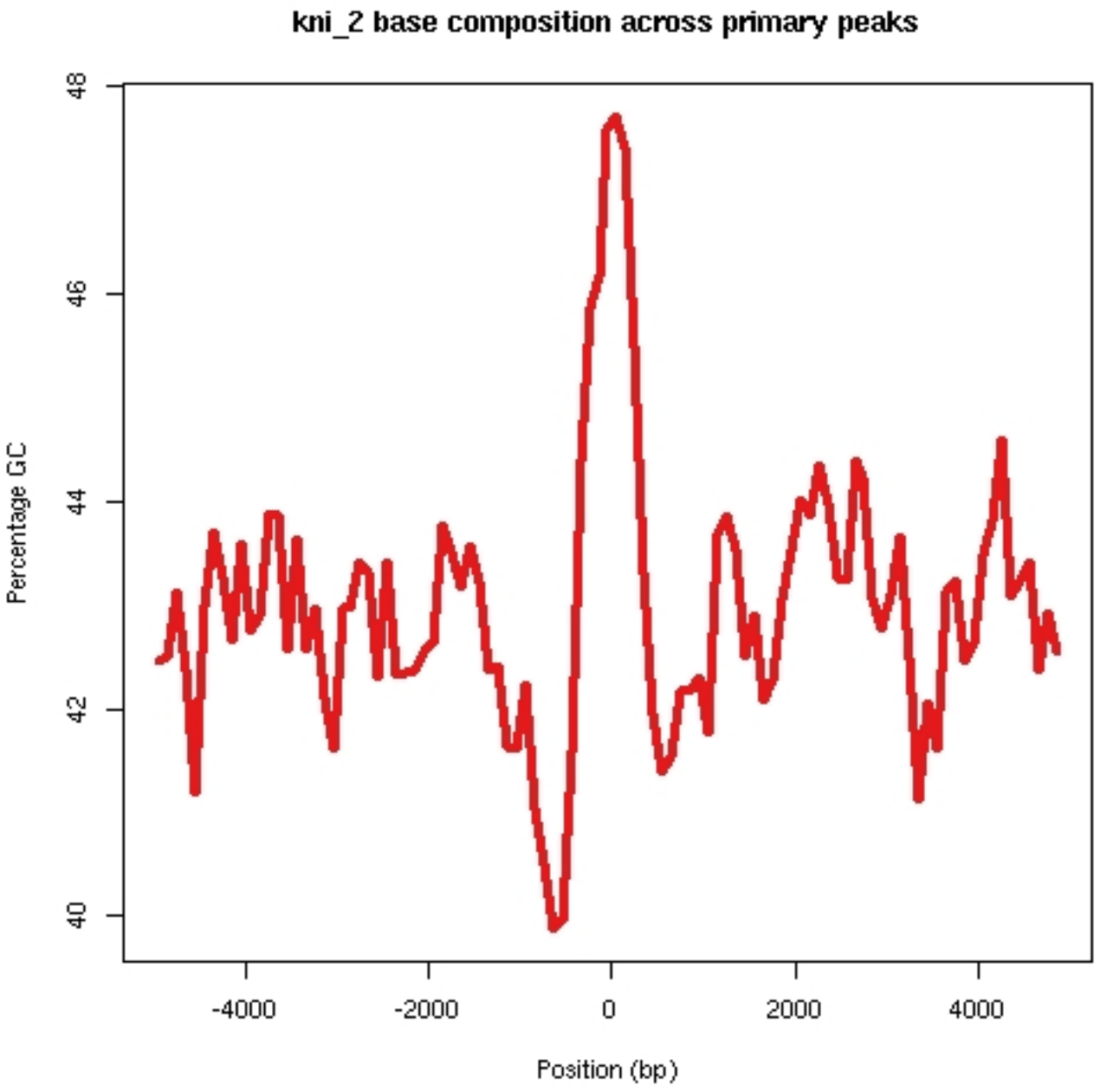
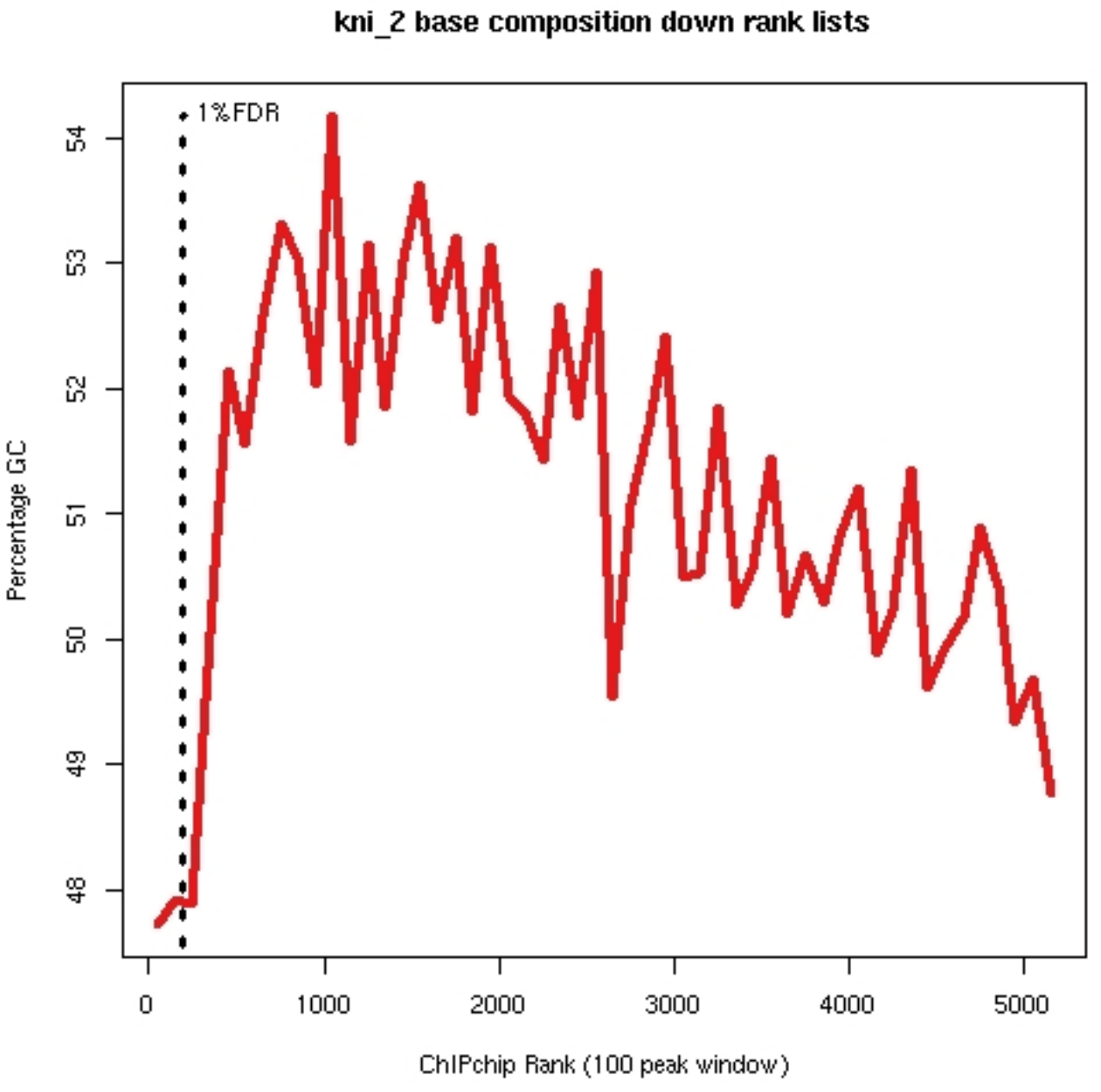
