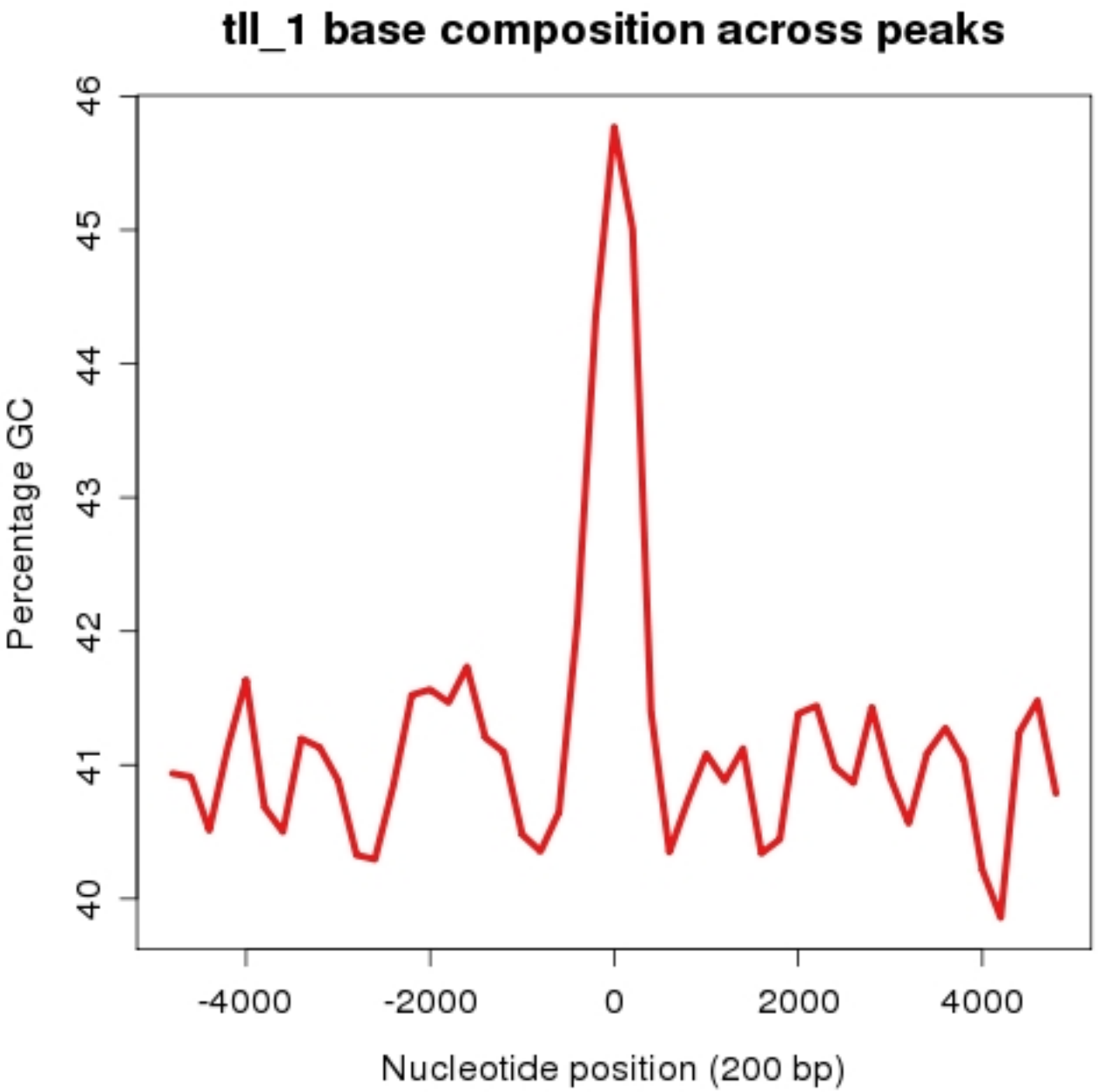
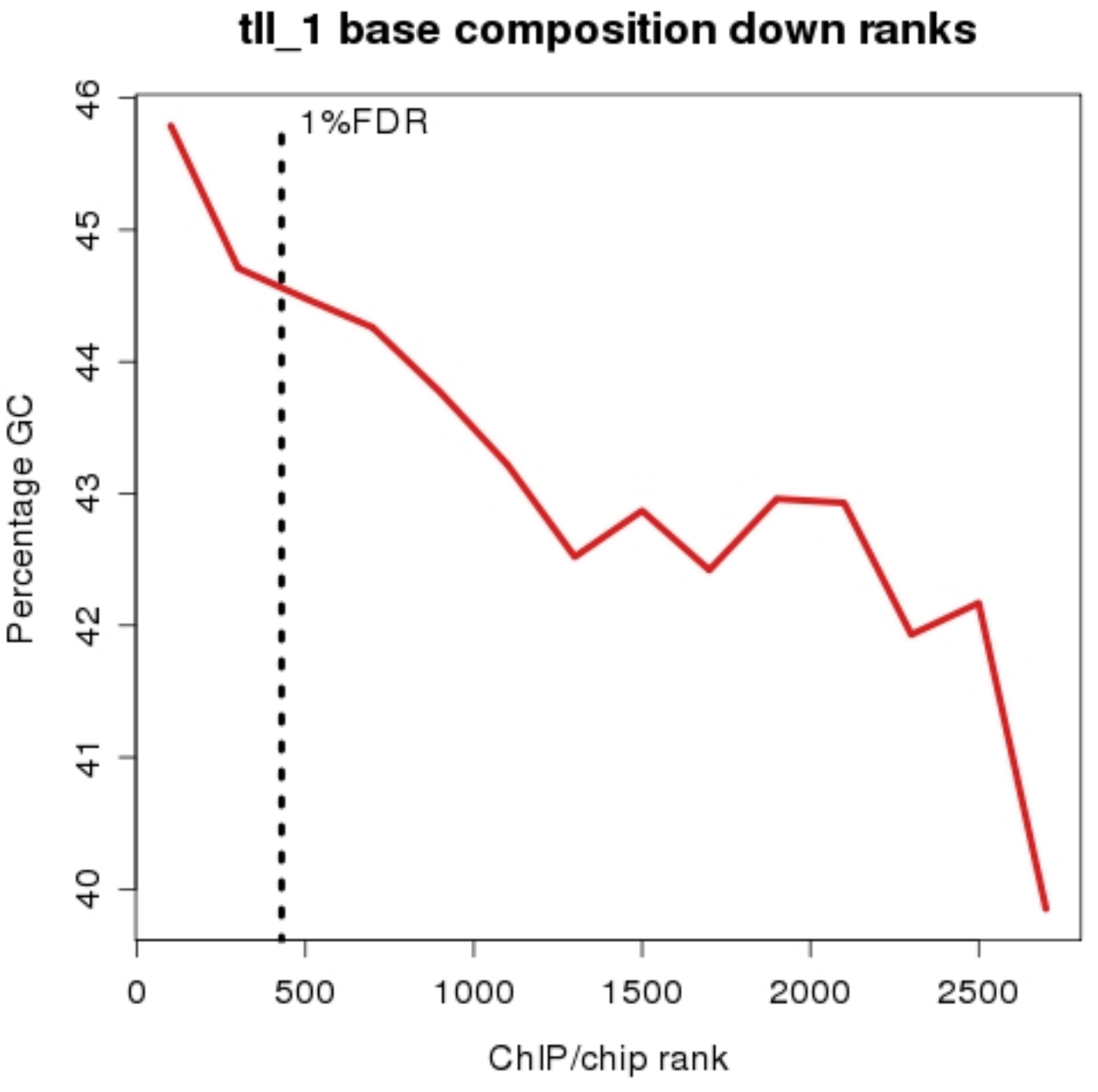
