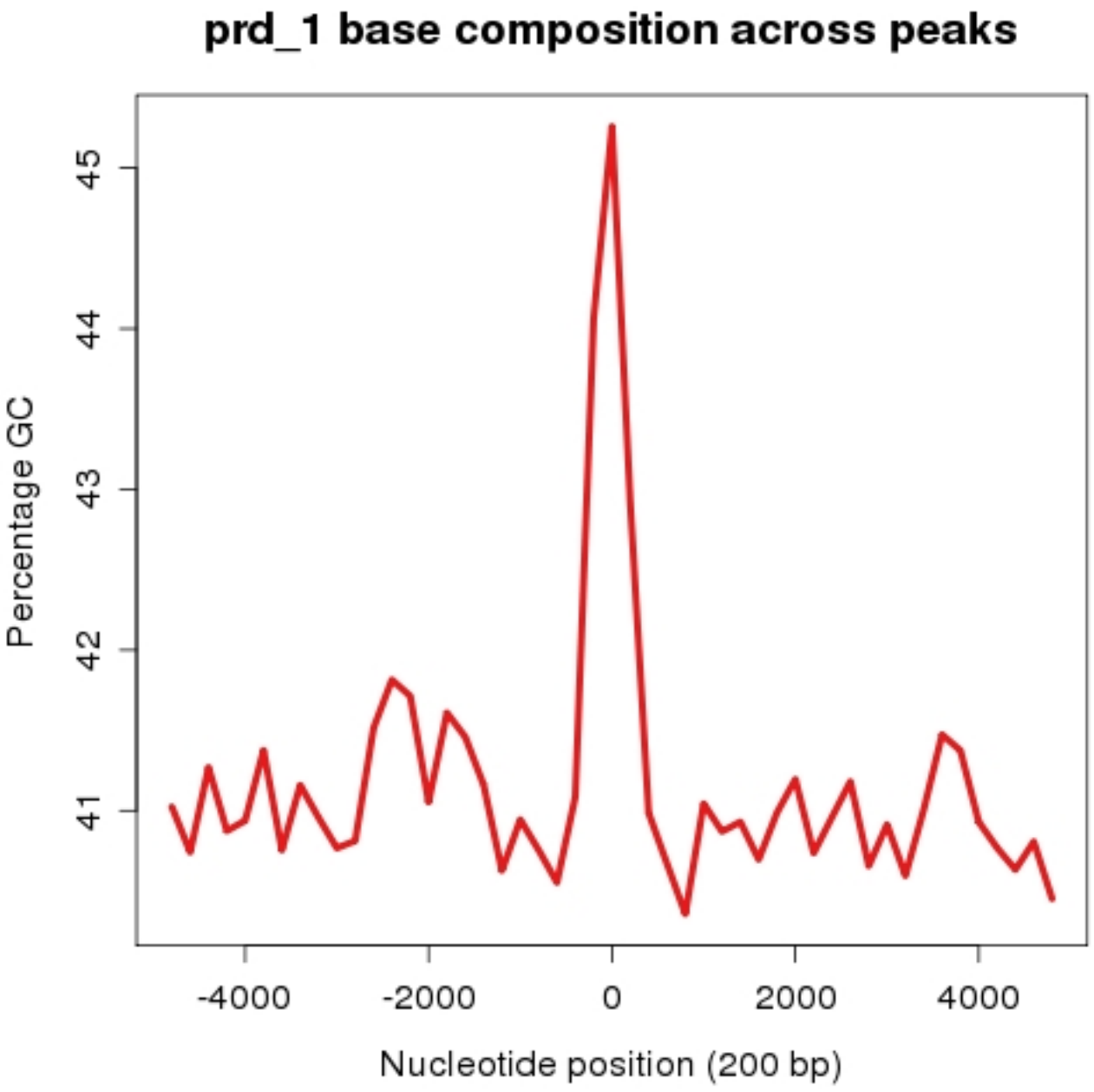
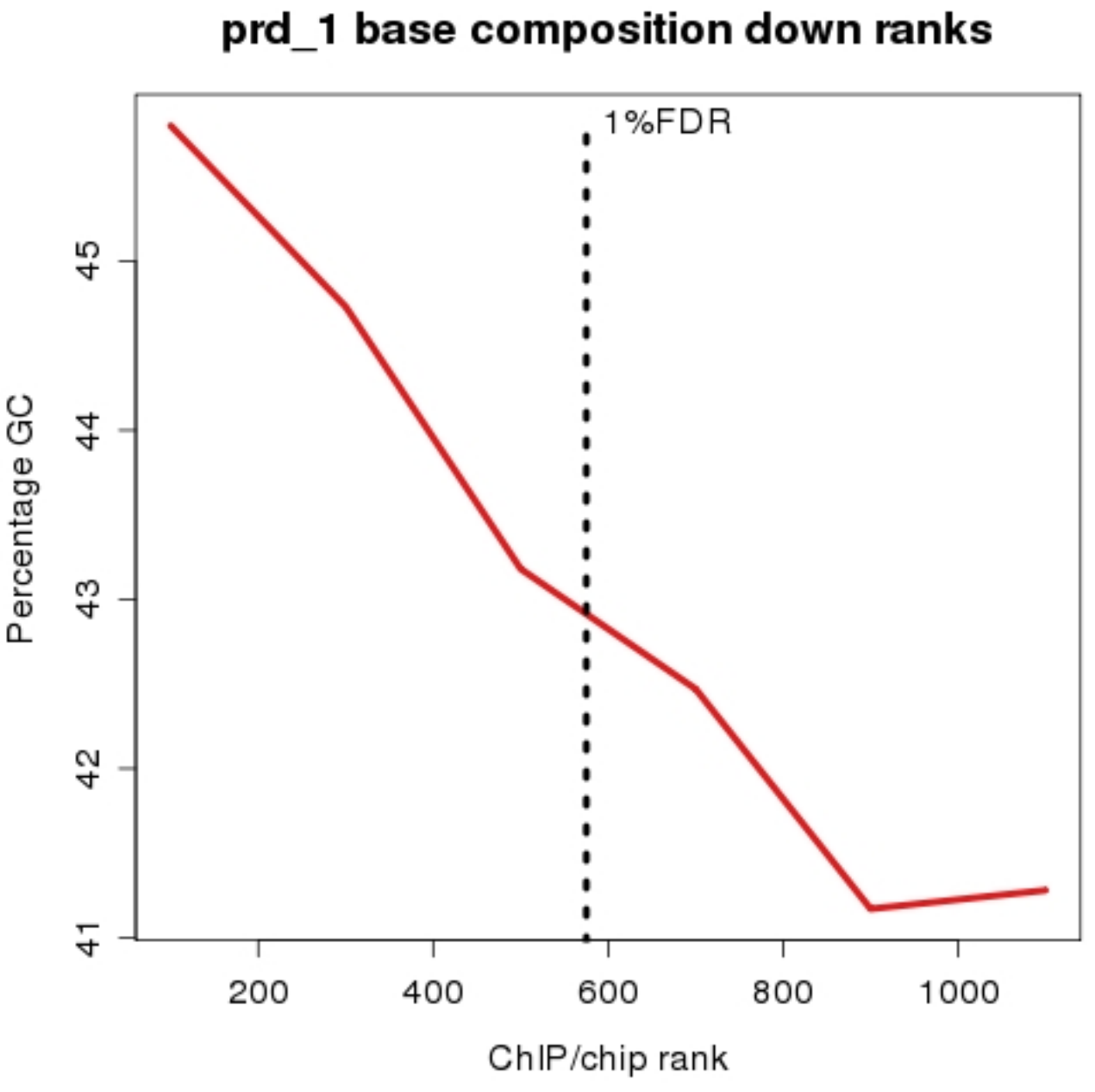