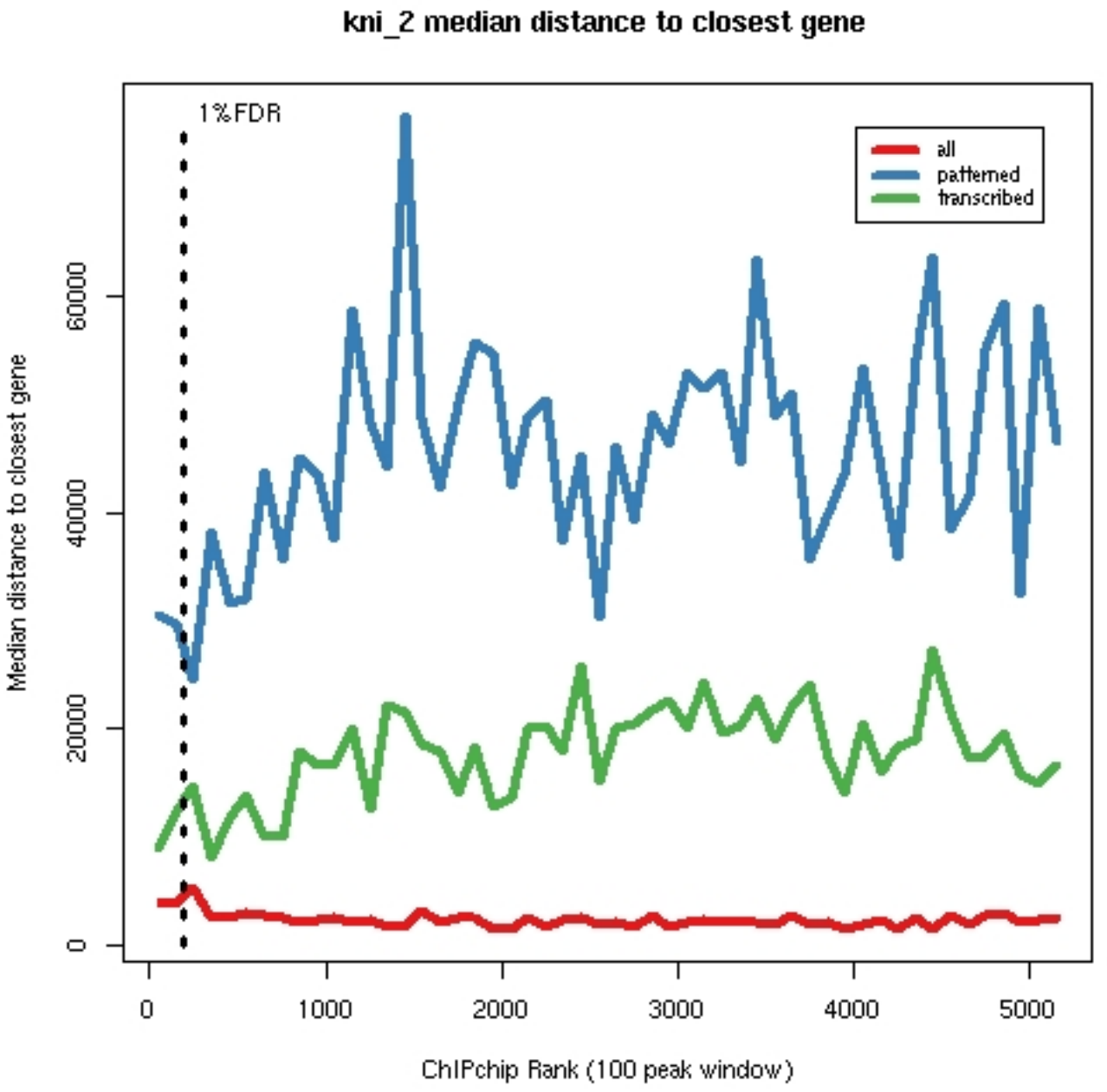
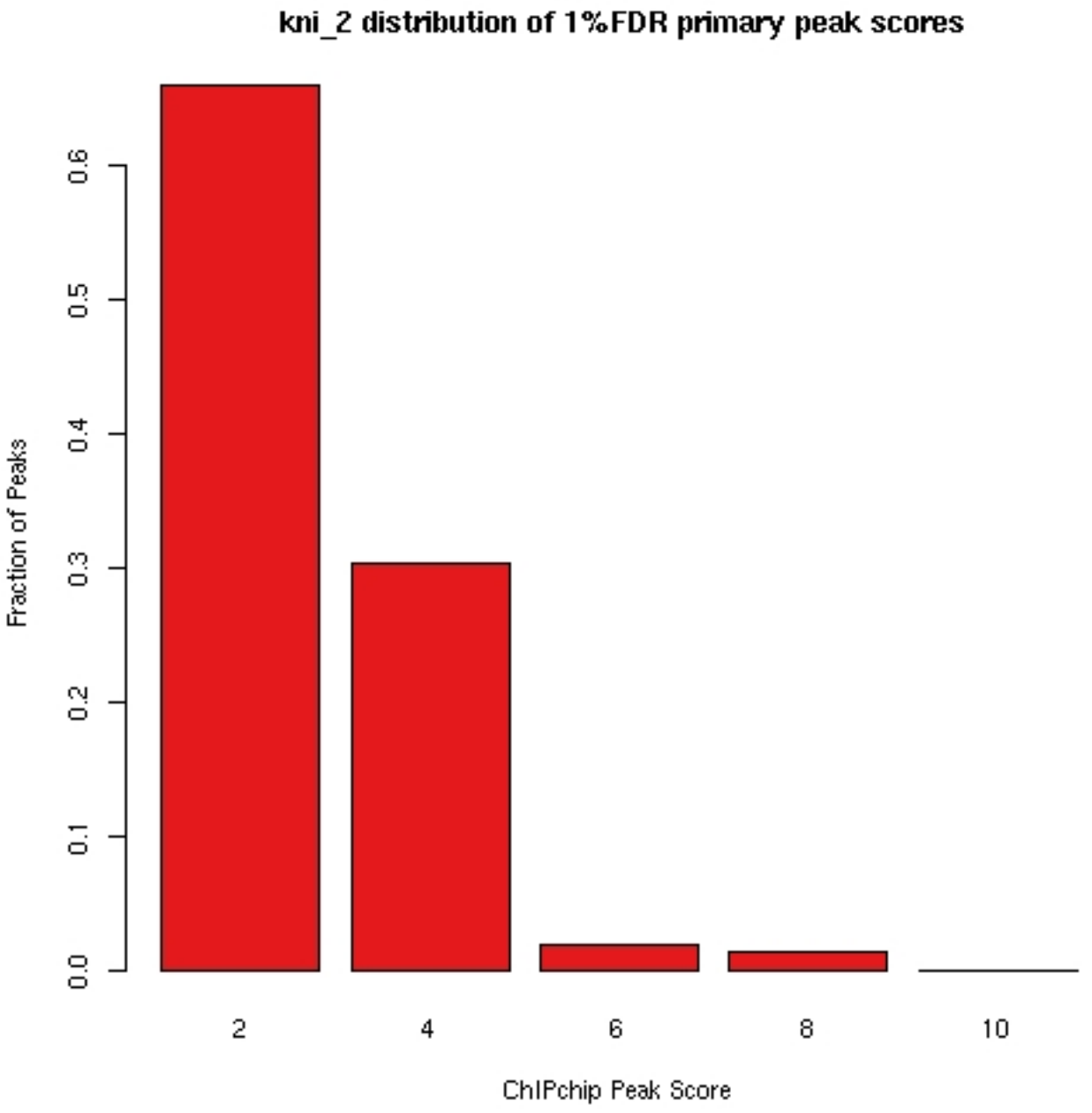
