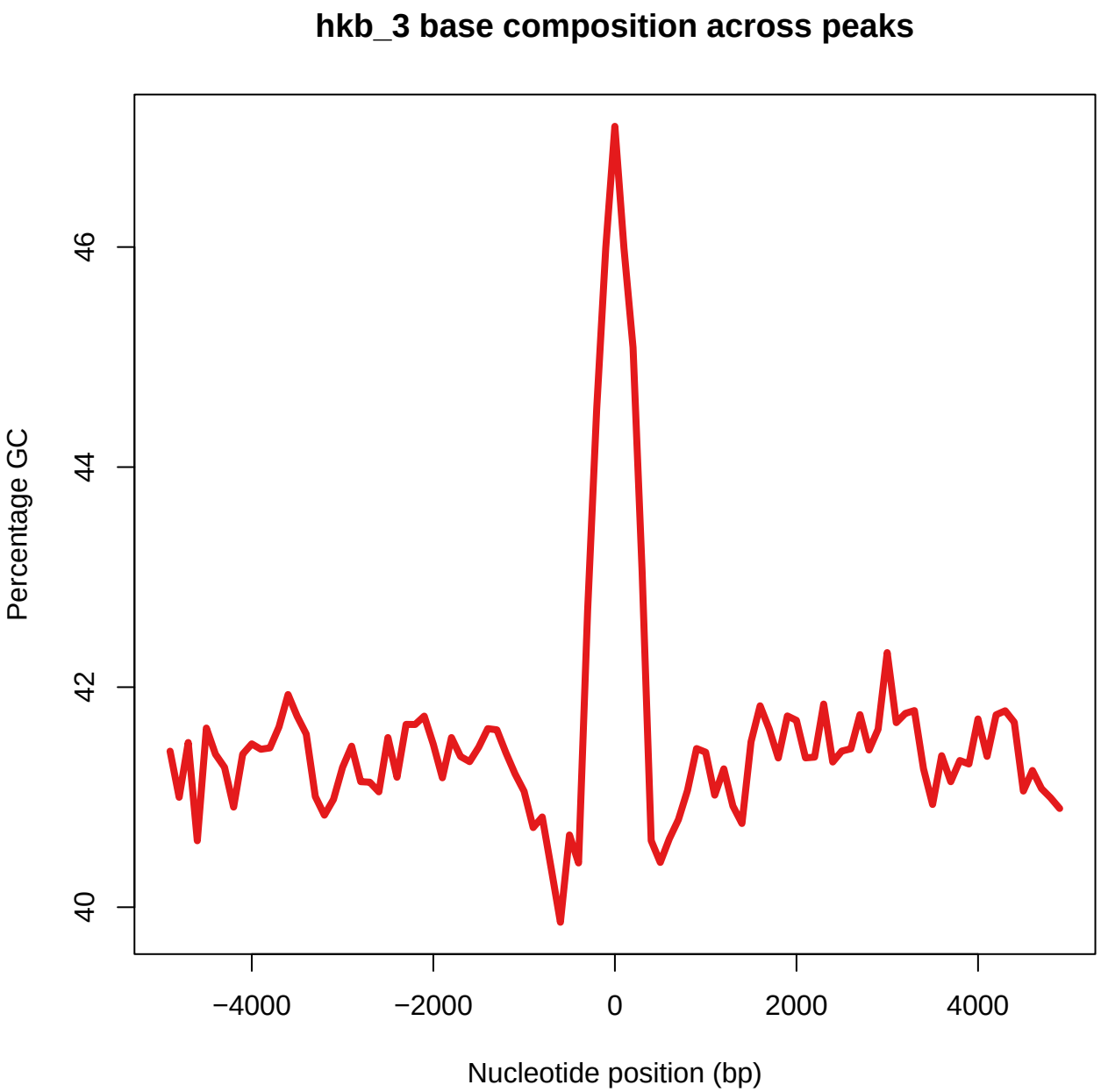
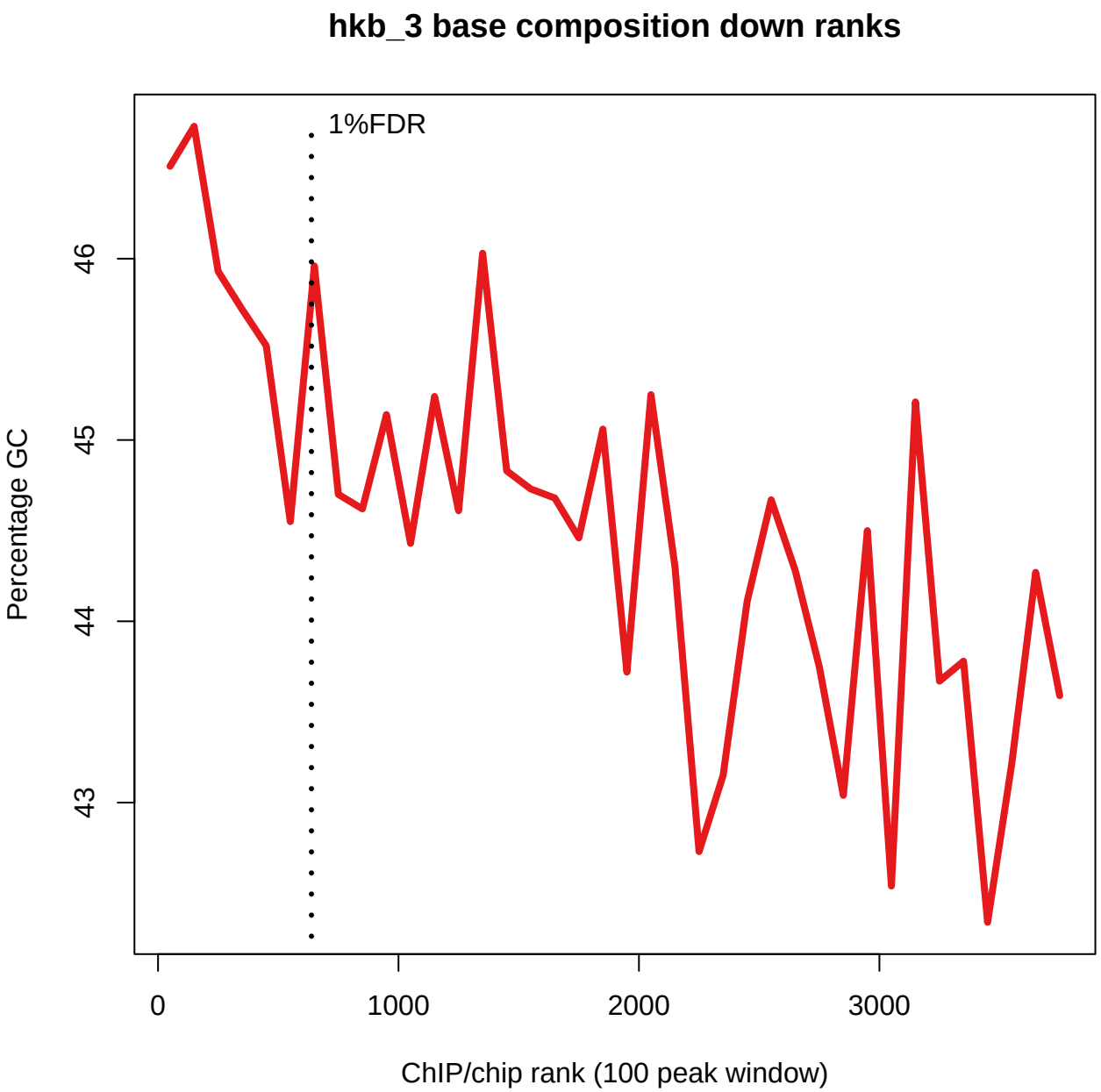