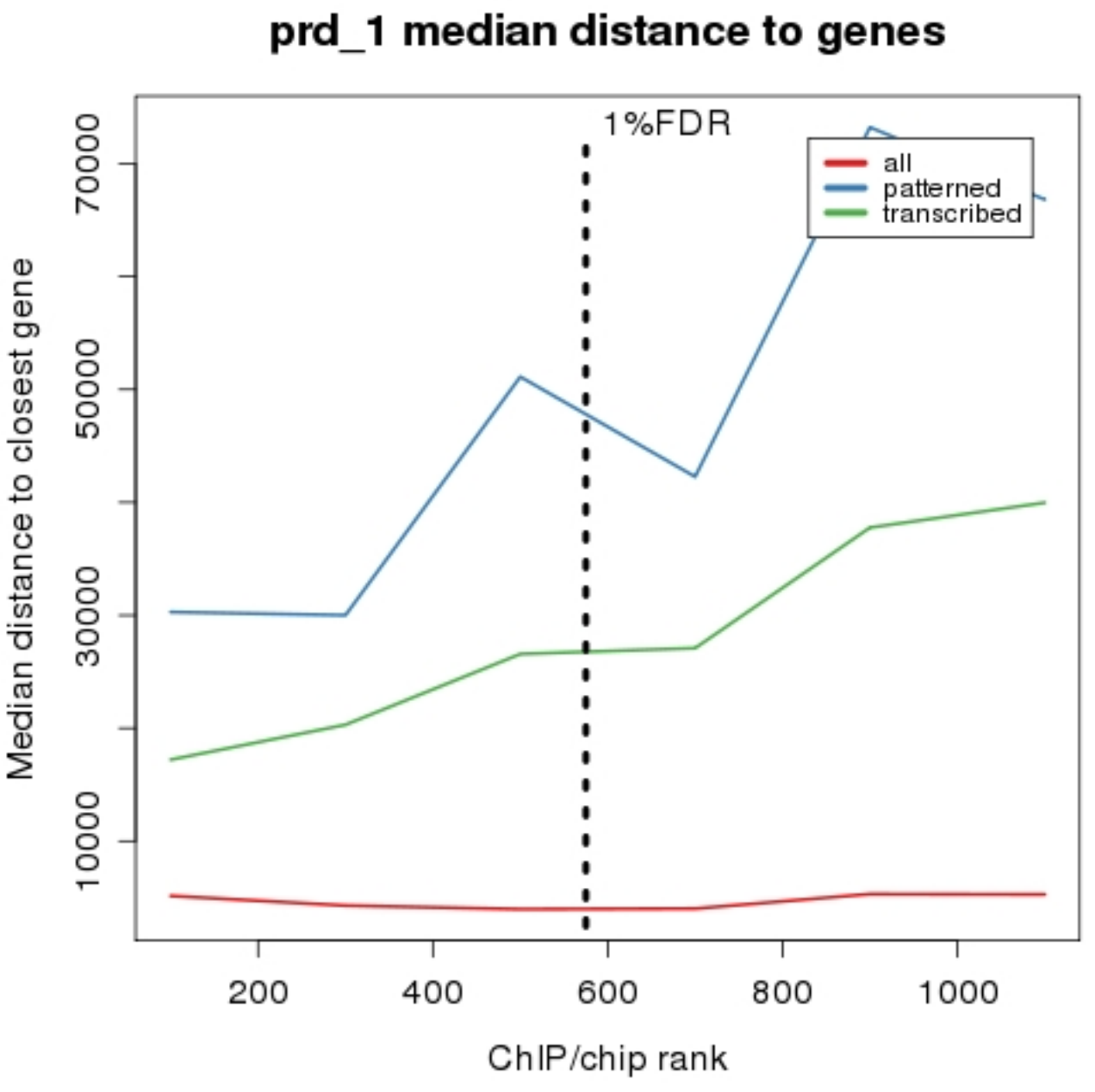
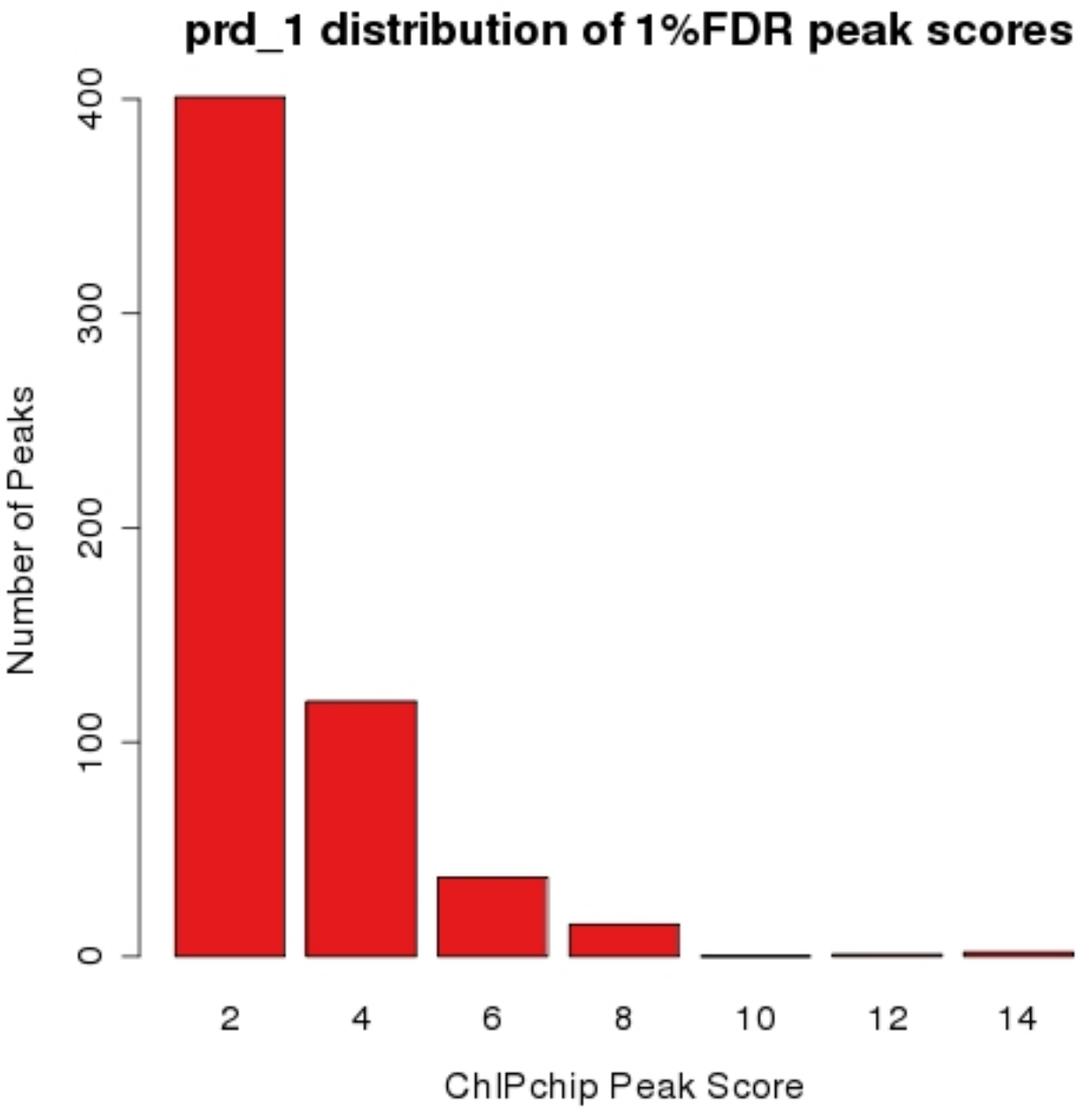
