	0.041090601	-2.81382246	ATP dependent RNA helicase	elongation zone	12 h
HORVU.MOREX.r3.4HG0333130.2	0.636394116	4.143810939	2.84823833	0.00624	0.049750126	-2.81483091	#N/A	elongation zone	12 h
HORVU.MOREX.r3.2HG0214780.1	0.642009635	7.100366582	3.016096865	0.00393	0.039645835	-2.81701574	3-isopropylmalate dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.5HG0511480.1	0.763476908	9.452511158	3.111927426	0.00299	0.035576158	-2.81738704	50S ribosomal protein L13	elongation zone	12 h
HORVU.MOREX.r3.1HG0085120.1	0.832060281	6.204576906	2.919710843	0.00513	0.045371176	-2.81879265	Asparagine synthetase	elongation zone	12 h
HORVU.MOREX.r3.5HG0470030.1	0.41422234	7.999201135	3.123173952	0.0029	0.035162818	-2.81954342	3-ketoacyl-CoA thiolase	elongation zone	12 h
HORVU.MOREX.r3.5HG0454500.1	1.501025022	6.350657597	2.87511062	0.0058	0.0479161	-2.82015067	Nucleolar protein 6	elongation zone	12 h
HORVU.MOREX.r3.1HG0058640.1	1.26786368	5.976990264	2.896805672	0.00547	0.046711054	-2.82192373	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.3HG0304370.1	-0.437780749	4.367817245	-2.984626745	0.00429	0.041182464	-2.82330507	Glutamyl-tRNA(Gln) amidotransferase subunit A	elongation zone	12 h
HORVU.MOREX.r3.6HG0626930.1	0.961169494	4.840472652	2.851967879	0.00618	0.049512564	-2.82751766	Ribonucleoside-diphosphate reductase	elongation zone	12 h
HORVU.MOREX.r3.1HG0026070.2	0.593610938	8.133614113	3.057955956	0.00349	0.037779464	-2.82951359	Ribosomal protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0323330.1	-0.711983369	1.397008086	-2.91170089	0.00525	0.04584899	-2.83074051	RNA binding protein, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0378160.1	0.638140267	8.929191593	3.084225279	0.00324	0.036928455	-2.83579339	Ribosomal protein L19	elongation zone	12 h
HORVU.MOREX.r3.6HG0630550.1	0.59599659	8.38745822	3.071862554	0.00335	0.037263411	-2.83738558	T-complex protein 1 subunit zeta	elongation zone	12 h
HORVU.MOREX.r3.3HG0293700.1	0.651253647	6.606906202	2.982670239	0.00431	0.041282541	-2.83810272	Protein downstream neighbor of Son	elongation zone	12 h
HORVU.MOREX.r3.2HG0114370.1	-0.432365803	4.135311302	-3.003748196	0.00406	0.040229538	-2.83966091	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0656440.1	0.459037497	5.106986071	2.897239242	0.00546	0.046711054	-2.83971021	Adenylyltransferase and sulfurtransferase MOCS3	elongation zone	12 h
HORVU.MOREX.r3.6HG0600000.1	-0.95245349	-0.219047099	-2.93321235	0.00495	0.044514543	-2.84159878	Blue copper protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0253650.1	0.591472893	6.25534348	2.957531088	0.00462	0.042776562	-2.84245131	WD40 repeat-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0606400.1	2.034984385	6.56878441	2.871575686	0.00586	0.048206582	-2.84638857	Replicase polyprotein 1a	elongation zone	12 h
HORVU.MOREX.r3.2HG0208810.1	0.276196684	6.69596435	3.02012744	0.00388	0.03943226	-2.84654953	Ubiquitin-conjugating enzyme E2	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.4HG0418460.1	-0.424970757	1.75953737	-3.005435829	0.00405	0.040178373	-2.84670388	Cysteine protease	elongation zone	12 h
HORVU.MOREX.r3.4HG0416710.1	0.554628132	7.831417977	3.037378067	0.0037	0.038671495	-2.84898358	Alanine--tRNA ligase	elongation zone	12 h
HORVU.MOREX.r3.7HG0695870.1	0.712695283	8.389980015	3.058398033	0.00348	0.037779464	-2.85061169	60S ribosomal protein L13	elongation zone	12 h
HORVU.MOREX.r3.5HG0480100.1	-0.34122956	8.360963836	-3.149010616	0.00269	0.033864708	-2.85237155	Cysteine protease	elongation zone	12 h
HORVU.MOREX.r3.6HG0596440.1	-0.412734698	4.52323359	-3.017585429	0.00391	0.039547618	-2.85270277	Hexosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0122080.1	-0.455747725	3.732881583	-3.009593546	0.004	0.039982662	-2.85450455	DUF630 family protein, putative (DUF630 and DUF632)	elongation zone	12 h
HORVU.MOREX.r3.4HG0378960.1	0.910911618	5.668628466	2.870631134	0.00587	0.048268753	-2.85504299	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.6HG0608390.1	-0.319042356	8.330662034	-3.137182221	0.00278	0.034272194	-2.85531538	Nuclear matrix constituent protein 1	elongation zone	12 h
HORVU.MOREX.r3.3HG0236670.1	0.682635025	5.680641273	2.919451102	0.00514	0.045371176	-2.85647188	Protein kinase	elongation zone	12 h
HORVU.MOREX.r3.7HG0645470.1	0.683109905	7.918742491	3.032554556	0.00375	0.038936762	-2.85659313	30S ribosomal protein S10	elongation zone	12 h
HORVU.MOREX.r3.1HG0022910.1	-0.43691274	3.569908814	-2.898564533	0.00544	0.046616466	-2.85756711	Villin	elongation zone	12 h
HORVU.MOREX.r3.6HG0591570.1	0.28005563	7.825511756	3.079774169	0.00328	0.036983216	-2.85790118	26S proteasome non-atpase regulatory subunit, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0230070.1	0.67076755	7.835026485	3.02268638	0.00385	0.039324804	-2.85915907	DNA/RNA helicase protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0411870.1	0.656925363	4.541599175	2.880712998	0.00571	0.047667054	-2.86426448	Cysteine-rich repeat secretory protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0185570.1	-0.675673331	1.316705398	-2.907282046	0.00531	0.04613544	-2.86698039	transcription repressor	elongation zone	12 h
HORVU.MOREX.r3.7HG0706100.1	0.273418969	5.89851201	2.983093033	0.00431	0.041274283	-2.86788506	Survival of motor neuron-related-splicing factor 30	elongation zone	12 h
HORVU.MOREX.r3.3HG0234970.1	-0.496604695	0.091121871	-2.915528379	0.00519	0.045616889	-2.86822932	6,7-dimethyl-8-ribityllumazine synthase	elongation zone	12 h
HORVU.MOREX.r3.7HG0690090.1	-0.723829946	0.298553998	-2.900723305	0.00541	0.046443727	-2.86982328	PLATZ transcription factor family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0087990.1	0.704487159	7.580271477	3.013703653	0.00395	0.039776135	-2.87315016	Ubiquitin	elongation zone	12 h
HORVU.MOREX.r3.5HG0445500.1	0.344881635	6.829254429	3.005940732	0.00404	0.040178373	-2.87926483	Tryptophan--tRNA ligase	elongation zone	12 h
HORVU.MOREX.r3.6HG0584160.1	1.037805479	6.882873618	2.938354705	0.00488	0.044176448	-2.8801219	40S ribosomal protein S24	elongation zone	12 h
HORVU.MOREX.r3.6HG0613040.1	-0.415035408	5.647164704	-3.062198398	0.00345	0.037646224	-2.88093822	2-oxoglutarate-dependent dioxygenase-related family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0285730.1	0.954238618	8.817427966	3.041549026	0.00365	0.0386017	-2.88271662	RNA binding protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0679370.1	0.630843443	7.662871406	3.024632055	0.00383	0.03925602	-2.88362663	60S ribosomal protein L31	elongation zone	12 h
HORVU.MOREX.r3.7HG0637320.1	0.696451143	5.613003444	2.879241274	0.00574	0.047754823	-2.88479224	ATP-dependent zinc metalloprotease FtsH	elongation zone	12 h
HORVU.MOREX.r3.1HG0085100.1	-0.311119626	6.524251428	-3.101286551	0.00308	0.036191331	-2.88575985	GDSL esterase/lipase	elongation zone	12 h
HORVU.MOREX.r3.6HG0619730.1	-0.447968364	8.659854696	-3.175085713	0.0025	0.032934053	-2.88710254	Nitrite reductase	elongation zone	12 h
HORVU.MOREX.r3.5HG0485430.1	0.647163297	6.220484243	2.935545378	0.00491	0.044383997	-2.88813927	#N/A	elongation zone	12 h
HORVU.MOREX.r3.4HG0386800.1	-0.295259663	5.120323725	-2.991421115	0.00421	0.040797666	-2.89010381	Ankyrin repeat family protein, putative, expressed	elongation zone	12 h
HORVU.MOREX.r3.6HG0543520.1	0.473619808	7.261198846	3.002118419	0.00408	0.040260354	-2.89029655	#N/A	elongation zone	12 h
HORVU.MOREX.r3.5HG0510490.1	0.681661916	5.205188872	2.861357987	0.00602	0.048806356	-2.89270771	ATP-dependent RNA helicase, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0113580.1	0.906906348	7.071697111	2.940567376	0.00485	0.043984368	-2.89344786	Ribosomal protein S8e/ribosomal biogenesis NSA2	elongation zone	12 h
HORVU.MOREX.r3.2HG0117790.1	-0.491307534	4.935391398	-2.963672269	0.00455	0.04241279	-2.89536306	Choline transporter-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0337120.1	0.503894442	5.989451331	2.968831873	0.00448	0.042098534	-2.89589202	Histone H1, putative	elongation zone	12 h
HORVU.MOREX.r3.6HG0552010.1	1.017414298	6.596518414	2.907100028	0.00532	0.046138583	-2.89602545	Ribosome biogenesis regulatory protein-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0219360.1	0.939198836	5.80749316	2.868921764	0.0059	0.048306767	-2.89798652	50S ribosomal protein L6	elongation zone	12 h
HORVU.MOREX.r3.2HG0172110.1	-0.482866133	5.282401422	-3.021876529	0.00386	0.039354132	-2.90053527	Dihydrofolate reductase	elongation zone	12 h
HORVU.MOREX.r3.6HG0626650.1	0.22636237	8.259288679	3.090303959	0.00318	0.036772996	-2.90116889	26S protease regulatory subunit-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0170030.1	-0.579536885	0.532968135	-2.926805909	0.00503	0.044862884	-2.90361559	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0498770.1	0.348105143	6.313632909	2.989252708	0.00423	0.040956128	-2.90402112	Hexosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0199260.1	-0.331633452	7.417796497	-3.122065114	0.00291	0.035232963	-2.90613251	Glycosyltransferase	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.7HG0732650.1	-0.56450035	3.272852308	-3.05921494	0.00348	0.037764638	-2.90712768	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.3HG0314880.1	-0.379770918	4.386487876	-2.987930534	0.00425	0.04102313	-2.9074713	Transmembrane protein 45B	elongation zone	12 h
HORVU.MOREX.r3.7HG0666290.1	-0.477354603	4.739589313	-3.002801122	0.00408	0.040241438	-2.90811092	Sphingoid base hydroxylase 2	elongation zone	12 h
HORVU.MOREX.r3.5HG0502750.1	0.808616124	6.985366873	2.98036559	0.00434	0.041353873	-2.90967097	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0710760.1	0.284793048	4.651152884	2.894660888	0.0055	0.046792558	-2.91131601	DGCR14 protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0231330.1	-0.457414868	4.950298797	-2.988120485	0.00425	0.04102313	-2.91293253	Transferase family protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0084340.1	0.812336969	9.276473428	3.065058229	0.00342	0.037489533	-2.91353575	Guanine nucleotide-binding protein subunit beta-1	elongation zone	12 h
HORVU.MOREX.r3.5HG0429680.1	-0.330450654	4.534926532	-2.937246053	0.00489	0.044253573	-2.91415648	GDP-L-galactose phosphorylase 1	elongation zone	12 h
HORVU.MOREX.r3.4HG0333090.1	0.550400892	5.57582127	2.89839826	0.00544	0.046616466	-2.91552992	Protein FAR1-RELATED SEQUENCE 5	elongation zone	12 h
HORVU.MOREX.r3.1HG0008510.2	-0.386472281	3.338317116	-2.865080812	0.00596	0.048546205	-2.9207363	Beta-hexosaminidase	elongation zone	12 h
HORVU.MOREX.r3.2HG0097950.1	0.655599546	10.61692335	3.140654391	0.00276	0.034208419	-2.92438622	Apyrase	elongation zone	12 h
HORVU.MOREX.r3.5HG0494320.1	0.456871429	7.049375017	2.998691461	0.00412	0.040338444	-2.93024445	Nuclear transport factor 2	elongation zone	12 h
HORVU.MOREX.r3.7HG0736870.1	-0.443466772	5.259227513	-2.989072074	0.00423	0.040956128	-2.93035009	Molybdenum cofactor sulfurase	elongation zone	12 h
HORVU.MOREX.r3.6HG0591080.1	0.933793576	6.734278286	2.911175258	0.00526	0.045859795	-2.93042939	Reticulocyte-binding protein 2 a	elongation zone	12 h
HORVU.MOREX.r3.1HG0039940.1	0.486137443	5.166253007	2.872013185	0.00585	0.048187648	-2.9310405	Inosine triphosphate pyrophosphatase	elongation zone	12 h
HORVU.MOREX.r3.6HG0587140.1	0.447733402	4.797451362	2.869951424	0.00589	0.048306767	-2.935158	Transmembrane 9 superfamily member	elongation zone	12 h
HORVU.MOREX.r3.1HG0001460.1	0.666875739	5.41419522	2.932998531	0.00495	0.044521339	-2.93541852	Transmembrane protein, putative (DUF247)	elongation zone	12 h
HORVU.MOREX.r3.4HG0393520.1	-0.65822398	3.798189813	-2.852357472	0.00617	0.049512065	-2.93626128	Microtubule associated protein family protein, putative, express	elongation zone	12 h
HORVU.MOREX.r3.4HG0362040.1	-0.205139225	7.194760833	-3.051400042	0.00355	0.037906495	-2.9374866	Armadillo repeat-containing protein 8	elongation zone	12 h
HORVU.MOREX.r3.4HG0406600.1	-0.635228829	0.071866549	-2.934446058	0.00493	0.044479997	-2.9392917	Heavy metal transport/detoxification superfamily protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0337460.1	0.87336602	6.171367141	2.869721411	0.00589	0.048306767	-2.94302396	Threonine dehydratase	elongation zone	12 h
HORVU.MOREX.r3.2HG0185340.1	-0.712015963	1.427350358	-2.87803426	0.00576	0.04776728	-2.94466808	Cationic amino acid transporter, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0536710.1	0.415450209	6.624728725	3.010737739	0.00399	0.039893403	-2.94512669	NAD/NADP-dependent betaine aldehyde dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.4HG0331420.1	1.206447566	6.43121596	2.84790724	0.00625	0.049762195	-2.94519079	Peptidyl-prolyl cis-trans isomerase	elongation zone	12 h
HORVU.MOREX.r3.4HG0388500.1	0.660947219	6.470028413	2.912484895	0.00524	0.045789106	-2.94524325	tRNA (Guanine(26)-N(2))-dimethyltransferase	elongation zone	12 h
HORVU.MOREX.r3.4HG0355680.1	0.702851985	6.142242249	2.912128613	0.00524	0.04581453	-2.94593008	stress response NST1-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0429940.1	1.312146121	6.908001713	2.886416706	0.00563	0.047232185	-2.94826134	ATP-dependent RNA helicase	elongation zone	12 h
HORVU.MOREX.r3.1HG0040610.1	0.566160565	8.863532503	3.050881459	0.00356	0.037942384	-2.94916757	60 kDa chaperonin	elongation zone	12 h
HORVU.MOREX.r3.2HG0144390.1	0.408694918	5.614147136	2.898654652	0.00544	0.046616466	-2.95178166	COP9 signalosome complex subunit-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0016810.1	0.606331134	5.521688944	2.864696748	0.00597	0.048574968	-2.95352833	Agenet domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0643670.1	2.197344058	8.84959673	2.922164796	0.0051	0.045258495	-2.95492219	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.7HG0643520.1	-0.513502199	3.174361277	-2.888356517	0.0056	0.047175894	-2.95567336	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	elongation zone	12 h
HORVU.MOREX.r3.6HG0618740.1	0.775927809	6.100205577	2.900829266	0.00541	0.046443727	-2.95579339	Separase, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0677230.1	0.912450606	4.893497944	3.054853471	0.00352	0.037808566	-2.95885902	Receptor protein kinase, putative	elongation zone	12 h
HORVU.MOREX.r3.3HG0229480.1	0.365025398	5.272770002	2.879150301	0.00574	0.047754823	-2.95895302	Actin/actin-like family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0525600.1	0.615274527	5.809975351	2.888878364	0.00559	0.047149582	-2.96102131	30S ribosomal protein S12	elongation zone	12 h
HORVU.MOREX.r3.4HG0402650.1	-0.726134963	1.552903388	-2.85655529	0.0061	0.049235401	-2.96248241	Annexin	elongation zone	12 h
HORVU.MOREX.r3.7HG0677570.1	-0.698420479	2.939774147	-2.899356602	0.00543	0.046579264	-2.96283712	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.3HG0219650.1	0.420483928	6.043803629	2.914158735	0.00521	0.045695322	-2.96303976	RNA polymerase II-associated factor 1	elongation zone	12 h
HORVU.MOREX.r3.7HG0656060.1	0.638811873	8.486727413	3.024000896	0.00384	0.039277346	-2.96343398	Pre-mRNA-processing-splicing factor 8	elongation zone	12 h
HORVU.MOREX.r3.2HG0173750.1	-0.334616471	8.547686714	-3.084475138	0.00324	0.036928455	-2.97060877	Aldehyde dehydrogenase	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.4HG0411270.1	0.719156992	6.58190466	2.921547679	0.00511	0.045296428	-2.97417688	N-acetyltransferase	elongation zone	12 h
HORVU.MOREX.r3.4HG0361420.2	0.403242517	5.485836237	2.888462465	0.00559	0.047175894	-2.97453951	ATP dependent RNA helicase	elongation zone	12 h
HORVU.MOREX.r3.2HG0181660.1	0.650683403	5.953972389	2.905970936	0.00533	0.04618095	-2.97872697	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	elongation zone	12 h
HORVU.MOREX.r3.7HG0748070.1	-1.038129431	-0.496958177	-2.856195625	0.00611	0.049242146	-2.97880041	Heavy metal transport/detoxification superfamily protein, putati	elongation zone	12 h
HORVU.MOREX.r3.2HG0130030.1	-0.537928889	1.30207633	-2.903268795	0.00537	0.046274876	-2.98207669	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0635720.1	0.826733187	5.955493906	2.861521059	0.00602	0.048803932	-2.98271477	50S ribosomal protein L9	elongation zone	12 h
HORVU.MOREX.r3.7HG0721650.1	0.265891299	5.578373097	2.960815936	0.00458	0.042615343	-2.98385671	Novel plant snare, putative	elongation zone	12 h
HORVU.MOREX.r3.5HG0484510.1	0.562714841	7.930415335	2.989785373	0.00423	0.040945934	-2.984392	60S ribosomal protein L34	elongation zone	12 h
HORVU.MOREX.r3.4HG0353520.1	0.656135916	9.059200888	3.04177951	0.00365	0.0386017	-2.98477117	30S ribosomal protein S9	elongation zone	12 h
HORVU.MOREX.r3.5HG0468420.1	0.292475491	6.568899246	2.959683777	0.0046	0.042694723	-2.98518932	#N/A	elongation zone	12 h
HORVU.MOREX.r3.1HG0076900.1	1.026661097	6.223225304	2.857979163	0.00608	0.049103351	-2.98562024	GATA transcription factor	elongation zone	12 h