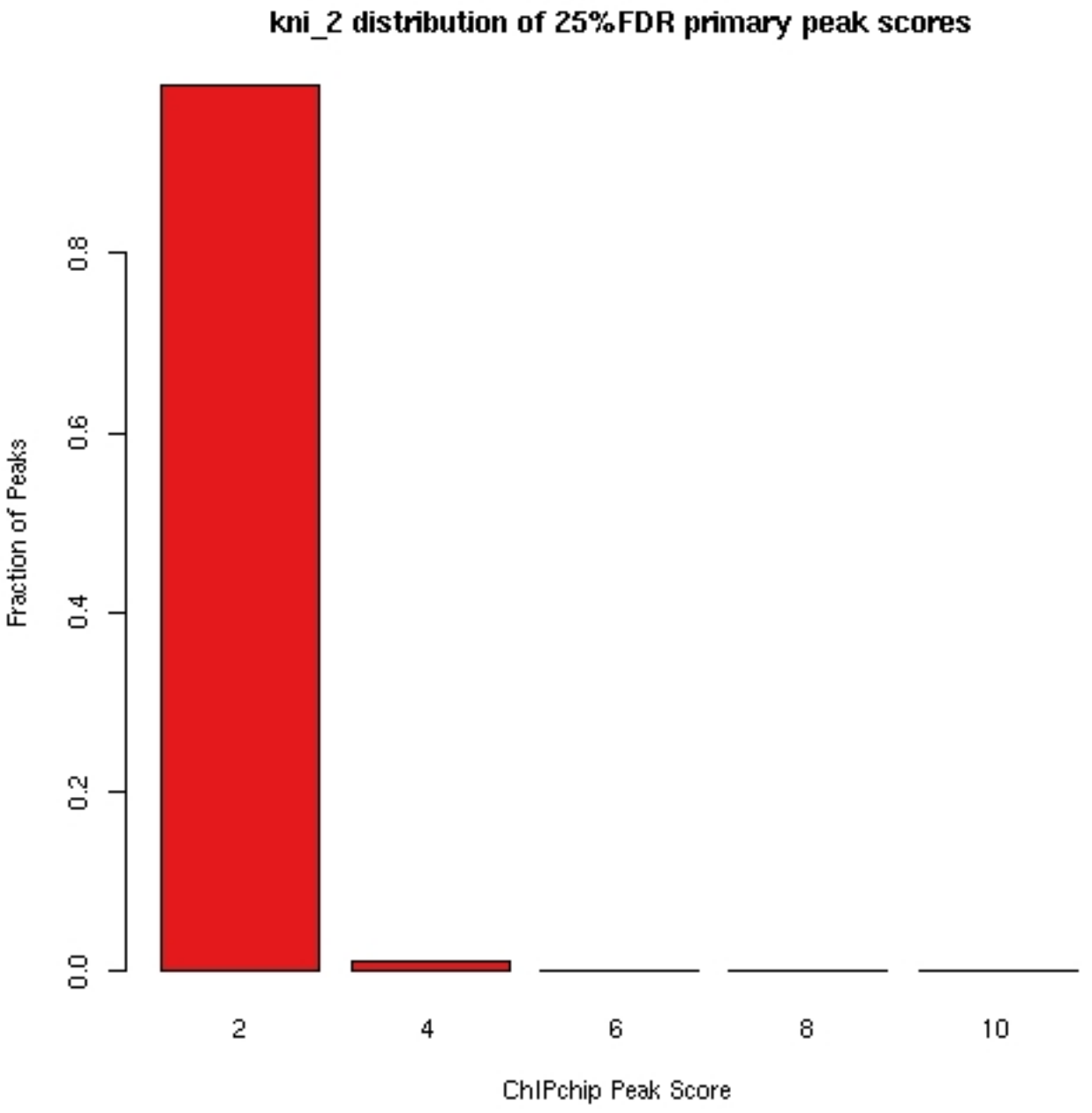
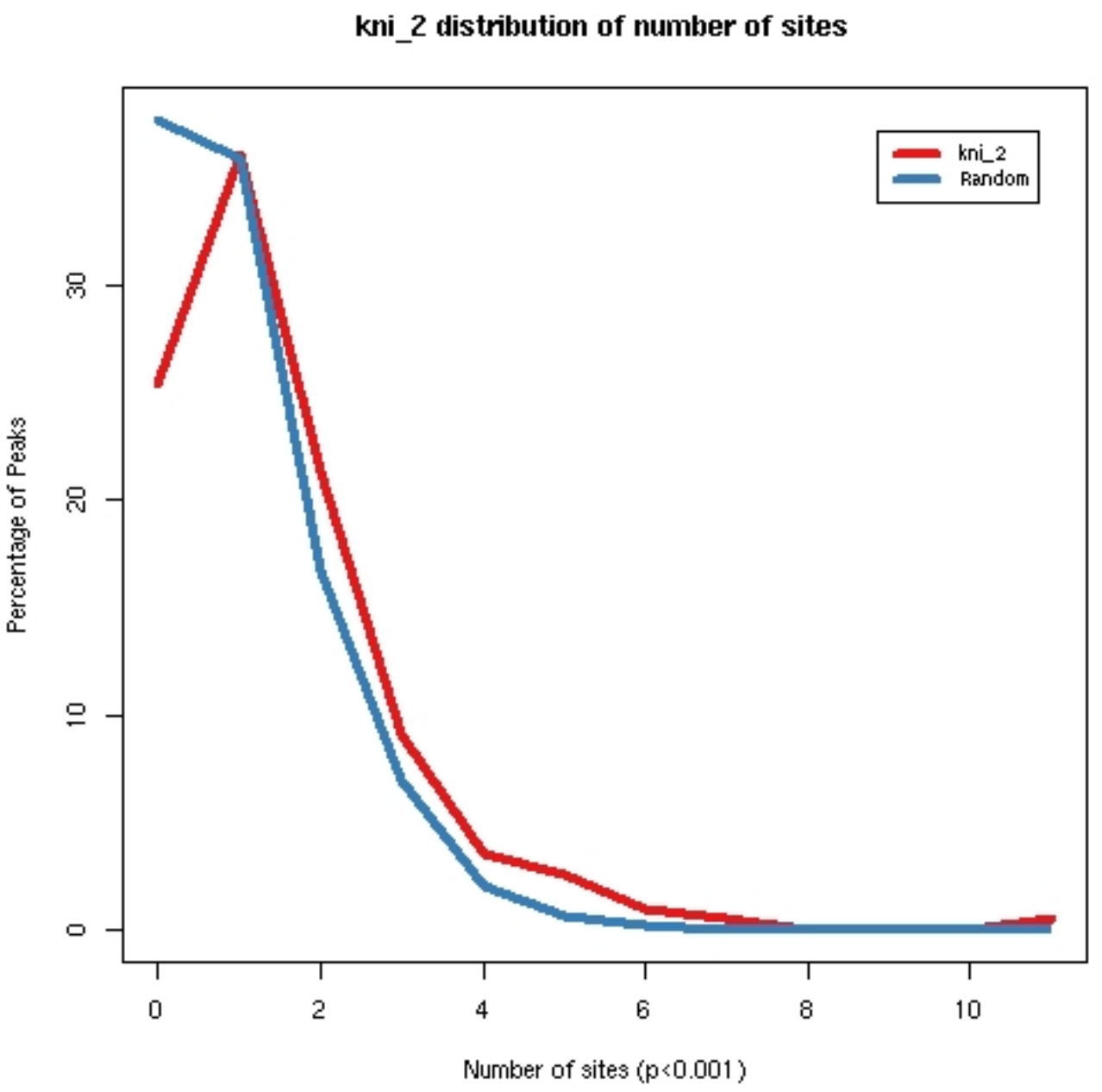