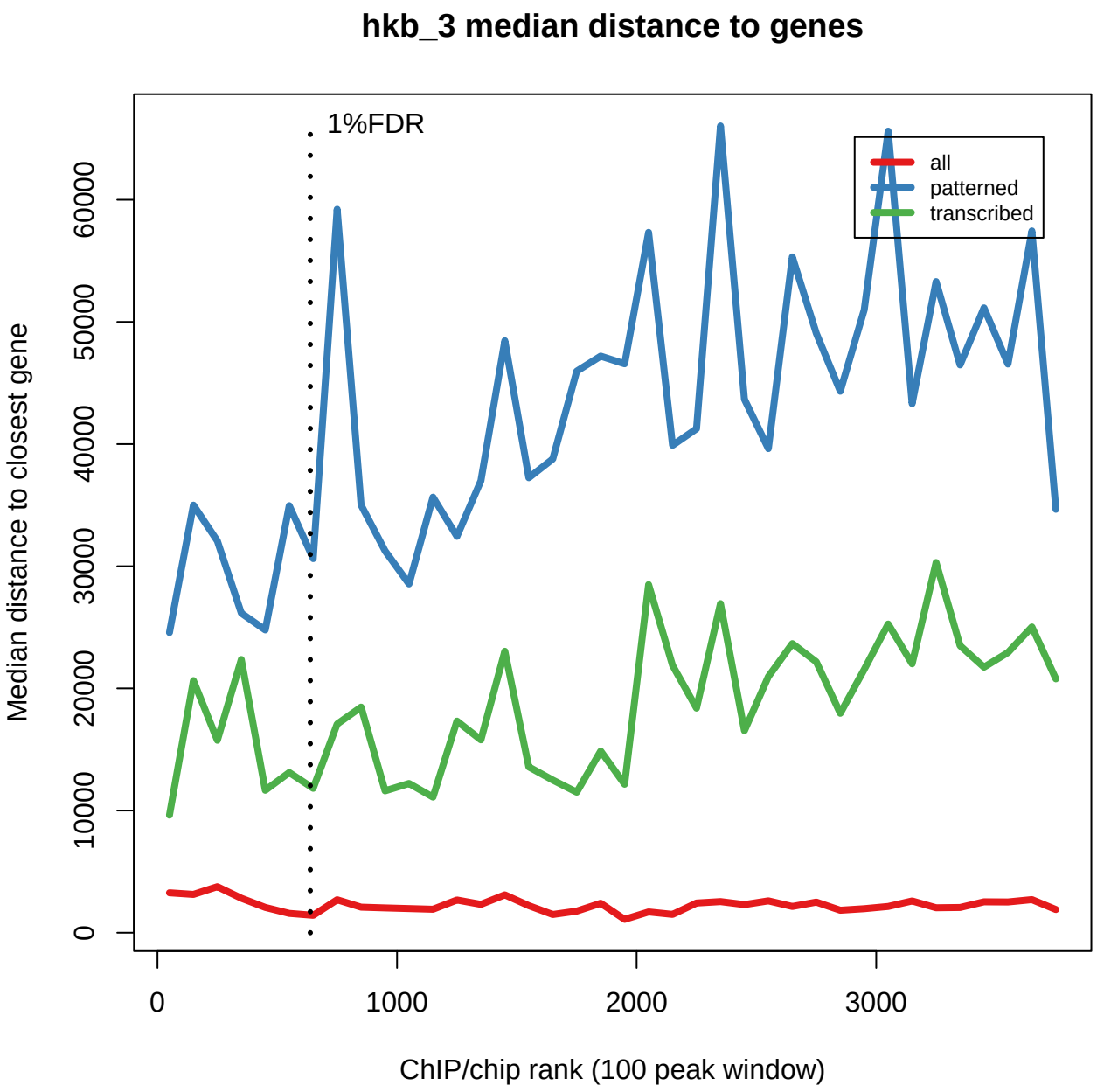