HORVU.MOREX.r3.2HG0191450.1	0.799065903	6.226559771	2.8632191	0.00599	0.048636131	-2.98679148	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subu	elongation zone	12 h
HORVU.MOREX.r3.3HG0254430.1	-0.292963101	8.132393812	-3.087400698	0.00321	0.036913075	-2.9872216	Oxidoreductase	elongation zone	12 h
HORVU.MOREX.r3.5HG0441770.1	0.803760799	6.5387839	2.89205986	0.00554	0.046904576	-2.98815294	Nuclear pore complex protein NUP93A	elongation zone	12 h
HORVU.MOREX.r3.1HG0061880.1	0.48140786	7.374139112	2.977462183	0.00437	0.041519226	-2.99010359	Ran-binding protein 1	elongation zone	12 h
HORVU.MOREX.r3.3HG0315410.1	-0.327532629	5.906295463	-2.978045673	0.00437	0.041506896	-2.99070801	Vesicle-associated protein 1-2	elongation zone	12 h
HORVU.MOREX.r3.1HG0073190.1	0.685119959	7.62223663	2.970400499	0.00446	0.041991983	-2.99093282	30S ribosomal protein S8, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0115970.1	0.892241871	3.355367576	2.86923845	0.0059	0.048306767	-2.9953444	NAD(P)H dehydrogenase (Quinone)	elongation zone	12 h
HORVU.MOREX.r3.5HG0457550.1	-0.391770239	4.931610725	-2.964344002	0.00454	0.04241279	-2.99801787	Plant/F1M20-13 protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0084910.1	0.558826204	5.655310184	2.873604319	0.00583	0.048075075	-3.00229015	50S ribosomal protein L7/L12	elongation zone	12 h
HORVU.MOREX.r3.2HG0120820.1	0.282294884	4.679691645	2.8696963	0.00589	0.048306767	-3.00379175	#N/A	elongation zone	12 h
HORVU.MOREX.r3.4HG0363150.1	0.552003928	5.976929467	2.885805319	0.00564	0.047276131	-3.00562762	WD40 repeat-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0179540.1	0.418720548	4.341715765	2.88421854	0.00566	0.047404516	-3.00810298	Ergosterol biosynthetic protein 28	elongation zone	12 h
HORVU.MOREX.r3.2HG0129980.1	0.580935985	5.921548911	2.875607441	0.00579	0.047903389	-3.01073136	SUMO-activating enzyme 2	elongation zone	12 h
HORVU.MOREX.r3.3HG0294340.1	-0.585854853	2.811533245	-2.863577618	0.00599	0.048636131	-3.01455225	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.5HG0512350.1	0.888676789	7.007305835	2.906237449	0.00533	0.04618095	-3.01640224	Cytochrome P450	elongation zone	12 h
HORVU.MOREX.r3.4HG0397450.1	0.720702425	7.797749659	2.960598863	0.00458	0.042615343	-3.01701975	T-complex protein 1 subunit beta	elongation zone	12 h
HORVU.MOREX.r3.3HG0280140.1	0.853977415	6.992266616	2.914392842	0.00521	0.045685378	-3.02469987	60S ribosomal protein L37a	elongation zone	12 h
HORVU.MOREX.r3.6HG0621950.1	0.789782524	7.314803764	2.933377255	0.00494	0.044514543	-3.02563555	60S ribosomal protein L35a-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0092810.1	0.791697614	7.116496563	2.895472183	0.00549	0.046758121	-3.02733781	Late embryogenesis abundant protein Lea14	elongation zone	12 h
HORVU.MOREX.r3.4HG0351070.1	-0.680823961	2.367322112	-2.859267049	0.00606	0.048988577	-3.02810769	STRUBBELIG-receptor family 5	elongation zone	12 h
HORVU.MOREX.r3.2HG0108680.1	-0.499951742	3.066286477	-2.922706815	0.00509	0.045229989	-3.02887277	Demethylmenaquinone methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.2HG0112180.1	-0.53789941	4.377395587	-2.887234133	0.00561	0.047204707	-3.02969937	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.5HG0477180.1	0.309915771	5.597570777	2.914786526	0.0052	0.045655368	-3.02985482	LAG1 longevity assurance-like protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0215610.1	0.929375841	6.340912174	2.959324862	0.0046	0.042717988	-3.02998687	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.2HG0168090.1	0.320024673	5.385495042	2.904533395	0.00535	0.046230732	-3.03029409	Sphingomyelin synthase-like domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0689490.1	0.549083273	6.098734945	2.883114873	0.00568	0.047427345	-3.03126766	Peptidyl-prolyl cis-trans isomerase	elongation zone	12 h
HORVU.MOREX.r3.7HG0739640.1	0.779701561	8.298465212	2.982652606	0.00431	0.041282541	-3.03234696	Auxin efflux carrier component	elongation zone	12 h
HORVU.MOREX.r3.1HG0063880.1	-0.566652859	4.61444207	-2.906214244	0.00533	0.04618095	-3.03457094	Glycosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0656430.1	0.300035593	6.915191761	2.943914995	0.0048	0.043752599	-3.03531619	Zinc finger CCCH domain protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0078910.1	-0.459548855	4.676362005	-2.93960023	0.00486	0.044063319	-3.03579908	p-loop containing nucleoside triphosphate hydrolases superfami	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.4HG0388980.2	0.342050984	5.157208042	2.883260022	0.00567	0.047427345	-3.03615129	#N/A	elongation zone	12 h
HORVU.MOREX.r3.4HG0389850.1	-0.380673133	6.082211287	-3.00105967	0.0041	0.040265883	-3.03687727	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0619540.1	0.339176199	5.67347569	2.869433815	0.00589	0.048306767	-3.03868711	THO complex subunit 5	elongation zone	12 h
HORVU.MOREX.r3.2HG0160270.2	0.607985534	9.915803777	3.060189158	0.00347	0.037761197	-3.04068471	40S ribosomal protein S8	elongation zone	12 h
HORVU.MOREX.r3.4HG0387150.1	0.871467136	6.899898072	2.911459842	0.00525	0.045859795	-3.04154365	Histone H2A	elongation zone	12 h
HORVU.MOREX.r3.3HG0312360.1	-0.239135493	7.147206035	-3.037752985	0.00369	0.038671495	-3.04442983	Coiled-coil domain-containing protein SCD2	elongation zone	12 h
HORVU.MOREX.r3.7HG0726700.1	0.73170601	7.183776553	2.918621601	0.00515	0.045408324	-3.04638955	Leucine-rich repeat protein kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0630670.1	2.093795787	8.145324526	2.856288785	0.00611	0.049242146	-3.0481649	rRNA 2'-O-methyltransferase fibrillarin 2	elongation zone	12 h
HORVU.MOREX.r3.7HG0655280.1	-0.455658489	1.566144439	-2.926338054	0.00504	0.044895531	-3.04949994	Galactoside 2-alpha-L-fucosyltransferase	elongation zone	12 h
HORVU.MOREX.r3.6HG0608780.1	0.399007469	7.822442469	3.009416855	0.004	0.039983	-3.05031984	Heat shock 70 kDa protein, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0160130.1	-0.478213173	3.662810319	-2.954697699	0.00466	0.042998159	-3.05115306	Basic helix-loop-helix transcription factor	elongation zone	12 h
HORVU.MOREX.r3.5HG0511110.3	-0.398906574	4.233551779	-2.927048358	0.00503	0.044862884	-3.0520262	Potassium channel	elongation zone	12 h
HORVU.MOREX.r3.5HG0530200.1	-0.284987088	8.300591094	-3.106295829	0.00304	0.035944821	-3.05248227	Actin	elongation zone	12 h
HORVU.MOREX.r3.7HG0654410.1	0.60383893	6.620820722	2.926893326	0.00503	0.044862884	-3.0527049	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.1HG0035400.1	-0.412076659	4.194434053	-2.904954322	0.00535	0.046230732	-3.05298171	Ras-related protein, expressed	elongation zone	12 h
HORVU.MOREX.r3.6HG0614500.1	0.321876284	5.054555082	2.861019963	0.00603	0.048830126	-3.05752066	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	elongation zone	12 h
HORVU.MOREX.r3.2HG0199300.1	1.062718027	7.23323174	2.871224724	0.00586	0.048231861	-3.05920162	Protein SDA1-like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0614840.1	-0.406983683	5.332590306	-2.956722796	0.00463	0.042834083	-3.06198672	Shikimate kinase	elongation zone	12 h
HORVU.MOREX.r3.7HG0656790.1	0.693229773	6.625384114	2.890726519	0.00556	0.047007942	-3.06284911	30S ribosomal protein S10	elongation zone	12 h
HORVU.MOREX.r3.1HG0076980.1	0.297279412	8.500485602	3.035850604	0.00371	0.038729899	-3.06393726	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase s	elongation zone	12 h
HORVU.MOREX.r3.3HG0305860.1	0.79863207	6.802235483	2.870517047	0.00588	0.048268753	-3.07892799	Nuclear transport factor 2 family protein with RNA binding doma	elongation zone	12 h
HORVU.MOREX.r3.2HG0213250.1	0.470164991	6.347478748	2.946782096	0.00476	0.043677865	-3.08025968	Choline transporter-related family protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0405780.1	-0.413383852	7.951420898	-3.075359572	0.00332	0.037190743	-3.08229569	Receptor-like protein kinase	elongation zone	12 h
HORVU.MOREX.r3.1HG0017750.1	-0.345287872	4.005500278	-2.854091136	0.00615	0.04938991	-3.08271584	Kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0625570.1	-0.457769965	5.941941183	-2.985102018	0.00428	0.041182136	-3.09233418	Transmembrane protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0515330.1	0.645838988	6.09421809	2.855085326	0.00613	0.049316553	-3.09511582	60S ribosomal protein L44	elongation zone	12 h
HORVU.MOREX.r3.2HG0126380.1	-0.453337732	5.874038041	-3.027913762	0.0038	0.039108923	-3.09826364	#N/A	elongation zone	12 h
HORVU.MOREX.r3.6HG0546420.1	0.811902893	9.042284244	2.976670348	0.00438	0.041550671	-3.09998281	60S ribosomal protein L13	elongation zone	12 h
HORVU.MOREX.r3.2HG0113880.1	-0.453881692	4.823614042	-2.872876746	0.00584	0.048151385	-3.1025005	Heavy metal transport/detoxification superfamily protein, putati	elongation zone	12 h
HORVU.MOREX.r3.1HG0056740.1	0.541835962	8.162242671	2.992578221	0.00419	0.040685115	-3.10546117	Pyruvate kinase	elongation zone	12 h
HORVU.MOREX.r3.3HG0263050.1	0.355124609	6.674660346	2.898306954	0.00545	0.046616466	-3.10673343	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfami	elongation zone	12 h
HORVU.MOREX.r3.4HG0393930.1	0.5709058	8.844580814	2.994184921	0.00417	0.040647009	-3.10797217	Ubiquitin	elongation zone	12 h
HORVU.MOREX.r3.2HG0176960.1	0.283907521	4.988465286	2.854672893	0.00614	0.049352603	-3.10993465	Kelch repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0187990.1	-0.353201691	5.49990496	-2.936215758	0.00491	0.044321273	-3.11068085	O-fucosyltransferase family protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0518560.1	-1.199400096	2.148281347	-2.853963524	0.00615	0.04938991	-3.11372973	Leucine-rich repeat protein kinase family protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0721760.1	0.289413786	8.421100262	3.02053987	0.00388	0.039407591	-3.11650123	Translocon-associated protein subunit alpha	elongation zone	12 h
HORVU.MOREX.r3.7HG0752370.1	-0.606400625	2.08824866	-2.919250656	0.00514	0.045371176	-3.11705672	NBS-LRR-like resistance protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0705860.1	-0.397078963	7.982365784	-3.065353788	0.00342	0.037489533	-3.11753886	Non-lysosomal glucosylceramidase	elongation zone	12 h
HORVU.MOREX.r3.7HG0681100.1	-0.280121191	5.610348477	-2.930832179	0.00498	0.044603947	-3.11893017	Glycine-rich domain-containing protein 2	elongation zone	12 h
HORVU.MOREX.r3.1HG0044310.1	0.603045083	7.299346006	2.90796892	0.0053	0.046106442	-3.11979322	Nascent polypeptide-associated complex subunit beta	elongation zone	12 h
HORVU.MOREX.r3.6HG0631360.1	-0.33504033	4.355721511	-2.86812664	0.00591	0.048306767	-3.12279946	Disease resistance protein RPM1	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.1HG0055230.1	0.667815911	7.59025634	2.955843608	0.00465	0.042900147	-3.12451366	Methyltransferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0457110.1	0.56952416	9.82719665	3.028770609	0.00379	0.039108923	-3.1301289	30S ribosomal protein S4	elongation zone	12 h
HORVU.MOREX.r3.4HG0389620.1	-0.361026935	4.010754431	-2.84958727	0.00622	0.049700096	-3.13055524	Glycogen synthase	elongation zone	12 h
HORVU.MOREX.r3.7HG0739480.1	0.656194298	7.565794341	2.92065256	0.00512	0.045330047	-3.13163572	Histone H2B	elongation zone	12 h
HORVU.MOREX.r3.2HG0189070.1	1.219226798	1.242983665	2.919860015	0.00513	0.045371176	-3.13231304	14 kDa proline-rich protein dc2.15	elongation zone	12 h
HORVU.MOREX.r3.3HG0301930.1	-0.445321284	4.019686283	-2.879328914	0.00574	0.047754823	-3.13447671	G patch domain protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0390230.1	0.393026691	6.080893711	2.862045233	0.00601	0.048753496	-3.13671945	Eukaryotic translation initiation factor 4E	elongation zone	12 h
HORVU.MOREX.r3.7HG0648810.1	-0.256091208	6.330560766	-2.971082351	0.00445	0.041967805	-3.13702423	Acyl-[acyl-carrier-protein] hydrolase	elongation zone	12 h
HORVU.MOREX.r3.3HG0223160.1	-0.547742168	5.278306557	-3.01161857	0.00398	0.03986915	-3.14083548	aberrant root formation protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0727290.1	-0.57864768	3.998416026	-2.894177742	0.00551	0.046806243	-3.14307341	#N/A	elongation zone	12 h
HORVU.MOREX.r3.1HG0074500.1	0.799384988	7.370525428	2.891596627	0.00555	0.046934592	-3.14670496	Histone H3	elongation zone	12 h
HORVU.MOREX.r3.2HG0200920.1	-0.59318877	3.047317061	-2.937004883	0.00489	0.044263597	-3.14692729	Agmatine coumaroyltransferase-2	elongation zone	12 h
HORVU.MOREX.r3.2HG0112690.1	-0.717408979	1.247172627	-2.951919897	0.0047	0.043259525	-3.14743163	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.3HG0255020.1	-0.699286777	3.485610317	-3.005991358	0.00404	0.040178373	-3.15157012	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.7HG0691650.1	0.333773703	7.880664191	2.948593932	0.00474	0.043517337	-3.15534981	RNA binding protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0424290.1	-0.341661281	9.703425568	-3.069823574	0.00337	0.037331432	-3.15654538	Cysteine synthase	elongation zone	12 h
HORVU.MOREX.r3.3HG0254950.1	-0.84685387	1.019759768	-2.878040936	0.00576	0.04776728	-3.17129481	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.1HG0022060.1	0.47671216	7.428714781	2.901011166	0.00541	0.046443727	-3.17705313	Cullin-1	elongation zone	12 h
HORVU.MOREX.r3.4HG0396220.1	0.304230092	8.114651828	2.980936502	0.00433	0.041314646	-3.17831158	Alpha-glucosidase like protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0566190.1	-0.513018484	5.134408532	-3.023600209	0.00384	0.039284359	-3.18368411	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.6HG0624630.1	0.330304524	6.985603223	2.928929207	0.005	0.044750195	-3.18488271	Aspartate aminotransferase	elongation zone	12 h
HORVU.MOREX.r3.5HG0489130.1	0.950825725	6.654428009	2.931957877	0.00496	0.044592291	-3.18490221	Receptor protein kinase, putative	elongation zone	12 h
HORVU.MOREX.r3.4HG0337740.1	-0.361726469	6.566981129	-2.943359643	0.00481	0.043773947	-3.18694458	Receptor protein kinase, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0041260.1	0.305520107	7.367448887	2.923765837	0.00508	0.045176231	-3.18999341	Eukaryotic translation initiation factor 4E	elongation zone	12 h
HORVU.MOREX.r3.6HG0614970.1	-0.315253944	5.579922669	-2.877932734	0.00576	0.04776728	-3.1916892	Kelch repeat-containing protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0051180.1	-0.428635896	5.081434726	-2.927453157	0.00503	0.044862884	-3.19442782	Rhomboid-like protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0272030.1	0.477768938	8.079674682	2.930587373	0.00498	0.044603947	-3.19450287	N-alpha-acetyltransferase 16, NatA auxiliary subunit	elongation zone	12 h
HORVU.MOREX.r3.6HG0549380.1	0.404296281	7.237694492	2.877918751	0.00576	0.04776728	-3.19525184	Gamma-glutamylcyclotransferase	elongation zone	12 h
HORVU.MOREX.r3.7HG0738190.1	-0.335818143	5.38770736	-2.915275459	0.0052	0.045616889	-3.20860932	Copper-transporting ATPase	elongation zone	12 h
HORVU.MOREX.r3.5HG0523150.1	0.248718051	6.194464004	2.845307162	0.00629	0.049959998	-3.2111347	Protein phosphatase 2c, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0006400.1	-0.551255078	6.387241341	-2.986506564	0.00427	0.041089957	-3.21165373	Beta-1,3-galactosyltransferase-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0379400.1	-0.694825149	1.850080654	-2.937905133	0.00488	0.044199271	-3.22032492	Protein kinase-like protein	elongation zone	12 h
HORVU.MOREX.r3.5HG0508450.1	-0.369809707	5.166935854	-2.865356915	0.00596	0.048546205	-3.22195598	Calmodulin-binding family protein, putative, expressed	elongation zone	12 h
HORVU.MOREX.r3.6HG0609420.1	-0.379903983	5.023973234	-2.903433263	0.00537	0.046274876	-3.22947899	phosphoenolpyruvate carboxykinase 2	elongation zone	12 h
HORVU.MOREX.r3.5HG0458450.1	-0.32439936	5.682873141	-2.8671452	0.00593	0.048385844	-3.23168701	TLD domain-containing protein 1	elongation zone	12 h
HORVU.MOREX.r3.1HG0066850.1	-0.389248488	4.235298003	-2.854277143	0.00614	0.04938644	-3.23343777	Adenine nucleotide alpha hydrolases-like superfamily	elongation zone	12 h
HORVU.MOREX.r3.5HG0507470.1	-0.34858237	5.264725422	-2.893468731	0.00552	0.046829376	-3.23578036	Arogenate dehydratase	elongation zone	12 h
HORVU.MOREX.r3.3HG0325580.1	-0.256987513	5.824048637	-2.871851942	0.00585	0.048189541	-3.23913609	MACPF domain-containing protein	elongation zone	12 h
HORVU.MOREX.r3.7HG0710920.1	-0.267048239	5.393550621	-2.852359858	0.00617	0.049512065	-3.24075752	TOM1-like protein 2	elongation zone	12 h
HORVU.MOREX.r3.6HG0602990.1	0.692651589	7.353646827	2.847211543	0.00626	0.04981773	-3.24091281	High mobility group family	elongation zone	12 h
HORVU.MOREX.r3.2HG0173880.1	0.201180376	6.785205192	2.887104102	0.00562	0.047204707	-3.24664055	UBX domain-containing protein, putative	elongation zone	12 h