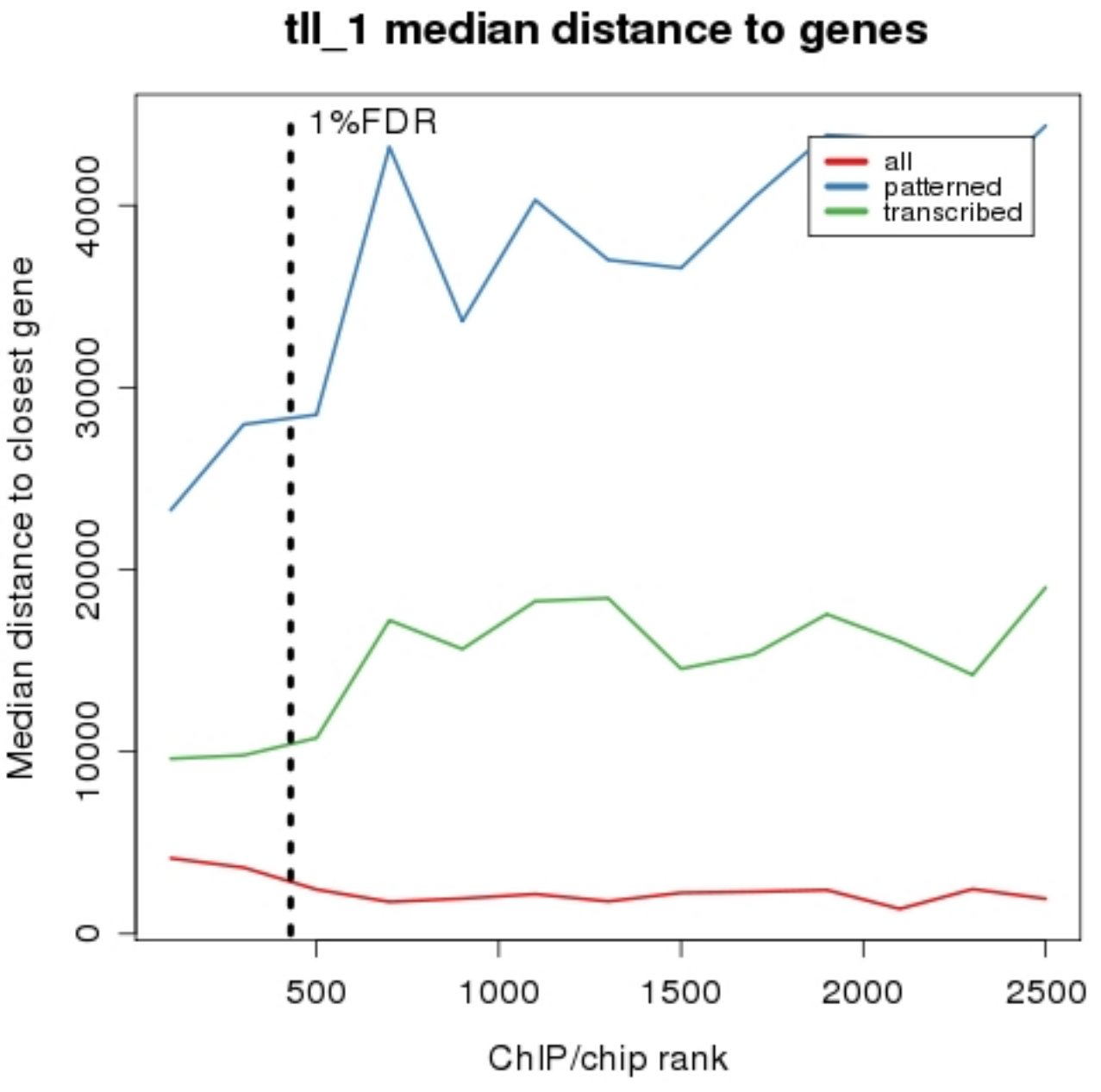
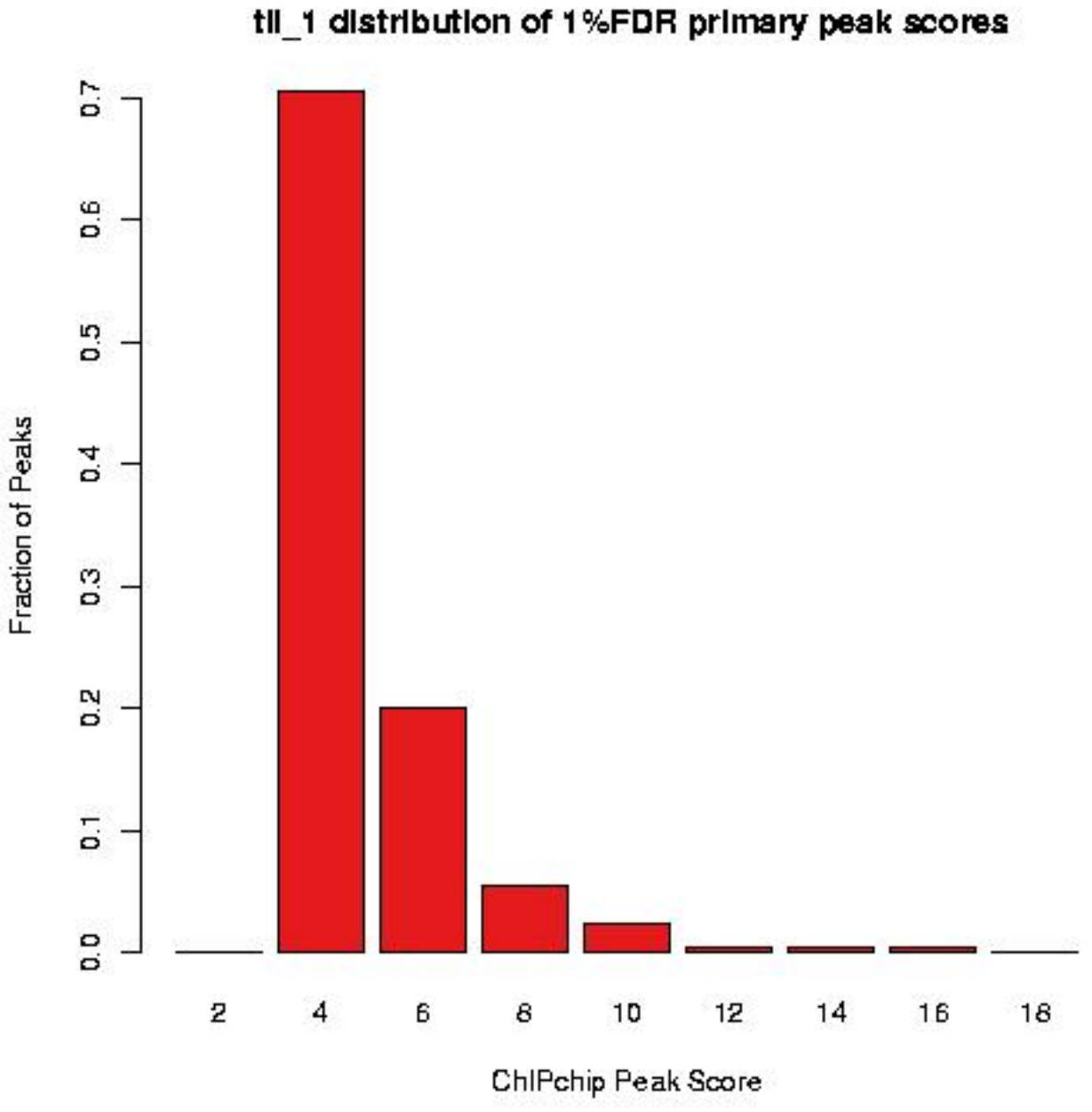