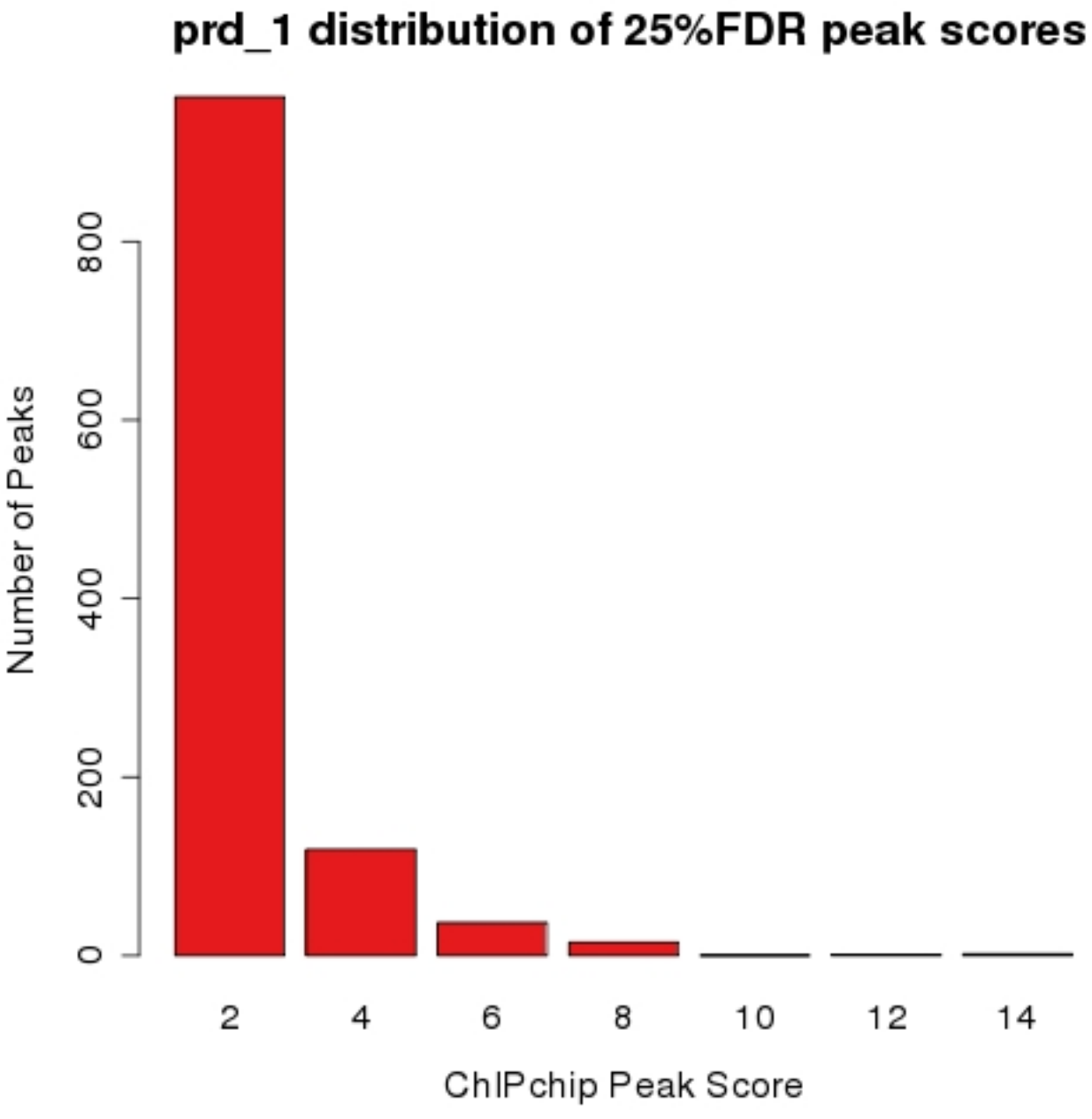
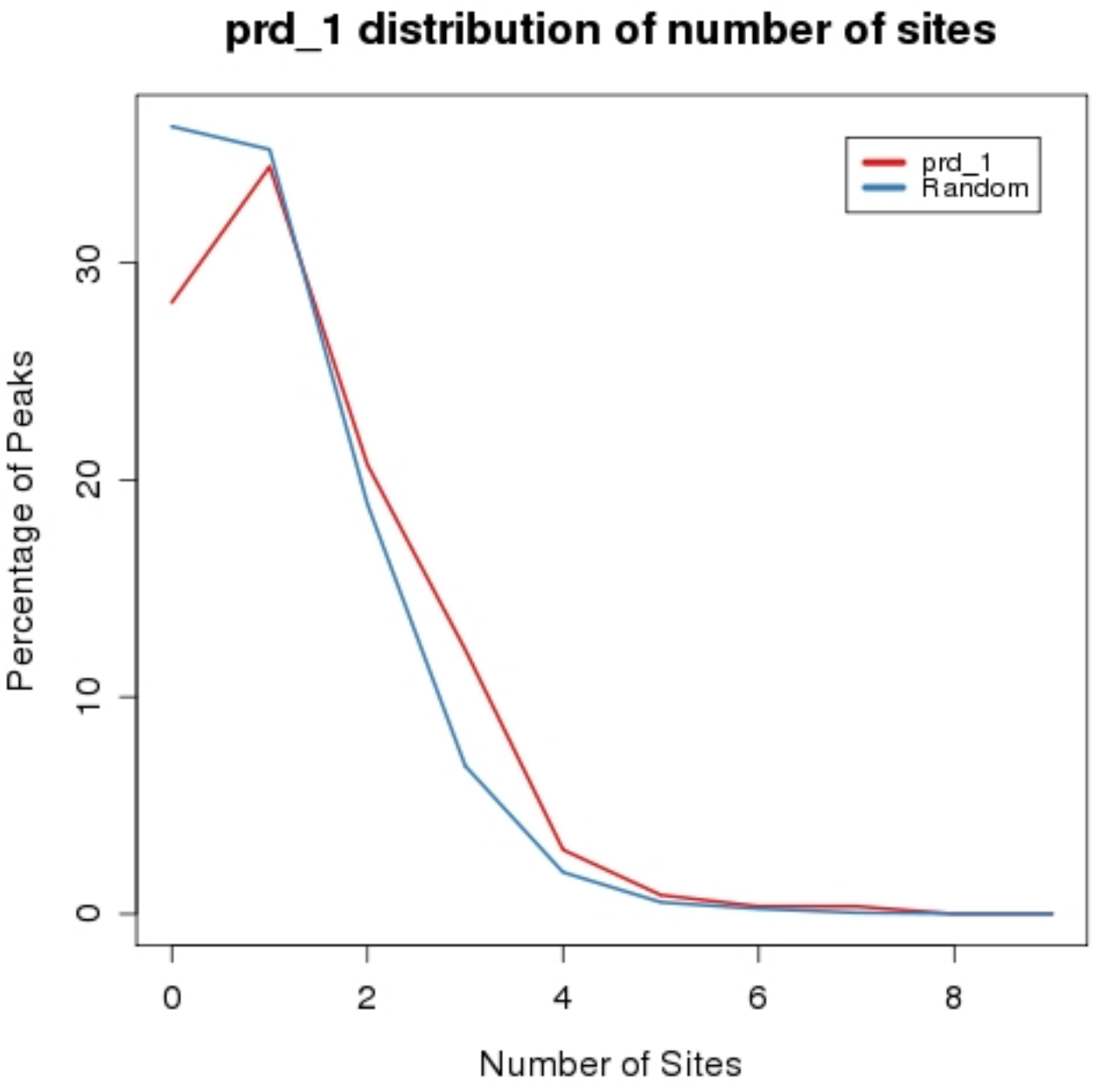