Table Sc Continued.

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	gene description	root zone	time point
HORVU.MOREX.r3.6HG0551180.1	0.35153076	7.241444096	2.859294997	0.00606	0.048988577	-3.25988646	3-isopropylmalate dehydratase large subunit	elongation zone	12 h
HORVU.MOREX.r3.1HG0022440.1	0.524341881	7.971656134	2.889309318	0.00558	0.047136585	-3.26086177	Chromatin remodeling factor, putative	elongation zone	12 h
HORVU.MOREX.r3.2HG0165200.1	-0.599333802	5.318500517	-2.958450791	0.00461	0.042747009	-3.263942	#N/A	elongation zone	12 h
HORVU.MOREX.r3.3HG0254150.1	-0.276211082	7.075489408	-2.949776176	0.00472	0.043452654	-3.26725358	Phosphoadenosine phosphosulfate reductase family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0292280.1	0.528467151	7.335521365	2.856072199	0.00611	0.049242146	-3.27711245	Ubiquitin carboxyl-terminal hydrolase-like protein	elongation zone	12 h
HORVU.MOREX.r3.4HG0369570.1	0.173927817	10.41352761	3.075501904	0.00332	0.037190743	-3.28443463	Alpha-1,4-glucan-protein synthase [UDP-forming]	elongation zone	12 h
HORVU.MOREX.r3.1HG0072860.1	0.733714287	8.053944148	2.868057399	0.00592	0.048306767	-3.28509427	30S ribosomal protein S12	elongation zone	12 h
HORVU.MOREX.r3.3HG0296600.1	0.583286833	9.192372739	2.930761361	0.00498	0.044603947	-3.29675842	60S ribosomal protein L24	elongation zone	12 h
HORVU.MOREX.r3.6HG0578930.1	0.203231026	7.54149509	2.892840608	0.00553	0.046871369	-3.29793007	Histone deacetylase	elongation zone	12 h
HORVU.MOREX.r3.3HG0314490.2	-0.490389483	3.653110454	-2.84923063	0.00623	0.049700096	-3.30769096	Receptor-like kinase	elongation zone	12 h
HORVU.MOREX.r3.7HG0704470.1	0.623393968	8.481284146	2.895382676	0.00549	0.046758121	-3.313952	60S acidic ribosomal protein P1	elongation zone	12 h
HORVU.MOREX.r3.6HG0550950.1	0.391071811	7.177293507	2.85042772	0.00621	0.049645466	-3.31624312	NADP dependent sorbitol 6-phosphate dehydrogenase family pr	elongation zone	12 h
HORVU.MOREX.r3.6HG0610930.1	0.405844507	7.991073157	2.899205799	0.00543	0.046579264	-3.31673128	Enhancer of mRNA-decapping protein 4	elongation zone	12 h
HORVU.MOREX.r3.6HG0628930.1	0.477342458	7.959731866	2.868692565	0.00591	0.048306767	-3.31743782	Alcohol dehydrogenase	elongation zone	12 h
HORVU.MOREX.r3.4HG0402000.1	0.526499416	8.180685451	2.91919627	0.00514	0.045371176	-3.32030656	Kinase interacting (KIP1-like) family protein, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0081060.1	0.429929803	7.924567077	2.881412582	0.0057	0.047595228	-3.3233397	Mitochondrial outer membrane porin	elongation zone	12 h
HORVU.MOREX.r3.5HG0491130.1	0.478289324	8.223604151	2.87775393	0.00576	0.04776728	-3.3376914	Chaperone DnaK	elongation zone	12 h
HORVU.MOREX.r3.2HG0167300.1	-0.472868125	4.945499856	-2.872404772	0.00585	0.04818291	-3.34747866	Late embryogenesis abundant (LEA) hydroxyproline-rich glycopr	elongation zone	12 h
HORVU.MOREX.r3.1HG0024510.1	-0.423164755	5.713562753	-2.90219879	0.00539	0.046372228	-3.35198611	Universal stress protein	elongation zone	12 h
HORVU.MOREX.r3.2HG0112820.1	0.592113834	9.728760634	2.932589139	0.00495	0.044552225	-3.35443581	Ribosomal protein L19	elongation zone	12 h
HORVU.MOREX.r3.6HG0593920.1	0.418633688	8.297449459	2.874308177	0.00582	0.048001992	-3.36223612	#N/A	elongation zone	12 h
HORVU.MOREX.r3.7HG0714620.1	-0.403076027	6.402884248	-2.886294075	0.00563	0.047232185	-3.36583951	3'-N-debenzoyl-2'-deoxytaxol N-benzoyltransferase	elongation zone	12 h
HORVU.MOREX.r3.1HG0039670.1	0.208126993	7.408424513	2.869064101	0.0059	0.048306767	-3.37822814	Calcium ion-binding protein	elongation zone	12 h
HORVU.MOREX.r3.6HG0564480.1	0.565485578	8.296340254	2.856799754	0.0061	0.04922198	-3.3869467	T-complex protein 1 subunit eta	elongation zone	12 h
HORVU.MOREX.r3.5HG0444520.1	-0.612373717	5.327750335	-2.909647079	0.00528	0.045952435	-3.38935312	NADP-dependent alkenal double bond reductase	elongation zone	12 h
HORVU.MOREX.r3.1HG0073380.1	0.685789953	8.454580573	2.851902871	0.00618	0.049512564	-3.39480067	60S ribosomal protein L36	elongation zone	12 h
HORVU.MOREX.r3.5HG0470270.1	0.56900555	9.530865348	2.903417876	0.00537	0.046274876	-3.39926061	50S ribosomal protein L22	elongation zone	12 h
HORVU.MOREX.r3.1HG0088510.1	0.695413918	9.089763599	2.867305181	0.00593	0.048383961	-3.41933361	60S ribosomal protein L18a	elongation zone	12 h
HORVU.MOREX.r3.7HG0641060.1	-0.398401199	7.954456485	-2.927079513	0.00503	0.044862884	-3.42045596	Kinase-like protein	elongation zone	12 h
HORVU.MOREX.r3.1HG0094710.1	0.331758591	8.999934807	2.892619549	0.00553	0.046880427	-3.43915997	Translation initiation factor if-2, putative	elongation zone	12 h
HORVU.MOREX.r3.7HG0718190.1	-0.572568363	6.009060521	-2.894367508	0.0055	0.046806243	-3.4554614	ABC transporter family protein	elongation zone	12 h
HORVU.MOREX.r3.3HG0254990.1	-0.389976397	7.164090125	-2.919074338	0.00514	0.045371176	-3.47010269	Peroxidase	elongation zone	12 h
HORVU.MOREX.r3.3HG0283130.1	-0.689769038	6.080795139	-2.850785274	0.0062	0.049624591	-3.47494432	Subtilisin-like protease	elongation zone	12 h
HORVU.MOREX.r3.2HG0197260.1	-0.277286229	7.52618409	-2.892396638	0.00553	0.046889731	-3.49218591	WEB family protein, chloroplastic	elongation zone	12 h
HORVU.MOREX.r3.3HG0236850.1	-0.234602448	8.690188681	-2.896704704	0.00547	0.046711054	-3.55190634	Malic enzyme	elongation zone	12 h
HORVU.MOREX.r3.7HG0711070.1	-0.323777753	7.633823382	-2.877825963	0.00576	0.04776728	-3.55382313	Receptor-like kinase, putative	elongation zone	12 h
HORVU.MOREX.r3.1HG0069420.1	-0.24401767	7.626353217	-2.86506656	0.00596	0.048546205	-3.5751131	Cytochrome P450	elongation zone	12 h
HORVU.MOREX.r3.2HG0202670.1	-0.28364566	8.97883709	-2.916950289	0.00517	0.045490951	-3.57983942	Plasma membrane ATPase	elongation zone	12 h
HORVU.MOREX.r3.3HG0222130.1	0.244033212	8.795276054	2.848139225	0.00625	0.049750126	-3.62747935	Transmembrane protein 214	elongation zone	12 h
HORVU.MOREX.r3.7HG0723600.1	-0.5677823	3.100437987	-2.857416629	0.00609	0.049158681	-3.64420562	Peroxidase	elongation zone	12 h