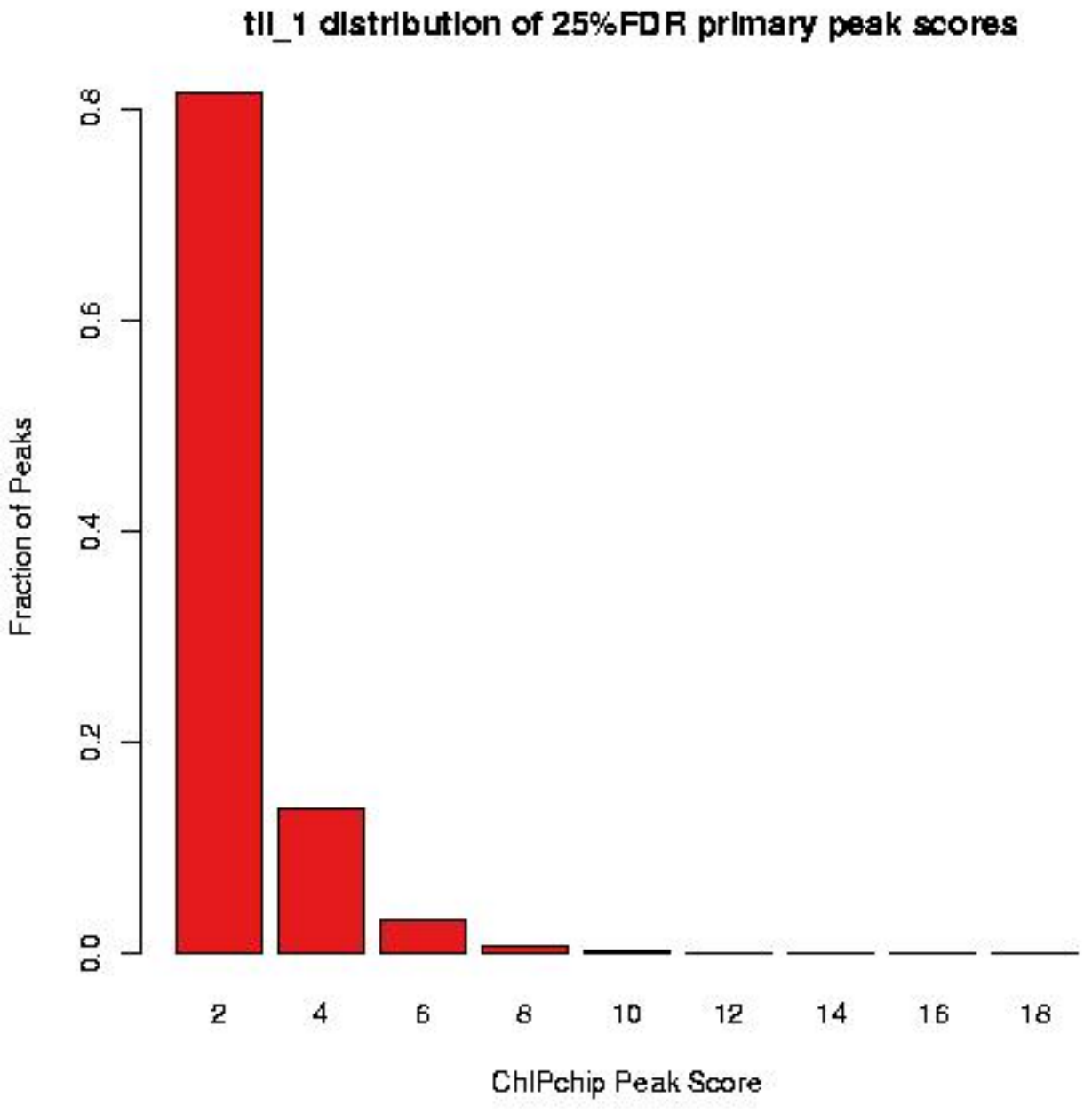
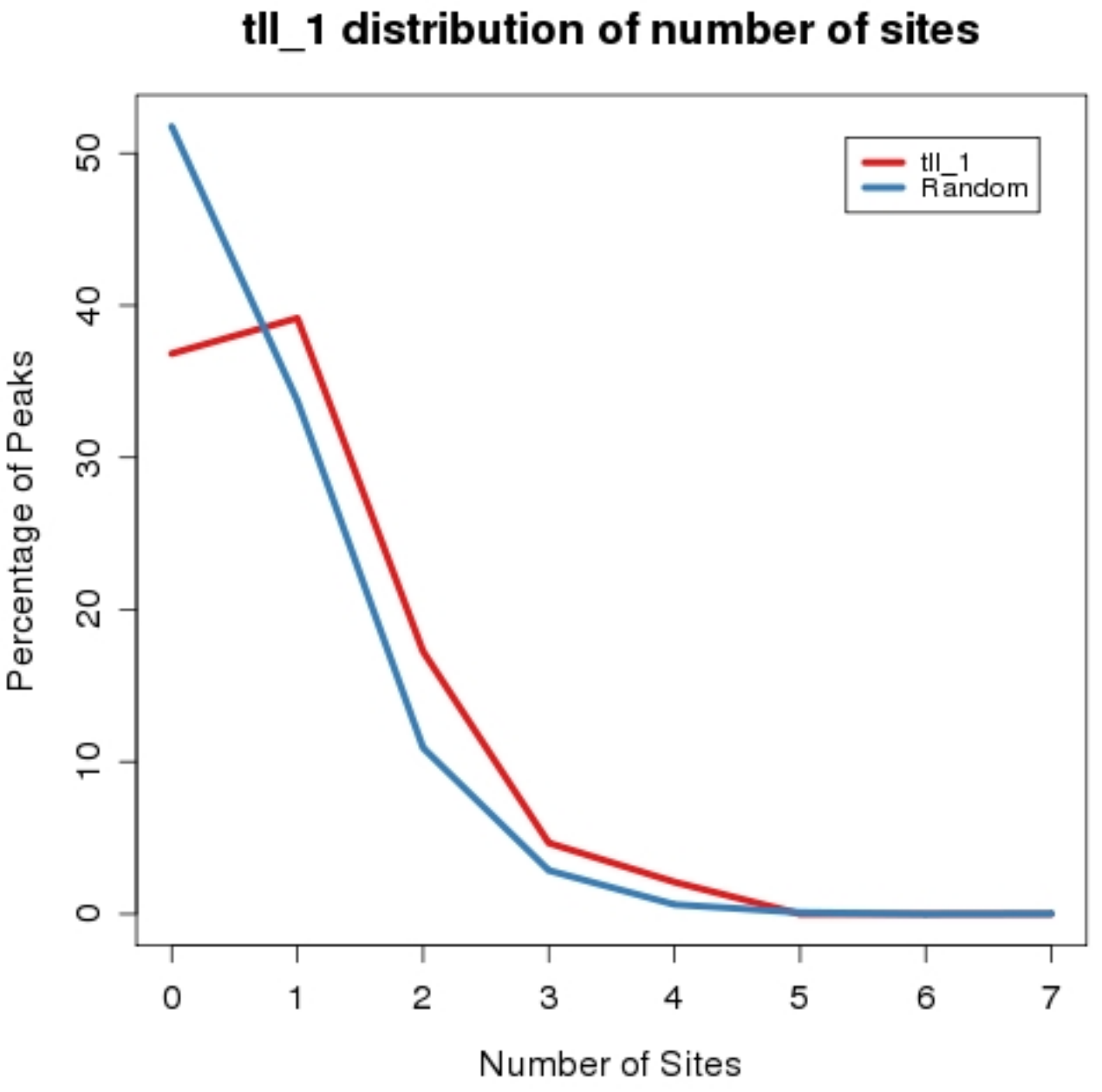

