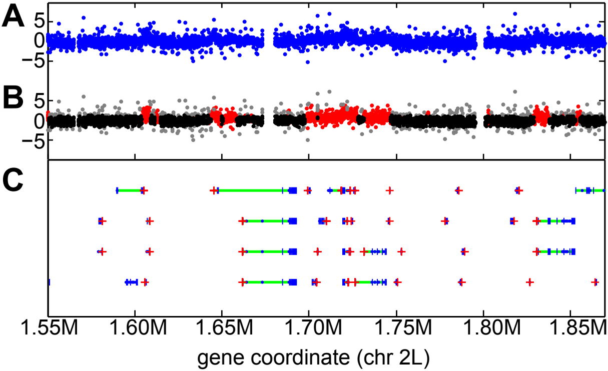

A
5
0
−5
B
5
0
−5
C
1.55M
1.60M
1.65M
1.70M
1.75M
1.80M
1.85M
gene coordinate (chr 2L)

Figure S1

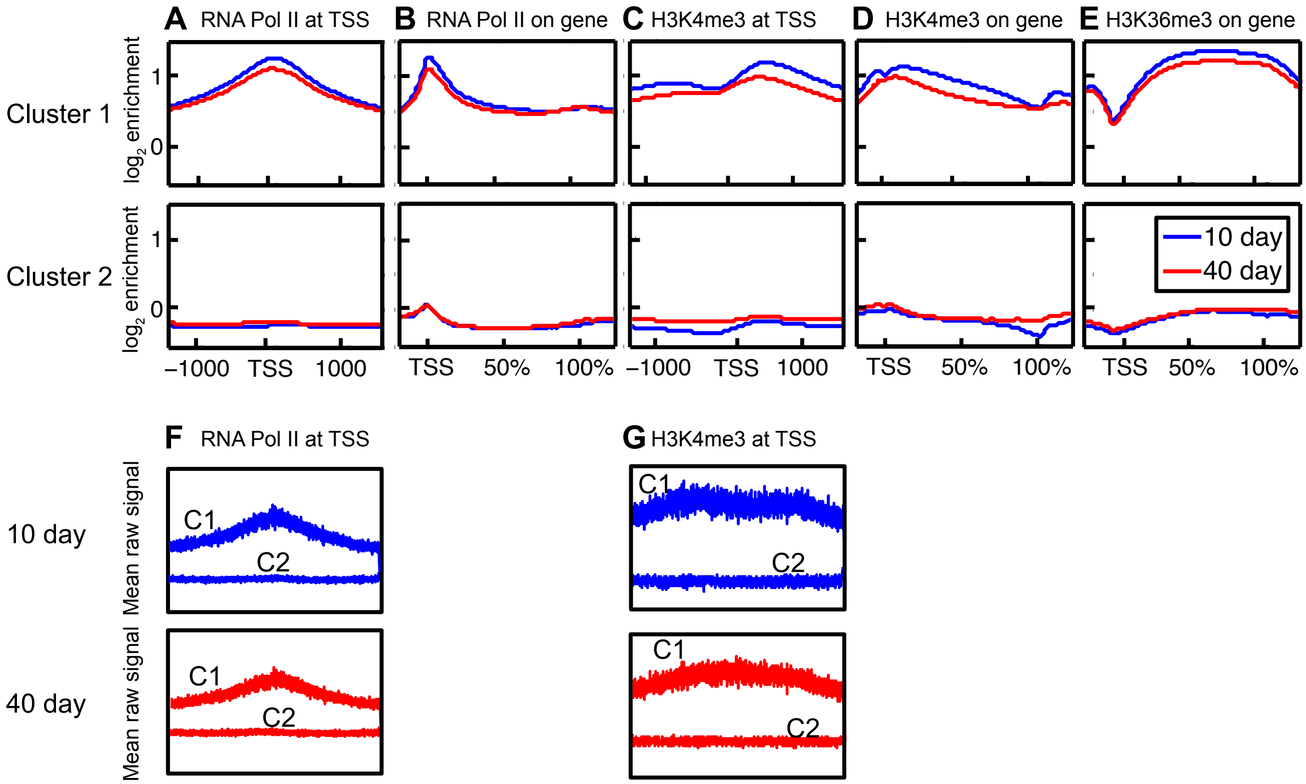

A RNA Pol II at TSS
B RNA Pol II on gene
C H3K4me3 at TSS
D H3K4me3 on gene
E H3K36me3 on gene
Cluster 1
Cluster 2
log2 enrichment
1
0
10 day
40 day
−1000
TSS
1000
50%
100%
F RNA Pol II at TSS
G H3K4me3 at TSS
10 day
40 day
Mean raw signal
C1
C2