Table STa Enriched biological processes terms among genes differentially expressed between wild type and *e gt2* (false discovery rate (FDR) <5%) root caps after a gravistimulation time-course experiment.

Go term	**description**	time points			
		0h	3h	6h	12h
GO:0031047	gene silencing by RNA	🟥	⬜	⬜	⬜
GO:0031122	cytoplasmic microtubule organization	🟥	🟥	🟥	🟥
GO:0030865	cortical cytoskeleton organization	🟥	🟥	🟥	🟥
GO:0010091	trichome branching	🟥	🟥	🟥	🟥
GO:0005978	glycogen biosynthetic process	🟥	⬜	🟥	🟥
GO:0016049	cell growth	🟥	🟥	⬜	⬜
GO:0009832	plant-type cell wall biogenesis	🟥	🟥	🟥	🟥
GO:0006730	one-carbon metabolic process	🟦	🟦	🟦	⬜
GO:0010951	negative regulation of endopeptidase act...	🟦	⬜	⬜	⬜
GO:0009611	response to wounding	🟦	⬜	⬜	⬜
GO:0006979	response to oxidative stress	⬜	🟥	⬜	⬜
GO:0042744	hydrogen peroxide catabolic process	⬜	🟥	⬜	⬜
GO:0006511	ubiquitin-dependent protein catabolic pr...	⬜	⬜	🟥	⬜
GO:0006829	zinc ion transport	⬜	⬜	🟥	⬜
GO:0039651	induction by virus of host cysteine-type endopeptidase activity involved in apoptotic process	⬜	⬜	🟥	⬜
GO:0075732	viral penetration into host nucleus	⬜	⬜	🟥	⬜
GO:0009231	riboflavin biosynthetic process	⬜	⬜	🟥	🟥
GO:0006839	mitochondrial transport	⬜	⬜	🟥	⬜
GO:0090502	RNA phosphodiester bond hydrolysis, endonucleolytic	⬜	⬜	🟥	⬜
GO:0009606	tropism	⬜	⬜	⬜	🟥
GO:0019882	antigen processing and presentation	⬜	⬜	⬜	🟥
GO:1990542	mitochondrial transmembrane transport	⬜	⬜	⬜	🟥
GO:0051603	proteolysis involved in cellular protein catabolic process	⬜	⬜	⬜	🟥
GO:0009637	response to blue light	⬜	⬜	⬜	🟥
GO:0006004	fucose metabolic process	⬜	⬜	⬜	🟥
GO:0044743	protein transmembrane import into intracellular organelle	⬜	⬜	⬜	🟥
GO:0006626	protein targeting to mitochondrion	⬜	⬜	⬜	🟥
GO:0065002	intracellular protein transmembrane transport	⬜	⬜	⬜	🟥
GO:0006354	DNA-templated transcription, elongation	⬜	⬜	⬜	🟥
GO:0009800	cinnamic acid biosynthetic process	⬜	⬜	⬜	🟦
GO:0006559	L-phenylalanine catabolic process	⬜	⬜	⬜	🟦

🟥 up-regulated
🟦 down-regulated

Table STb Enriched biological processes terms among genes differentially expressed between wild type and *egt2* (false discovery rate (FDR) <5%) meristems after a gravistimulation time-course experiment.