kni_2 base composition across primary peaks
Percentage GC
40
42
44
46
48
-4000
-2000
0
2000
4000
Position (bp)

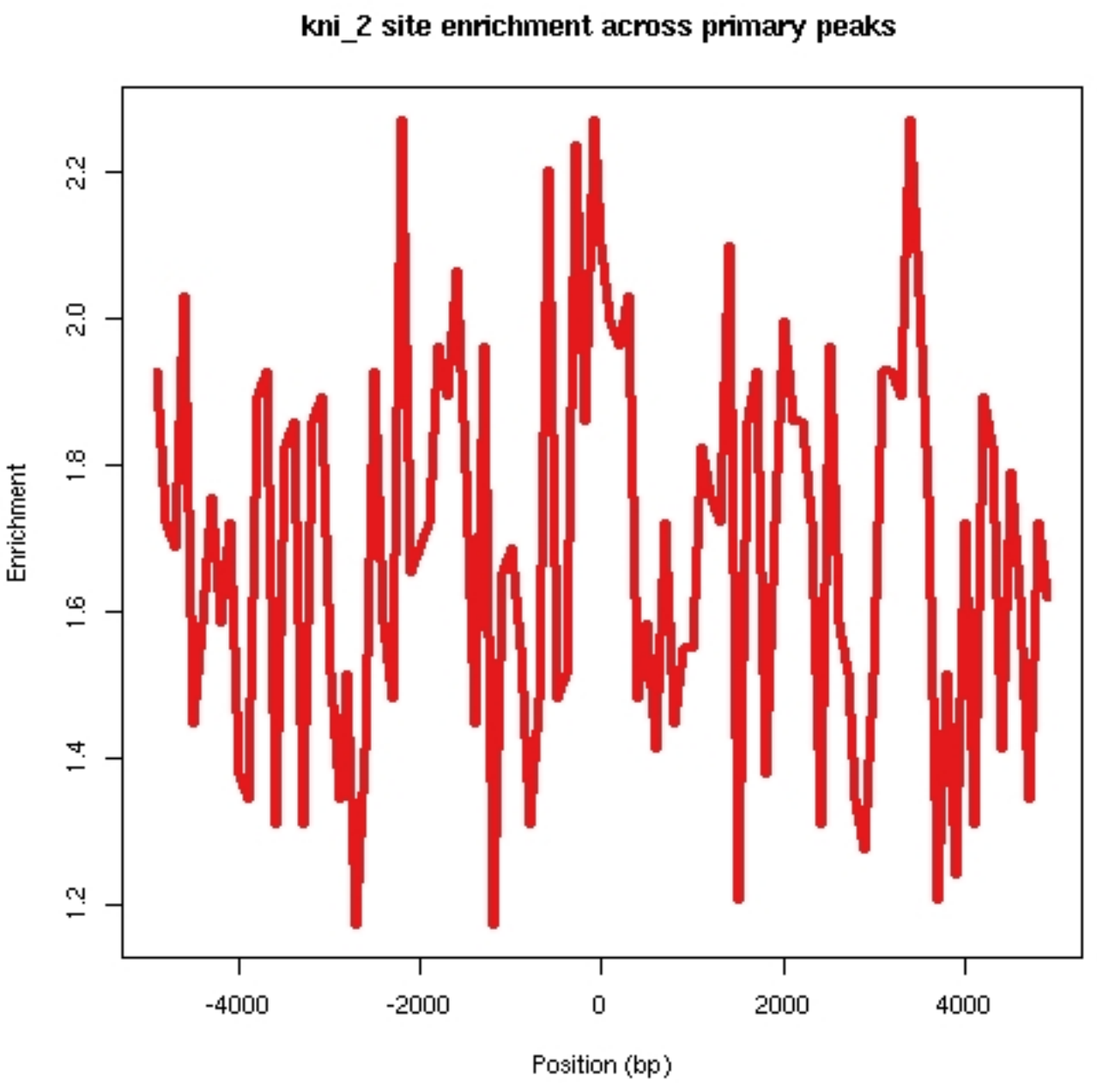

kni_2 base composition down rank lists
1%FDR
Percentage GC
48
49
50
51
52
53
54
0
1000
2000
3000
4000
5000
ChIPchip Rank (100 peak window)