Figure S2

Figure S3

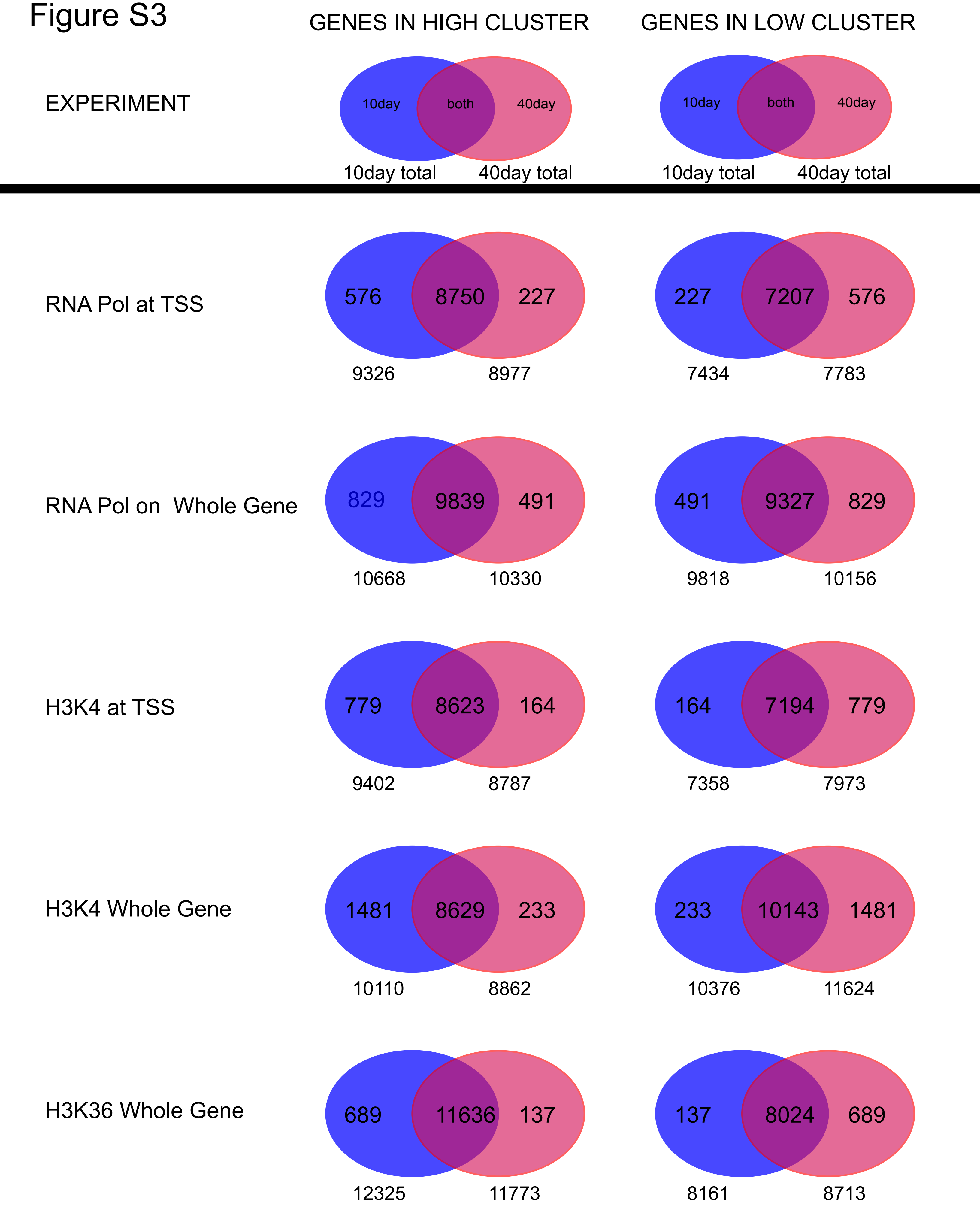

GENES IN HIGH CLUSTER
GENES IN LOW CLUSTER
EXPERIMENT
10day
both
40day
10day total
40day total
10day
both
40day
10day total
40day total
RNA Pol at TSS
576
8750
227
9326
8977
227
7207
576
7434
7783
RNA Pol on Whole Gene
829
9839
491
10668
10330
491
9327
829
9818
10156
H3K4 at TSS
779
8623
164
9402
8787
164
7194
779
7358
7973
H3K4 Whole Gene
1481
8629
233
10110
8862
233
10143
1481
10376
11624
H3K36 Whole Gene
689
11636
137
12325
11773
137
8024
689
8161
8713

