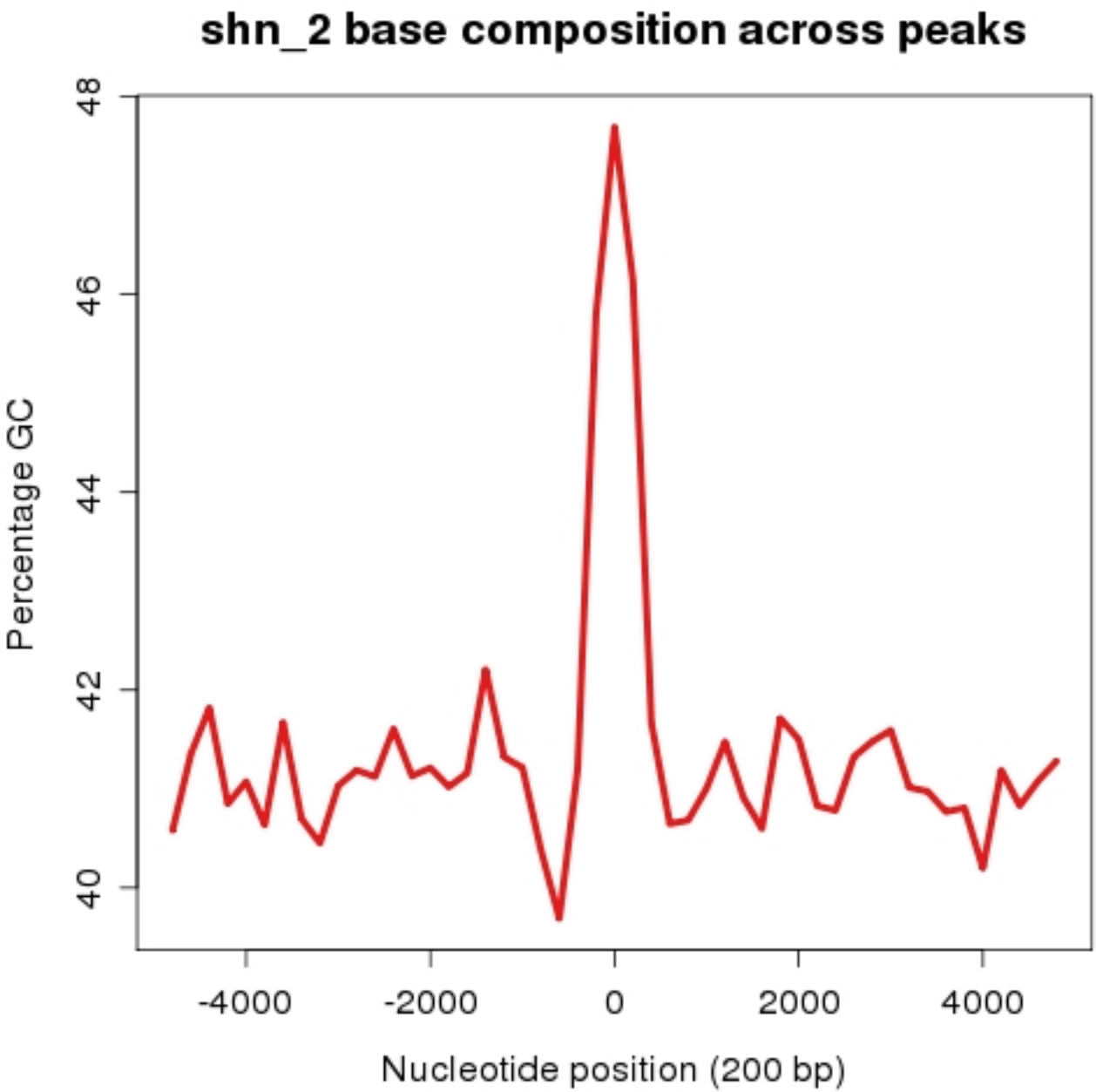
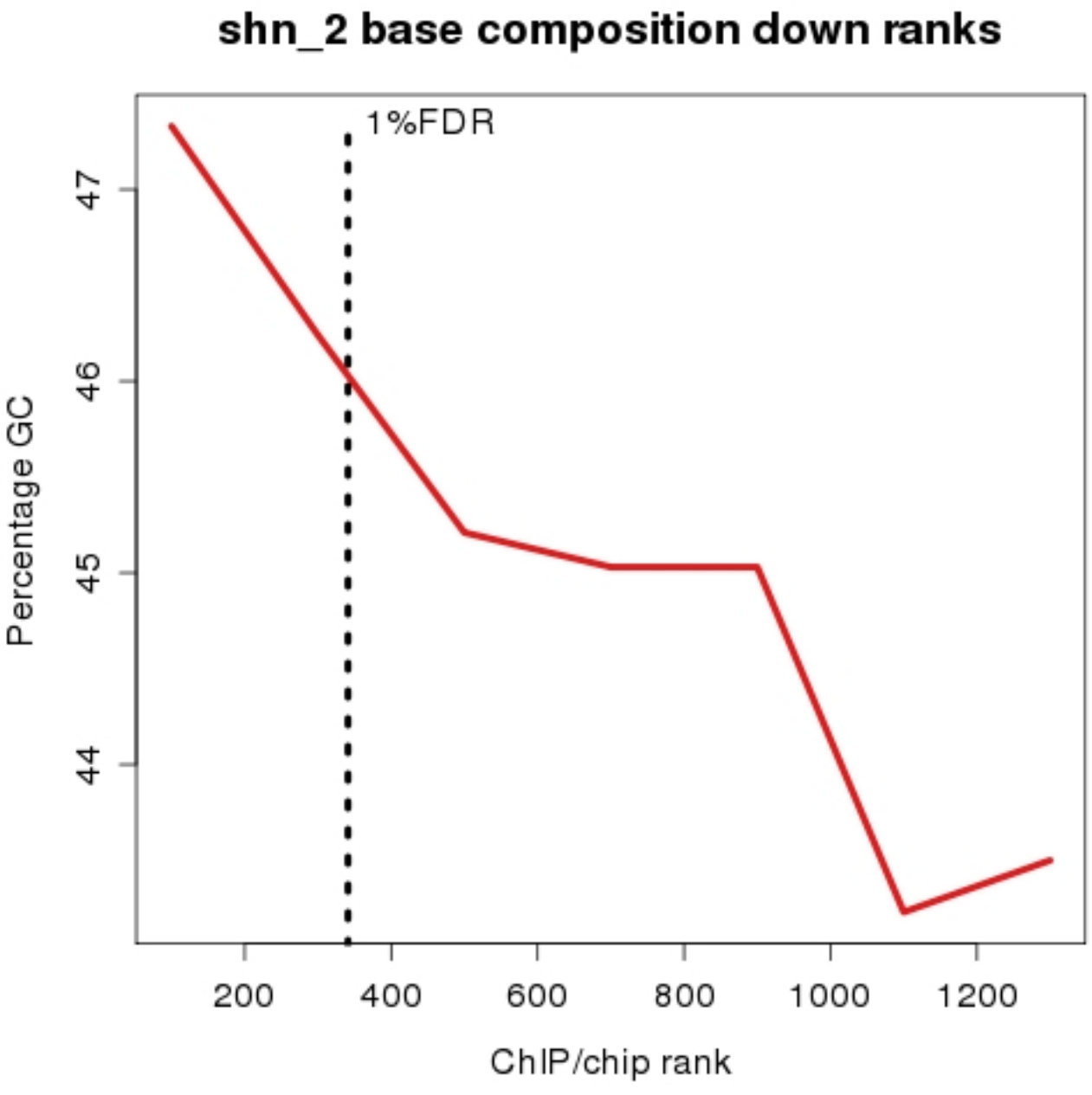
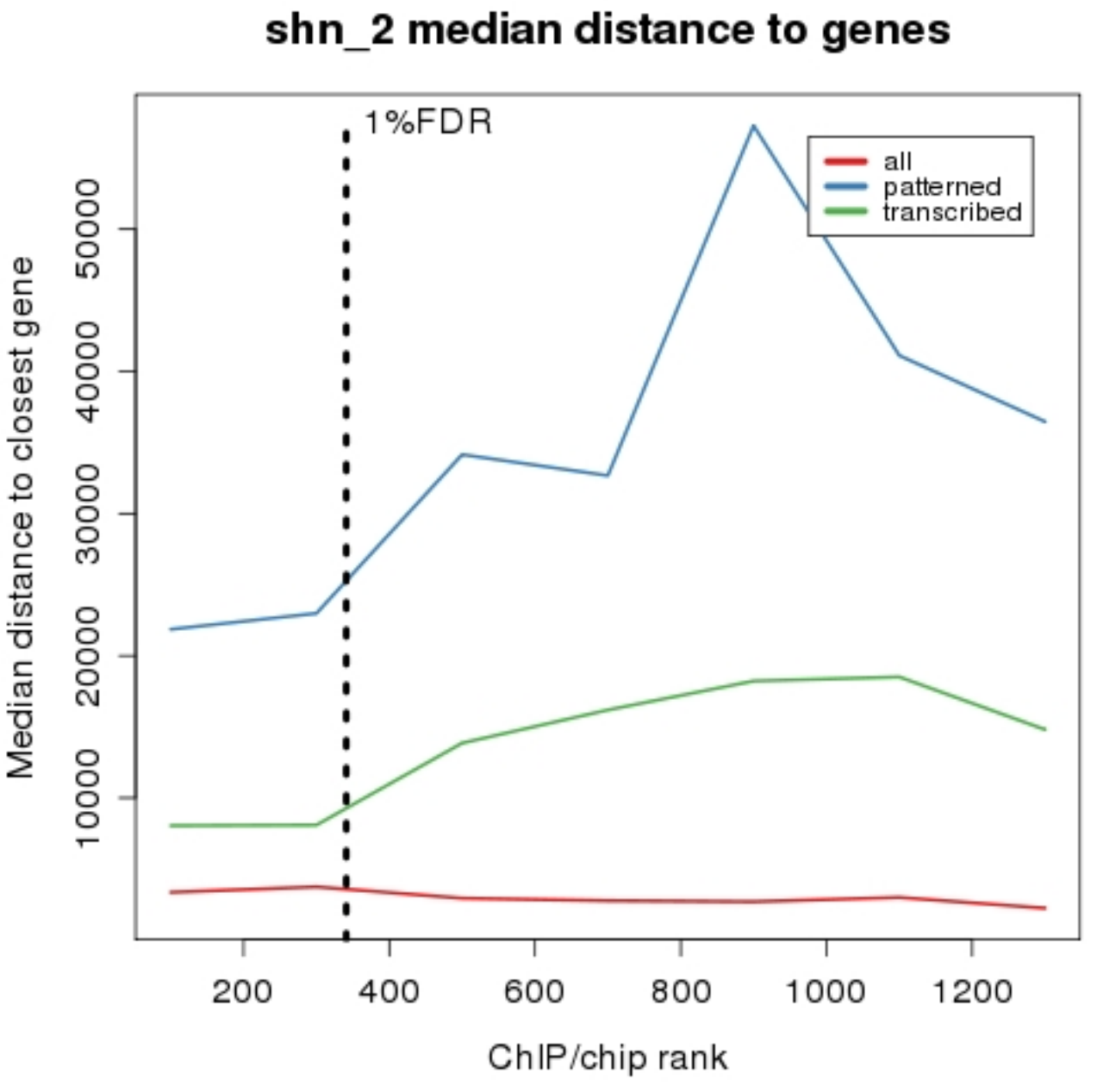

