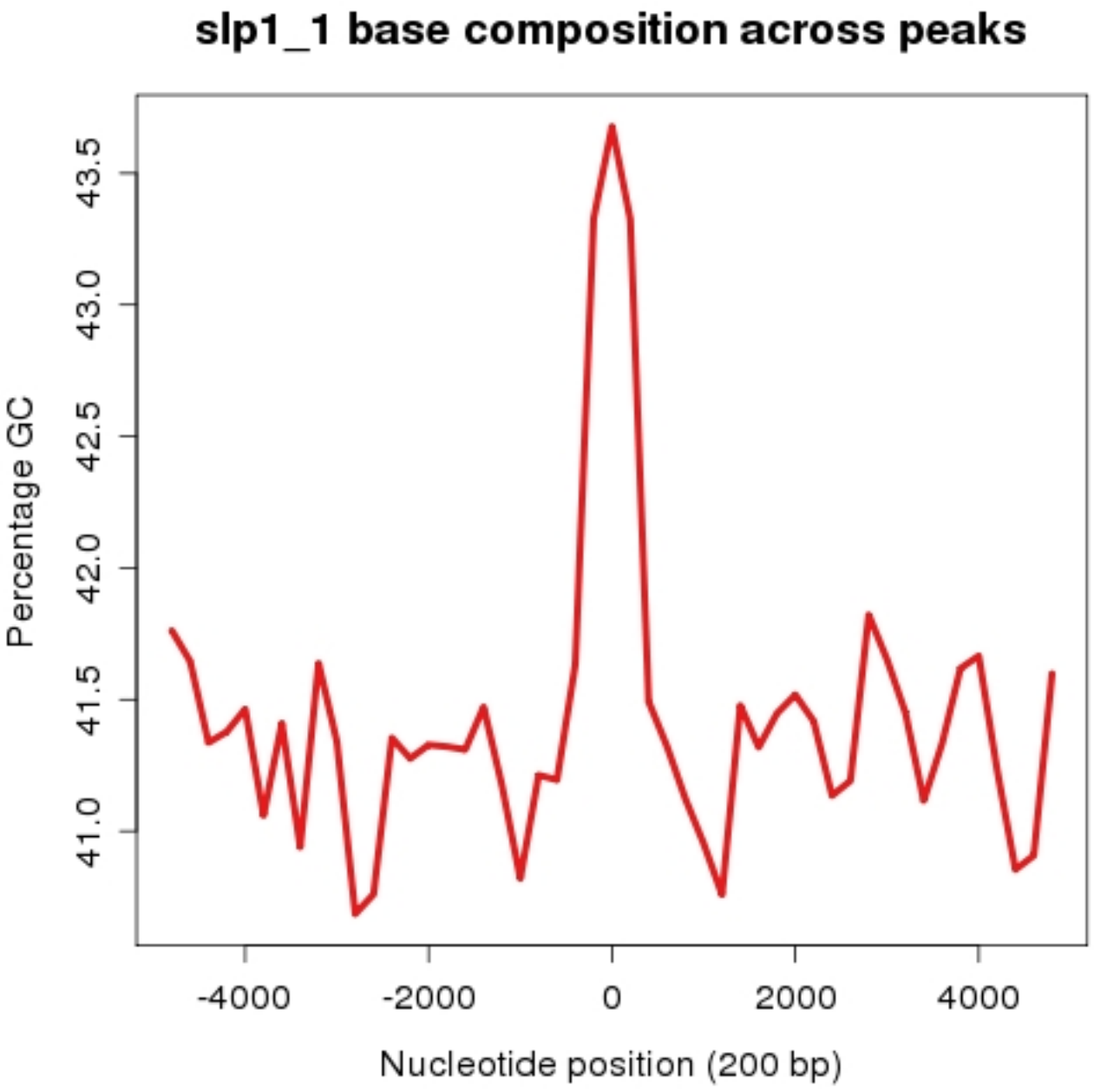
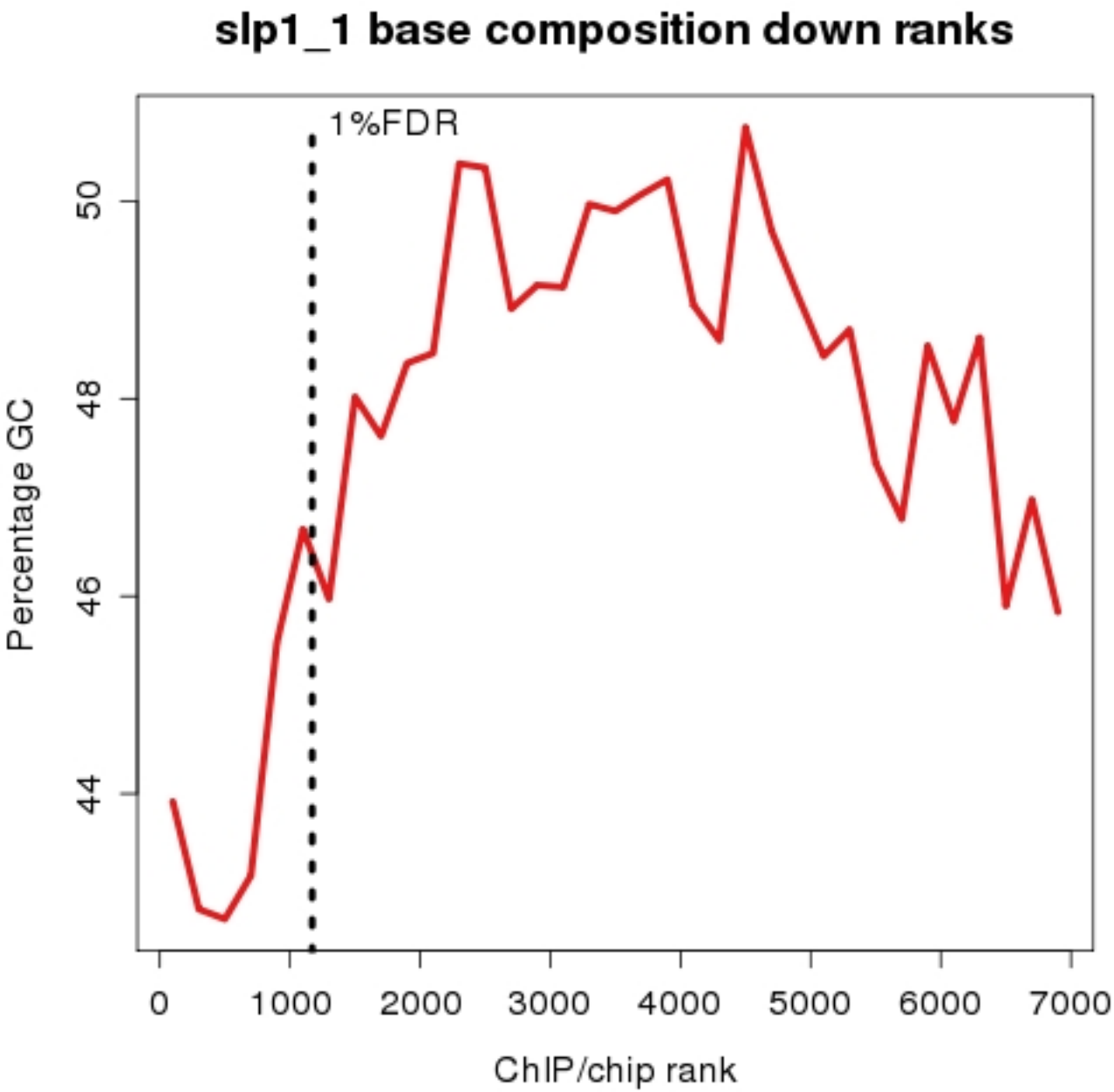