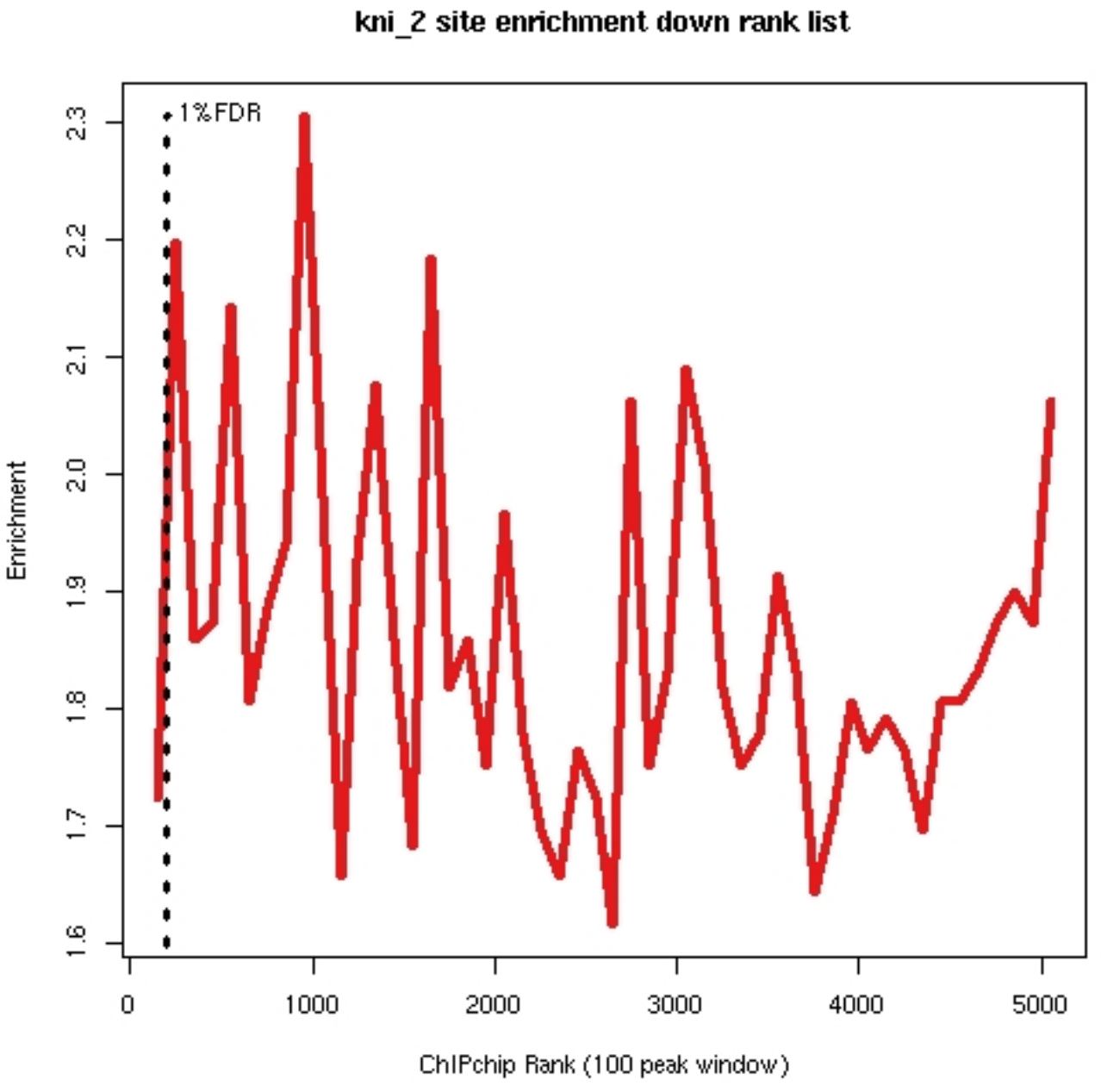

kni_2 median distance to closest gene
1%FDR
all
patterned
transcribed
Median distance to closest gene
0
20000
40000
60000
0
1000
2000
3000
4000
5000
ChIPchip Rank (100 peak window)