tll_1 base composition across peaks
Percentage GC
40
41
42
43
44
45
46
-4000
-2000
0
2000
4000
Nucleotide position (200 bp)

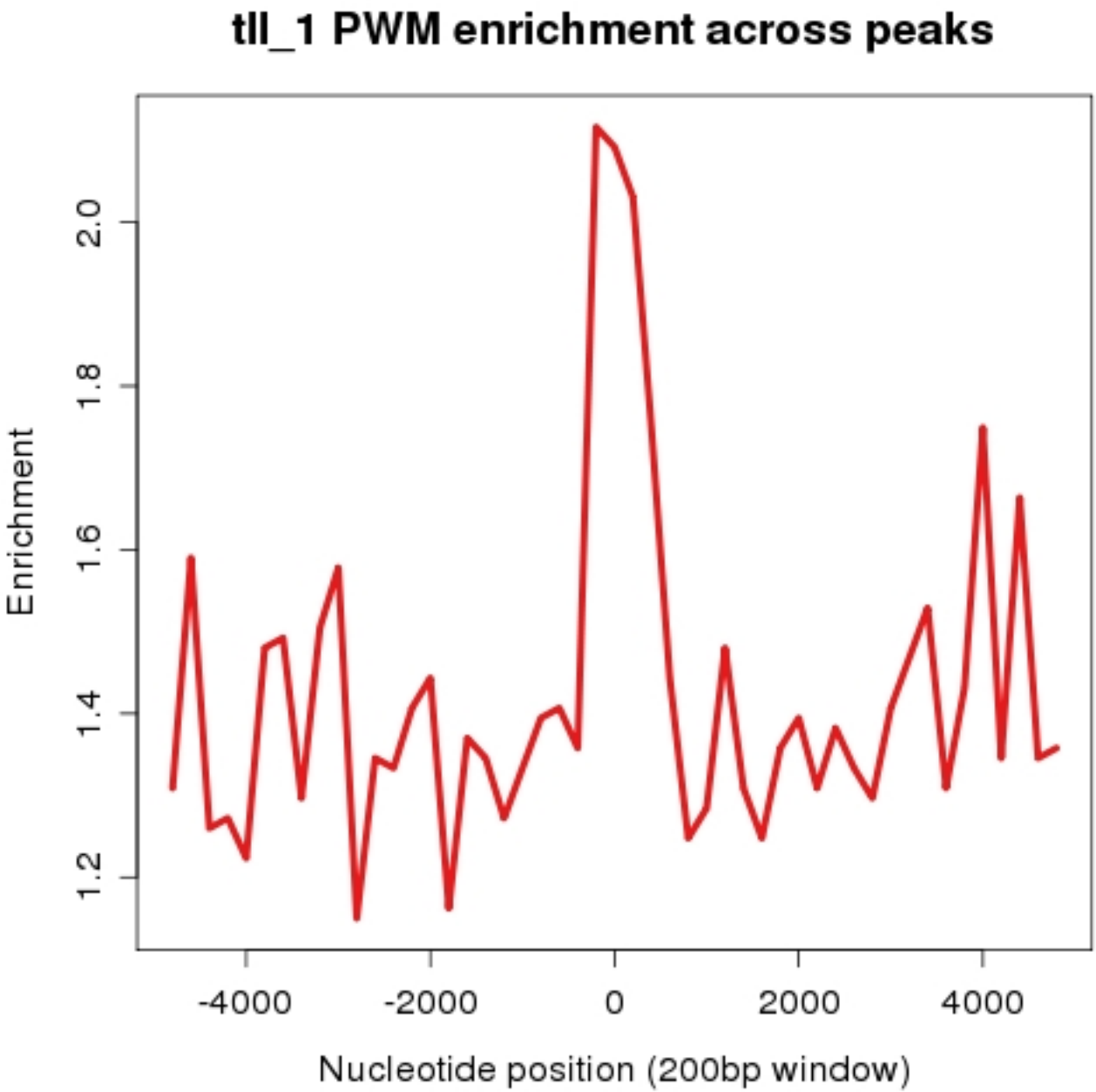

tll_1 base composition down ranks
1%FDR
Percentage GC
40
41
42
43
44
45
46
0
500
1000
1500
2000
2500
ChIP/chip rank