Go term	**description**	time points			
		0h	3h	6h	12h
GO:0031122	cytoplasmic microtubule organization	🟥	🟥	🟥	🟥
GO:0030865	cortical cytoskeleton organization	🟥	🟥	🟥	🟥
GO:0010091	trichome branching	🟥	🟥	🟥	🟥
GO:0009231	riboflavin biosynthetic process	🟥	⬜	⬜	⬜
GO:0016049	cell growth	🟥	🟥	🟥	🟥
GO:0005978	glycogen biosynthetic process	🟥	⬜	🟥	🟥
GO:0009832	plant-type cell wall biogenesis	🟥	🟥	🟥	🟥
GO:0006730	one-carbon metabolic process	🟦	🟦	🟦	🟦
GO:0006979	response to oxidative stress	⬜	🟥	⬜	⬜
GO:0042744	hydrogen peroxide catabolic process	⬜	🟥	⬜	⬜
GO:0006511	ubiquitin-dependent protein catabolic process	⬜	🟥	⬜	⬜
GO:0016567	protein ubiquitination	⬜	🟥	⬜	⬜
GO:0006352	DNA-templated transcription, initiation	⬜	⬜	🟥	🟥
GO:0006413	translational initiation	⬜	⬜	🟥	🟥
GO:0006813	potassium ion transport	⬜	⬜	⬜	🟥
GO:0030488	tRNA methylation	⬜	⬜	⬜	🟥
GO:0030001	metal ion transport	⬜	⬜	⬜	🟦

🟥 up-regulated
🟦 down-regulated

Table STc Enriched biological processes terms among genes differentially expressed between wild type and *egt2* (false discovery rate (FDR) <5%) elongation zones after a gravistimulation time-course experiment.

Go term	description	time points			
		0h	3h	6h	12h
GO:0006352	DNA-templated transcription, initiation	🟥	🟥	🟥	⬜
GO:0006813	potassium ion transport	🟥	⬜	⬜	⬜
GO:0010091	trichome branching	🟥	🟥	🟥	⬜
GO:0031122	cytoplasmic microtubule organization	🟥	🟥	🟥	⬜
GO:0030865	cortical cytoskeleton organization	🟥	🟥	⬜	⬜
GO:0016049	cell growth	🟥	🟥	⬜	⬜
GO:0009832	plant-type cell wall biogenesis	🟥	🟥	🟥	⬜
GO:0006308	DNA catabolic process	🟥	⬜	⬜	⬜
GO:0006413	translational initiation	🟥	🟥	🟥	⬜
GO:0006458	'de novo' protein folding	🟦	🟦	⬜	🟥
GO:0010951	negative regulation of endopeptidase activity	🟦	🟦	⬜	🟦
GO:0019511	peptidyl-proline hydroxylation	🟦	⬜	🟥	🟦
GO:1990542	mitochondrial transmembrane transport	🟦	🟦	⬜	🟥
GO:0006730	one-carbon metabolic process	🟦	🟦	⬜	🟥
GO:0044743	protein transmembrane import into intracellular organelle	🟦	🟦	⬜	🟥
GO:0006626	protein targeting to mitochondrion	🟦	🟦	⬜	🟥
GO:0065002	intracellular protein transmembrane transport	🟦	🟦	⬜	🟥
GO:0006433	prolyl-tRNA aminoacylation	⬜	🟥	🟥	⬜
GO:0070588	calcium ion transmembrane transport	⬜	🟦	⬜	⬜
GO:0009744	response to sucrose	⬜	⬜	🟥	🟥
GO:0009664	plant-type cell wall organization	⬜	⬜	🟪	⬜
GO:0045489	pectin biosynthetic process	⬜	⬜	🟥	🟥
GO:0070592	cell wall polysaccharide biosynthetic process	⬜	⬜	🟥	⬜
GO:0006457	protein folding	⬜	⬜	🟥	🟥
GO:0032507	maintenance of protein location in cell	⬜	⬜	🟥	⬜
GO:0006886	intracellular protein transport	⬜	⬜	🟥	⬜
GO:0072595	maintenance of protein localization in organelle	⬜	⬜	🟥	⬜
GO:0046149	pigment catabolic process	⬜	⬜	🟥	⬜
GO:0006099	tricarboxylic acid cycle	⬜	⬜	🟥	⬜
GO:0008299	isoprenoid biosynthetic process	⬜	⬜	🟥	⬜
GO:0006636	unsaturated fatty acid biosynthetic process	⬜	⬜	🟥	⬜
GO:0016126	sterol biosynthetic process	⬜	⬜	🟥	⬜
GO:0001676	long-chain fatty acid metabolic process	⬜	⬜	🟥	⬜
GO:0019285	glycine betaine biosynthetic process from choline	⬜	⬜	🟥	⬜
GO:0006487	protein N-linked glycosylation	⬜	⬜	🟥	⬜
GO:0006004	fucose metabolic process	⬜	⬜	🟥	🟦
GO:0006044	N-acetylglucosamine metabolic process	⬜	⬜	🟥	⬜
GO:0007030	Golgi organization	⬜	⬜	🟥	⬜
GO:0048532	anatomical structure arrangement	⬜	⬜	🟥	⬜
GO:0010016	shoot system morphogenesis	⬜	⬜	🟥	⬜
GO:0006637	acyl-CoA metabolic process	⬜	⬜	🟥	⬜
GO:0043101	purine-containing compound salvage	⬜	⬜	🟥	⬜
GO:0009100	glycoprotein metabolic process	⬜	⬜	🟥	⬜
GO:0006979	response to oxidative stress	⬜	⬜	🟦	🟦
GO:0042744	hydrogen peroxide catabolic process	⬜	⬜	🟦	🟦
GO:0048146	positive regulation of fibroblast proliferation	⬜	⬜	🟦	⬜
GO:0071805	potassium ion transmembrane transport	⬜	⬜	🟦	⬜
GO:0034220	ion transmembrane transport	⬜	⬜	🟦	⬜
GO:0016119	carotene metabolic process	⬜	⬜	🟦	⬜
GO:0010411	xyloglucan metabolic process	⬜	⬜	🟦	⬜
GO:0042546	cell wall biogenesis	⬜	⬜	🟦	⬜
GO:0005975	carbohydrate metabolic process	⬜	⬜	🟦	⬜
GO:0035377	transepithelial water transport	⬜	⬜	🟦	⬜
GO:0006468	protein phosphorylation	⬜	⬜	🟦	🟦
GO:0032941	secretion by tissue	⬜	⬜	🟦	⬜
GO:0031960	response to corticosteroid	⬜	⬜	🟦	⬜
GO:0021670	lateral ventricle development	⬜	⬜	🟦	⬜
GO:0006696	ergosterol biosynthetic process	⬜	⬜	🟦	⬜
GO:0071474	cellular hyperosmotic response	⬜	⬜	🟦	⬜
GO:0046689	response to mercury ion	⬜	⬜	🟦	⬜
GO:0046274	lignin catabolic process	⬜	⬜	🟦	🟦

🟥 up-regulated
🟦 down-regulated
🟪 up and down-regulation

Table STc Continued.

Go term	description	time points			
		0h	3h	6h	12h
GO:0043525	positive regulation of neuron apoptotic process	⬜	⬜	🟦	⬜
GO:0006359	regulation of transcription by RNA polymerase III	⬜	⬜	⬜	🟥
GO:0009737	response to abscisic acid	⬜	⬜	⬜	🟥
GO:0071369	cellular response to ethylene stimulus	⬜	⬜	⬜	🟥
GO:0002183	cytoplasmic translational initiation	⬜	⬜	⬜	🟥
GO:0006913	nucleocytoplasmic transport	⬜	⬜	⬜	🟥
GO:0007018	microtubule-based movement	⬜	⬜	⬜	🟥
GO:0042254	ribosome biogenesis	⬜	⬜	⬜	🟥
GO:0042274	ribosomal small subunit biogenesis	⬜	⬜	⬜	🟥
GO:0006364	rRNA processing	⬜	⬜	⬜	🟥
GO:0009451	RNA modification	⬜	⬜	⬜	🟥
GO:0006189	'de novo' IMP biosynthetic process	⬜	⬜	⬜	🟥
GO:0009116	nucleoside metabolic process	⬜	⬜	⬜	🟥
GO:0009113	purine nucleobase biosynthetic process	⬜	⬜	⬜	🟥
GO:0009165	nucleotide biosynthetic process	⬜	⬜	⬜	🟥
GO:0006541	glutamine metabolic process	⬜	⬜	⬜	🟥
GO:0006529	asparagine biosynthetic process	⬜	⬜	⬜	🟥
GO:0006542	glutamine biosynthetic process	⬜	⬜	⬜	🟥
GO:0009089	lysine biosynthetic process via diaminopimelate	⬜	⬜	⬜	🟥
GO:0016575	histone deacetylation	⬜	⬜	⬜	🟥
GO:0006260	DNA replication	⬜	⬜	⬜	🟥
GO:0006270	DNA replication initiation	⬜	⬜	⬜	🟥
GO:0006271	DNA strand elongation involved in DNA replication	⬜	⬜	⬜	🟥
GO:0006269	DNA replication, synthesis of RNA primer	⬜	⬜	⬜	🟥
GO:0009658	chloroplast organization	⬜	⬜	⬜	🟥
GO:0018022	peptidyl-lysine methylation	⬜	⬜	⬜	🟥
GO:0051567	histone H3-K9 methylation	⬜	⬜	⬜	🟥
GO:0030488	tRNA methylation	⬜	⬜	⬜	🟥
GO:0034227	tRNA thio-modification	⬜	⬜	⬜	🟥
GO:0006418	tRNA aminoacylation for protein translation	⬜	⬜	⬜	🟥
GO:0002098	tRNA wobble uridine modification	⬜	⬜	⬜	🟥
GO:0006412	translation	⬜	⬜	⬜	🟥
GO:0010039	response to iron ion	⬜	⬜	⬜	🟥
GO:0046654	tetrahydrofolate biosynthetic process	⬜	⬜	⬜	🟥
GO:0009231	riboflavin biosynthetic process	⬜	⬜	⬜	🟥
GO:0016579	protein deubiquitination	⬜	⬜	⬜	🟥
GO:0043628	ncRNA 3'-end processing	⬜	⬜	⬜	🟥
GO:0006265	DNA topological change	⬜	⬜	⬜	🟥
GO:0048285	organelle fission	⬜	⬜	⬜	🟥
GO:0031509	subtelomeric heterochromatin assembly	⬜	⬜	⬜	🟥
GO:0006334	nucleosome assembly	⬜	⬜	⬜	🟥
GO:0030466	silent mating-type cassette heterochromatin assembly	⬜	⬜	⬜	🟥
GO:0007076	mitotic chromosome condensation	⬜	⬜	⬜	🟥
GO:0032508	DNA duplex unwinding	⬜	⬜	⬜	🟥
GO:0000183	rDNA heterochromatin assembly	⬜	⬜	⬜	🟥
GO:0030261	chromosome condensation	⬜	⬜	⬜	🟥
GO:0006414	translational elongation	⬜	⬜	⬜	🟥
GO:0006302	double-strand break repair	⬜	⬜	⬜	🟥
GO:0000377	nucleophile	⬜	⬜	⬜	🟥
GO:0071549	cellular response to dexamethasone stimulus	⬜	⬜	⬜	🟦
GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	⬜	⬜	⬜	🟦
GO:0009103	lipopolysaccharide biosynthetic process	⬜	⬜	⬜	🟦

