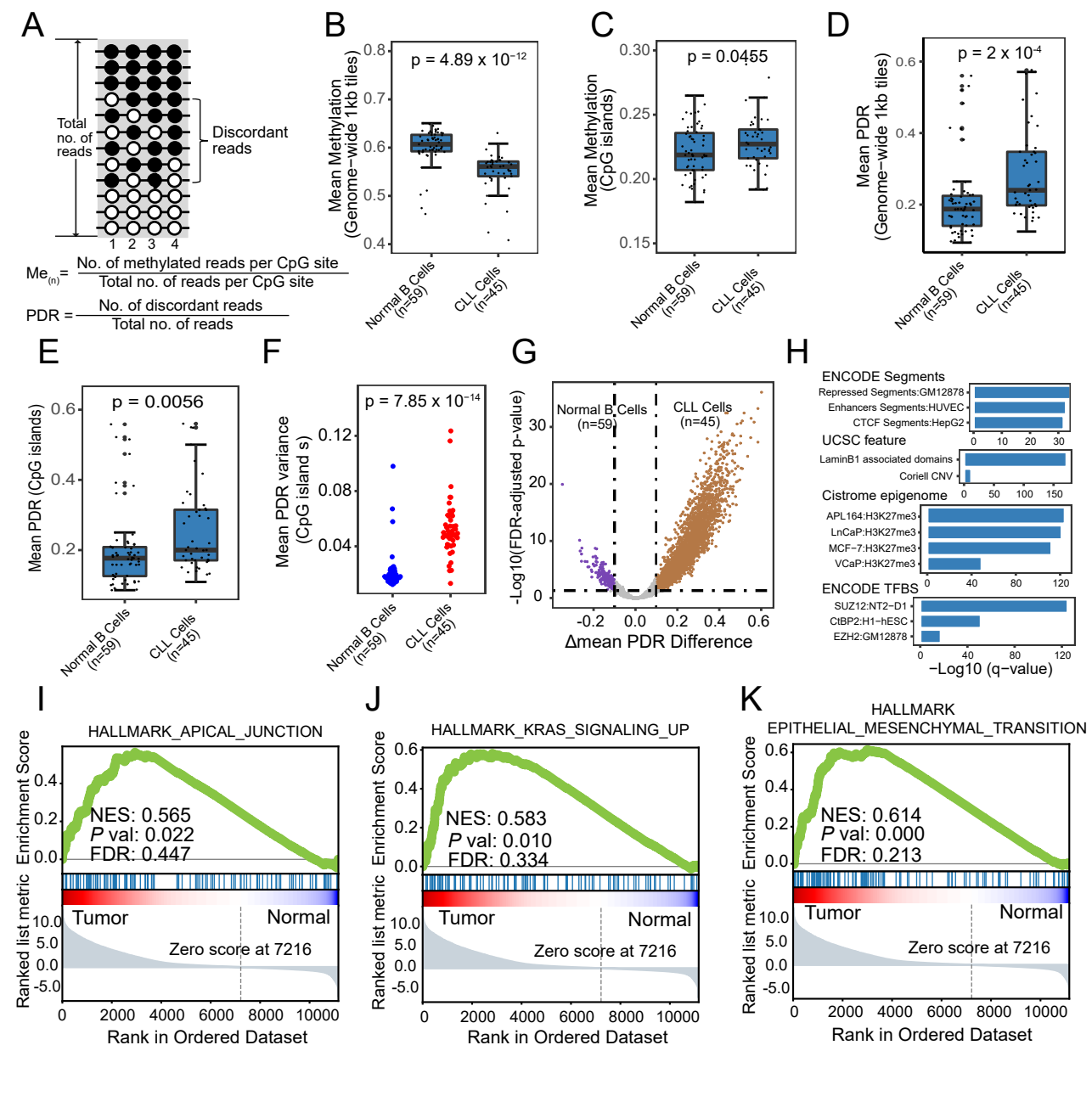
A
Total no. of reads
Discordant reads
1 2 3 4
Me(n) = No. of methylated reads per CpG site / Total no. of reads per CpG site
PDR = No. of discordant reads / Total no. of reads
B
p = 4.89 x 10-12
Mean Methylation (Genome-wide 1kb tiles)
Normal B Cells (n=59)
CLL Cells (n=45)
C
p = 0.0455
Mean Methylation (CpG islands)
D
p = 2 x 10-4
Mean PDR (Genome-wide 1kb tiles)
E
p = 0.0056
Mean PDR (CpG islands)
F
p = 7.85 x 10-14
Mean PDR variance (CpG island s)
G
Normal B Cells (n=59)
CLL Cells (n=45)
-Log10(FDR-adjusted p-value)
Δmean PDR Difference
H
ENCODE Segments
Repressed Segments:GM12878
Enhancers Segments:HUVEC
CTCF Segments:HepG2
UCSC feature
LaminB1 associated domains
Coriell CNV
Cistrome epigenome
APL164:H3K27me3
LnCaP:H3K27me3
MCF-7:H3K27me3
VCaP:H3K27me3
ENCODE TFBS
SUZ12:NT2-D1
CtBP2:H1-hESC
EZH2:GM12878
-Log10 (q-value)
I
HALLMARK_APICAL_JUNCTION
NES: 0.565
P val: 0.022
FDR: 0.447
Enrichment Score
Ranked list metric
Tumor
Normal
Zero score at 7216
Rank in Ordered Dataset
J
HALLMARK_KRAS_SIGNALING_UP
NES: 0.583
P val: 0.010
FDR: 0.334
K
HALLMARK EPITHELIAL_MESENCHYMAL_TRANSITION
NES: 0.614
P val: 0.000
FDR: 0.213