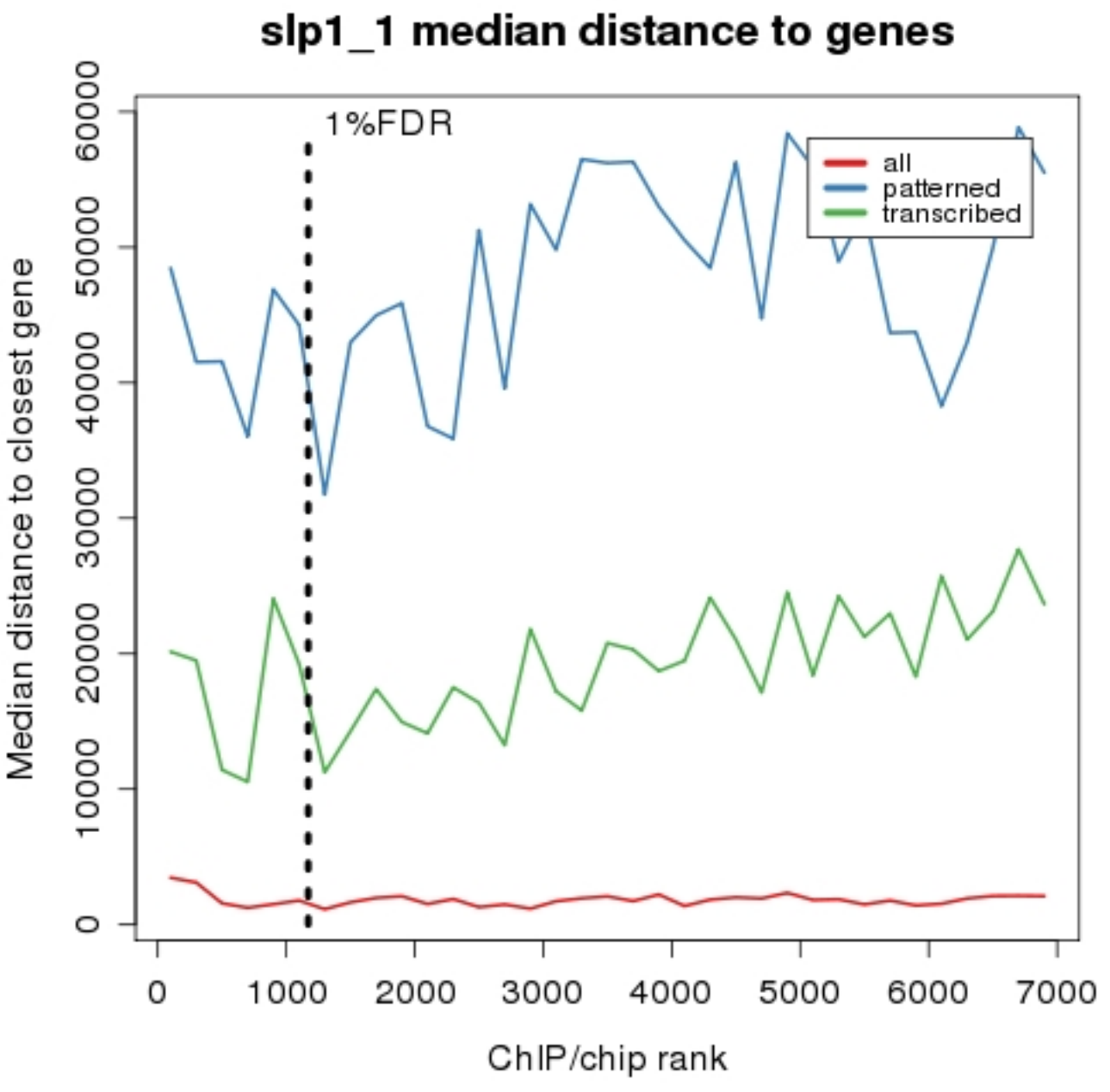
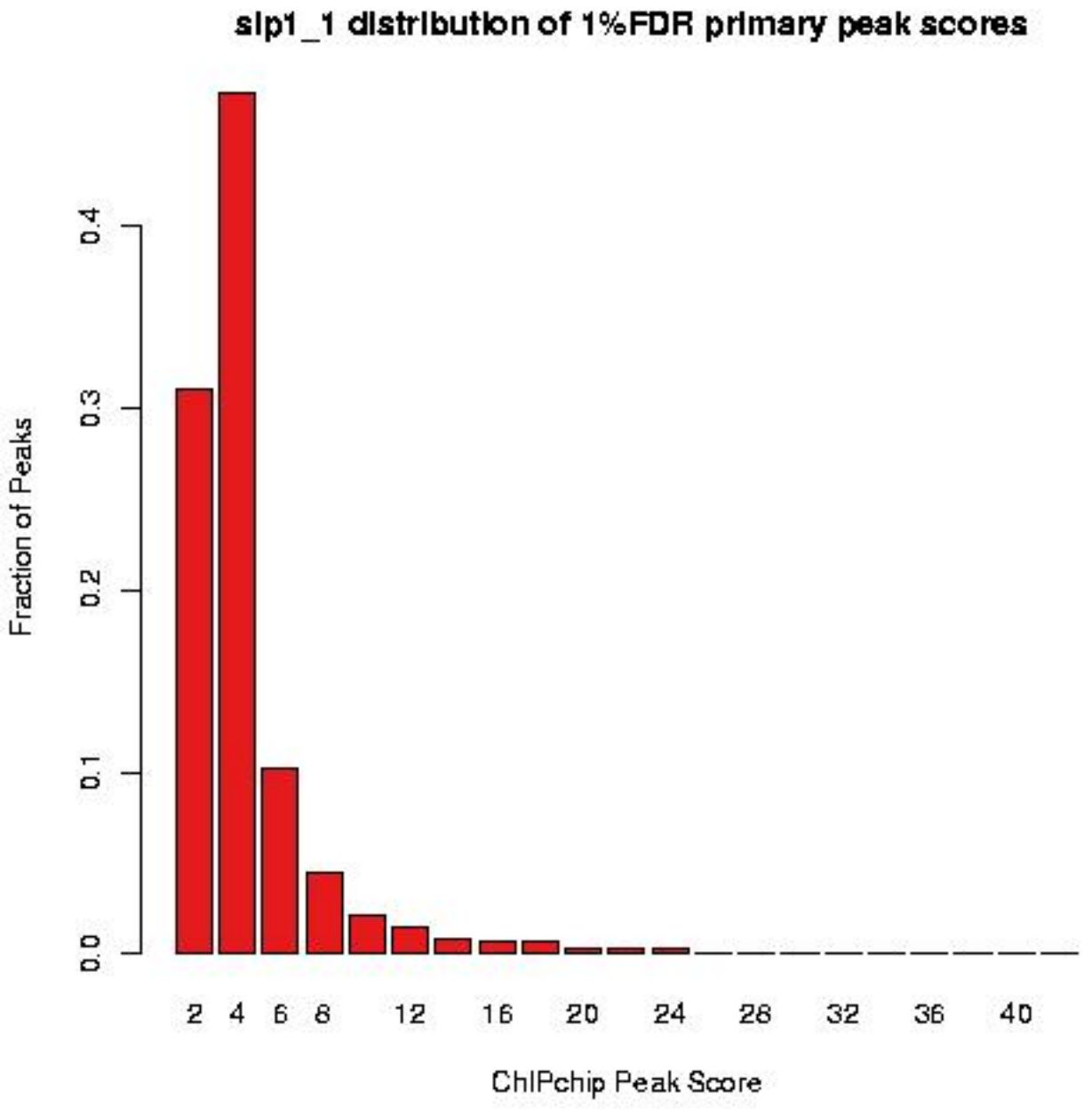