Table Sy Overlapping genes among differentially expressed genes in the wild type time course experiment and *egt2* vs wild type comparisons.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.1HG0003270.1	🟥 yes		🟥 yes			🟥 yes		root cap
HORVU.MOREX.r3.1HG0062030.1			🟦 yes			🟥 yes		root cap
HORVU.MOREX.r3.1HG0092900.1			🟦 yes				🟥 yes	root cap
HORVU.MOREX.r3.2HG0113590.1			🟦 yes			🟥 yes	🟥 yes	root cap
HORVU.MOREX.r3.2HG0125600.1			🟦 yes				🟥 yes	root cap
HORVU.MOREX.r3.2HG0197550.1			🟦 yes				🟥 yes	root cap
HORVU.MOREX.r3.4HG0382640.1			🟦 yes				🟥 yes	root cap
HORVU.MOREX.r3.5HG0455240.1			🟦 yes				🟥 yes	root cap
HORVU.MOREX.r3.5HG0495750.1			🟦 yes				🟥 yes	root cap
HORVU.MOREX.r3.6HG0548800.1			🟦 yes				🟥 yes	root cap
HORVU.MOREX.r3.7HG0635050.1			🟦 yes				🟥 yes	root cap
HORVU.MOREX.r3.7HG0663550.1			🟦 yes	🟦 yes				root cap
HORVU.MOREX.r3.7HG0725940.1			🟥 yes				🟦 yes	root cap
HORVU.MOREX.r3.7HG0752370.1			🟥 yes				🟦 yes	elongation zone
HORVU.MOREX.r3.7HG0751110.1			🟦 yes			🟥 yes	🟥 yes	elongation zone
HORVU.MOREX.r3.7HG0751060.1		🟦 yes				🟥 yes		elongation zone
HORVU.MOREX.r3.7HG0750000.1		🟥 yes	🟥 yes			🟦 yes	🟦 yes	elongation zone
HORVU.MOREX.r3.7HG0749870.1			🟥 yes			🟦 yes	🟦 yes	elongation zone
HORVU.MOREX.r3.7HG0749150.1			🟦 yes				🟥 yes	elongation zone
HORVU.MOREX.r3.7HG0748670.1		🟥 yes				🟦 yes		elongation zone
HORVU.MOREX.r3.7HG0748070.1		🟥 yes	🟥 yes			🟦 yes	🟦 yes	elongation zone
HORVU.MOREX.r3.7HG0747940.1		🟥 yes	🟥 yes				🟦 yes	elongation zone
HORVU.MOREX.r3.7HG0747230.1		🟥 yes	🟥 yes			🟦 yes		elongation zone
HORVU.MOREX.r3.7HG0746770.1		🟦 yes	🟦 yes			🟥 yes	🟥 yes	elongation zone
HORVU.MOREX.r3.7HG0744540.1			🟦 yes				🟥 yes	elongation zone
HORVU.MOREX.r3.7HG0743900.1			🟥 yes				🟦 yes	elongation zone
HORVU.MOREX.r3.7HG0742080.1		🟥 yes	🟥 yes			🟦 yes		elongation zone
HORVU.MOREX.r3.7HG0739910.1		🟦 yes	🟦 yes	🟥 yes	🟥 yes	🟥 yes	🟥 yes	elongation zone
HORVU.MOREX.r3.7HG0739640.1			🟦 yes				🟥 yes	elongation zone
HORVU.MOREX.r3.7HG0739490.1			🟦 yes				🟥 yes	elongation zone
HORVU.MOREX.r3.7HG0739480.1			🟦 yes				🟥 yes	elongation zone
HORVU.MOREX.r3.7HG0739230.1		🟥 yes	🟥 yes			🟦 yes		elongation zone
HORVU.MOREX.r3.7HG0739030.1			🟥 yes			🟦 yes		elongation zone
HORVU.MOREX.r3.7HG0737340.1		🟥 yes	🟥 yes			🟦 yes		elongation zone
HORVU.MOREX.r3.7HG0736960.1		🟦 yes	🟦 yes			🟥 yes	🟥 yes	elongation zone

🟥	up-regulated
🟦	down-regualted

Table Sy Continued.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.7HG0736870.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0736860.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0736150.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.7HG0735840.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.7HG0734670.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.7HG0732610.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0731560.1		yes				yes		elongation zone
HORVU.MOREX.r3.7HG0731320.1		yes				yes		elongation zone
HORVU.MOREX.r3.7HG0730510.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.7HG0730070.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0729150.1			yes	yes	yes	yes	yes	elongation zone
HORVU.MOREX.r3.7HG0728630.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0728190.1			yes			yes		elongation zone
HORVU.MOREX.r3.7HG0728060.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.7HG0728000.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.7HG0727460.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0727350.1			yes			yes		elongation zone
HORVU.MOREX.r3.7HG0727290.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0726790.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.7HG0726770.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.7HG0726700.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0725060.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0724060.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.7HG0722360.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.7HG0721930.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0721760.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.7HG0721320.1		yes				yes		elongation zone
HORVU.MOREX.r3.7HG0720790.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.7HG0720670.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0719410.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0719170.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0719070.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0718540.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0718190.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.7HG0718170.1			yes			yes		elongation zone

Table Sy Continued.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.7HG0717610.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.7HG0716900.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.7HG0715570.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.7HG0714910.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0714900.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0714660.1		yes				yes		elongation zone
HORVU.MOREX.r3.7HG0714510.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0714400.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.7HG0712850.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.7HG0711890.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.7HG0709860.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0709230.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0708820.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0708120.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0708050.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0707700.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.7HG0706330.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0706310.1			yes			yes		elongation zone
HORVU.MOREX.r3.7HG0705860.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0704450.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.7HG0704060.1		yes					yes	elongation zone
HORVU.MOREX.r3.7HG0703580.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0702190.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0702050.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0700930.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0700270.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.7HG0697940.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0696190.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0690090.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0689490.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0688870.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.7HG0687630.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.7HG0685970.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0685920.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.7HG0684880.1		yes	yes			yes	yes	elongation zone

Table Sy Continued.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.7HG0680960.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.7HG0679350.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.7HG0679060.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0679050.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.7HG0677860.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0677580.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0677510.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.7HG0677230.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0676040.1		yes				yes	yes	elongation zone
HORVU.MOREX.r3.7HG0674990.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.7HG0674750.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0674720.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.7HG0674590.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0674480.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0674320.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.7HG0671880.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0670020.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0669580.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0668820.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.7HG0667730.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0667060.1		yes				yes		elongation zone
HORVU.MOREX.r3.7HG0666340.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.7HG0665990.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.7HG0665040.1		yes				yes		elongation zone
HORVU.MOREX.r3.7HG0664720.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.7HG0664130.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0663940.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.7HG0663730.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0662830.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0662210.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0662160.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0661890.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.7HG0661490.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.7HG0661480.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.7HG0658560.1		yes				yes		elongation zone

Table Sy Continued.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.7HG0656440.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0656430.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0656030.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0655210.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.7HG0654410.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0652830.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0650970.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0650300.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0649950.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.7HG0649240.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.7HG0648600.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0648460.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0647950.1		yes				yes		elongation zone
HORVU.MOREX.r3.7HG0647930.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0647520.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0642520.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.7HG0641750.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.7HG0641160.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0640560.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.7HG0636750.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0636630.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.7HG0635550.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0635160.1			yes				yes	elongation zone
HORVU.MOREX.r3.7HG0634520.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.6HG0634260.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0633420.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0632980.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0632320.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.6HG0632270.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.6HG0632020.2			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0631760.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0631710.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.6HG0631400.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0630650.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0628930.1			yes				yes	elongation zone

Table Sy Continued.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.6HG0628790.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.6HG0627570.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.6HG0627090.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0626650.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.6HG0626030.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.6HG0626020.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.6HG0625570.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.6HG0624650.1			yes			yes		elongation zone
HORVU.MOREX.r3.6HG0624630.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0624580.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0624390.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.6HG0623920.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0623830.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0622740.1		yes				yes		elongation zone
HORVU.MOREX.r3.6HG0621690.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0620520.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.6HG0619540.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0618170.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0617080.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0616960.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0616790.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0616480.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0616300.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.6HG0616240.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.6HG0616130.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0615840.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.6HG0615710.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0615130.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.6HG0614840.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0614500.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0614110.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0613230.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.6HG0612180.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.6HG0611290.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0610980.1		yes	yes			yes		elongation zone

Table Sy Continued.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.6HG0610500.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.6HG0609720.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.6HG0609520.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.6HG0608780.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.6HG0608390.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0608180.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0607590.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.6HG0607360.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.6HG0607000.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0606940.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0606930.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.6HG0605940.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.6HG0605290.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0605130.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0604860.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0604200.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.6HG0601830.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.6HG0601670.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.6HG0601260.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.6HG0600910.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.6HG0600000.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.6HG0598750.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0597640.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0597590.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.6HG0597360.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0595860.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0595190.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.6HG0589860.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.6HG0588350.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.6HG0587460.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0587140.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0586570.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0582480.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.6HG0582230.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0581020.1		yes	yes			yes		elongation zone

Table Sy Continued.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.6HG0581010.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0577220.1		yes				yes		elongation zone
HORVU.MOREX.r3.6HG0576550.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.6HG0576010.1		yes				yes		elongation zone
HORVU.MOREX.r3.6HG0575530.1		yes				yes		elongation zone
HORVU.MOREX.r3.6HG0574510.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0573870.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0573150.1			yes			yes		elongation zone
HORVU.MOREX.r3.6HG0570960.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0570230.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.6HG0569990.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0569490.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0569480.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0568910.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0568390.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0567780.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.6HG0567330.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0566940.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.6HG0566930.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0564690.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0564590.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.6HG0564510.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0560290.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0560140.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.6HG0558880.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0558800.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0558430.1		yes				yes		elongation zone
HORVU.MOREX.r3.6HG0557920.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.6HG0555700.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.6HG0555660.2		yes	yes			yes		elongation zone
HORVU.MOREX.r3.6HG0554520.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0554050.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.6HG0553310.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0553290.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0552860.1			yes				yes	elongation zone

Table Sy Continued.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.6HG0552800.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0551740.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0550950.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0550700.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0550670.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0550600.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.6HG0549990.1		yes				yes		elongation zone
HORVU.MOREX.r3.6HG0549510.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0548670.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0547570.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0546160.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.6HG0546140.1			yes			yes		elongation zone
HORVU.MOREX.r3.6HG0545970.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.6HG0545630.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0545620.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.6HG0545460.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0543800.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0543780.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0543770.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0543740.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0543730.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0542970.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0541940.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.6HG0541250.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.6HG0540620.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0540280.1			yes				yes	elongation zone
HORVU.MOREX.r3.6HG0540020.1		yes				yes	yes	elongation zone
HORVU.MOREX.r3.5HG0537150.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.5HG0536710.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.5HG0536490.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0536200.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.5HG0535780.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0534640.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0533630.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0533230.1		yes	yes			yes		elongation zone

Table Sy Continued.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.5HG0532630.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0532150.1	yes	yes	yes			yes		elongation zone
HORVU.MOREX.r3.5HG0532140.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.5HG0532120.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.5HG0531850.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0530750.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0529130.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0529120.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0528890.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0527890.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0527650.1			yes			yes		elongation zone
HORVU.MOREX.r3.5HG0527310.1		yes				yes		elongation zone
HORVU.MOREX.r3.5HG0526940.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0526250.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.5HG0526200.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.5HG0524060.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.5HG0523860.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.5HG0523150.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0520260.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0519810.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.5HG0519120.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.5HG0518560.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.5HG0517740.1	yes	yes	yes			yes		elongation zone
HORVU.MOREX.r3.5HG0517490.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0516720.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0516470.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0515610.1			yes		yes			elongation zone
HORVU.MOREX.r3.5HG0514790.3			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0514790.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0514490.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0514110.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0514100.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0513980.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.5HG0513810.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.5HG0513740.1			yes				yes	elongation zone

Table Sy Continued.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.5HG0513440.1			yes			yes		elongation zone
HORVU.MOREX.r3.5HG0513020.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.5HG0512510.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0512350.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0512230.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.5HG0511820.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.5HG0511450.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.5HG0511090.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.5HG0510940.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0508190.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0504160.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0502760.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0502750.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0502130.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0501980.1			yes			yes		elongation zone
HORVU.MOREX.r3.5HG0501270.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0500680.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.5HG0499490.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0498770.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0498150.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0494320.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0494040.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.5HG0493850.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.5HG0493070.1			yes			yes		elongation zone
HORVU.MOREX.r3.5HG0492650.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0491230.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.5HG0489840.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0489130.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0488050.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.5HG0488040.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.5HG0486660.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.5HG0486070.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0485610.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.5HG0485410.1		yes	yes	yes				elongation zone
HORVU.MOREX.r3.5HG0483980.1		yes	yes			yes	yes	elongation zone

Table Sy Continued.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.5HG0483860.1		yes				yes		elongation zone
HORVU.MOREX.r3.5HG0480980.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.5HG0479210.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0478390.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0477750.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.5HG0477180.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.5HG0477040.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.5HG0476380.1			yes			yes		elongation zone
HORVU.MOREX.r3.5HG0474540.1		yes				yes		elongation zone
HORVU.MOREX.r3.5HG0473970.1		yes				yes		elongation zone
HORVU.MOREX.r3.5HG0472880.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0472840.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0472810.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.5HG0472770.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.5HG0471960.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0470170.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.5HG0470030.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.5HG0469340.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.5HG0469300.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.5HG0467880.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0467870.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.5HG0466020.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0466010.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0465260.1			yes			yes		elongation zone
HORVU.MOREX.r3.5HG0463350.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0462450.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.5HG0462380.1			yes	yes				elongation zone
HORVU.MOREX.r3.5HG0462220.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.5HG0461950.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.5HG0461830.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0461280.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.5HG0461170.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0460720.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0459320.1			yes			yes		elongation zone
HORVU.MOREX.r3.5HG0458890.1		yes	yes				yes	elongation zone

Table Sy Continued.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.5HG0458010.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.5HG0450470.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0450100.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0447720.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0444350.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.5HG0442460.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0441420.1		yes				yes		elongation zone
HORVU.MOREX.r3.5HG0439710.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0438160.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0437610.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0435800.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0430460.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0430050.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.5HG0428840.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.5HG0427370.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0427060.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0426480.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0426110.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.5HG0420980.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0420970.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0420630.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.5HG0420480.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.5HG0420410.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0420210.1			yes				yes	elongation zone
HORVU.MOREX.r3.5HG0419590.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.4HG0418640.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0418530.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0418460.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.4HG0417920.1	yes	yes	yes			yes		elongation zone
HORVU.MOREX.r3.4HG0417410.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0417010.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.4HG0416730.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0416070.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0415600.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0415590.1		yes	yes				yes	elongation zone