Figure S4

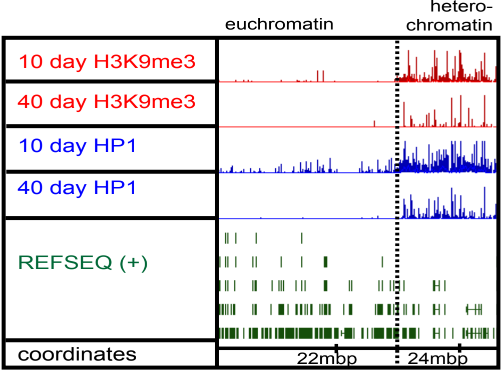
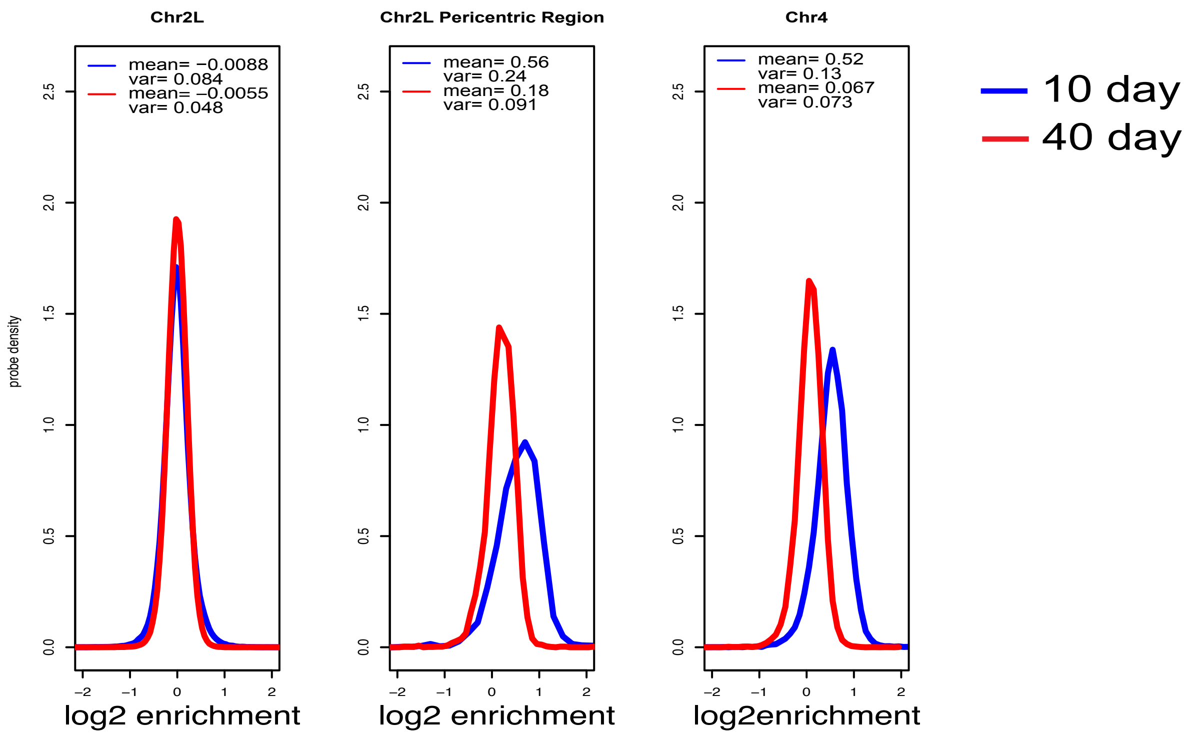

euchromatin
hetero-chromatin
10 day H3K9me3
40 day H3K9me3
10 day HP1
40 day HP1
REFSEQ (+)
coordinates
22mbp
24mbp

Figure S5

A H3K9me3 Signal:



B

H3k9me3 enrichment in pericentric regions + chr4 from each individual replicate
pvalue (10day v. 40day term in 2 way anova) = 0.