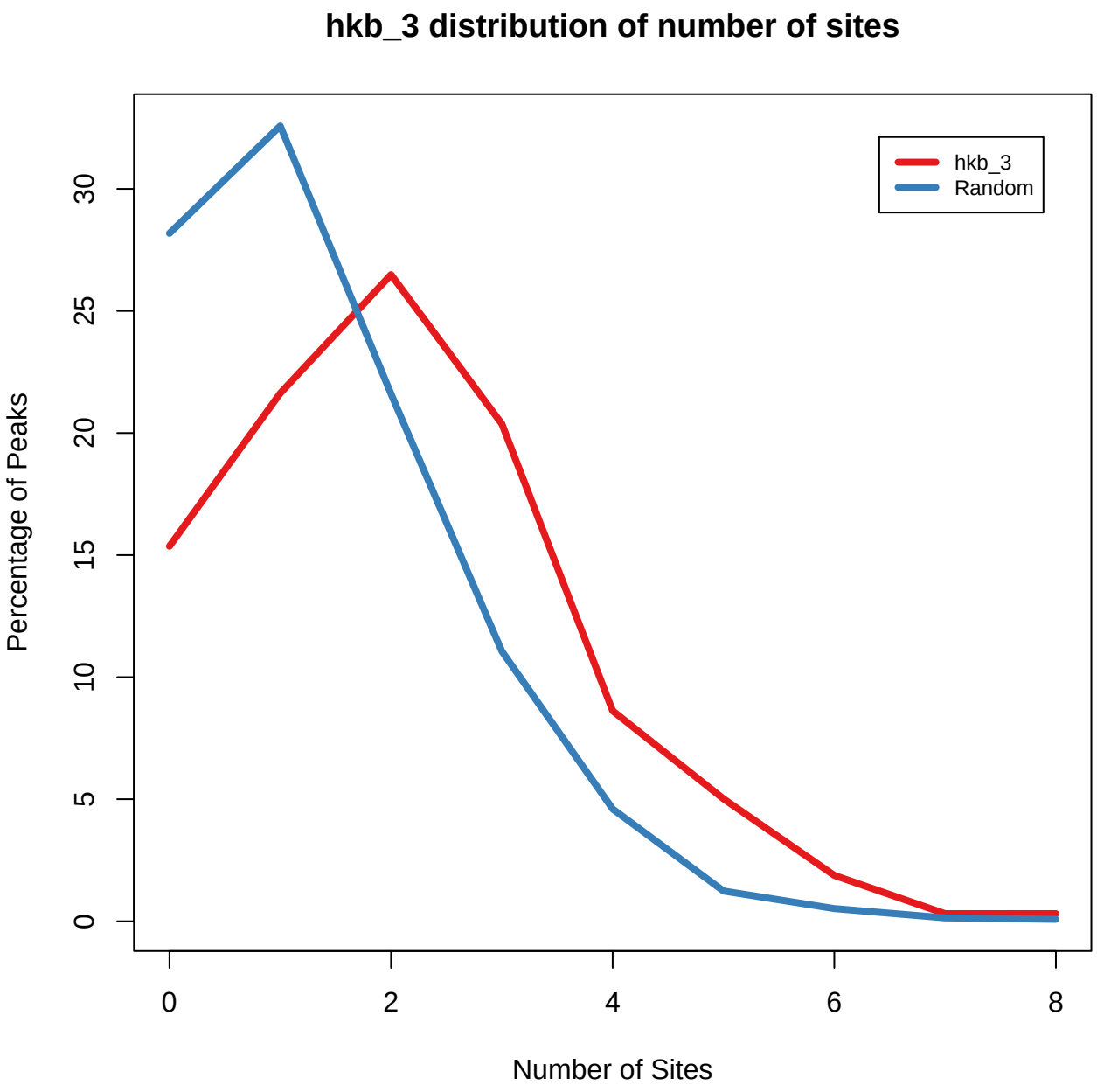
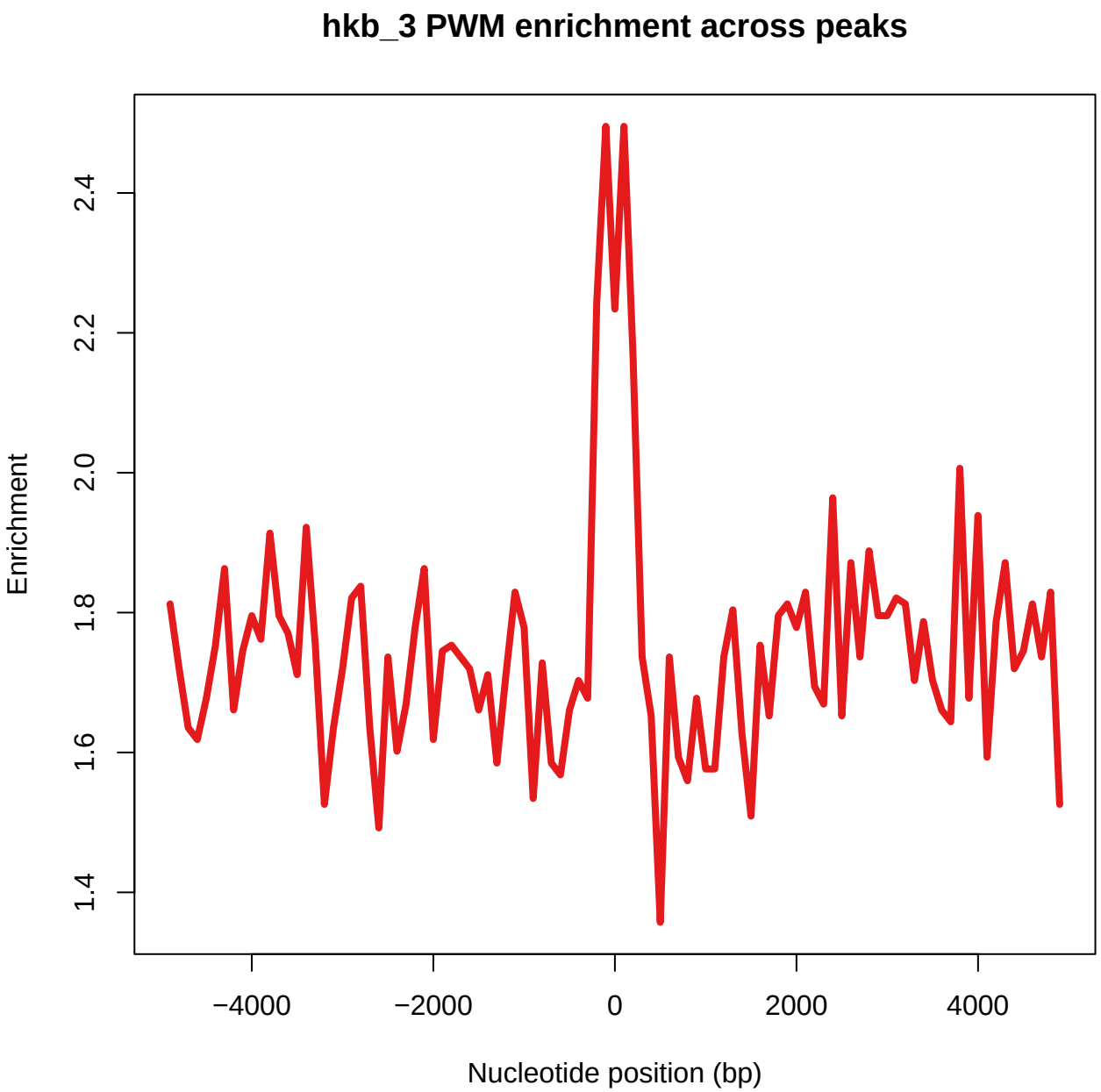
