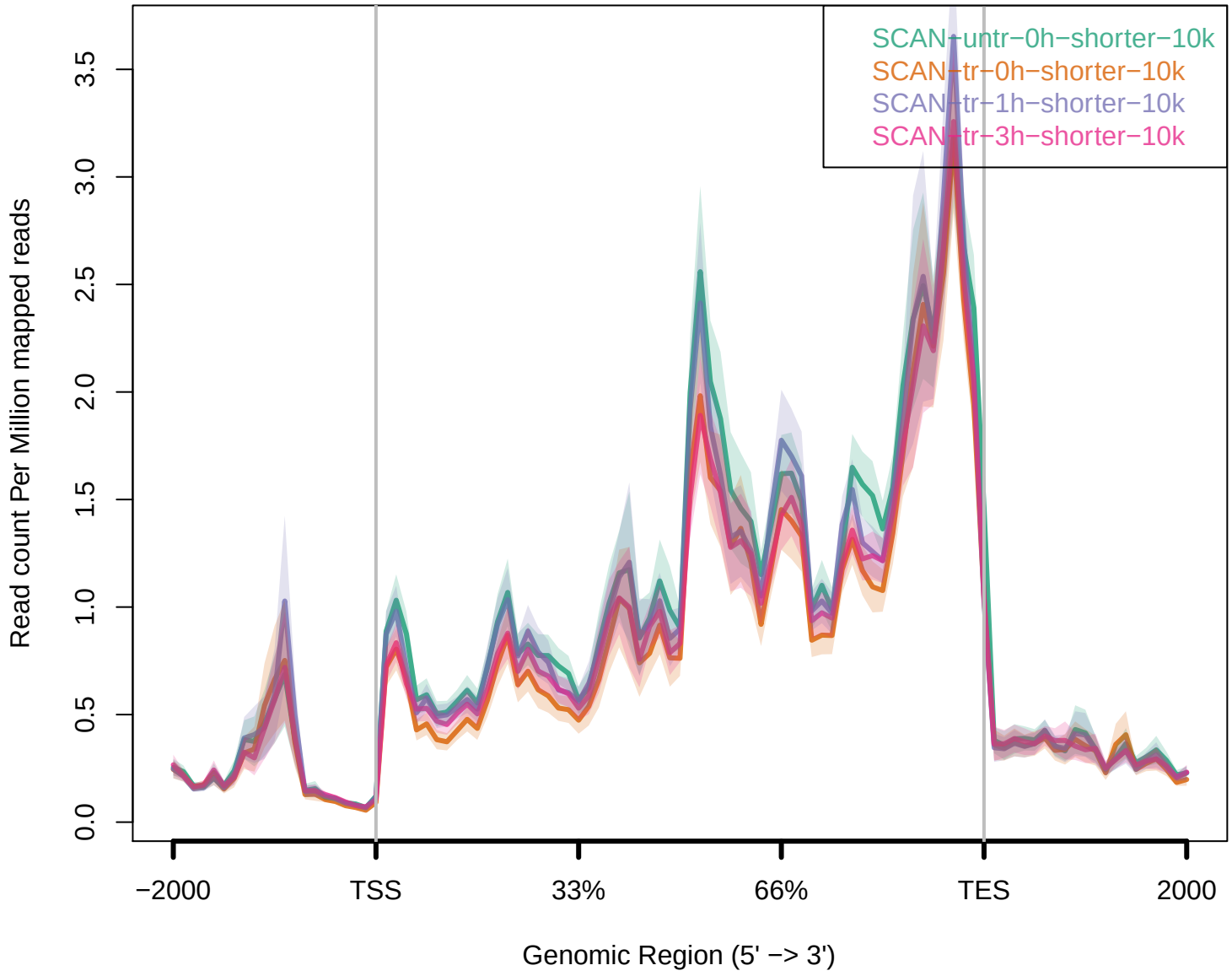
SCAN−untr−0h−shorter−10k
SCAN−tr−0h−shorter−10k
SCAN−tr−1h−shorter−10k
SCAN−tr−3h−shorter−10k
Read count Per Million mapped reads
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
−2000
TSS
33%
66%
TES
2000
Genomic Region (5' −> 3')