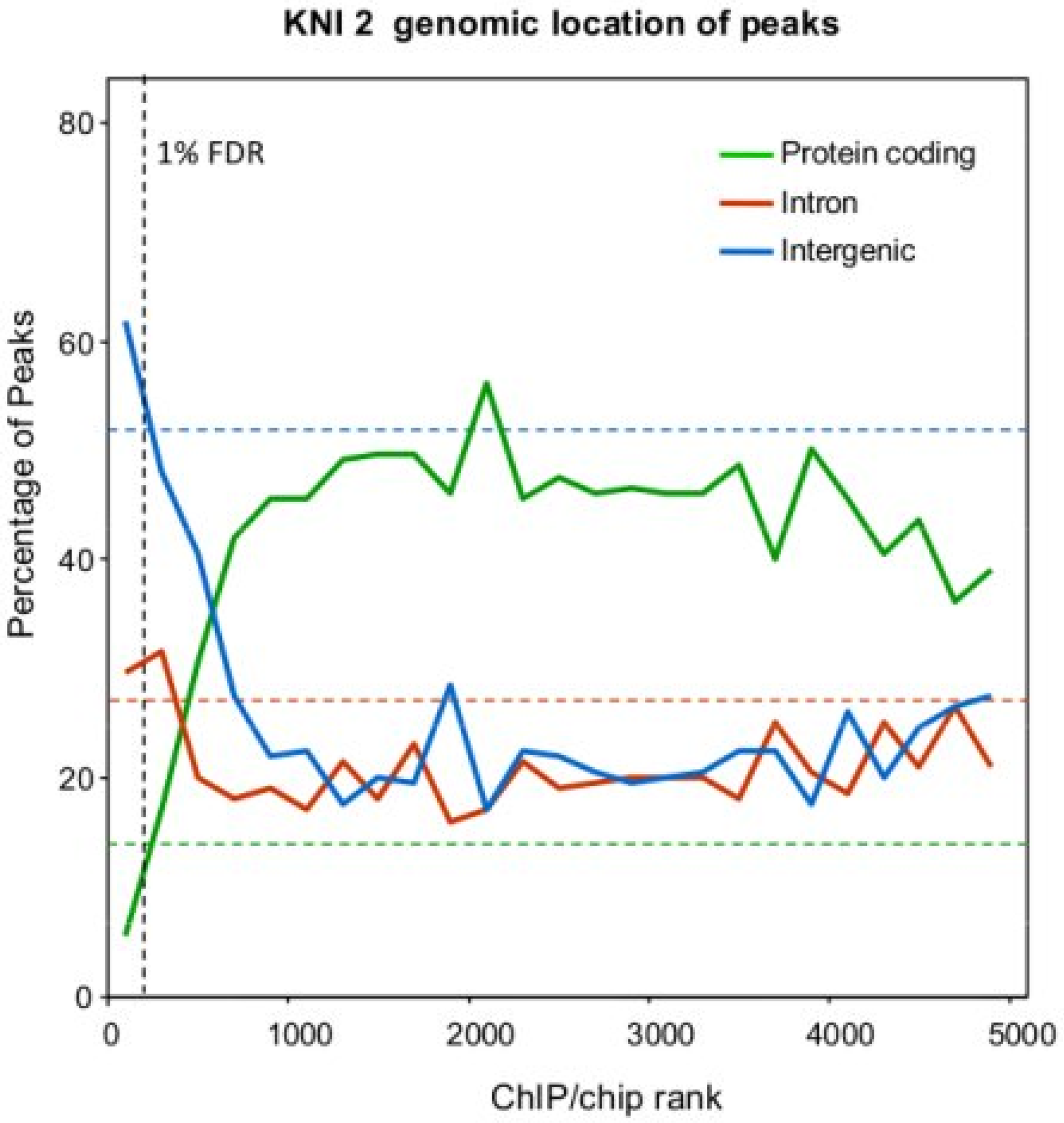

kni_2 distribution of 1%FDR primary peak scores
Fraction of Peaks
0.0
0.1
0.2
0.3
0.4
0.5
0.6
2
4
6
8
10
ChIPchip Peak Score

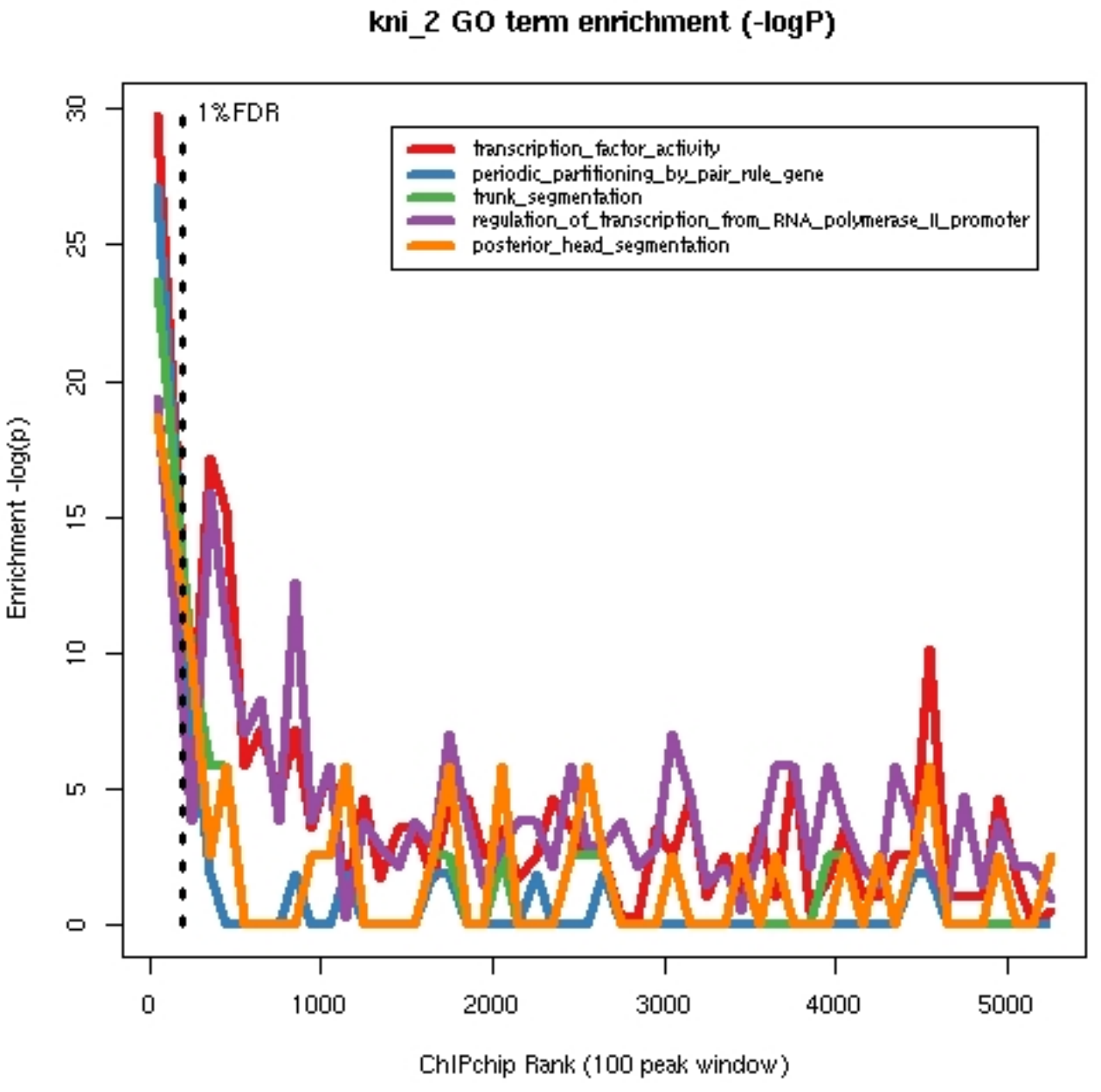

kni_2 distribution of 25%FDR primary peak scores
Fraction of Peaks
0.0
0.2
0.4
0.6
0.8
2
4
6
8
10
ChIPchip Peak Score

