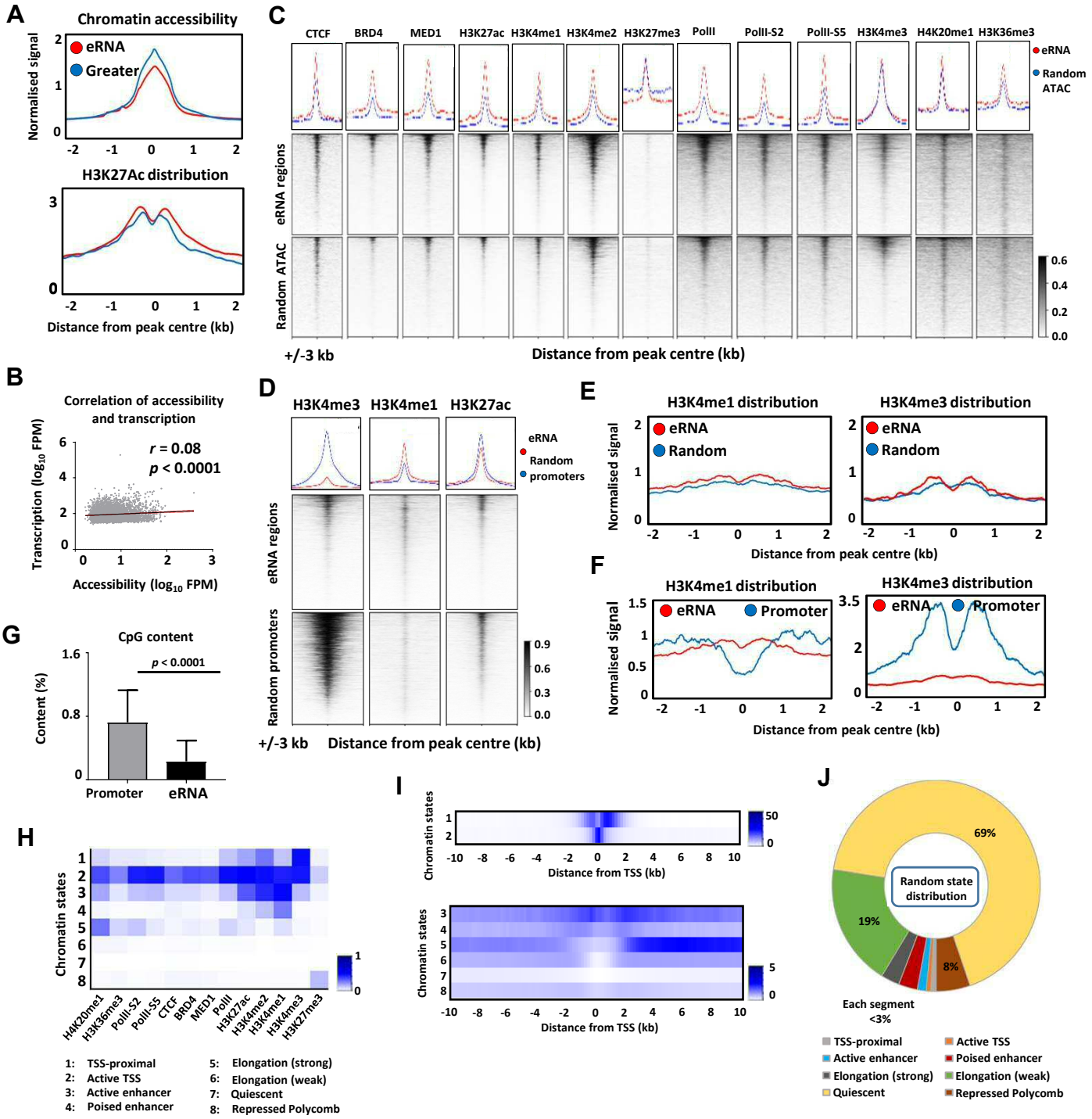
A
Chromatin accessibility
eRNA
Greater
Normalised signal
H3K27Ac distribution
Distance from peak centre (kb)
B
Correlation of accessibility and transcription
r = 0.08
p < 0.0001
Transcription (log10 FPM)
Accessibility (log10 FPM)
C
CTCF
BRD4
MED1
H3K27ac
H3K4me1
H3K4me2
H3K27me3
PolII
PolII-S2
PolII-S5
H3K4me3
H4K20me1
H3K36me3
eRNA
Random ATAC
eRNA regions
Random ATAC
+/-3 kb
Distance from peak centre (kb)
D
H3K4me3
H3K4me1
H3K27ac
eRNA
Random promoters
eRNA regions
Random promoters
+/-3 kb
Distance from peak centre (kb)
E
H3K4me1 distribution
H3K4me3 distribution
eRNA
Random
Normalised signal
Distance from peak centre (kb)
F
H3K4me1 distribution
H3K4me3 distribution
eRNA
Promoter
Normalised signal
Distance from peak centre (kb)
G
CpG content
p < 0.0001
Content (%)
Promoter
eRNA
H
Chromatin states
H4K20me1
H3K36me3
PolII-S2
PolII-S5
CTCF
BRD4
MED1
PolII
H3K27ac
H3K4me2
H3K4me1
H3K4me3
H3K27me3
1: TSS-proximal
2: Active TSS
3: Active enhancer
4: Poised enhancer
5: Elongation (strong)
6: Elongation (weak)
7: Quiescent
8: Repressed Polycomb
I
Chromatin states
Distance from TSS (kb)
J
69%
19%
8%
Random state distribution
Each segment <3%
TSS-proximal
Active TSS
Active enhancer
Poised enhancer
Elongation (strong)
Elongation (weak)
Quiescent
Repressed Polycomb