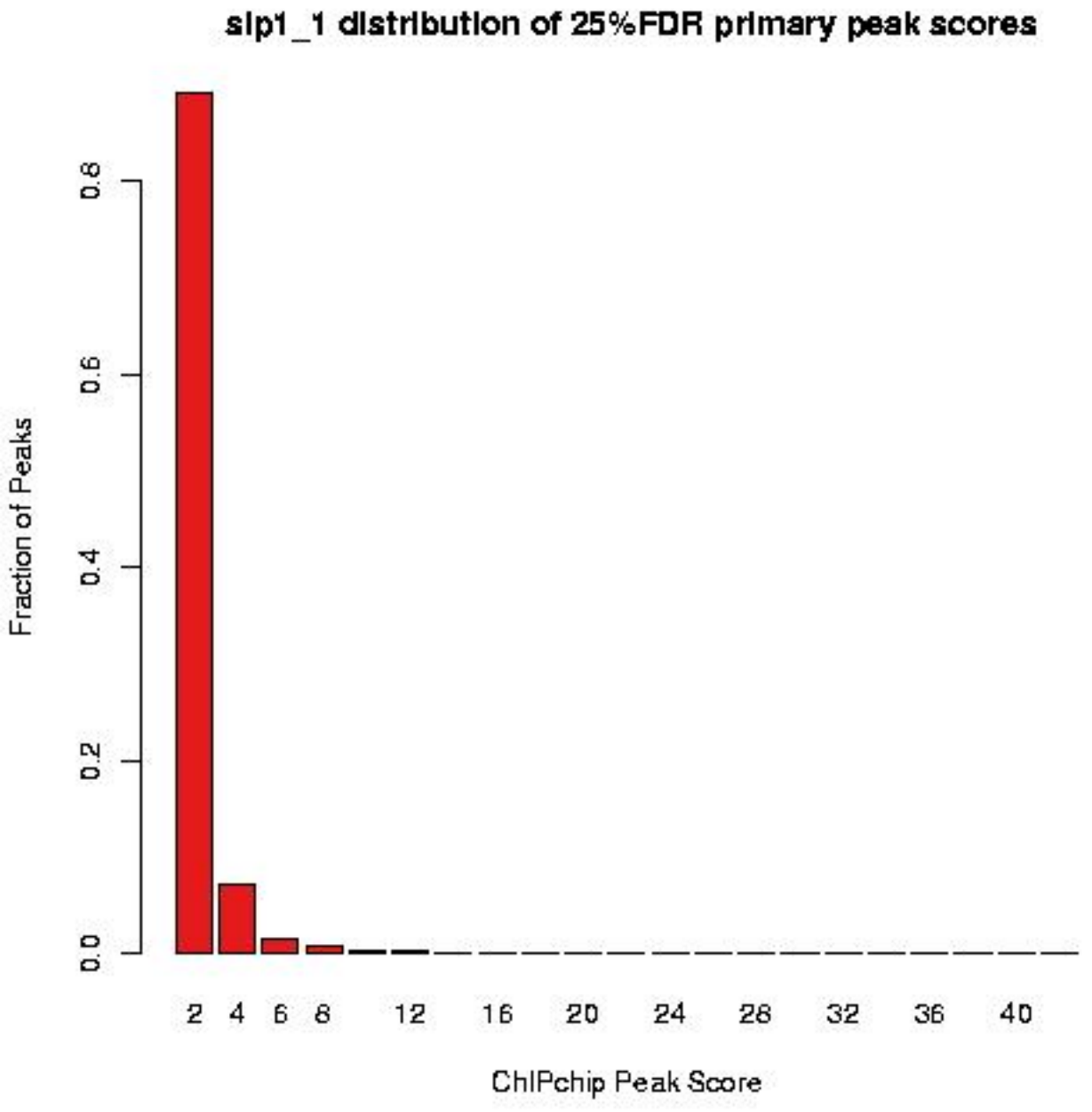
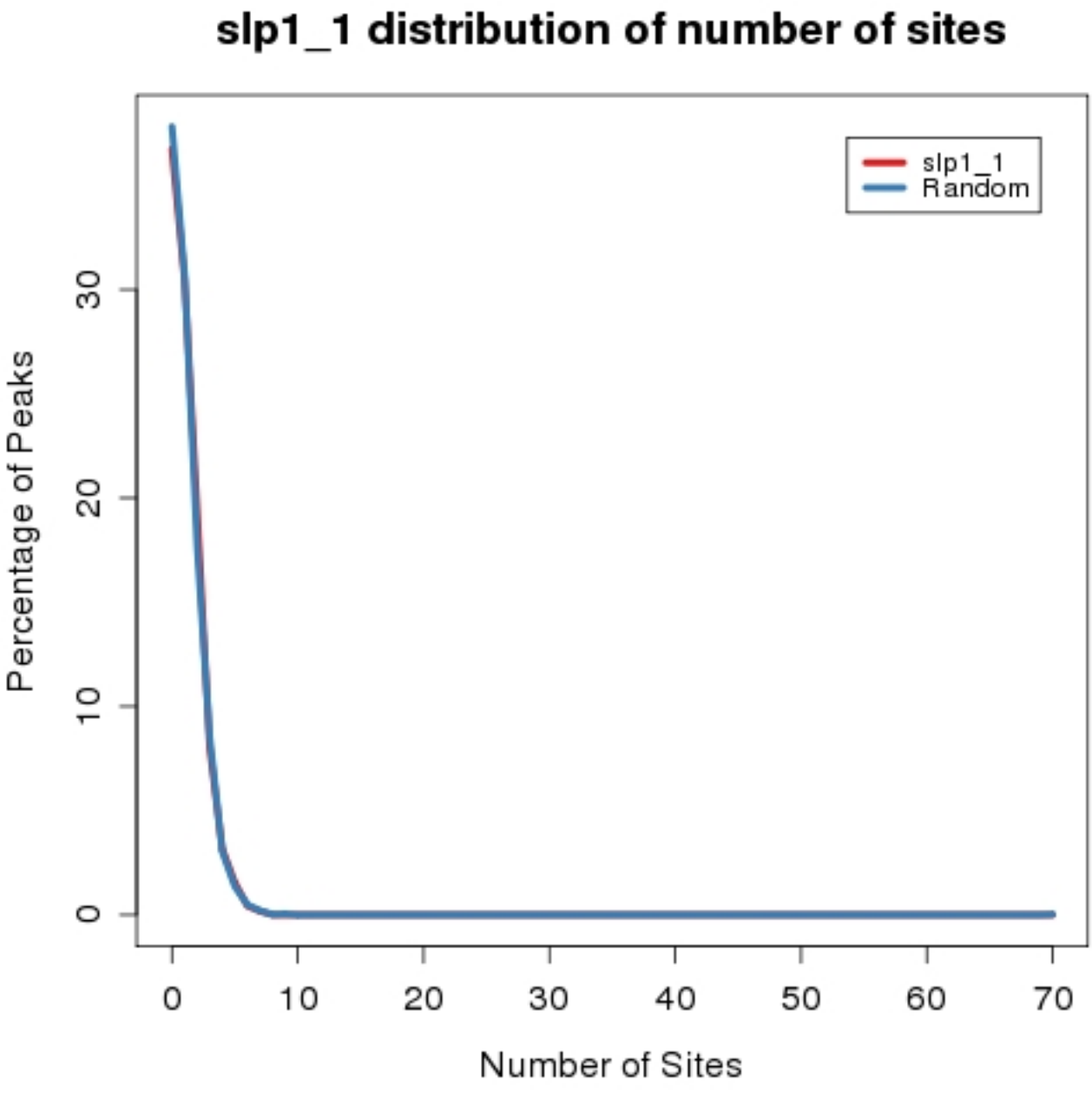