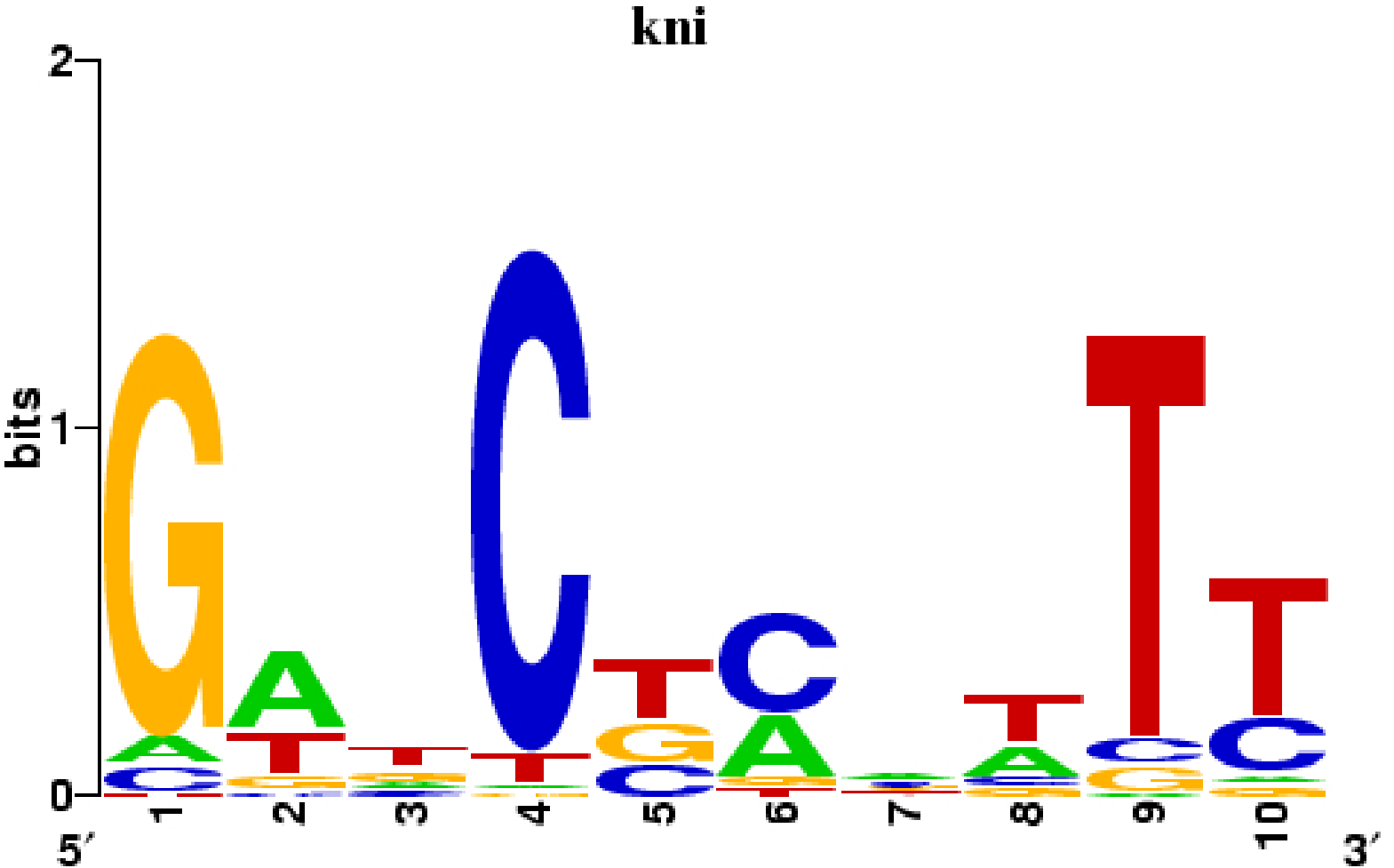

kni_2 distribution of number of sites
kni_2
Random
Percentage of Peaks
0
10
20
30
0
2
4
6
8
10
Number of sites (p<0.001)