prd_1 base composition across peaks
Percentage GC
41
42
43
44
45
-4000
-2000
0
2000
4000
Nucleotide position (200 bp)

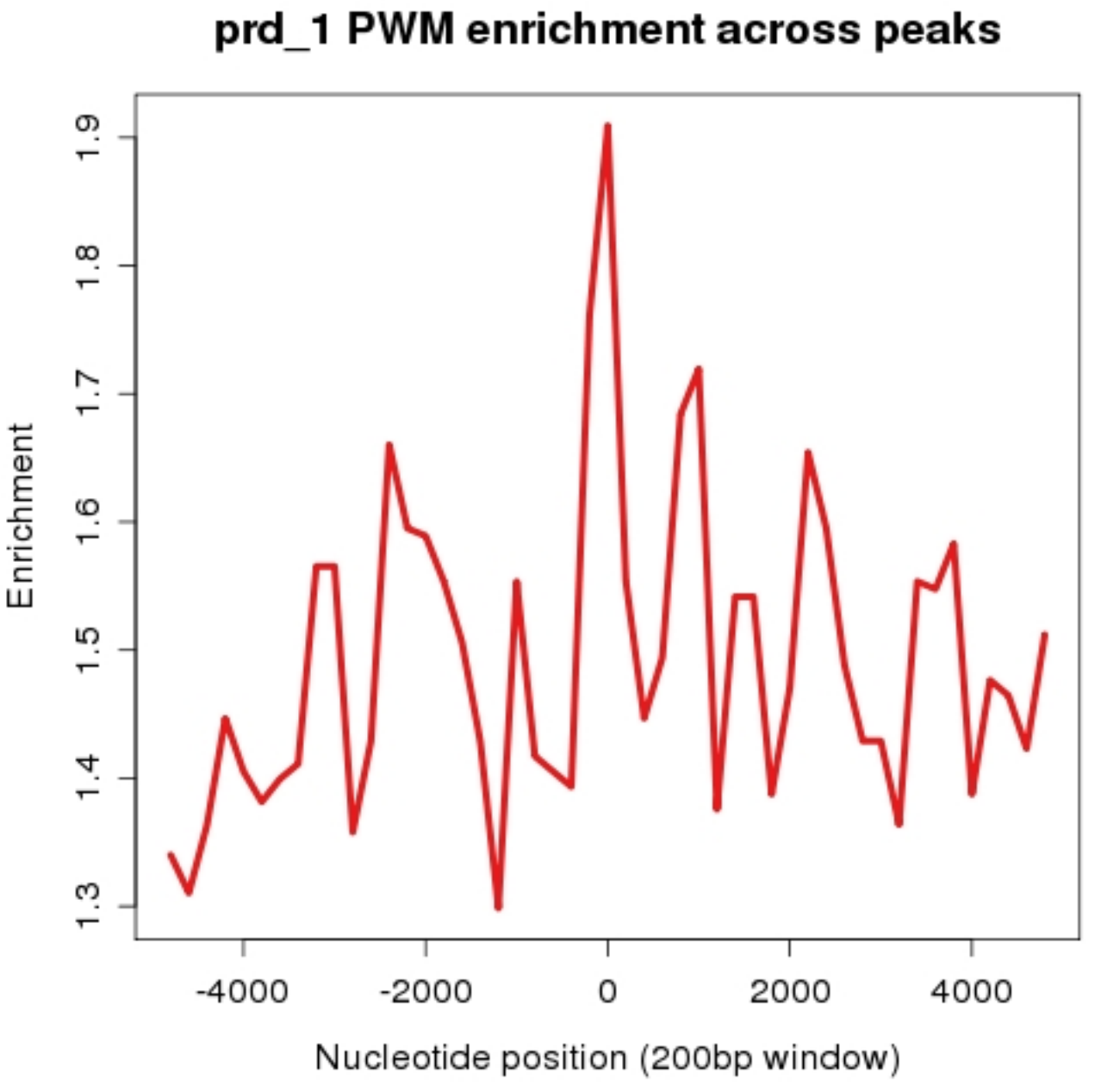

prd_1 base composition down ranks
1%FDR
Percentage GC
41
42
43
44
45
200
400
600
800
1000
ChIP/chip rank


prd_1 median distance to genes
1%FDR
all
patterned
transcribed
Median distance to closest gene
10000
30000
50000
70000
200
400
600
800
1000
ChIP/chip rank


prd_1 distribution of 1%FDR peak scores
Number of Peaks
0
100
200
300
400
2
4
6
8
10
12
14
ChIPchip Peak Score


prd_1 distribution of 25%FDR peak scores
Number of Peaks
0
200
400
600
800
2
4
6
8
10
12
14
ChIPchip Peak Score


prd_1 distribution of number of sites
prd_1
Random
Percentage of Peaks
0
10
20
30
0
2
4
6
8
Number of Sites


prd_1 PWM enrichment across peaks
Enrichment
1.3
1.4
1.5
1.6
1.7
1.8
1.9
-4000
-2000
0
2000
4000
Nucleotide position (200bp window)