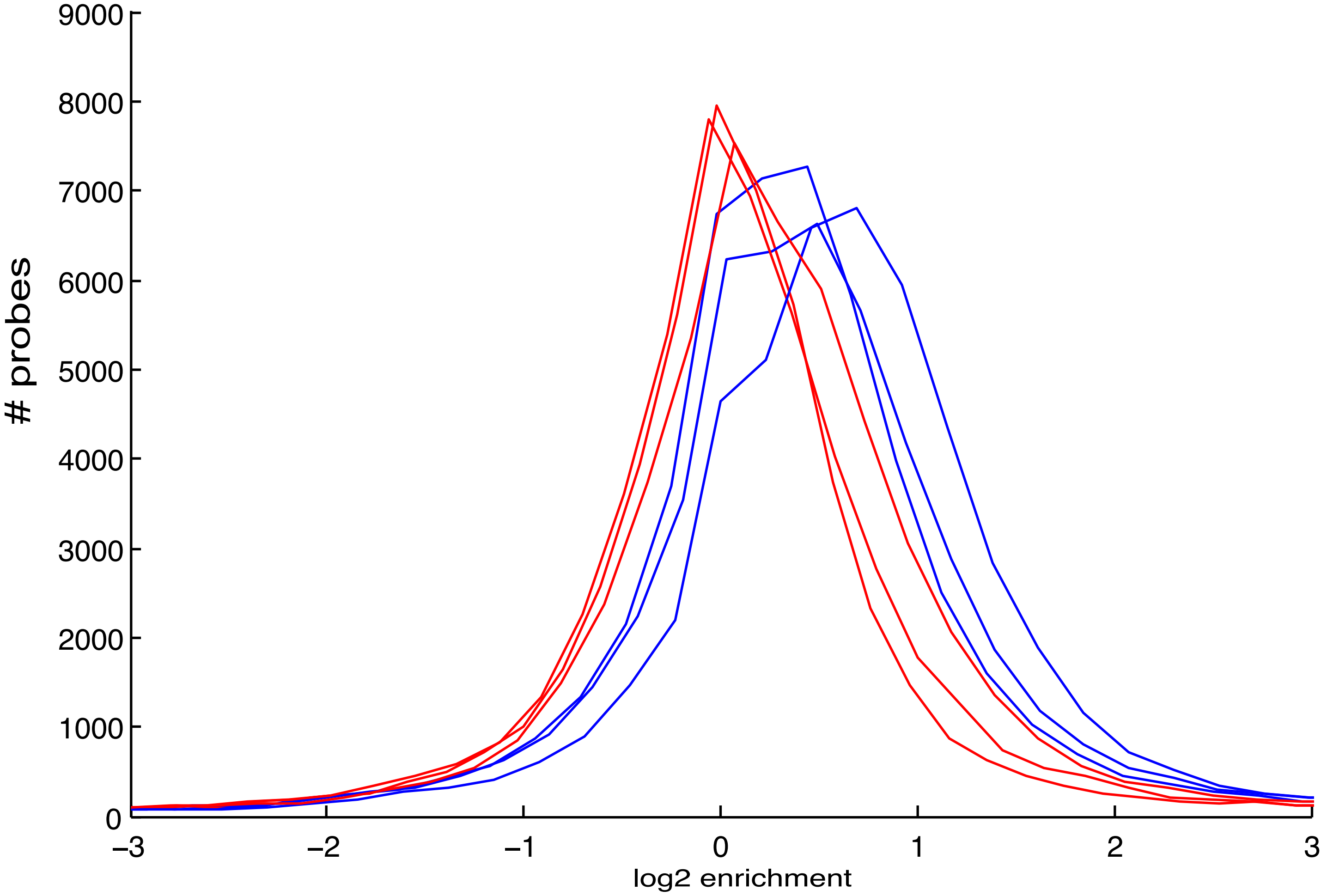