slp1_1 base composition across peaks
Percentage GC
41.0
41.5
42.0
42.5
43.0
43.5
-4000
-2000
0
2000
4000
Nucleotide position (200 bp)

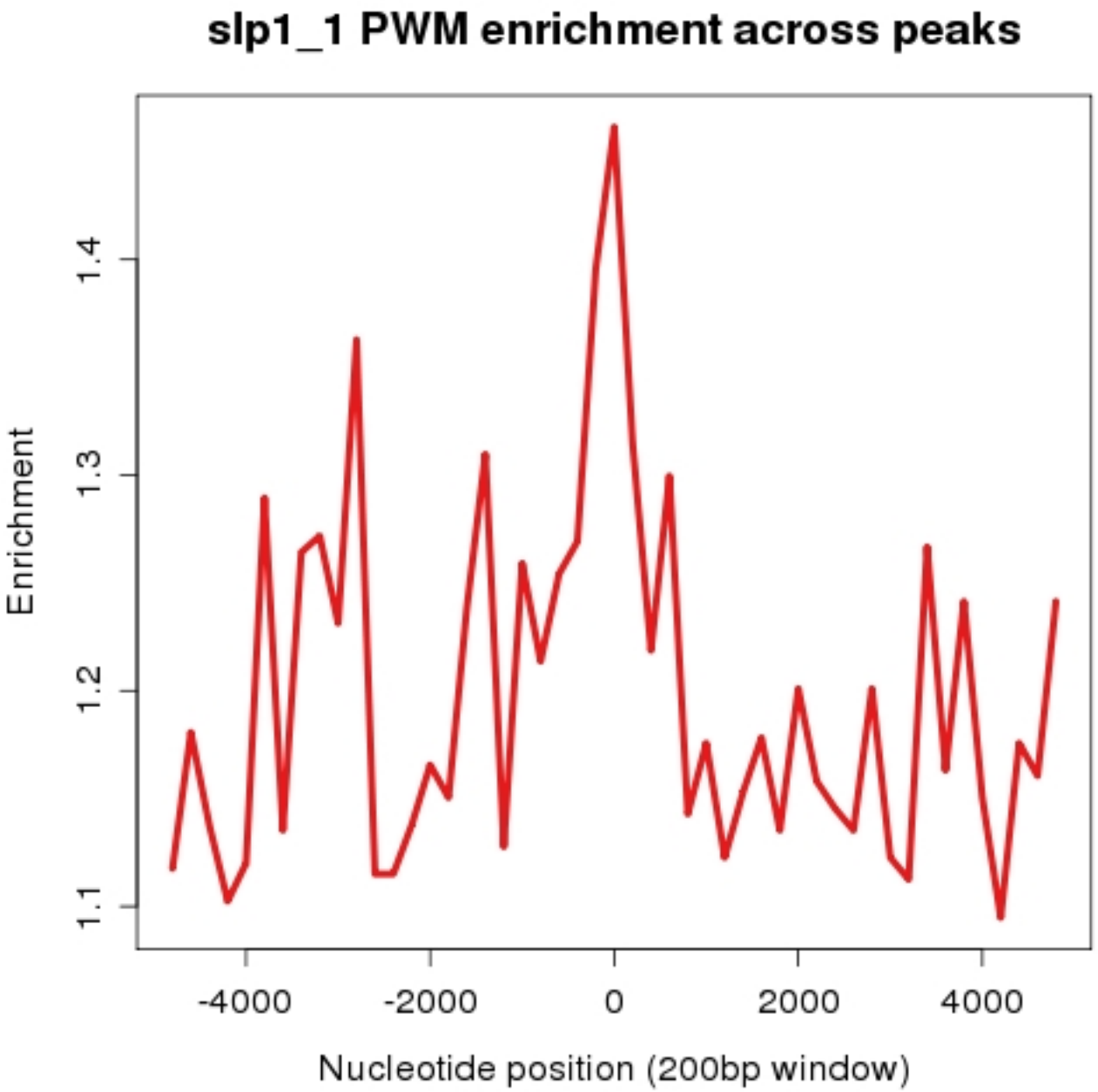

slp1_1 base composition down ranks
1%FDR
Percentage GC
44
46
48
50
0
1000
2000
3000
4000
5000
6000
7000
ChIP/chip rank