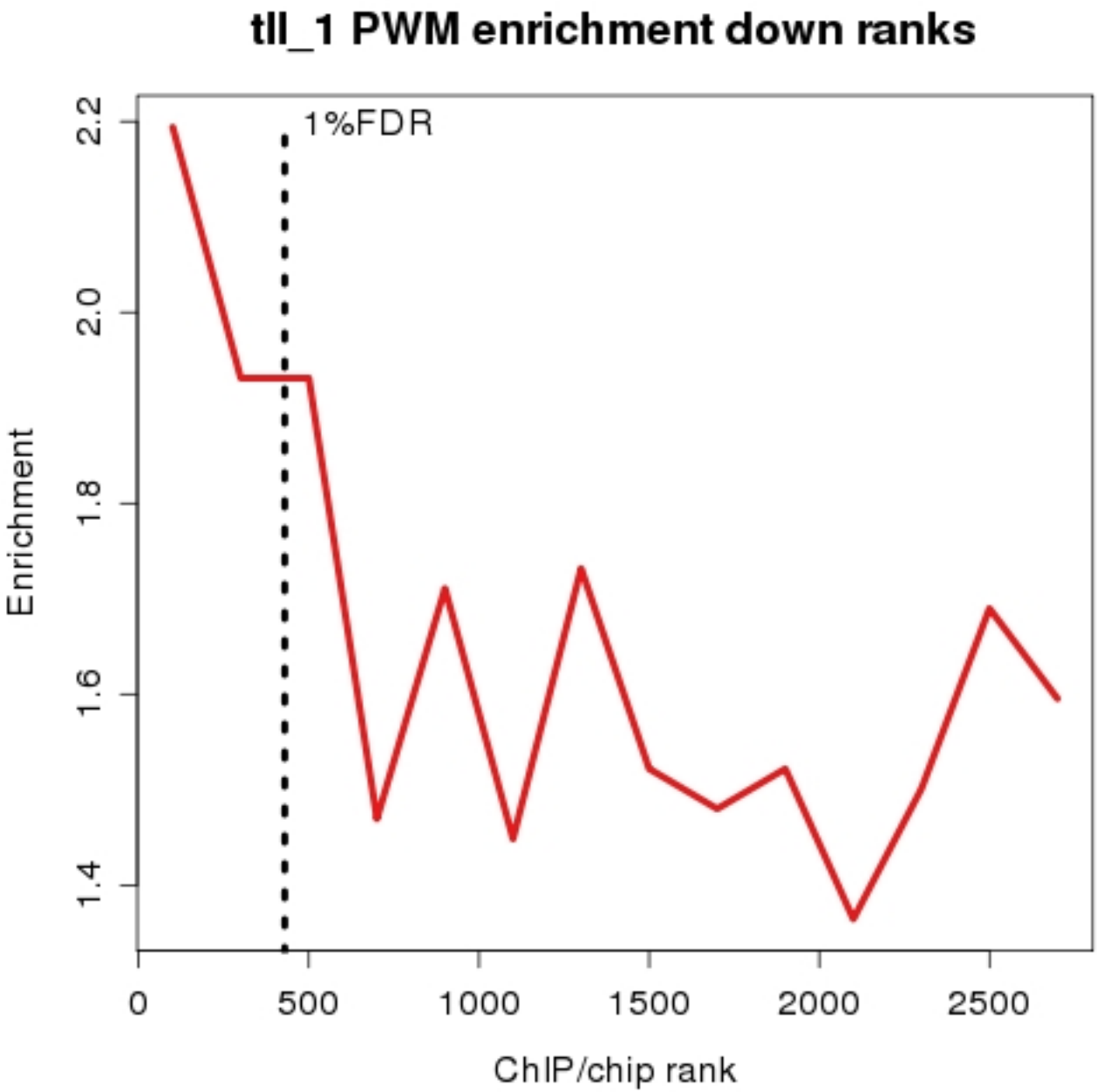

tll_1 median distance to genes
1%FDR
all
patterned
transcribed
Median distance to closest gene
0
10000
20000
30000
40000
500
1000
1500
2000
2500
ChIP/chip rank