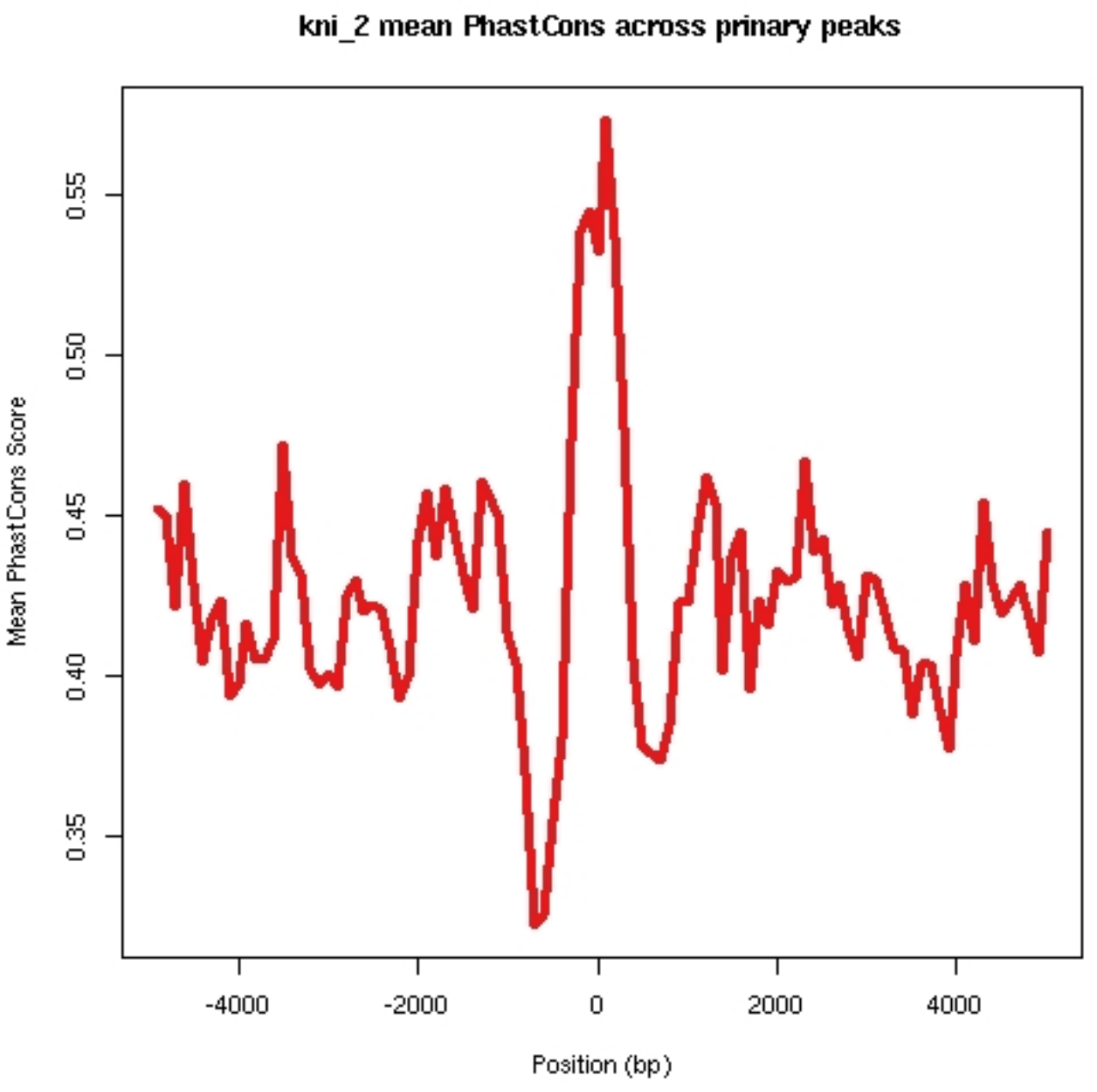

kni_2 site enrichment across primary peaks
Enrichment
1.2
1.4
1.6
1.8
2.0
2.2
-4000
-2000
0
2000
4000
Position (bp)

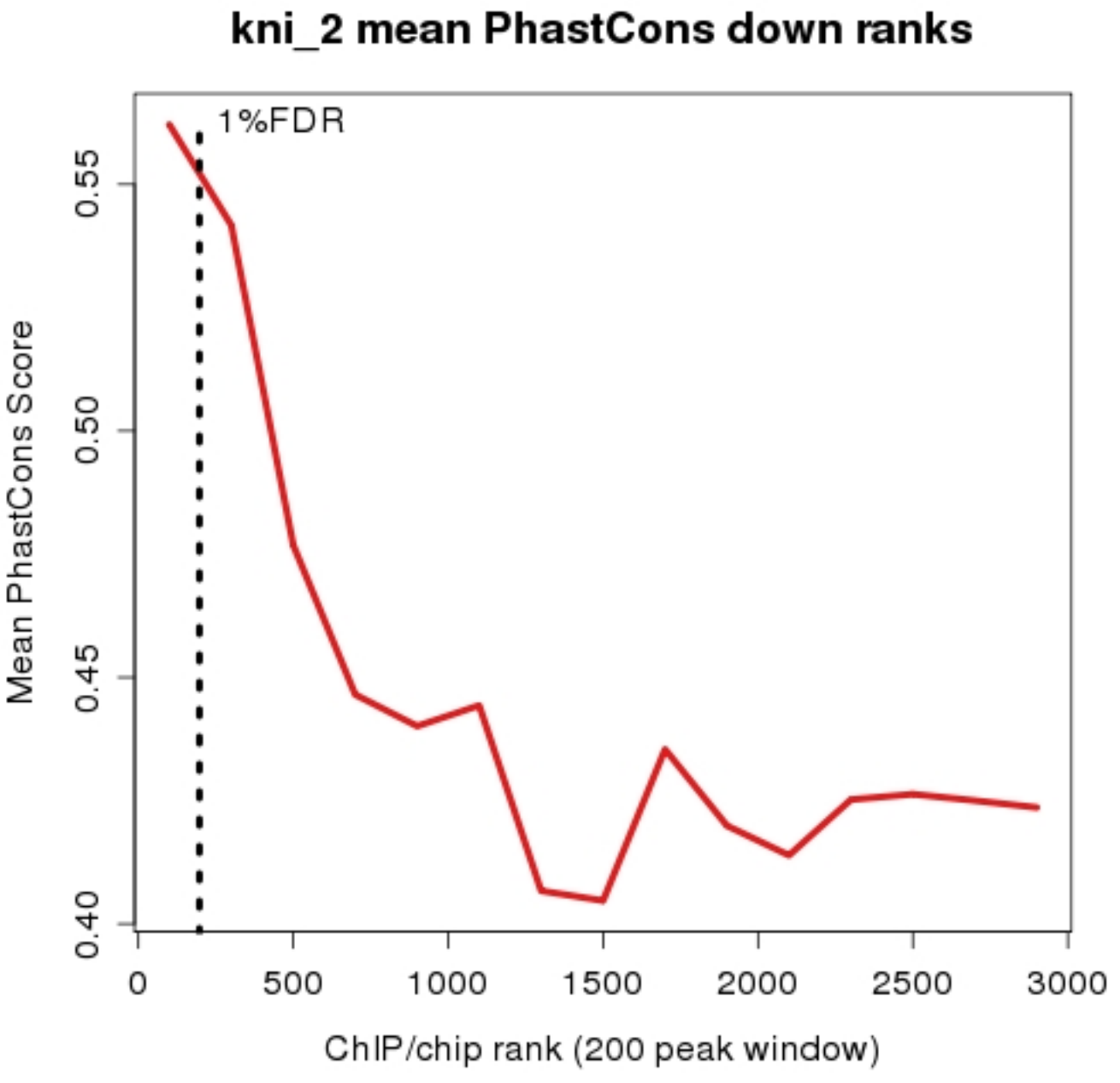

kni_2 site enrichment down rank list
1%FDR
Enrichment
2.3
2.2
2.1
2.0
1.9
1.8
1.7
1.6
0
1000
2000
3000
4000
5000
ChIPchip Rank (100 peak window)


KNI 2 genomic location of peaks
1% FDR
Protein coding
Intron
Intergenic
Percentage of Peaks
0
20
40
60
80
0
1000
2000
3000
4000
5000
ChIP/chip rank


kni_2 GO term enrichment (-logP)
1%FDR
transcription_factor_activity
periodic_partitioning_by_pair_rule_gene
trunk_segmentation
regulation_of_transcription_from_RNA_polymerase_II_promoter
posterior_head_segmentation
Enrichment -log(p)
0
5
10
15
20
25
30
0
1000
2000
3000
4000
5000
ChIPchip Rank (100 peak window)


kni
bits
2
1
0
5′
3′
1
2
3
4
5
6
7
8
9
10


kni_2 mean PhastCons across prinary peaks
Mean PhastCons Score
0.35
0.40
0.45
0.50
0.55
-4000
-2000
0
2000
4000
Position (bp)


kni_2 mean PhastCons down ranks
1%FDR
Mean PhastCons Score
0.40
0.45
0.50
0.55
0
500
1000
1500
2000
2500
3000
ChIP/chip rank (200 peak window)