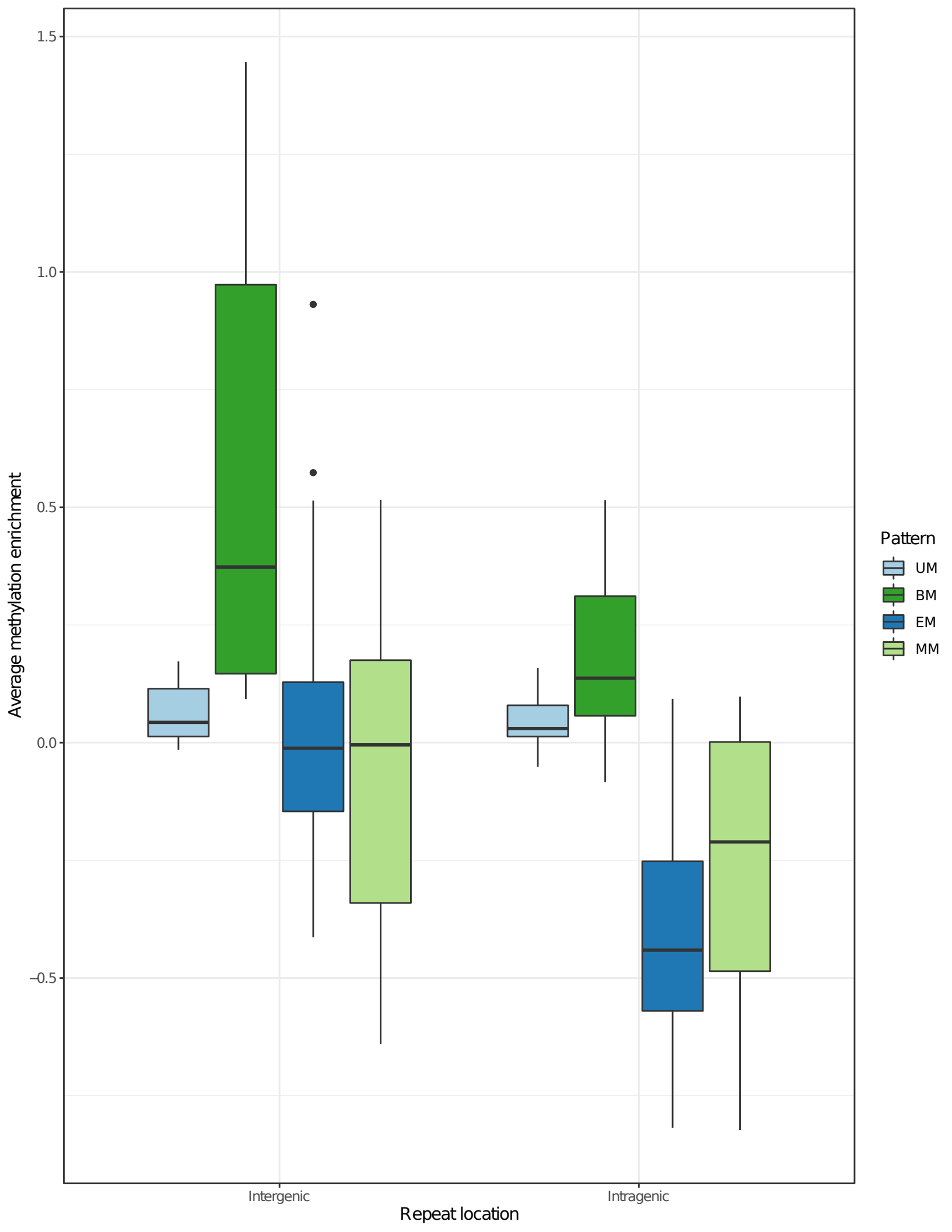
1.5
1.0
0.5
0.0
−0.5
Average methylation enrichment
Intergenic
Intragenic
Repeat location
Pattern
UM
BM
EM
MM