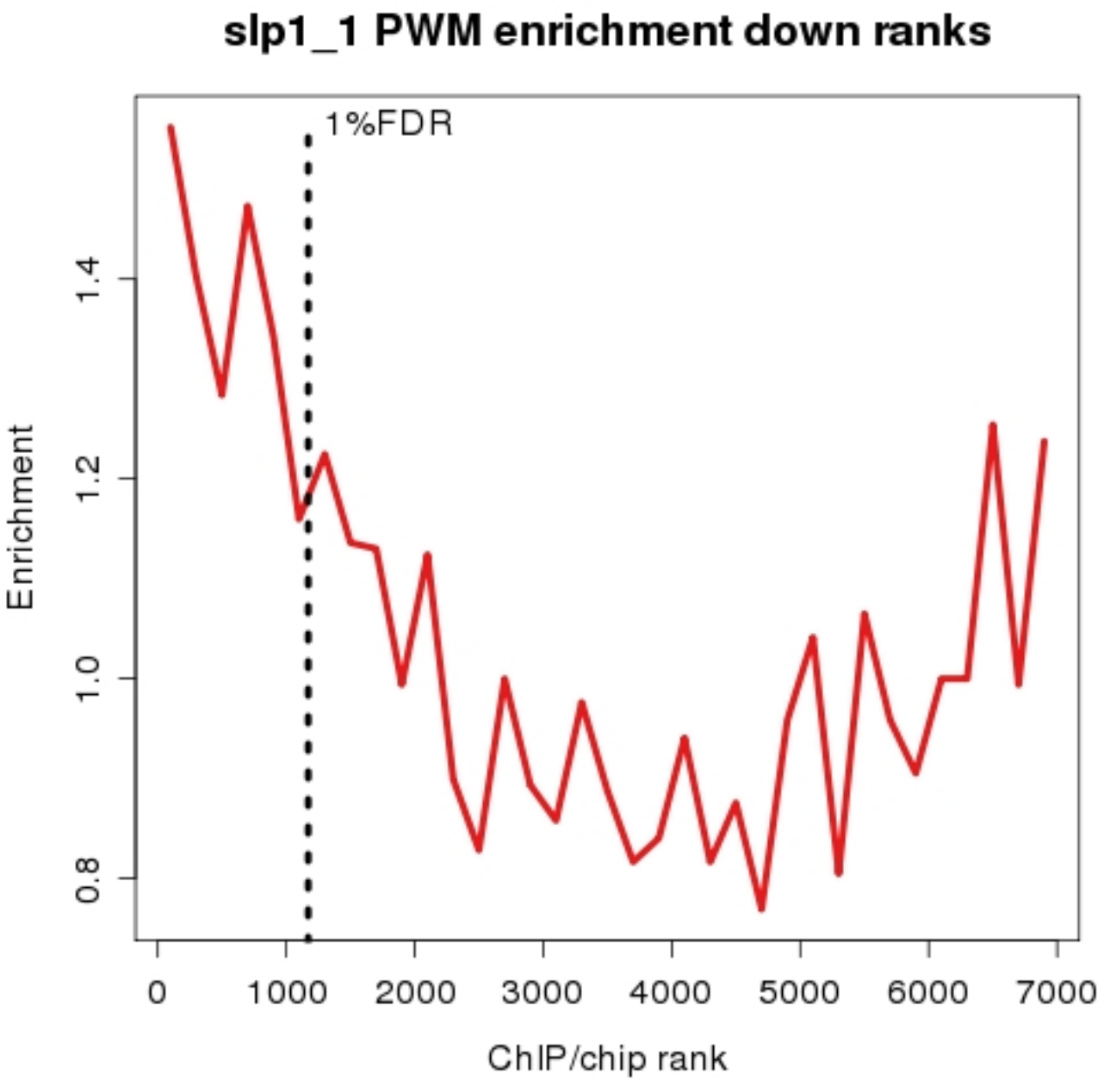

slp1_1 median distance to genes
1%FDR
all
patterned
transcribed
Median distance to closest gene
0
10000
20000
30000
40000
50000
60000
0
1000
2000
3000
4000
5000
6000
7000
ChIP/chip rank