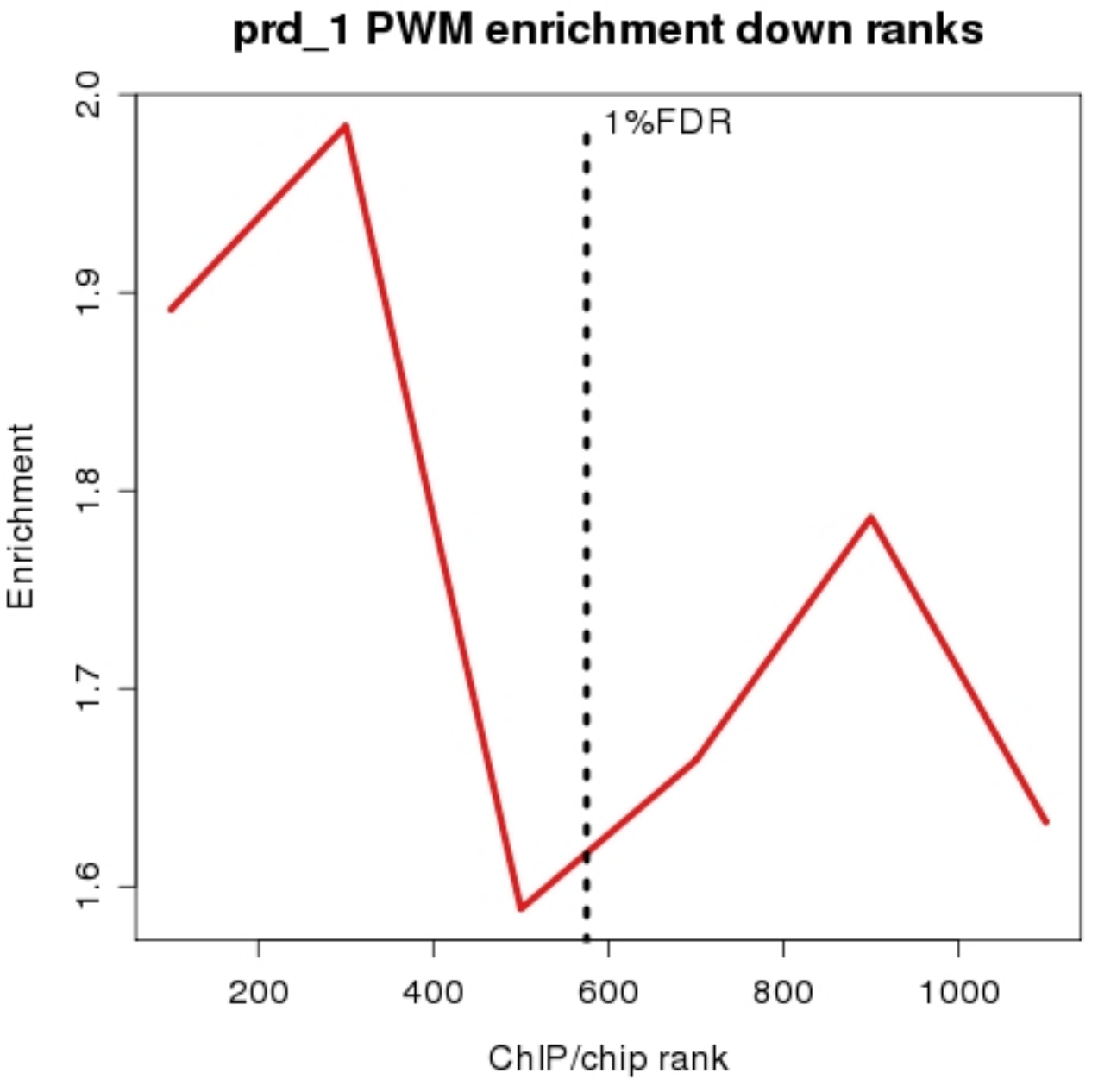
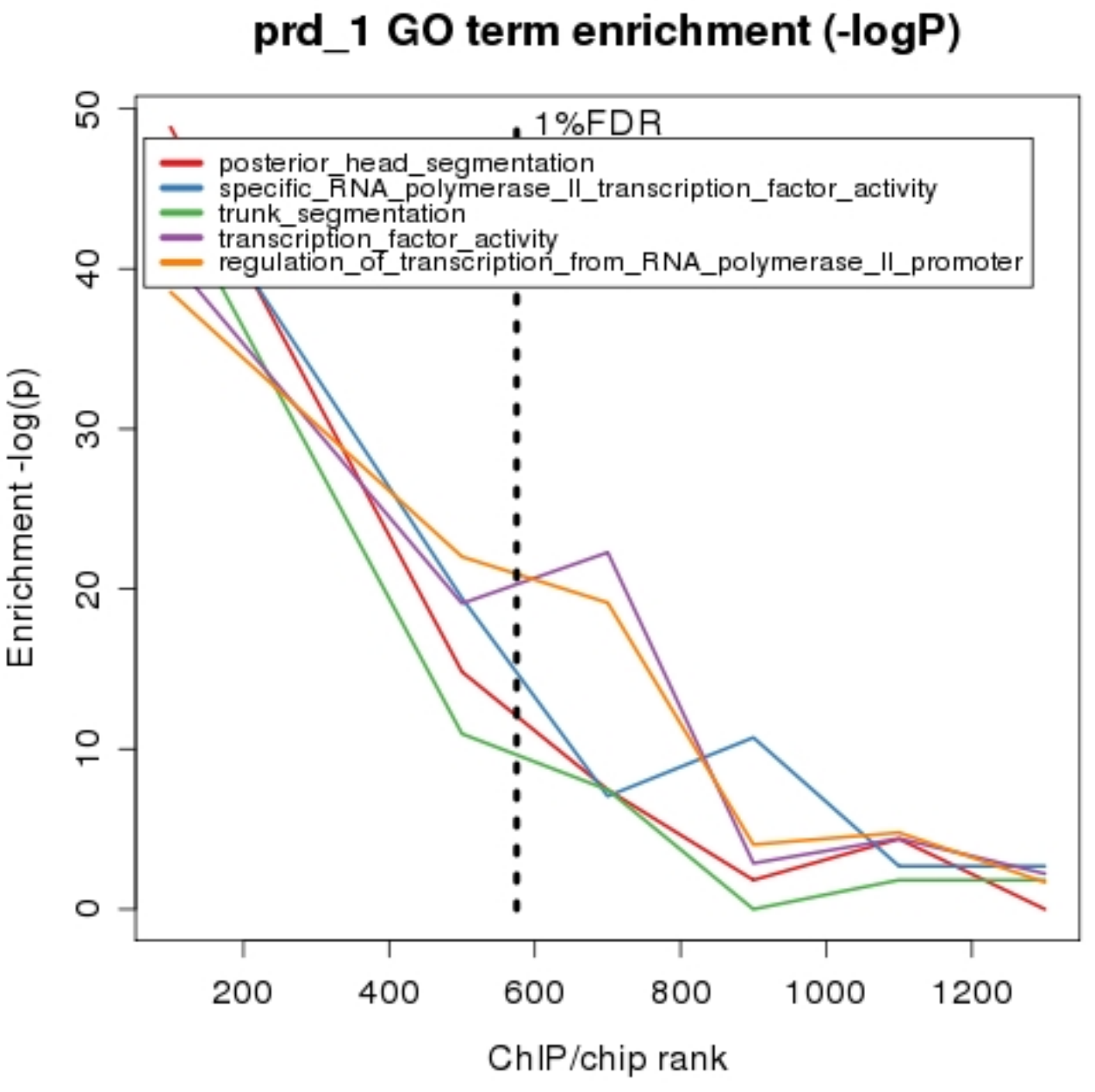