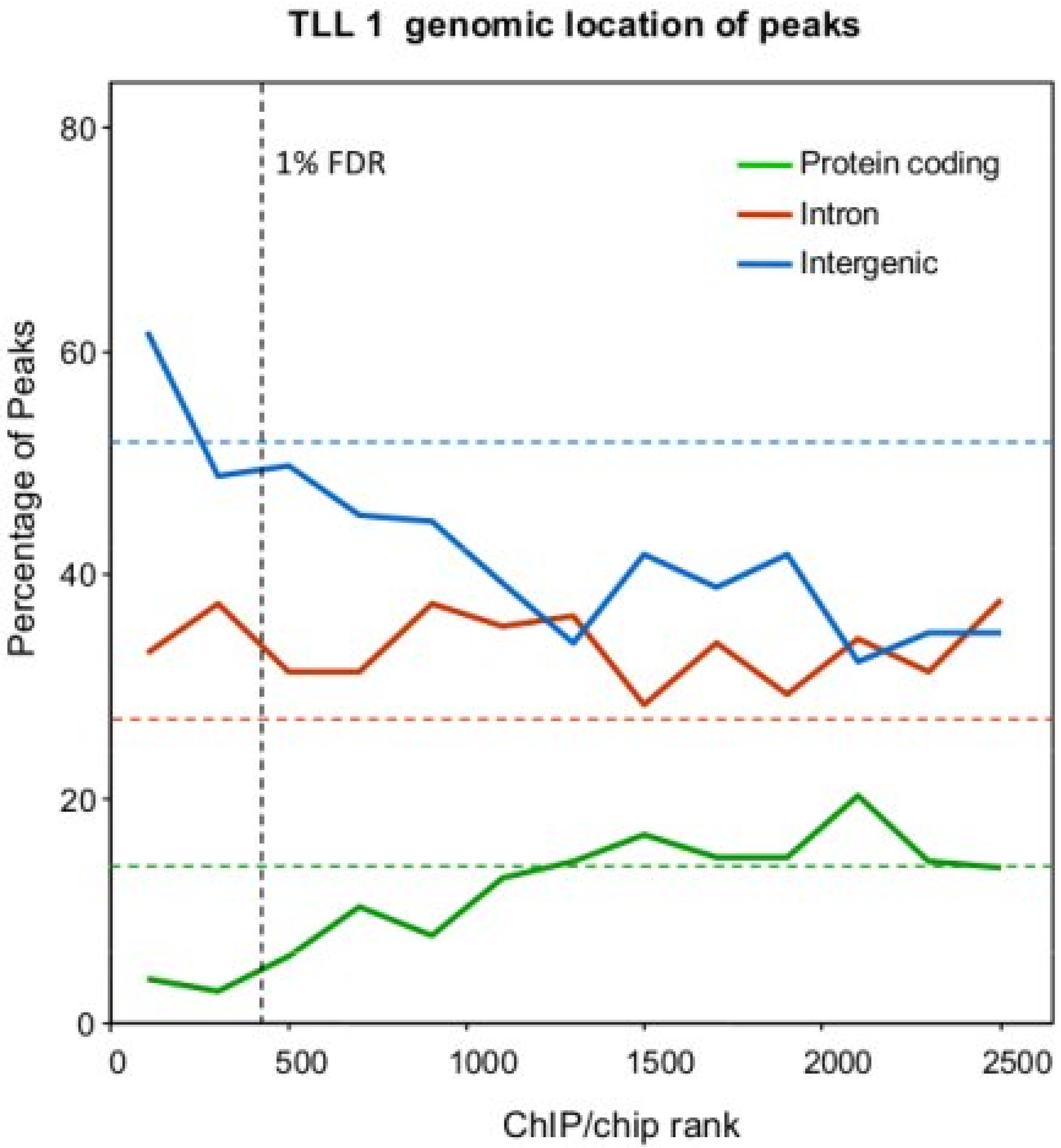

tll_1 distribution of 1%FDR primary peak scores
Fraction of Peaks
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
2
4
6
8
10
12
14
16
18
ChIPchip Peak Score

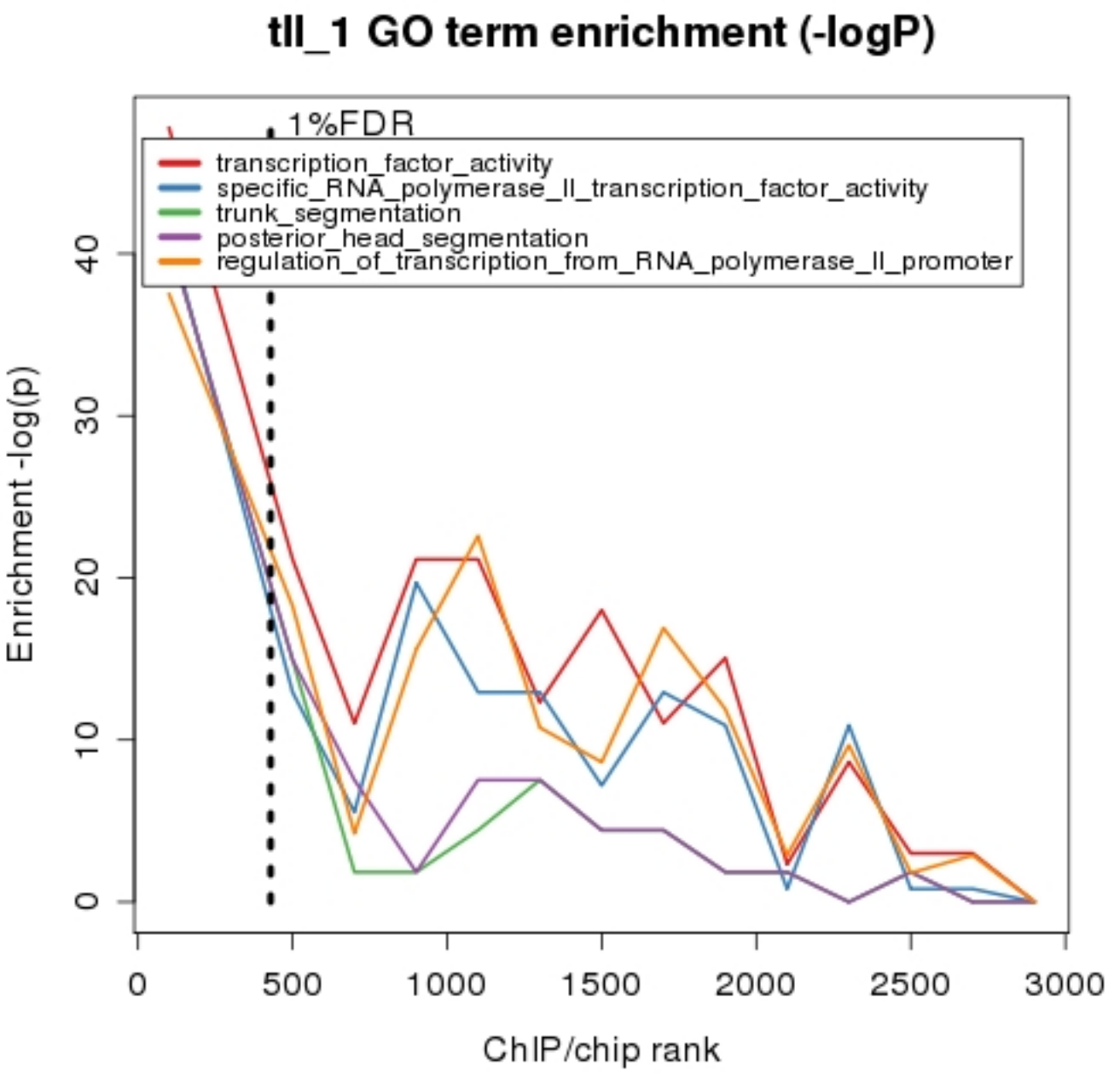

tll_1 distribution of 25%FDR primary peak scores
Fraction of Peaks
0.0
0.2
0.4
0.6
0.8
2
4
6
8
10
12
14
16
18
ChIPchip Peak Score

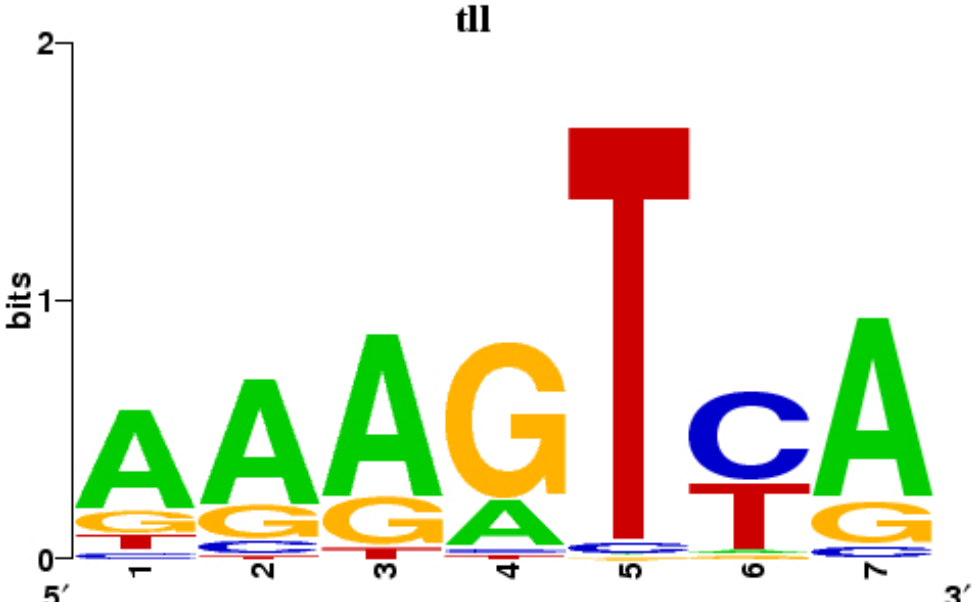

tll_1 distribution of number of sites
tll_1
Random
Percentage of Peaks
0
10
20
30
40
50
0
1
2
3
4
5
6
7
Number of Sites