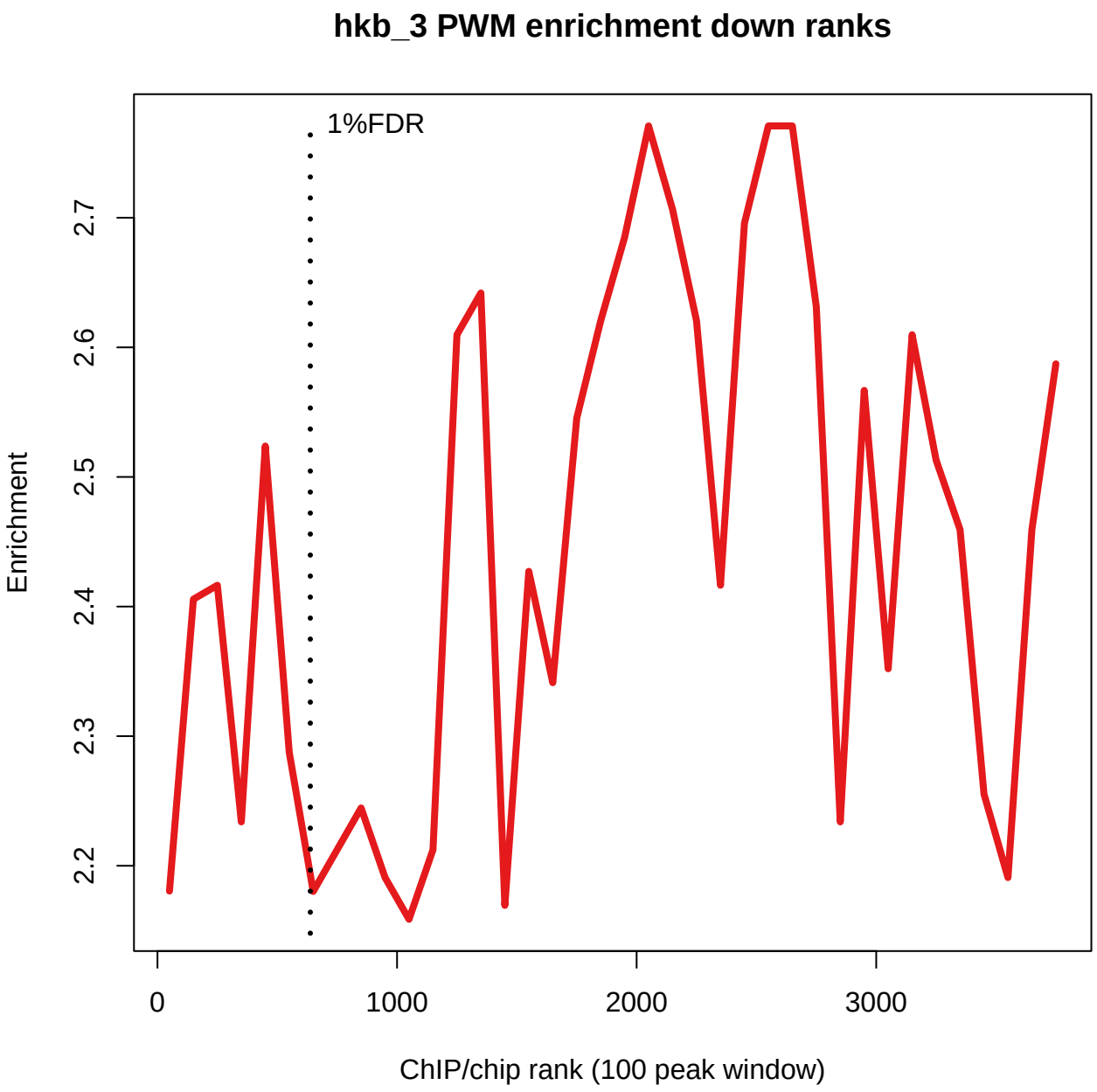