Table Sy Continued.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.4HG0415490.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.4HG0415420.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.4HG0413410.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0413320.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.4HG0412370.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.4HG0411270.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0410640.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.4HG0409600.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0408780.1		yes	yes		yes			elongation zone
HORVU.MOREX.r3.4HG0408270.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.4HG0407230.1		yes				yes		elongation zone
HORVU.MOREX.r3.4HG0406600.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.4HG0406380.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0406140.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.4HG0405920.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.4HG0405780.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0405400.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.4HG0404740.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.4HG0403620.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.4HG0403250.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0403070.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0402730.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.4HG0402650.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0402600.2			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0402030.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.4HG0402000.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.4HG0401720.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0401710.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0400740.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.4HG0400520.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.4HG0400040.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0398910.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0398900.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0396660.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0396220.1			yes				yes	elongation zone

Table Sy Continued.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.4HG0395540.1	yes	yes	yes			yes		elongation zone
HORVU.MOREX.r3.4HG0394830.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.4HG0394460.1		yes				yes		elongation zone
HORVU.MOREX.r3.4HG0393520.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.4HG0393260.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0392160.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0391330.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.4HG0389250.1		yes				yes		elongation zone
HORVU.MOREX.r3.4HG0388470.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0388310.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.4HG0387150.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0387120.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0386830.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0386800.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0385300.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0385270.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0384390.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.4HG0384230.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.4HG0383870.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0383780.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.4HG0383530.3			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0383340.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0383070.1			yes			yes		elongation zone
HORVU.MOREX.r3.4HG0382500.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.4HG0380540.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.4HG0379960.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0379400.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.4HG0379290.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.4HG0378960.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0378580.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.4HG0375550.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0372280.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0370520.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0364210.1		yes				yes		elongation zone
HORVU.MOREX.r3.4HG0364050.1		yes	yes			yes	yes	elongation zone

Table Sy Continued.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.4HG0361420.2			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0358890.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0357230.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0355210.1		yes				yes		elongation zone
HORVU.MOREX.r3.4HG0354980.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.4HG0354970.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.4HG0354540.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0354010.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.4HG0353450.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0353330.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0353200.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0352780.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0352200.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.4HG0351750.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.4HG0351070.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0350900.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.4HG0350800.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0349310.1		yes				yes		elongation zone
HORVU.MOREX.r3.4HG0349170.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0348800.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.4HG0347760.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0346830.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.4HG0346720.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.4HG0345810.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0344990.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0344830.1		yes			yes	yes	yes	elongation zone
HORVU.MOREX.r3.4HG0344370.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.4HG0343050.1			yes			yes		elongation zone
HORVU.MOREX.r3.4HG0342950.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0342640.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0342160.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.4HG0342080.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.4HG0341080.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0338400.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0337950.1		yes	yes			yes		elongation zone

Table Sy Continued.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.4HG0337770.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0337120.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0337110.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.4HG0336310.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0335450.1		yes				yes		elongation zone
HORVU.MOREX.r3.4HG0335110.1			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0334360.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.4HG0333550.2			yes				yes	elongation zone
HORVU.MOREX.r3.4HG0333450.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.4HG0332930.1		yes				yes		elongation zone
HORVU.MOREX.r3.4HG0331420.1		yes					yes	elongation zone
HORVU.MOREX.r3.3HG0330980.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.3HG0330200.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.3HG0330120.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0329950.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.3HG0329870.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.3HG0329040.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.3HG0328480.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0327630.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0327170.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.3HG0326430.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.3HG0323810.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0323600.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.3HG0322660.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0321700.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.3HG0320840.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0319570.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0318700.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.3HG0318400.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0316280.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.3HG0316000.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0315410.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0314820.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0314070.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.3HG0313320.1		yes				yes		elongation zone

Table Sy Continued.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.3HG0313090.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.3HG0310540.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.3HG0310210.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0309820.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0309410.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.3HG0308980.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0308420.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0307850.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.3HG0307400.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.3HG0307310.1		yes				yes	yes	elongation zone
HORVU.MOREX.r3.3HG0307240.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.3HG0307120.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.3HG0306420.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0306210.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0305500.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0305440.1		yes				yes		elongation zone
HORVU.MOREX.r3.3HG0304660.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0304490.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.3HG0304420.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0304370.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0303970.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0303380.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.3HG0303330.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0302860.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0301930.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0299990.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0299820.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0298790.1		yes					yes	elongation zone
HORVU.MOREX.r3.3HG0298750.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.3HG0298340.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0297940.1			yes	yes	yes	yes	yes	elongation zone
HORVU.MOREX.r3.3HG0297330.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.3HG0297180.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0296490.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0295680.1			yes				yes	elongation zone

Table Sy Continued.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.3HG0293700.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0293570.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.3HG0293310.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.3HG0293130.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.3HG0293040.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0292680.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.3HG0291490.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0291030.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.3HG0290180.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0289070.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0288420.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0287690.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.3HG0287070.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.3HG0287000.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.3HG0286160.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0285840.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0285440.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.3HG0284780.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.3HG0283990.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0283250.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0281860.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0280970.1			yes			yes		elongation zone
HORVU.MOREX.r3.3HG0280960.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.3HG0280630.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.3HG0280160.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0280060.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.3HG0278170.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.3HG0277330.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0277200.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0276120.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.3HG0275530.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0275090.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.3HG0274100.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0273790.2			yes			yes		elongation zone
HORVU.MOREX.r3.3HG0272430.1			yes			yes	yes	elongation zone

Table Sy Continued.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.3HG0269960.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0264440.1		yes				yes		elongation zone
HORVU.MOREX.r3.3HG0259660.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0257680.1		yes				yes		elongation zone
HORVU.MOREX.r3.3HG0257310.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.3HG0256580.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0256300.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0255580.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0255020.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.3HG0254950.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.3HG0254940.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.3HG0254850.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0254430.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0253860.1		yes				yes		elongation zone
HORVU.MOREX.r3.3HG0252610.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.3HG0252240.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0251830.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0250060.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.3HG0249590.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0248280.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.3HG0247250.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0246670.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.3HG0246560.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0246500.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.3HG0246300.1		yes				yes		elongation zone
HORVU.MOREX.r3.3HG0246030.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0245250.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.3HG0245120.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.3HG0244240.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0244040.1		yes				yes		elongation zone
HORVU.MOREX.r3.3HG0244010.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0243920.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0243130.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.3HG0242030.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0241320.1		yes				yes		elongation zone

Table Sy Continued.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.3HG0240450.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0239980.1		yes				yes	yes	elongation zone
HORVU.MOREX.r3.3HG0238180.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.3HG0237990.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.3HG0237870.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0236000.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0235030.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.3HG0234970.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.3HG0234470.1		yes				yes		elongation zone
HORVU.MOREX.r3.3HG0234000.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.3HG0233990.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.3HG0233150.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0231880.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0231780.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0231630.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0230970.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0230190.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0230090.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0229480.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0224680.1			yes			yes		elongation zone
HORVU.MOREX.r3.3HG0223950.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0223160.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0222830.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.3HG0222130.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.3HG0221460.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0220360.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.3HG0219810.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0219650.1			yes				yes	elongation zone
HORVU.MOREX.r3.3HG0219410.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.3HG0219380.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.3HG0218560.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.3HG0218330.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0218010.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.2HG0217550.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0217090.1		yes	yes			yes		elongation zone

Table Sy Continued.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.2HG0215550.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0215310.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0215250.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0215220.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0214240.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.2HG0214090.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0214070.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.2HG0213250.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.2HG0213020.1		yes				yes		elongation zone
HORVU.MOREX.r3.2HG0212990.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0212900.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0212570.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.2HG0210510.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.2HG0210420.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0209030.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0207860.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.2HG0207790.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.2HG0207720.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.2HG0206470.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.2HG0205990.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.2HG0205760.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0205680.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0205550.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0205050.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0204960.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0204940.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.2HG0204920.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0204340.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.2HG0203500.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0203080.1		yes				yes		elongation zone
HORVU.MOREX.r3.2HG0200640.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0200630.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0199600.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0199560.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0197560.1			yes				yes	elongation zone

Table Sy Continued.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.2HG0197260.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0196960.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0196800.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.2HG0196630.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0195910.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0195690.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.2HG0195110.2			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0194620.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.2HG0194450.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0193220.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0192900.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0192000.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.2HG0190710.1			yes			yes		elongation zone
HORVU.MOREX.r3.2HG0189800.1			yes			yes		elongation zone
HORVU.MOREX.r3.2HG0189670.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.2HG0188300.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.2HG0187640.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0187450.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.2HG0186750.1		yes					yes	elongation zone
HORVU.MOREX.r3.2HG0186650.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0185840.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0185570.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0183740.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0182400.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.2HG0181680.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.2HG0181660.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0181550.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0181390.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0180580.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0180060.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0180010.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.2HG0179560.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.2HG0179540.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0178160.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.2HG0178050.1		yes	yes				yes	elongation zone

Table Sy Continued.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.2HG0176920.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0176290.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0173960.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.2HG0173550.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0173380.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0173340.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0173210.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0173190.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0172730.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.2HG0172050.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0171780.1		yes				yes		elongation zone
HORVU.MOREX.r3.2HG0171550.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.2HG0170560.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0170230.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.2HG0168730.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0168700.1		yes				yes		elongation zone
HORVU.MOREX.r3.2HG0168090.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.2HG0167620.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0167500.2			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0165840.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.2HG0165250.1			yes			yes		elongation zone
HORVU.MOREX.r3.2HG0165200.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0163090.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0161020.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0160690.1		yes				yes		elongation zone
HORVU.MOREX.r3.2HG0160550.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0160130.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.2HG0159500.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0158180.1			yes			yes		elongation zone
HORVU.MOREX.r3.2HG0157290.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0156810.1		yes				yes		elongation zone
HORVU.MOREX.r3.2HG0155810.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0152140.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0150450.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.2HG0147770.1			yes				yes	elongation zone

Table Sy Continued.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.2HG0142740.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0141140.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.2HG0140700.1		yes				yes		elongation zone
HORVU.MOREX.r3.2HG0140170.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.2HG0139810.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.2HG0139050.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0136670.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0136010.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0135860.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0135650.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0134300.1		yes					yes	elongation zone
HORVU.MOREX.r3.2HG0128230.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0127260.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.2HG0126380.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0125870.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0125780.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0124990.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0124660.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.2HG0124470.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0122720.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0122080.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0121570.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.2HG0121410.1		yes				yes		elongation zone
HORVU.MOREX.r3.2HG0120830.1		yes				yes		elongation zone
HORVU.MOREX.r3.2HG0120320.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.2HG0119360.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0117980.1		yes				yes		elongation zone
HORVU.MOREX.r3.2HG0117880.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.2HG0116870.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0115970.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0113880.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0113700.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0112690.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.2HG0111570.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0111130.1			yes				yes	elongation zone

Table Sy Continued.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.2HG0110060.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0108490.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0107900.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.2HG0107450.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0106750.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0105680.3			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0104510.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0104480.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0101220.2			yes		yes			elongation zone
HORVU.MOREX.r3.2HG0099780.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0099160.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0099010.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0098420.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0097950.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0097390.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.2HG0096800.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.2HG0096760.1			yes				yes	elongation zone
HORVU.MOREX.r3.2HG0096600.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.2HG0096230.1		yes				yes		elongation zone
HORVU.MOREX.r3.2HG0095970.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0094980.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.1HG0094770.1		yes				yes	yes	elongation zone
HORVU.MOREX.r3.1HG0094110.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.1HG0093050.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.1HG0092810.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0091820.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.1HG0091360.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.1HG0091240.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0088530.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.1HG0087170.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.1HG0086480.1		yes				yes		elongation zone
HORVU.MOREX.r3.1HG0086390.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.1HG0086370.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.1HG0086010.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0085420.1			yes				yes	elongation zone

Table Sy Continued.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.1HG0085380.1			yes			yes		elongation zone
HORVU.MOREX.r3.1HG0085140.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0084890.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0084850.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0084760.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0083980.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0083440.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0082770.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.1HG0082750.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0081950.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.1HG0080760.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0080230.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0080180.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.1HG0079870.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.1HG0079810.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0079800.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.1HG0079750.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.1HG0079280.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0079250.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0079140.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.1HG0078910.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0078370.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0078040.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0077950.1			yes			yes		elongation zone
HORVU.MOREX.r3.1HG0077880.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0077170.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0076980.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.1HG0076540.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0075730.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.1HG0075590.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.1HG0075440.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.1HG0074500.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0074490.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0073460.1		yes				yes		elongation zone
HORVU.MOREX.r3.1HG0073430.1		yes				yes		elongation zone