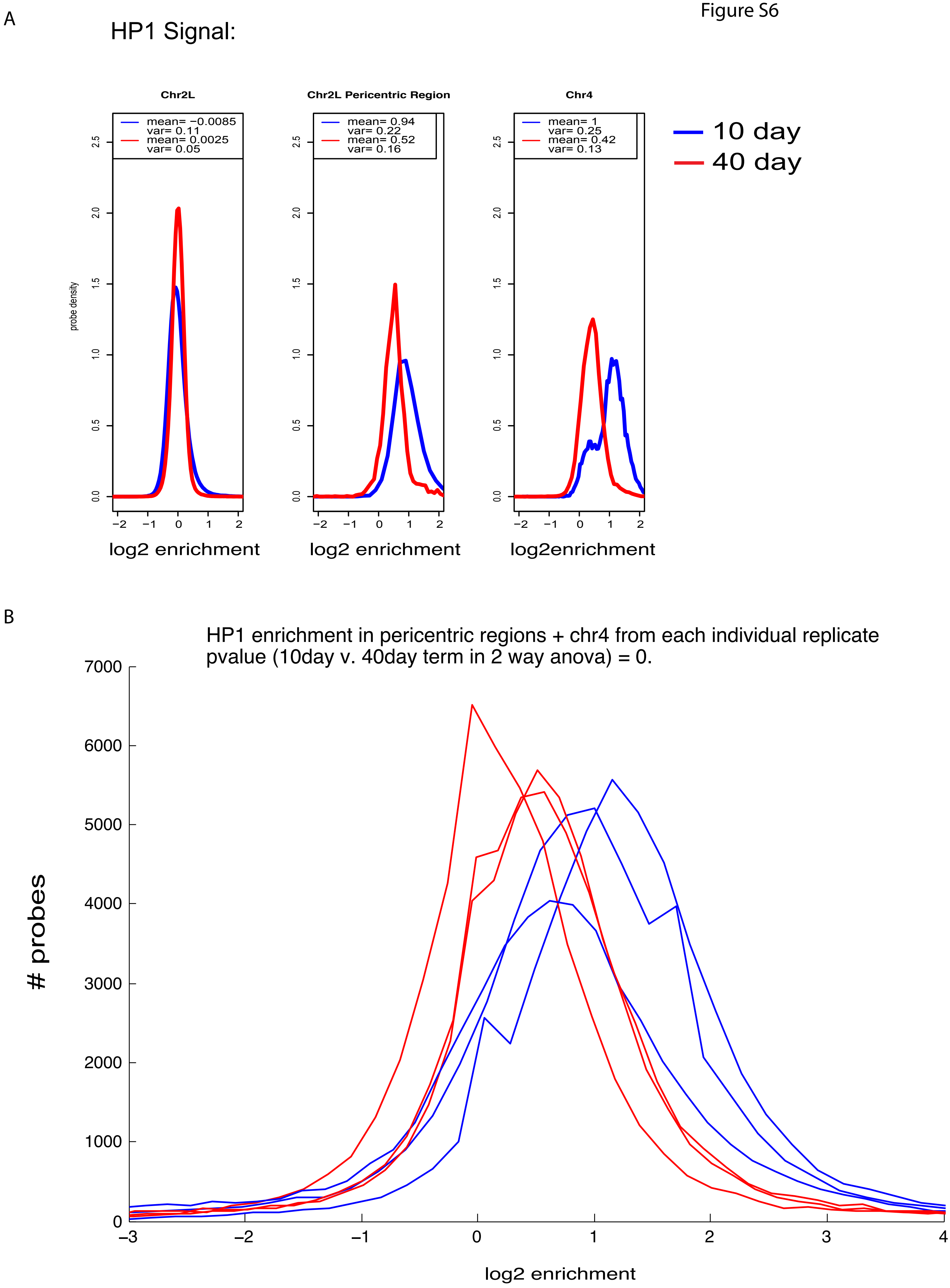