hkb_3 base composition across peaks
Percentage GC
40
42
44
46
−4000
−2000
0
2000
4000
Nucleotide position (bp)

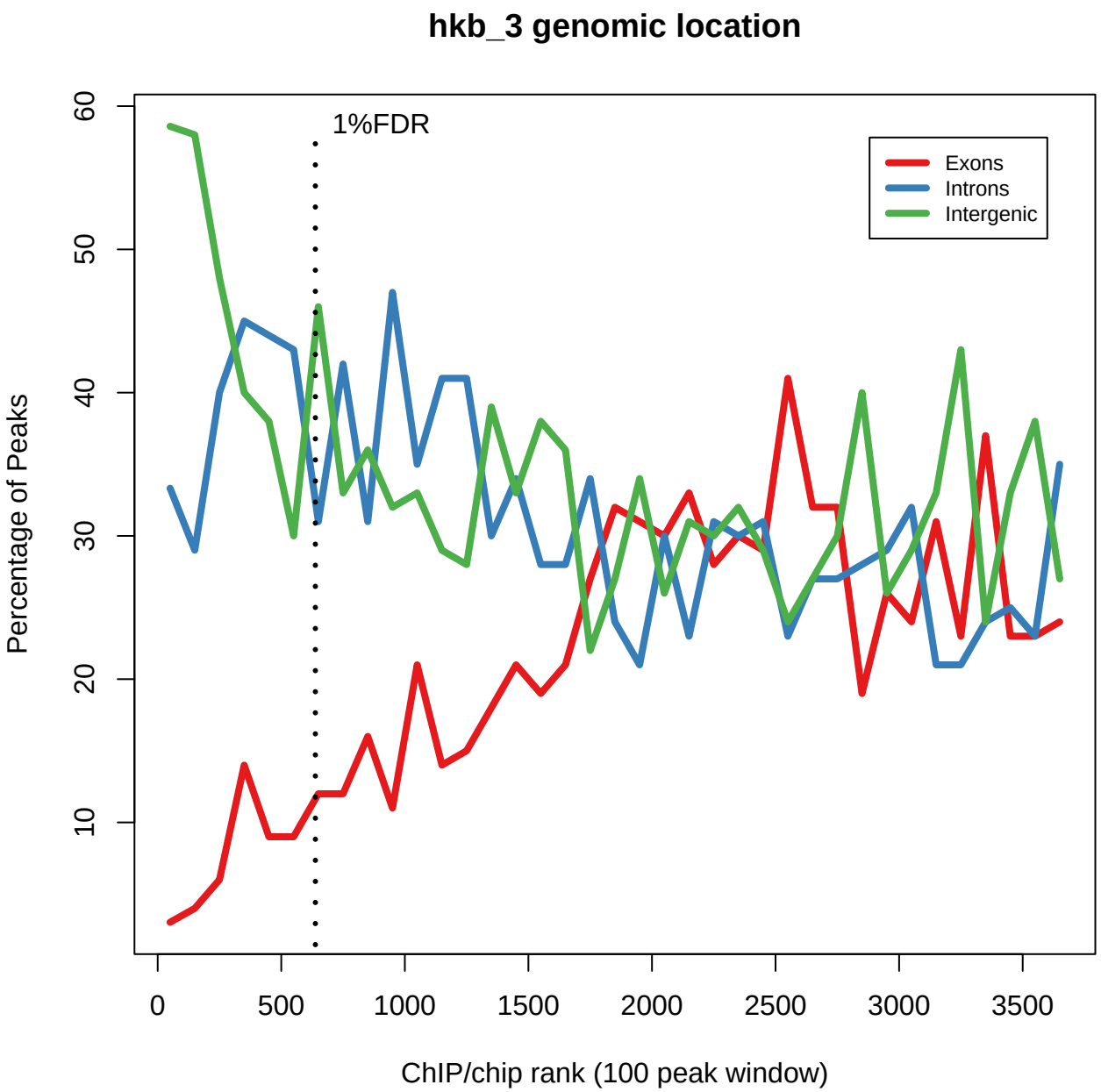

hkb_3 base composition down ranks
1%FDR
Percentage GC
43
44
45
46
0
1000
2000
3000
ChIP/chip rank (100 peak window)