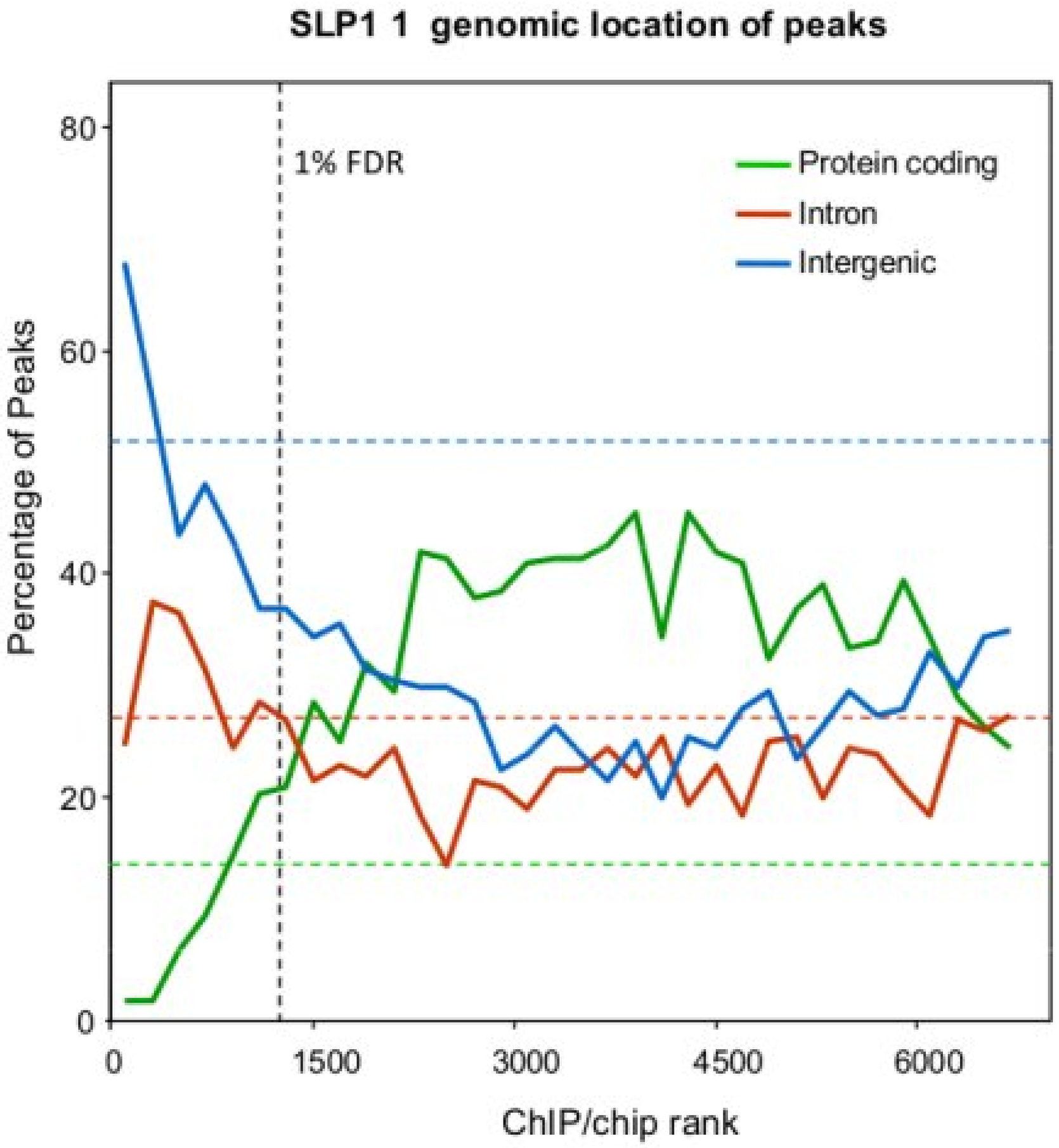

slp1_1 distribution of 1%FDR primary peak scores
Fraction of Peaks
0.0
0.1
0.2
0.3
0.4
2
4
6
8
12
16
20
24
28
32
36
40
ChIPchip Peak Score

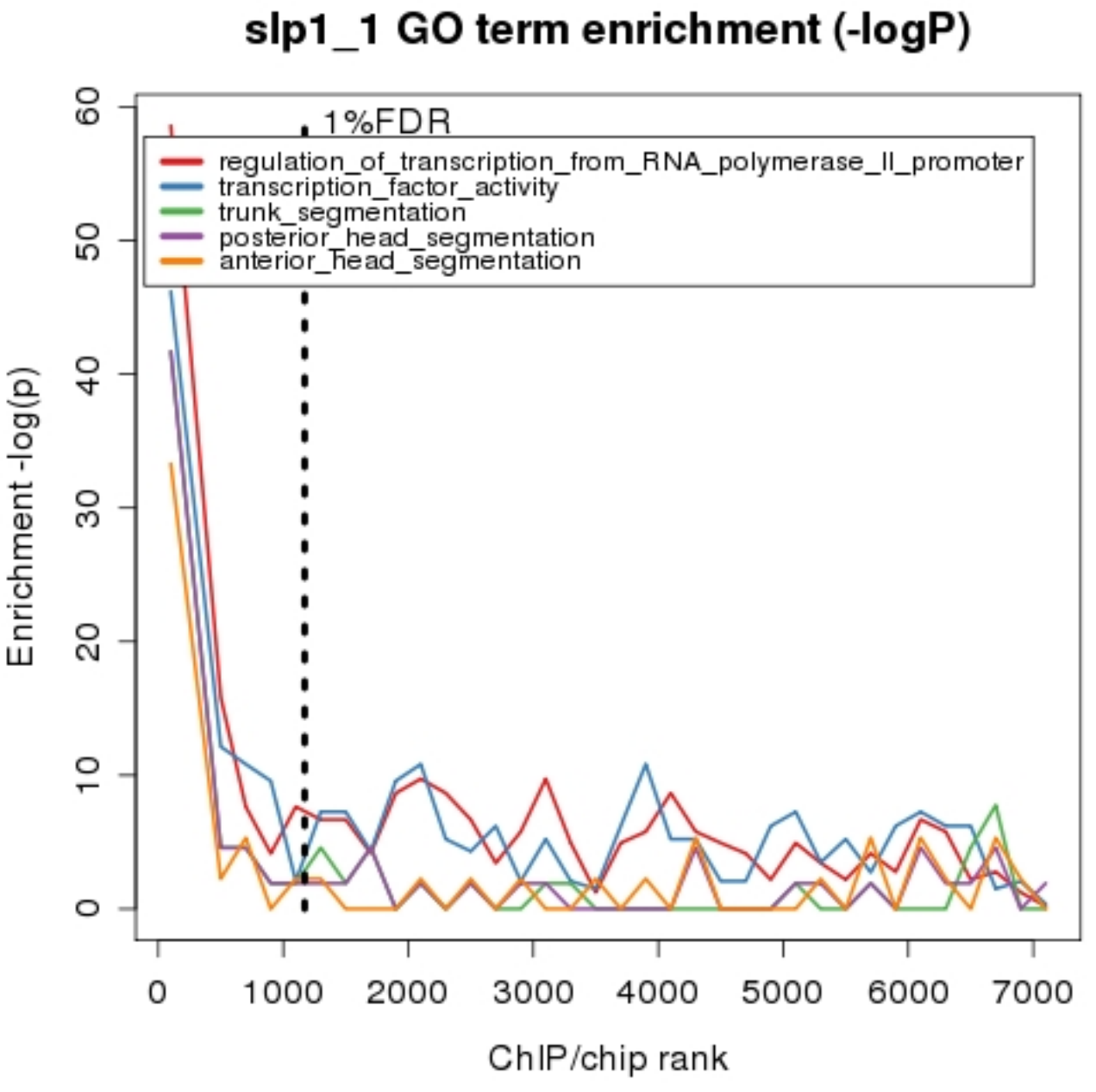

slp1_1 distribution of 25%FDR primary peak scores
Fraction of Peaks
0.0
0.2
0.4
0.6
0.8
2
4
6
8
12
16
20
24
28
32
36
40
ChIPchip Peak Score

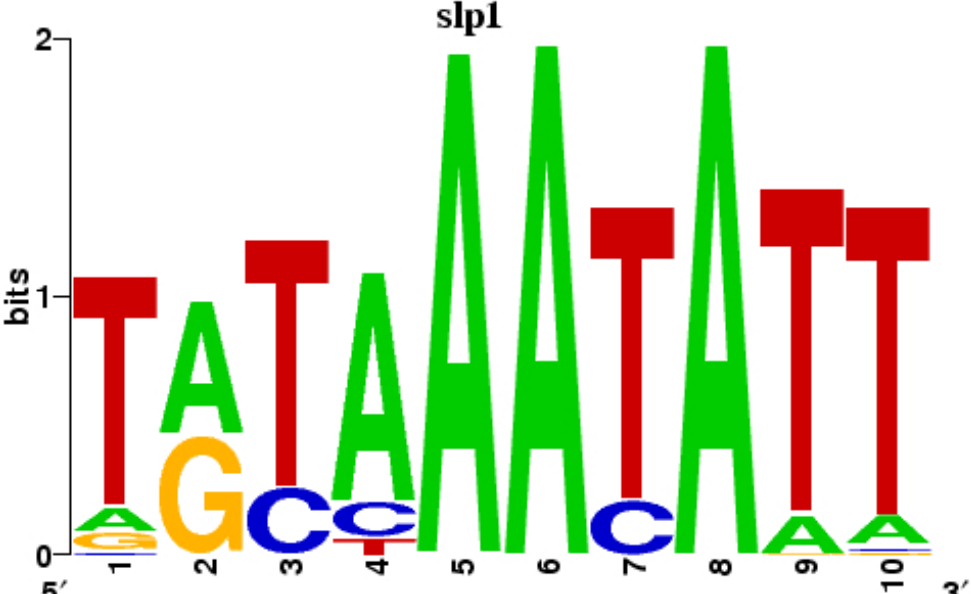

slp1_1 distribution of number of sites
slp1_1
Random
Percentage of Peaks
0
10
20
30
0
10
20
30
40
50
60
70
Number of Sites