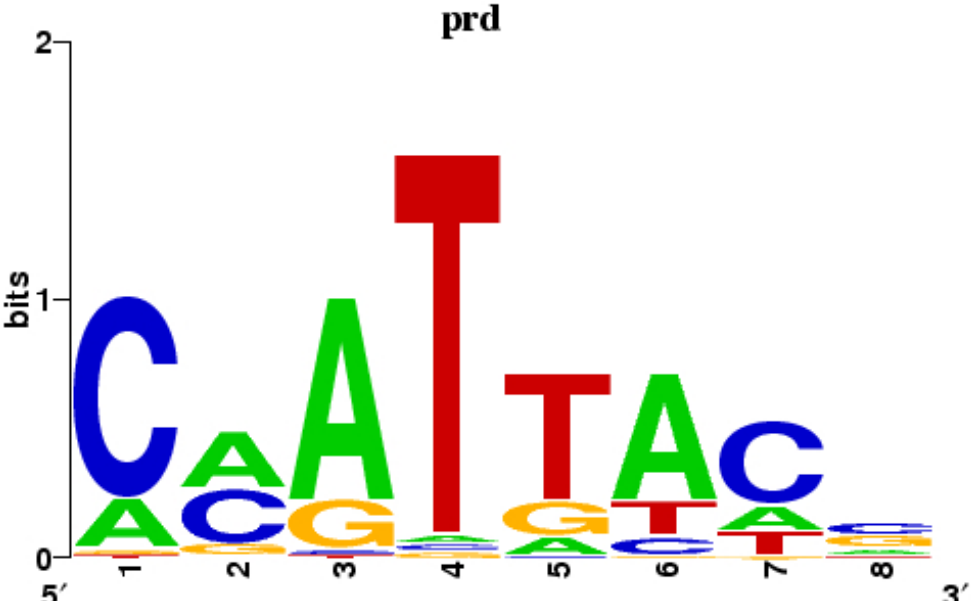