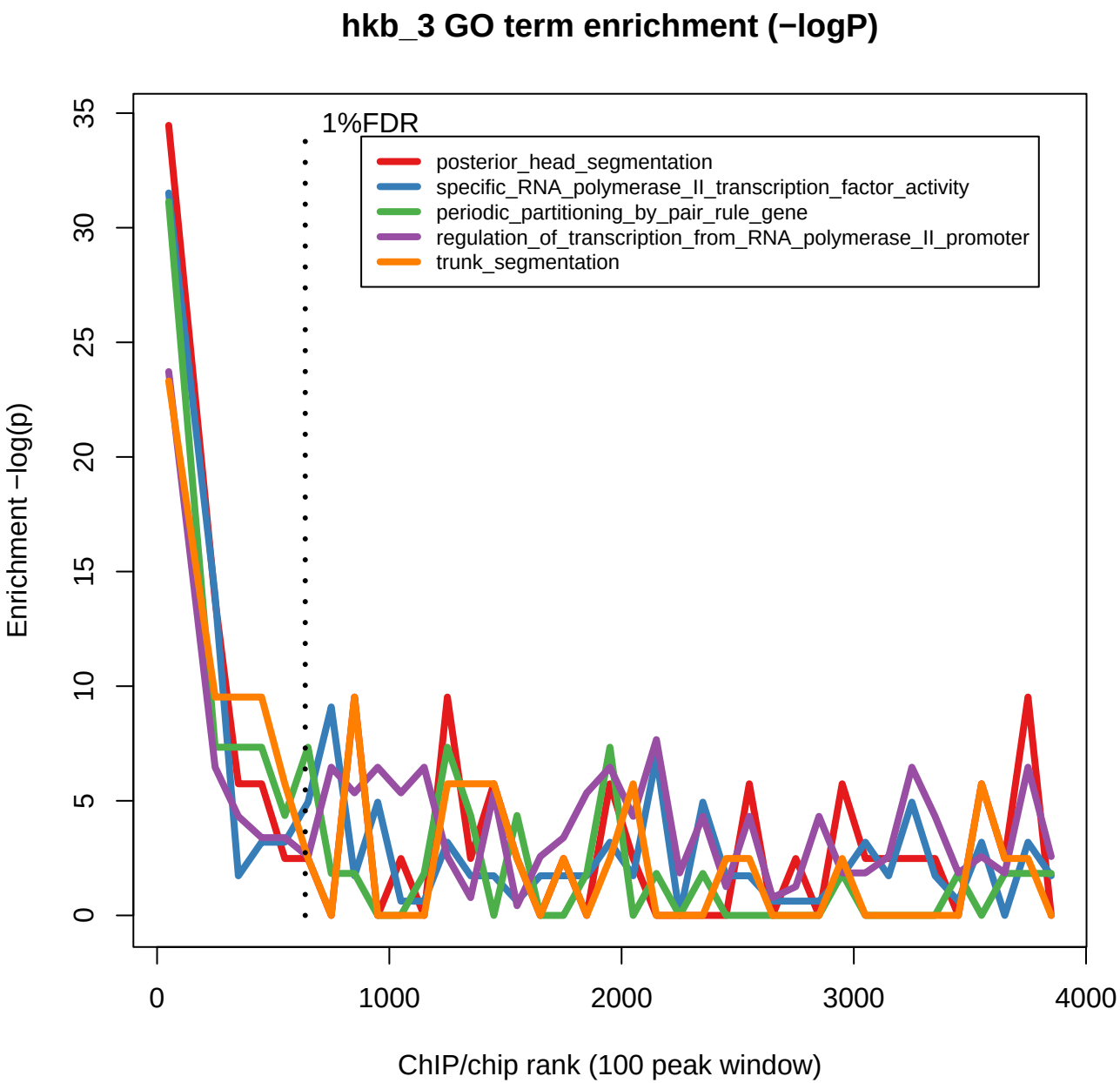

hkb_3 median distance to genes
1%FDR
all
patterned
transcribed
Median distance to closest gene
0
10000
20000
30000
40000
50000
60000
0
1000
2000
3000
ChIP/chip rank (100 peak window)

