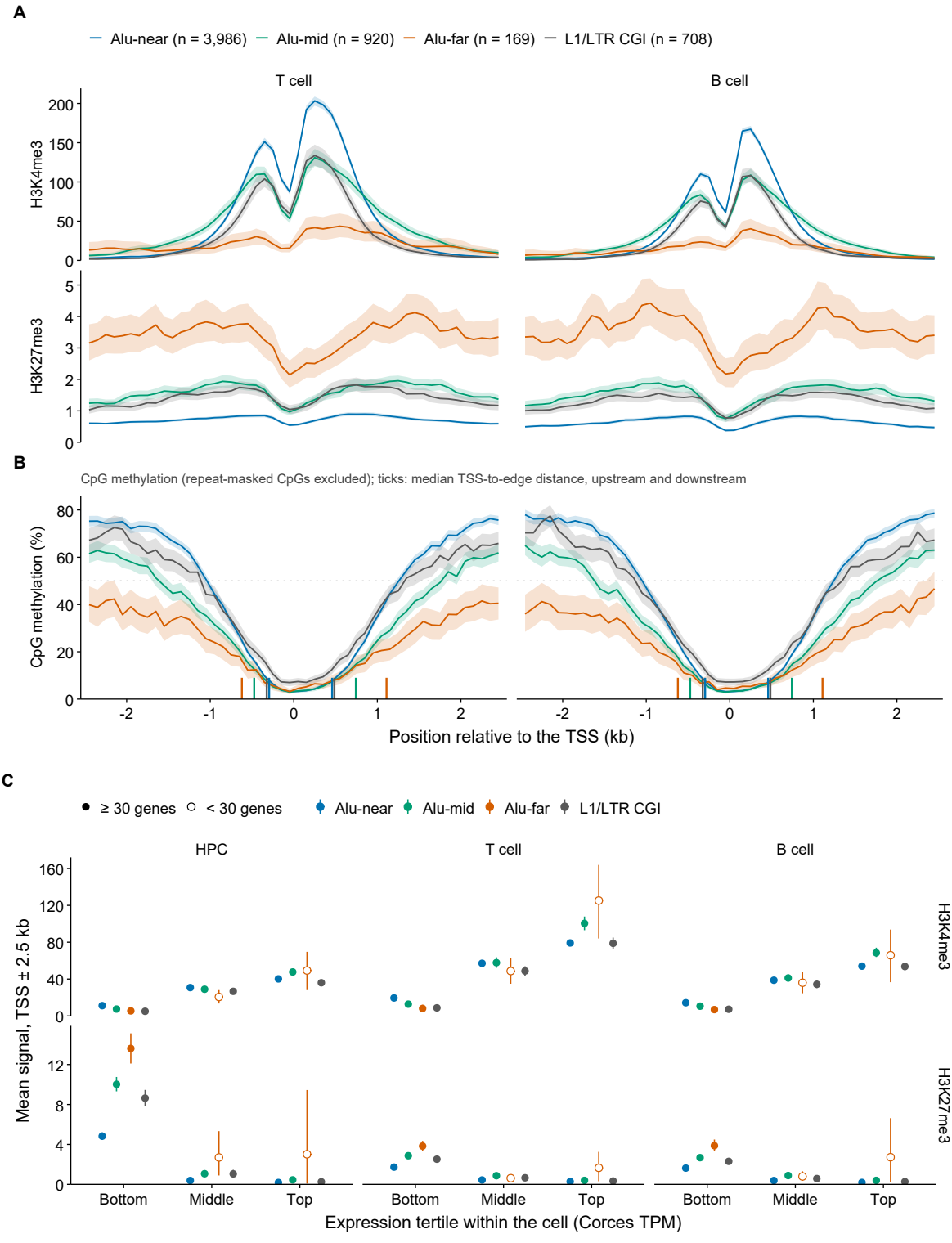

A
Alu-near (n = 3,986)
Alu-mid (n = 920)
Alu-far (n = 169)
L1/LTR CGI (n = 708)
T cell
B cell
H3K4me3
H3K27me3
B
CpG methylation (repeat-masked CpGs excluded); ticks: median TSS-to-edge distance, upstream and downstream
CpG methylation (%)
Position relative to the TSS (kb)
C
≥ 30 genes
< 30 genes
Alu-near
Alu-mid
Alu-far
L1/LTR CGI
HPC
T cell
B cell
Mean signal, TSS ± 2.5 kb
Bottom
Middle
Top
Expression tertile within the cell (Corces TPM)