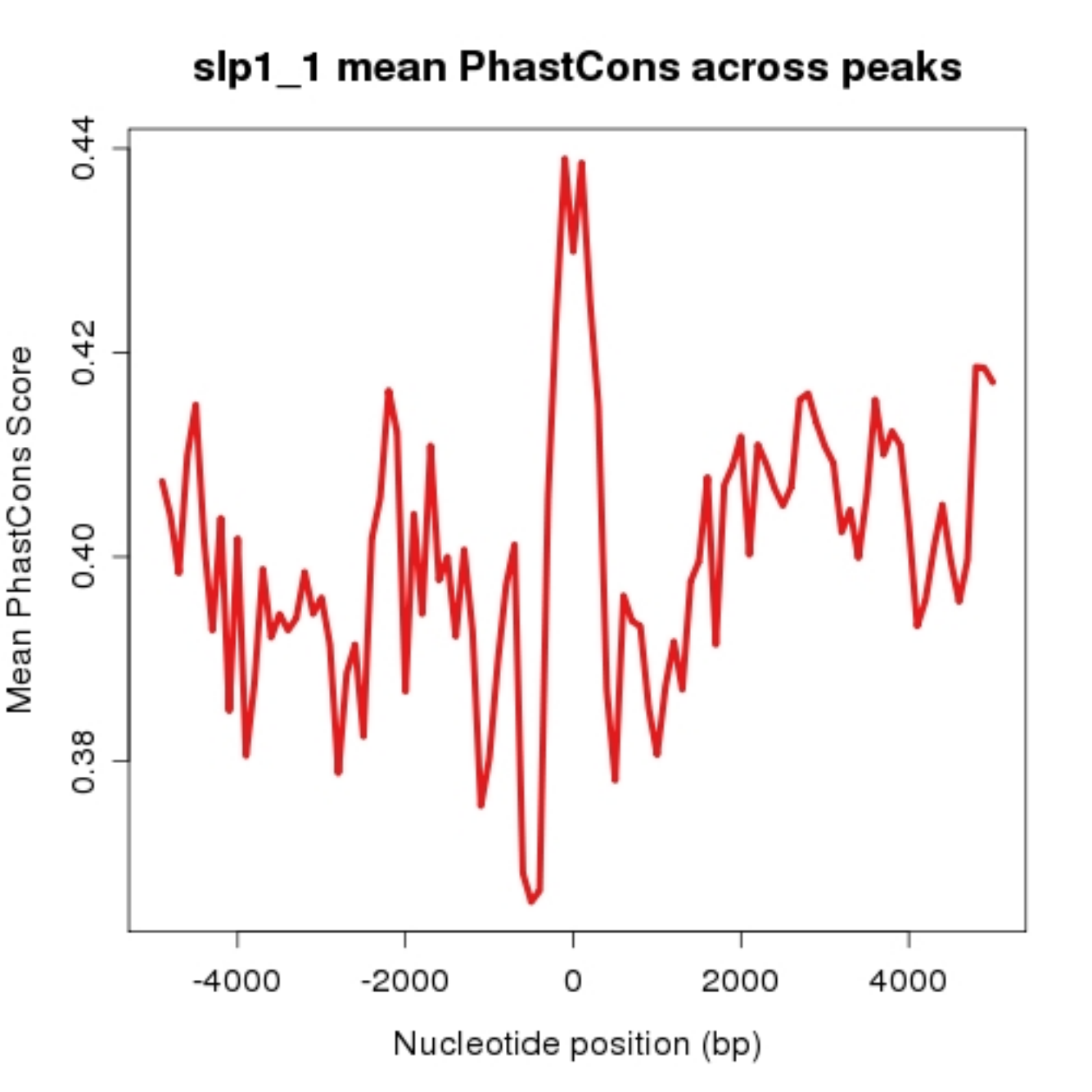

slp1_1 PWM enrichment across peaks
Enrichment
1.1
1.2
1.3
1.4
-4000
-2000
0
2000
4000
Nucleotide position (200bp window)