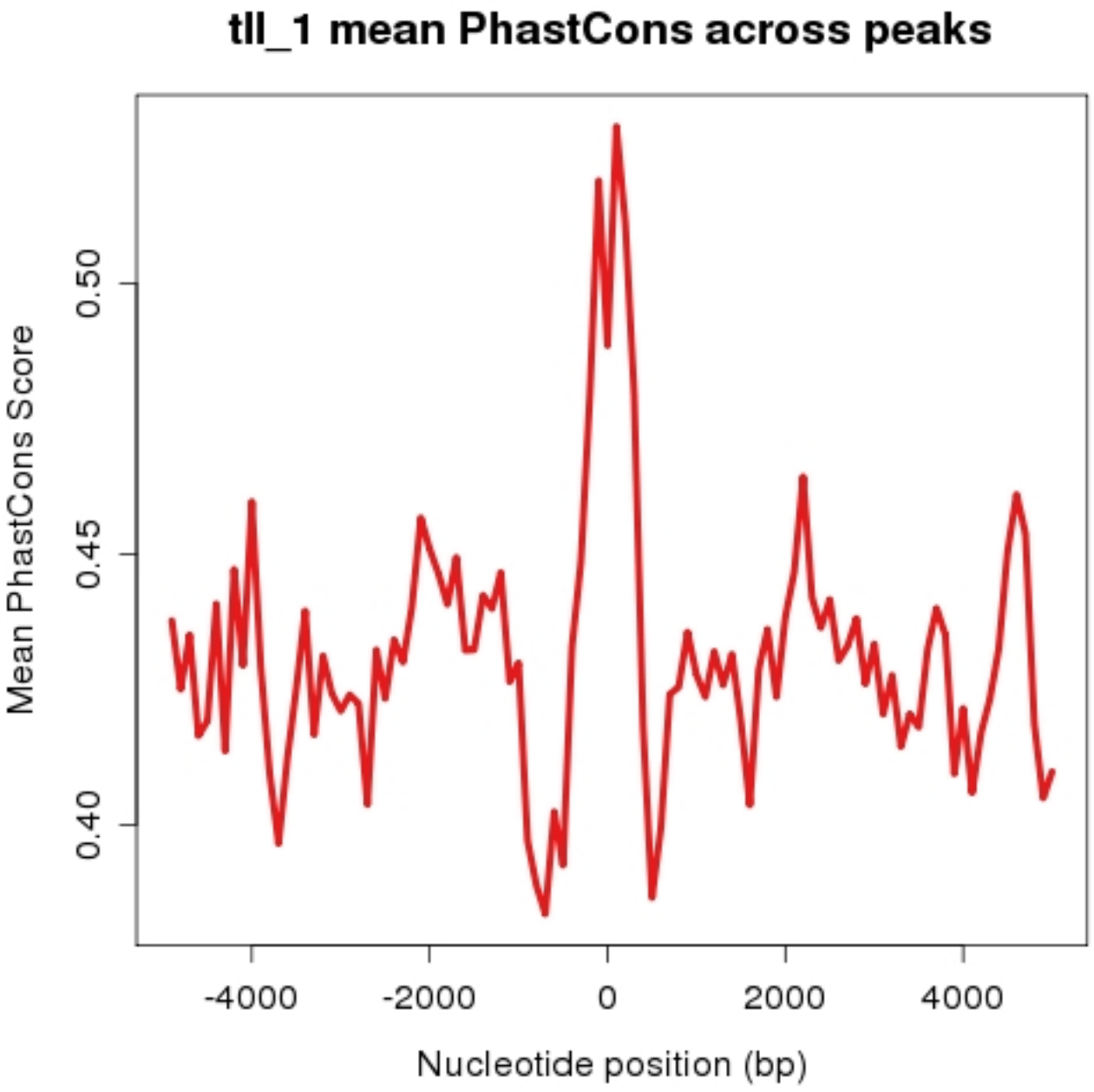

tll_1 PWM enrichment across peaks
Enrichment
2.0
1.8
1.6
1.4
1.2
-4000
-2000
0
2000
4000
Nucleotide position (200bp window)