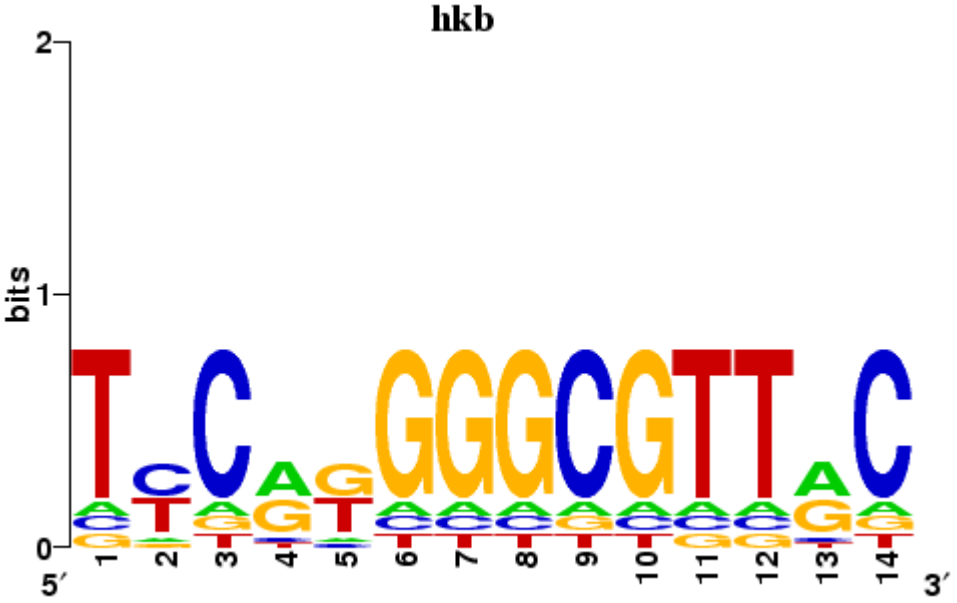

hkb_3 distribution of number of sites
hkb_3
Random
Percentage of Peaks
0
5
10
15
20
25
30
0
2
4
6
8
Number of Sites

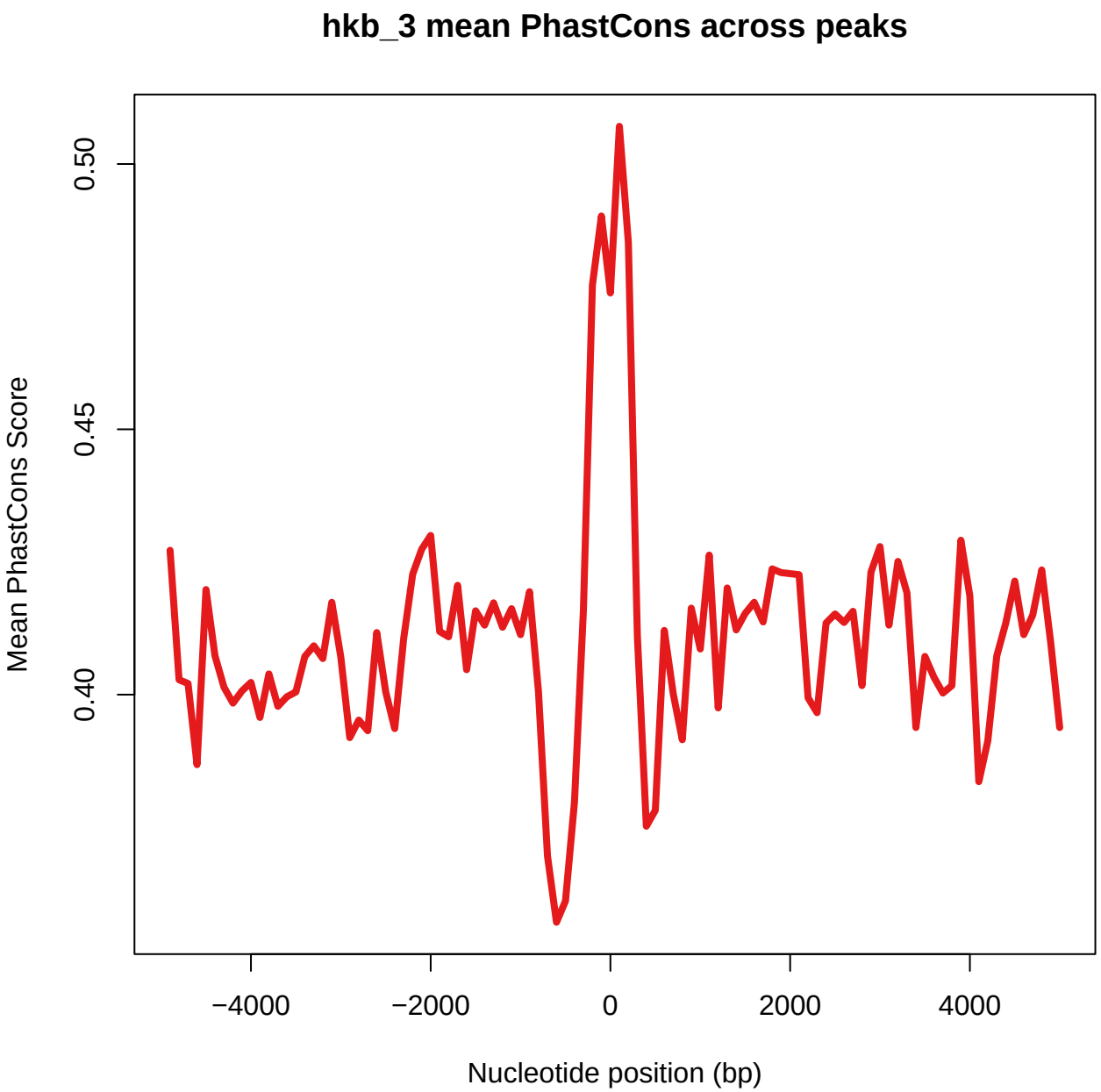

hkb_3 PWM enrichment across peaks
Enrichment
1.4
1.6
1.8
2.0
2.2
2.4
−4000
−2000
0
2000
4000
Nucleotide position (bp)