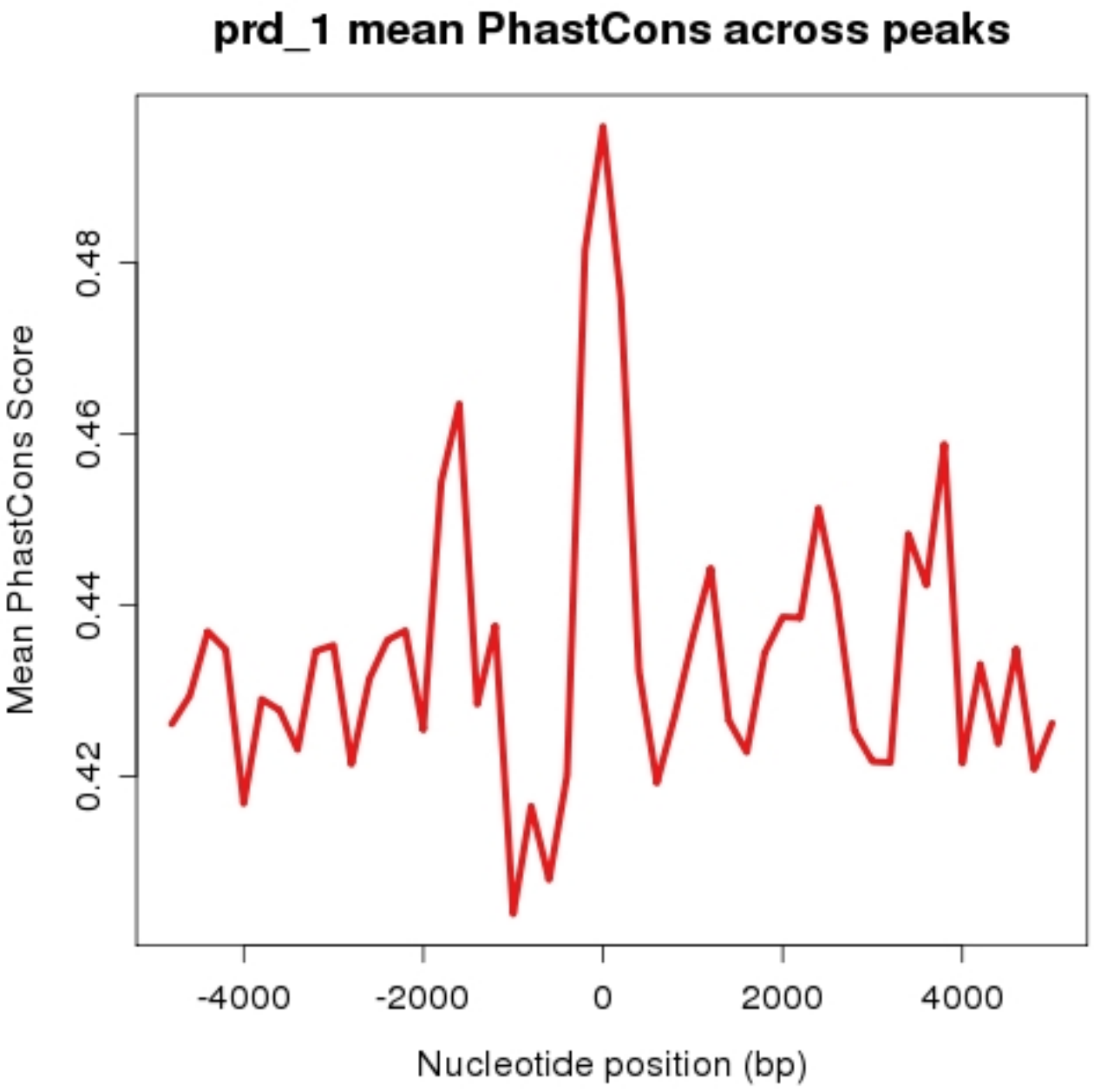
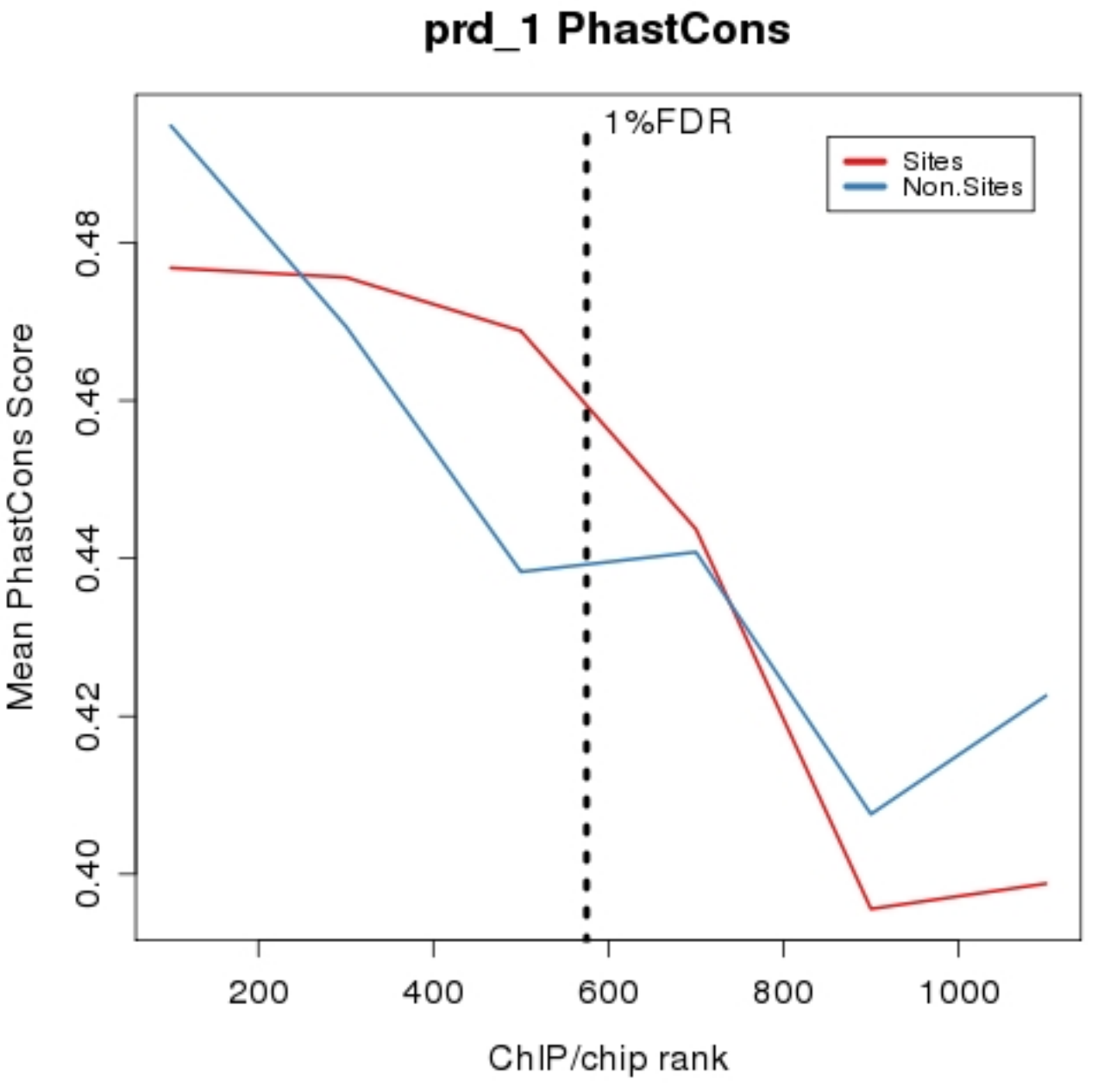