Figure S6



A
HP1 Signal:
Chr2L
mean= −0.0085
var= 0.11
mean= 0.0025
var= 0.05
Chr2L Pericentric Region
mean= 0.94
var= 0.22
mean= 0.52
var= 0.16
Chr4
mean= 1
var= 0.25
mean= 0.42
var= 0.13
10 day
40 day
probe density
0.0
0.5
1.0
1.5
2.0
2.5
−2
−1
0
1
2
log2 enrichment
log2 enrichment
log2enrichment
B
HP1 enrichment in pericentric regions + chr4 from each individual replicate
pvalue (10day v. 40day term in 2 way anova) = 0.
probes
0
1000
2000
3000
4000
5000
6000
7000
−3
−2
−1
0
1
2
3
4
log2 enrichment

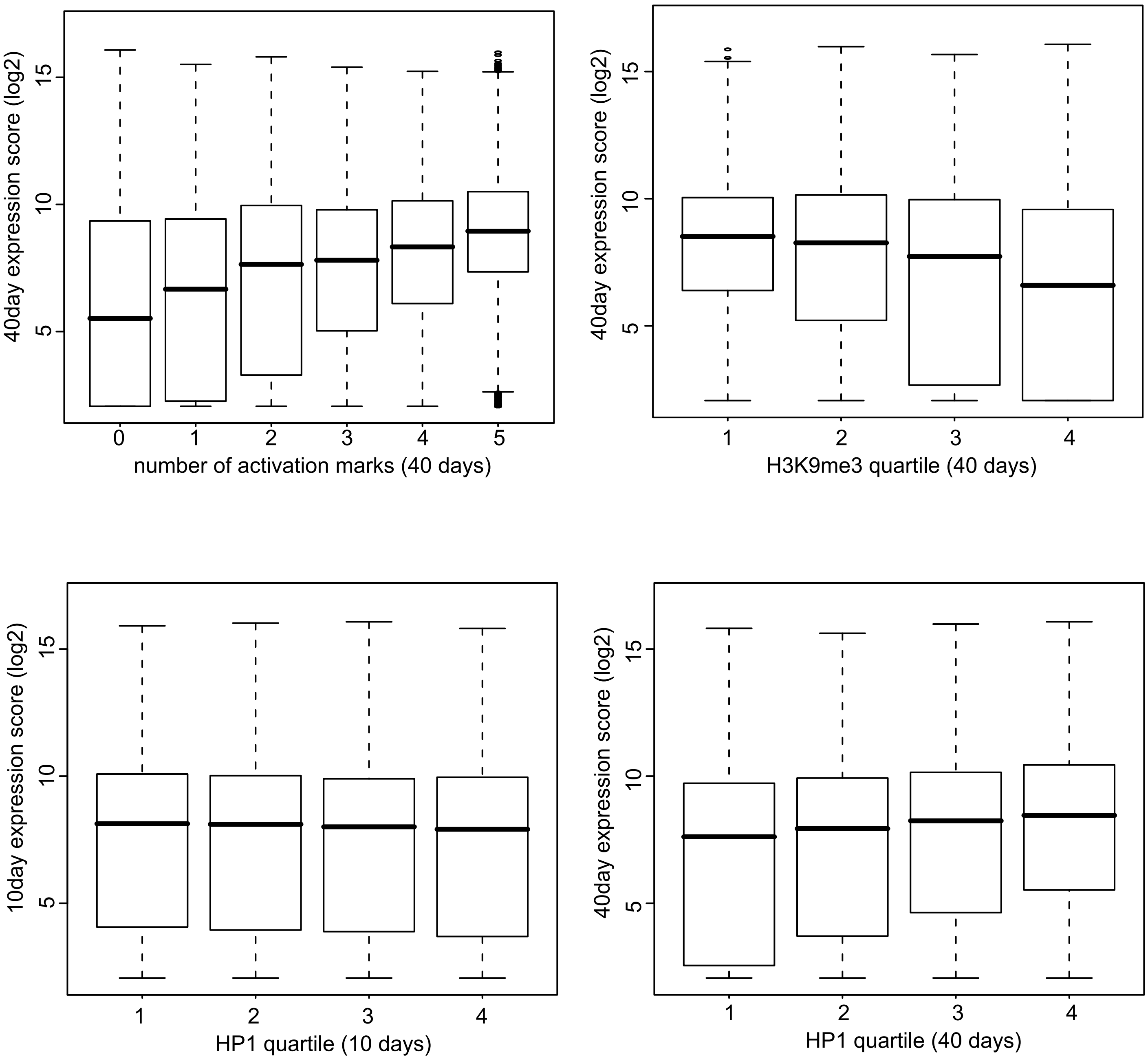
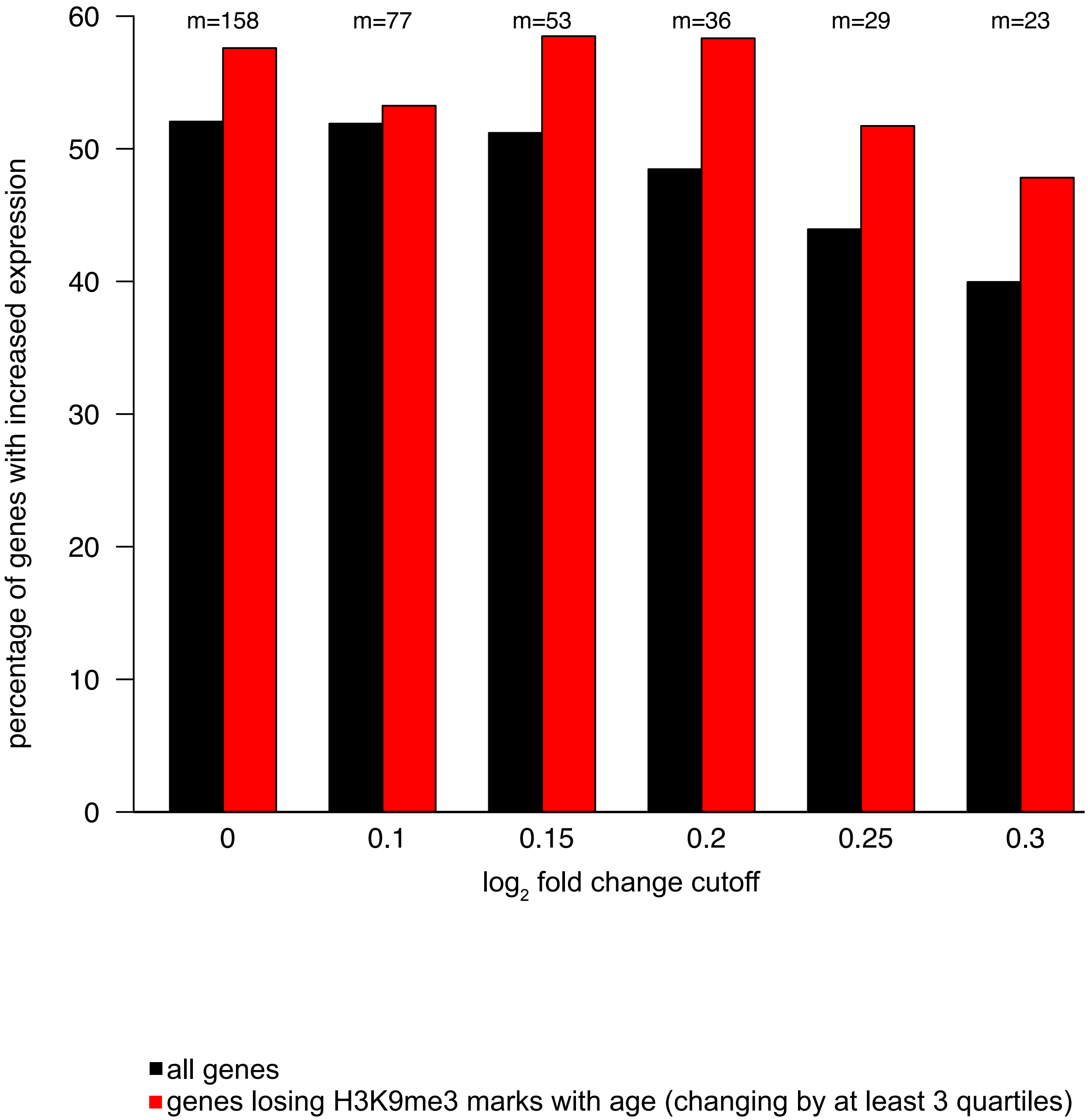

40day expression score (log2)
5
10
15
0
1
2
3
4
5
number of activation marks (40 days)
40day expression score (log2)
5
10
15
1
2
3
4
H3K9me3 quartile (40 days)
10day expression score (log2)
5
10
15
1
2
3
4
HP1 quartile (10 days)
40day expression score (log2)
5
10
15
1
2
3
4
HP1 quartile (40 days)

Figure S7

Figure S8



m is the number of genes that meet both the foldchange restriction and lose H3K9me3 by at least 3 quartiles (See supplemental methods)