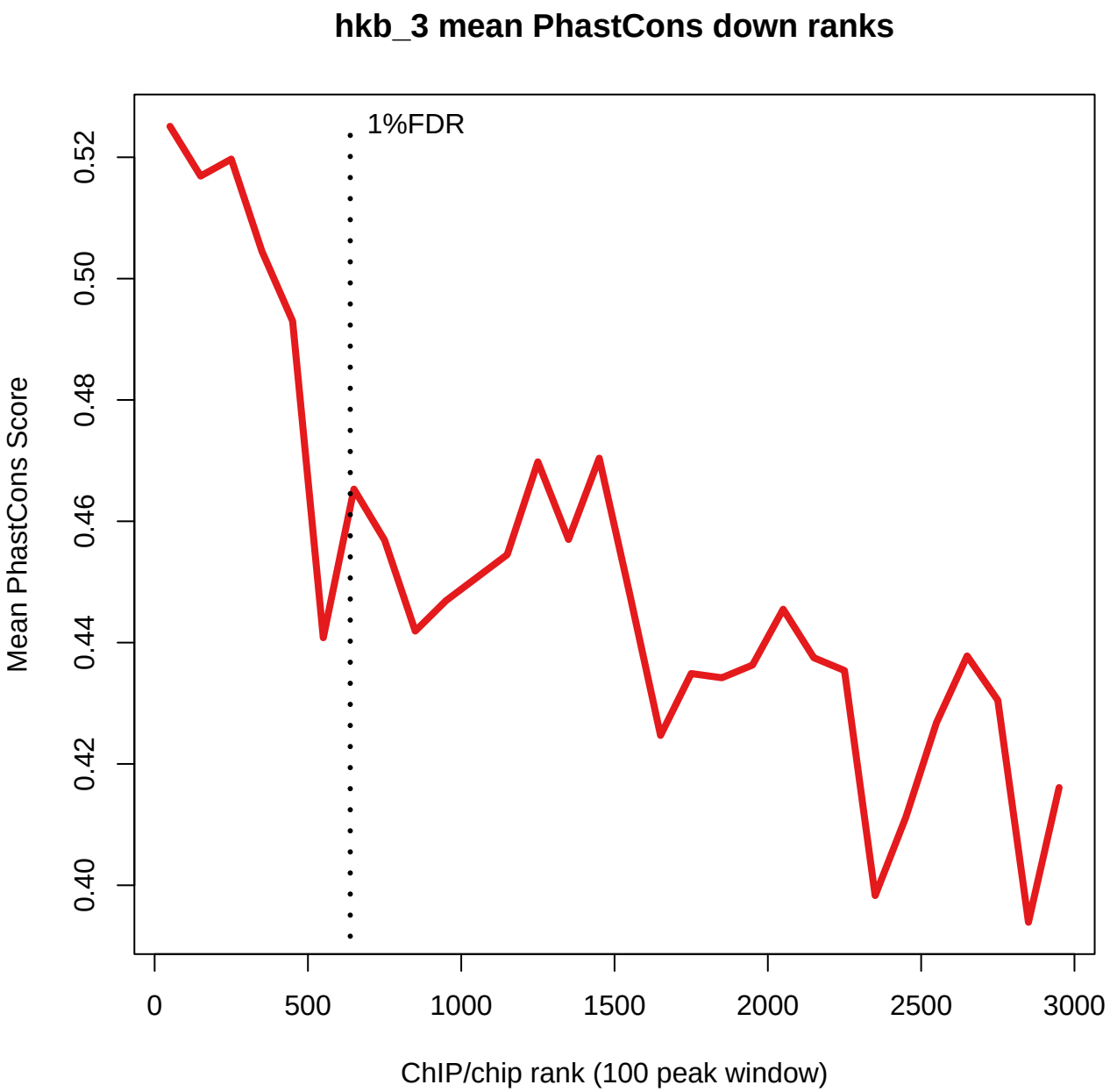

hkb_3 PWM enrichment down ranks
1%FDR
Enrichment
2.2
2.3
2.4
2.5
2.6
2.7
0
1000
2000
3000
ChIP/chip rank (100 peak window)


hkb_3 genomic location
1%FDR
Exons
Introns
Intergenic
Percentage of Peaks
10
20
30
40
50
60
0
500
1000
1500
2000
2500
3000
3500
ChIP/chip rank (100 peak window)


hkb_3 GO term enrichment (−logP)
1%FDR
posterior_head_segmentation
specific_RNA_polymerase_II_transcription_factor_activity
periodic_partitioning_by_pair_rule_gene
regulation_of_transcription_from_RNA_polymerase_II_promoter
trunk_segmentation
Enrichment −log(p)
0
5
10
15
20
25
30
35
0
1000
2000
3000
4000
ChIP/chip rank (100 peak window)


hkb
bits
2
1
0
5′
3′
1
2
3
4
5
6
7
8
9
10
11
12
13
14


hkb_3 mean PhastCons across peaks
Mean PhastCons Score
0.40
0.45
0.50
−4000
−2000
0
2000
4000
Nucleotide position (bp)


hkb_3 mean PhastCons down ranks
1%FDR
Mean PhastCons Score
0.40
0.42
0.44
0.46
0.48
0.50
0.52
0
500
1000
1500
2000
2500
3000
ChIP/chip rank (100 peak window)