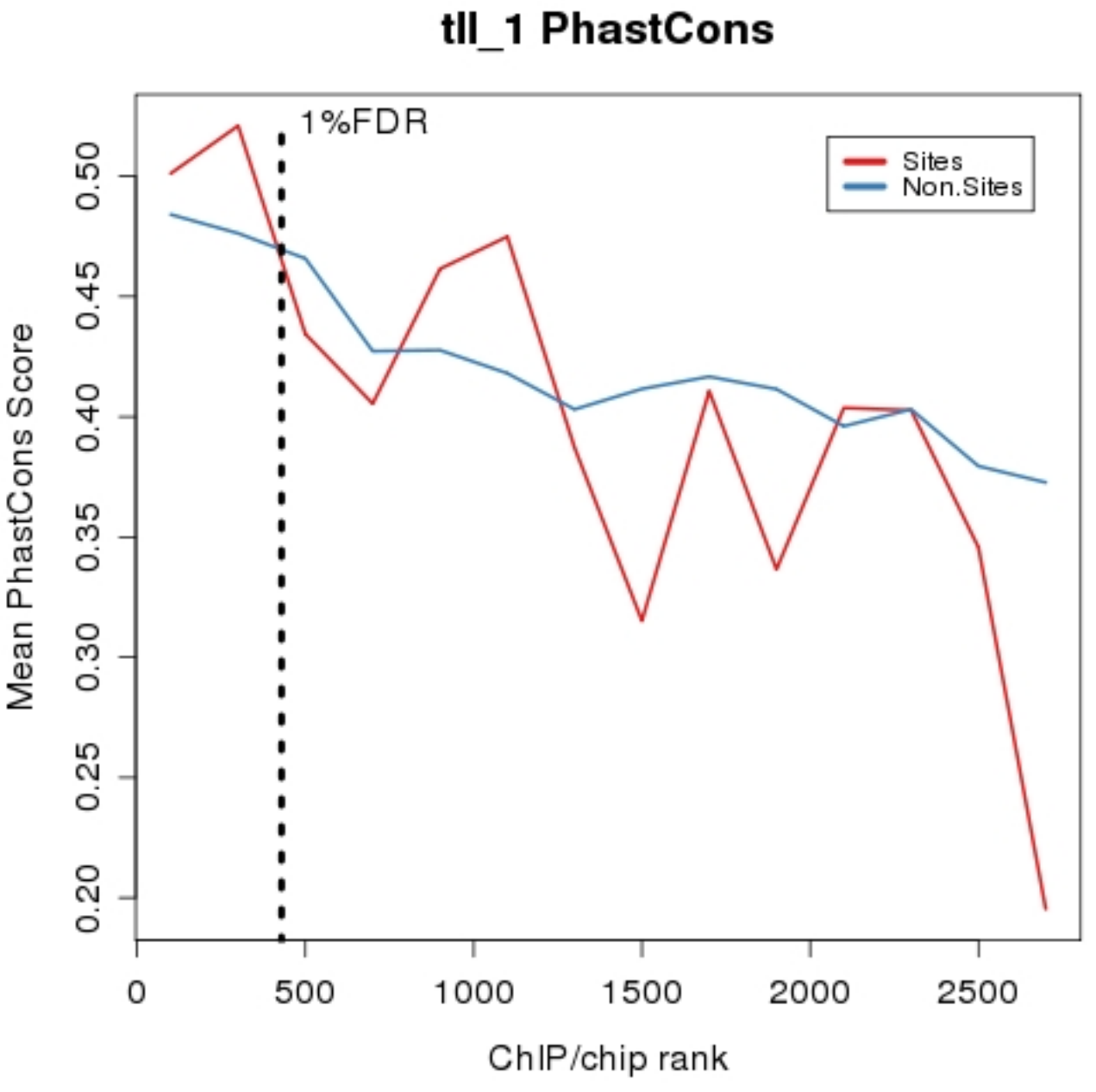

tll_1 PWM enrichment down ranks
1%FDR
Enrichment
2.2
2.0
1.8
1.6
1.4
0
500
1000
1500
2000
2500
ChIP/chip rank

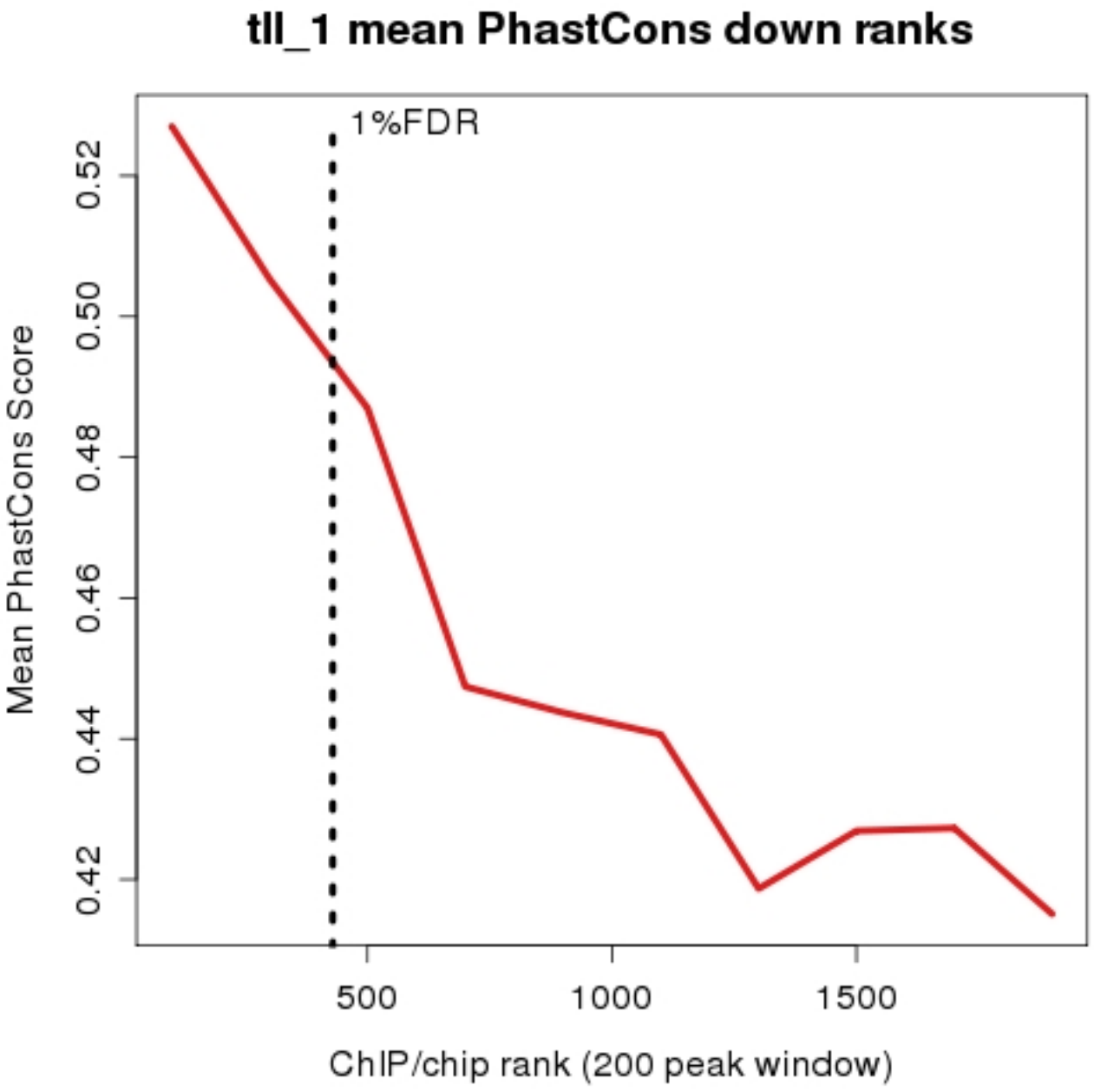

TLL 1 genomic location of peaks
1% FDR
Protein coding
Intron
Intergenic
Percentage of Peaks
0
20
40
60
80
0
500
1000
1500
2000
2500
ChIP/chip rank


tll_1 GO term enrichment (-logP)
1%FDR
transcription_factor_activity
specific_RNA_polymerase_II_transcription_factor_activity
trunk_segmentation
posterior_head_segmentation
regulation_of_transcription_from_RNA_polymerase_II_promoter
Enrichment -log(p)
0
10
20
30
40
0
500
1000
1500
2000
2500
3000
ChIP/chip rank


tll
bits
2
1
0
5′
3′
1
2
3
4
5
6
7


tll_1 mean PhastCons across peaks
Mean PhastCons Score
0.40
0.45
0.50
-4000
-2000
0
2000
4000
Nucleotide position (bp)


tll_1 PhastCons
1%FDR
Sites
Non.Sites
Mean PhastCons Score
0.20
0.25
0.30
0.35
0.40
0.45
0.50
0
500
1000
1500
2000
2500
ChIP/chip rank


tll_1 mean PhastCons down ranks
1%FDR
Mean PhastCons Score
0.42
0.44
0.46
0.48
0.50
0.52
500
1000
1500
ChIP/chip rank (200 peak window)