Table Sy Continued.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.1HG0073170.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.1HG0073160.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0072910.2		yes	yes			yes		elongation zone
HORVU.MOREX.r3.1HG0072580.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.1HG0072540.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0072520.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0070480.1			yes	yes	yes	yes	yes	elongation zone
HORVU.MOREX.r3.1HG0070340.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.1HG0069940.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0069870.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0069410.1		yes				yes		elongation zone
HORVU.MOREX.r3.1HG0069380.1		yes	yes	yes	yes	yes	yes	elongation zone
HORVU.MOREX.r3.1HG0069030.1		yes	yes		yes	yes	yes	elongation zone
HORVU.MOREX.r3.1HG0067930.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0067720.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.1HG0067630.1			yes			yes		elongation zone
HORVU.MOREX.r3.1HG0067410.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.1HG0066800.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.1HG0066530.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0065860.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.1HG0065370.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0065020.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0064740.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0064610.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0064320.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0063870.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0063810.1		yes				yes		elongation zone
HORVU.MOREX.r3.1HG0062110.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.1HG0061710.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.1HG0061390.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0061220.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0060320.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0059790.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0059000.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0058800.1			yes				yes	elongation zone

Table Sy Continued.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.1HG0058640.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0058050.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0057990.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.1HG0057620.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0057030.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.1HG0056740.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0056620.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.1HG0056560.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0055240.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.1HG0055230.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0054500.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0054200.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0054010.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.1HG0053530.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0053060.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.1HG0052120.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.1HG0052080.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0051960.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.1HG0051020.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0050990.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0050920.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.1HG0050700.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.1HG0049550.1			yes	yes	yes			elongation zone
HORVU.MOREX.r3.1HG0046180.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.1HG0042740.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.1HG0039670.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.1HG0039230.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0038960.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0038800.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.1HG0036930.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0035400.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.1HG0032910.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0032230.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0028320.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.1HG0027200.1		yes	yes			yes		elongation zone

Table Sy Continued.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.1HG0026830.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.1HG0026080.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.1HG0026070.2			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0025870.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.1HG0025320.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.1HG0024510.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0024280.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0024230.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0024040.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.1HG0023610.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0020980.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0018810.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0017310.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0017280.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.1HG0016810.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0015750.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.1HG0014410.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0012330.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0010340.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.1HG0008510.2			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0008200.1			yes			yes	yes	elongation zone
HORVU.MOREX.r3.1HG0008190.1			yes	yes	yes			elongation zone
HORVU.MOREX.r3.1HG0007670.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0007570.1			yes	yes	yes	yes	yes	elongation zone
HORVU.MOREX.r3.1HG0006650.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0006610.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0006400.1		yes	yes				yes	elongation zone
HORVU.MOREX.r3.1HG0006230.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.1HG0005840.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0004300.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0003620.1		yes	yes			yes	yes	elongation zone
HORVU.MOREX.r3.1HG0003150.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0002960.1		yes	yes			yes		elongation zone
HORVU.MOREX.r3.1HG0001510.1			yes				yes	elongation zone
HORVU.MOREX.r3.1HG0001460.1			yes				yes	elongation zone

Table Sy Continued.

ID	WT_3 h	WT_6 h	WT_12 h	*egt2* vsWT_0 h	*egt2* vsWT_3 h	*egt* 2vsWT_6 h	*egt2* vsWT_12 h	root zone
HORVU.MOREX.r3.1HG0000050.1		yes	yes			yes		elongation zone

Table Sɸ Overview of the candidates interacting with EGT2 identified by yeast-two-hybrid (Y2H) screening.

ID_version 3(2021)	Description	cuptered times		confirmation		differentially expressed genes in *egt2*		differentially expressed genes in rotated WT	
		1st	2nd	by 1-no-1 Y2H	by BiFC	FDR < 0.05	FDR < 5%; Log2FC ≥ 1	FDR < 0.05	FDR < 5%; Log2FC ≥ 1
HORVU.MOREX.r3.1HG0078770.1	NADH-quinone oxidoreductase, subunit E	7	12	yes, #1				yes	
HORVU.MOREX.r3.3HG0330120.1	O-methyltransferase	0	2	yes, OMT	yes	yes	yes	yes	yes
HORVU.MOREX.r3.6HG0548050.1	Acetyl-coenzyme A synthetase	2	10	Yes, #2					
HORVU.MOREX.r3.5HG0480100.1	Cysteine protease	2	1	yes, #15		yes			
HORVU.MOREX.r3.1HG0053480.1	Cinnamoyl-CoA reductase-like protein	1	3	yes, #9					
HORVU.MOREX.r3.7HG0726360.1	12-oxophytodienoate reductase	1	1	yes, #28		yes			
HORVU.MOREX.r3.1HG0085590.1	Non specific phospholipase C	1	3	yes, #10					
HORVU.MOREX.r3.5HG0475360.1	Mitochondrial outer membrane porin	1	5	yes, #5					
HORVU.MOREX.r3.7HG0721830.1/HORVU.MOREX.r3.7HG0721840.1 (two genes with high similarity)	Germin-like protein	1	3	yes, #11					
HORVU.MOREX.r3.6HG0599140.1	Kinesin-like protein	1	1	yes, #29					
HORVU.MOREX.r3.7HG0736300.1	Glycosyltransferase	0	2	yes, GTF		yes	yes		
HORVU.MOREX.r3.1HG0006660.1	Inorganic pyrophosphatase family protein	0	3	yes, #12				yes	
HORVU.MOREX.r3.2HG0197110.1	AT hook motif DNA-binding family protein	0	4	yes, #7				yes	
HORVU.MOREX.r3.3HG0269000.1	zinc finger FYVE domain protein	1	1	yes, #30					
HORVU.MOREX.r3.3HG0244960.1	TPR repeat-containing thioredoxin TTL1	0	2	yes, #24					
HORVU.MOREX.r3.5HG0423100.1	Pathogenesis-related thaumatin family protein	1	2	yes, #14					
HORVU.MOREX.r3.5HG0523150.1/ HORVU.MOREX.r3.5HG0523140.1	Protein phosphatase 2c, putative/ DNA ligase-like protein	1	1	yes, #31		yes		yes	
HORVU.MOREX.r3.5HG0517090.1	Chaperone protein dnaJ, putative	0	4	yes, #8					
HORVU.MOREX.r3.6HG0607930.1	Ring box protein	0	6	yes, #4					
HORVU.MOREX.r3.2HG0108780.1	26S protease regulatory subunit	7	0	yes, #6				yes	
HORVU.MOREX.r3.6HG0571770.1	Glycine cleavage system H protein	1	2	yes, #13					
HORVU.MOREX.r3.3HG0292400.1	Histone-lysine N-methyltransferase	3	0	yes, #16					
HORVU.MOREX.r3.6HG0608910.1	Heavy metal transport/detoxification superfamily protein	0	7	yes, #3				yes	yes
HORVU.MOREX.r3.6HG0572880.1	Alpha/beta-Hydrolases superfamily protein	0	2			yes			
HORVU.MOREX.r3.6HG0626440.1	Aldehyde dehydrogenase	0	1						
HORVU.MOREX.r3.5HG0462200.1	Metacaspase	0	1					yes	yes
HORVU.MOREX.r3.7HG0663950.1	Alpha/beta-Hydrolases superfamily protein	0	2						
HORVU.MOREX.r3.1HG0016210.1	Endoglucanase	0	1						
HORVU.MOREX.r3.6HG0630640.1	Aconitate hydratase	0	2						
HORVU.MOREX.r3.4HG0336620.1	GAI-like protein 1	0	1						
HORVU.MOREX.r3.4HG0410090.1	Hypersensitive-induced response protein 1	0	2					yes	
HORVU.MOREX.r3.7HG0709860.1	Polyadenylate-binding protein	0	1		no	yes		yes	
HORVU.MOREX.r3.3HG0282230.1	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	0	2						
HORVU.MOREX.r3.6HG0630520.1	AT hook motif DNA-binding family protein	0	1						
HORVU.MOREX.r3.6HG0613040.1	2-oxoglutarate-dependent dioxygenase-related family protein	0	1			yes			
HORVU.MOREX.r3.4HG0413890.1	Alpha/beta-Hydrolases superfamily protein	0	2					yes	
HORVU.MOREX.r3.6HG0608920.2	DegP protease-like	0	7						
HORVU.MOREX.r3.3HG0223160.1	aberrant root formation protein	0	1			yes		yes	
HORVU.MOREX.r3.4HG0383750.2	26S protease regulatory subunit	0	1						
HORVU.MOREX.r3.7HG0721230.1	UPF0183 protein	0	1						
HORVU.MOREX.r3.3HG0292280.1	Ubiquitin carboxyl-terminal hydrolase-like protein	0	1			yes			
HORVU.MOREX.r3.4HG0333780.1	Glucan endo-1,3-beta-glucosidase	0	1						
HORVU.MOREX.r3.5HG0423110.1	Thaumatin-like protein	0	1						
HORVU.MOREX.r3.5HG0511040.1	Heavy metal transport/detoxification superfamily protein	0	1					yes	

Table Sϕ Continued.

ID_version 3(2021)	Description	cuptered times		confirmation		differentially expressed genes in *egt2*		differentially expressed genes in rotated WT	
		1st	2nd	by 1-no-1 Y2H	by BiFC	FDR < 0.05	FDR < 5%; Log2FC ≥ 1	FDR < 0.05	FDR < 5%; Log2FC ≥ 1
HORVU.MOREX.r3.3HG0278140.1	WRKY transcription factor	0	1						
HORVU.MOREX.r3.1HG0000050.1	RING-finger ubiquitin ligase	0	1		no	yes		yes	
HORVU.MOREX.r3.6HG0564530.1	glucuronoxylan 4-O-methyltransferase-like protein (DUF579)	0	1						
HORVU.MOREX.r3.6HG0620720.1	Ribonuclease	0	1					yes	
HORVU.MOREX.r3.7HG0749870.1	Glucuronoxylan 4-O-methyltransferase	0	1		yes	yes		yes	
HORVU.MOREX.r3.1HG0001180.1	Leucine-rich repeat protein kinase family protein	0	1						
HORVU.MOREX.r3.2HG0191150.1	Polygalacturonase QRT3	0	1					yes	
HORVU.MOREX.r3.7HG0732480.1	Zinc finger CCCH domain protein	0	1						
HORVU.MOREX.r3.3HG0230590.1	Triosephosphate isomerase	0	1						
HORVU.MOREX.r3.2HG0205420.1	Heavy metal transport/detoxification superfamily protein	0	1					yes	
HORVU.MOREX.r3.6HG0572960.1	Chlorophyll a-b binding protein, chloroplastic	0	1					yes	yes
HORVU.MOREX.r3.5HG0512400.1	GDSL esterase/lipase	0	1						
HORVU.MOREX.r3.6HG0625570.1	Transmembrane protein	0	2			yes		yes	
HORVU.MOREX.r3.5HG0487040.1	Alpha/beta-Hydrolases superfamily protein, putative	0	1					yes	
HORVU.MOREX.r3.5HG0516310.1	Patatin	0	1					yes	
HORVU.MOREX.r3.2HG0163850.1	Phosphoribosylformylglycinamidine synthase	0	1						
HORVU.MOREX.r3.2HG0126380.1	Heavy metal transport/detoxification superfamily protein	0	1		yes	yes		yes	
HORVU.MOREX.r3.5HG0499760.1	Cysteine proteinase	0	2						
HORVU.MOREX.r3.1HG0074750.1	Ferredoxin	2	0						
HORVU.MOREX.r3.7HG0721250.1	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9	1	0						
HORVU.MOREX.r3.1HG0057560.1	RNA-binding KH domain-containing protein	1	0						
HORVU.MOREX.r3.2HG0146530.1	ATP synthase epsilon chain	1	0						
HORVU.MOREX.r3.2HG0161130.1	Eukaryotic translation initiation factor 3 subunit H	2	0						
HORVU.MOREX.r3.2HG0176810.2	F-box family protein	2	0						
HORVU.MOREX.r3.4HG0395480.1	calcium/calcium/calmodulin-dependent Serine/Threonine-kinase	1	0						
HORVU.MOREX.r3.3HG0291750.1	Lipoyl synthase	1	0						
HORVU.MOREX.r3.7HG0655800.1	Caffeoyl-CoA O-methyltransferase	1	0						
HORVU.MOREX.r3.1HG0043190.1	Malate dehydrogenase	1	0						
HORVU.MOREX.r3.1HG0018270.1	Bushy growth protein	1	0						
HORVU.MOREX.r3.7HG0636530.1	MADS-box transcription factor 8	1	0					yes	
HORVU.MOREX.r3.2HG0107060.1	IAA-amino acid hydrolase ILR1	1	0						
HORVU.MOREX.r3.4HG0413910.1	Cell wall invertase	1	0						
HORVU.MOREX.r3.5HG0444520.1	NADP-dependent alkenal double bond reductase	1	0			yes			
HORVU.MOREX.r3.4HG0416190.1	Coatomer subunit alpha	1	0			yes			
HORVU.MOREX.r3.6HG0571760.1	Splicing factor, arginine/serine-rich 12	1	0						