prd_1 PWM enrichment down ranks
1%FDR
Enrichment
2.0
1.9
1.8
1.7
1.6
200
400
600
800
1000
ChIP/chip rank

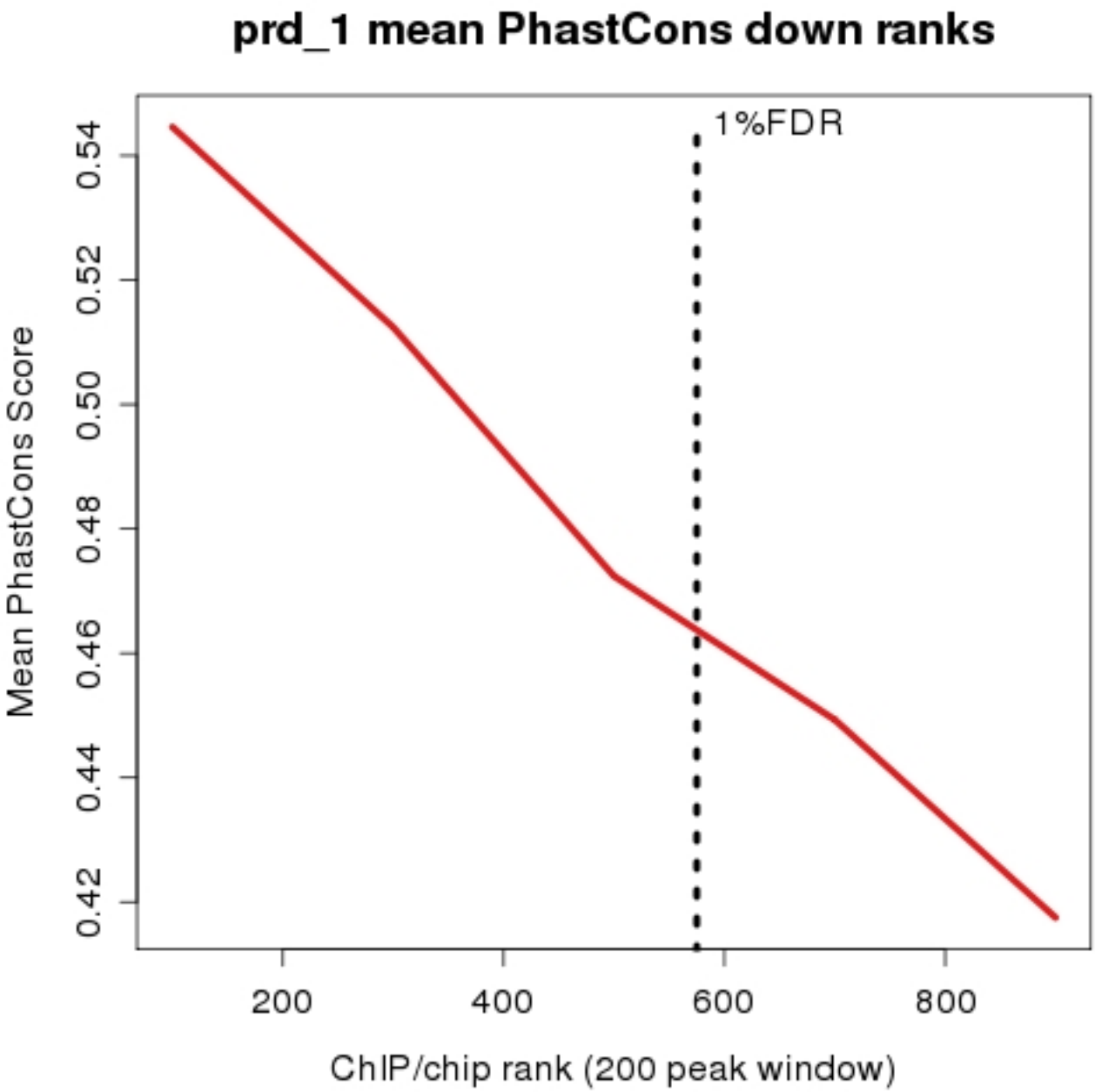
figure not available


prd_1 GO term enrichment (-logP)
1%FDR
posterior_head_segmentation
specific_RNA_polymerase_II_transcription_factor_activity
trunk_segmentation
transcription_factor_activity
regulation_of_transcription_from_RNA_polymerase_II_promoter
Enrichment -log(p)
0
10
20
30
40
50
200
400
600
800
1000
1200
ChIP/chip rank


prd
bits
2
1
0
1
2
3
4
5
6
7
8
5′
3′


prd_1 mean PhastCons across peaks
Mean PhastCons Score
0.42
0.44
0.46
0.48
-4000
-2000
0
2000
4000
Nucleotide position (bp)


prd_1 PhastCons
1%FDR
Sites
Non.Sites
Mean PhastCons Score
0.40
0.42
0.44
0.46
0.48
200
400
600
800
1000
ChIP/chip rank


prd_1 mean PhastCons down ranks
1%FDR
Mean PhastCons Score
0.42
0.44
0.46
0.48
0.50
0.52
0.54
200
400
600
800
ChIP/chip rank (200 peak window)