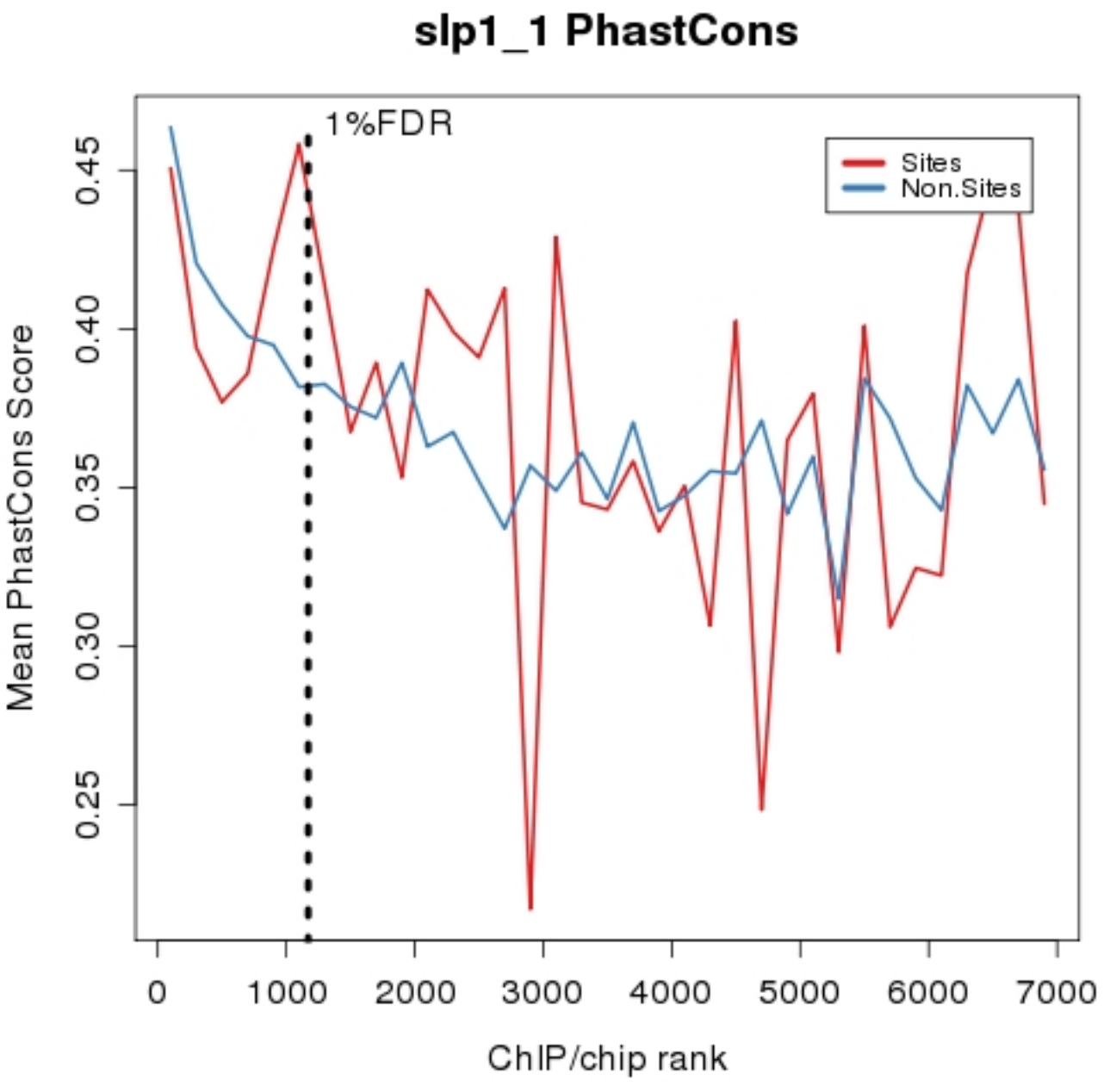

slp1_1 PWM enrichment down ranks
1%FDR
Enrichment
0.8
1.0
1.2
1.4
0
1000
2000
3000
4000
5000
6000
7000
ChIP/chip rank

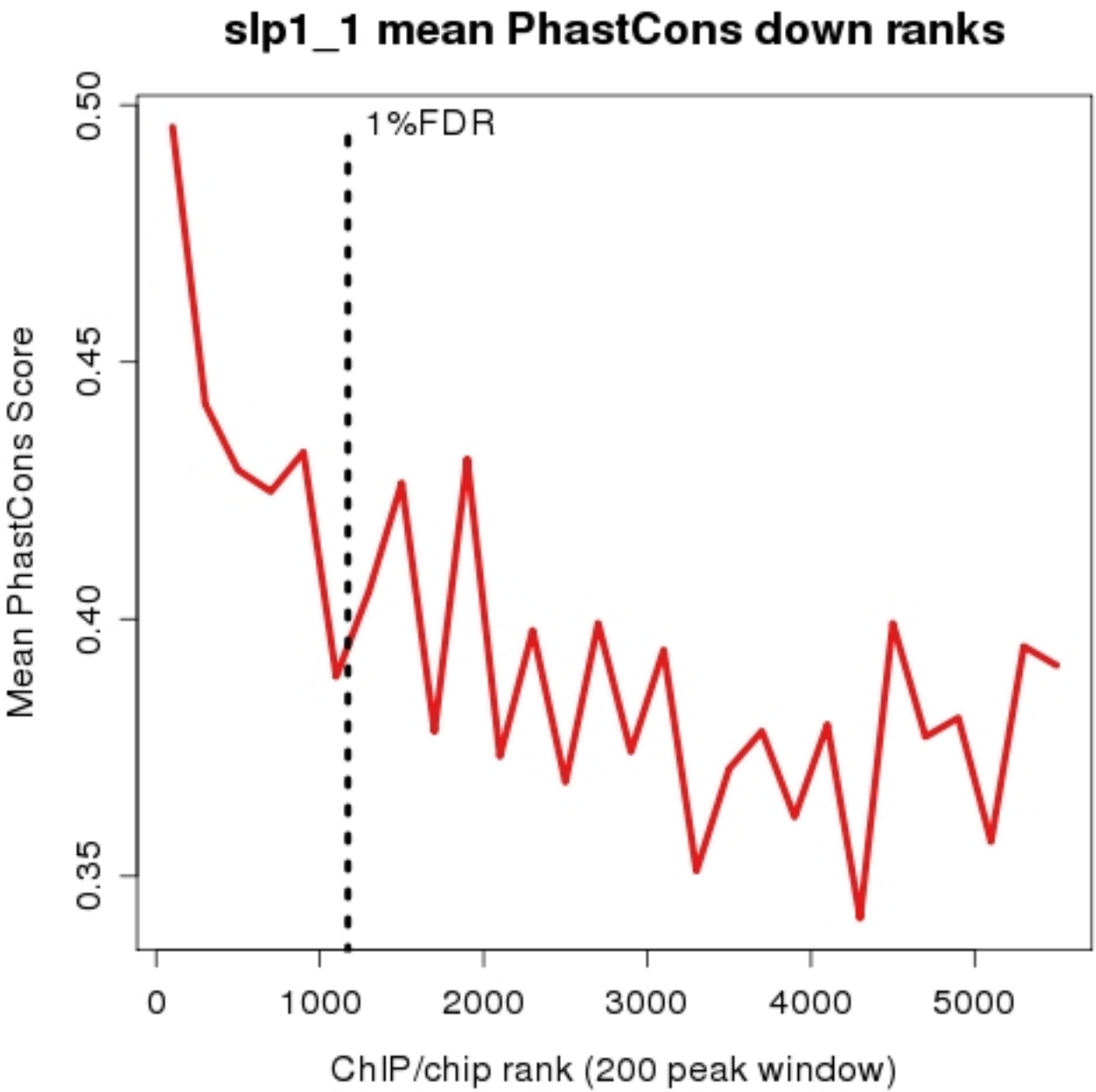

SLP1 1 genomic location of peaks
1% FDR
Protein coding
Intron
Intergenic
Percentage of Peaks
0
20
40
60
80
0
1500
3000
4500
6000
ChIP/chip rank


slp1_1 GO term enrichment (-logP)
1%FDR
regulation_of_transcription_from_RNA_polymerase_II_promoter
transcription_factor_activity
trunk_segmentation
posterior_head_segmentation
anterior_head_segmentation
Enrichment -log(p)
0
10
20
30
40
50
60
0
1000
2000
3000
4000
5000
6000
7000
ChIP/chip rank


slp1
bits
2
1
0
5′
1
2
3
4
5
6
7
8
9
10
3′


slp1_1 mean PhastCons across peaks
Mean PhastCons Score
0.38
0.40
0.42
0.44
-4000
-2000
0
2000
4000
Nucleotide position (bp)


slp1_1 PhastCons
1%FDR
Sites
Non.Sites
Mean PhastCons Score
0.25
0.30
0.35
0.40
0.45
0
1000
2000
3000
4000
5000
6000
7000
ChIP/chip rank


slp1_1 mean PhastCons down ranks
1%FDR
Mean PhastCons Score
0.35
0.40
0.45
0.50
0
1000
2000
3000
4000
5000
ChIP/chip rank (200 peak window)