shn_2 base composition across peaks
Percentage GC
40
42
44
46
48
-4000
-2000
0
2000
4000
Nucleotide position (200 bp)


shn_2 base composition down ranks
1%FDR
Percentage GC
44
45
46
47
200
400
600
800
1000
1200
ChIP/chip rank


shn_2 median distance to genes
1%FDR
all
patterned
transcribed
Median distance to closest gene
10000
20000
30000
40000
50000
200
400
600
800
1000
1200
ChIP/chip rank

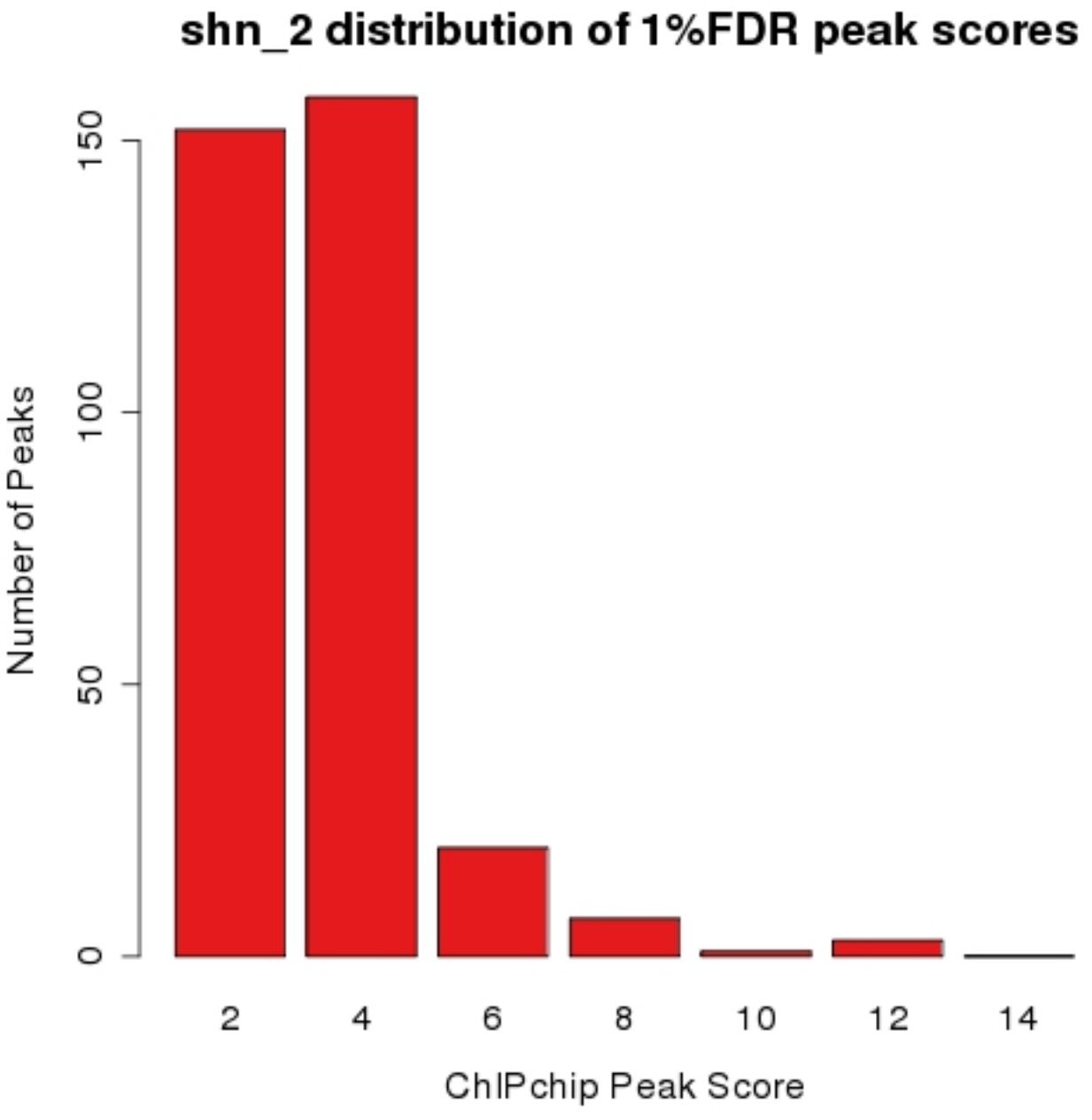
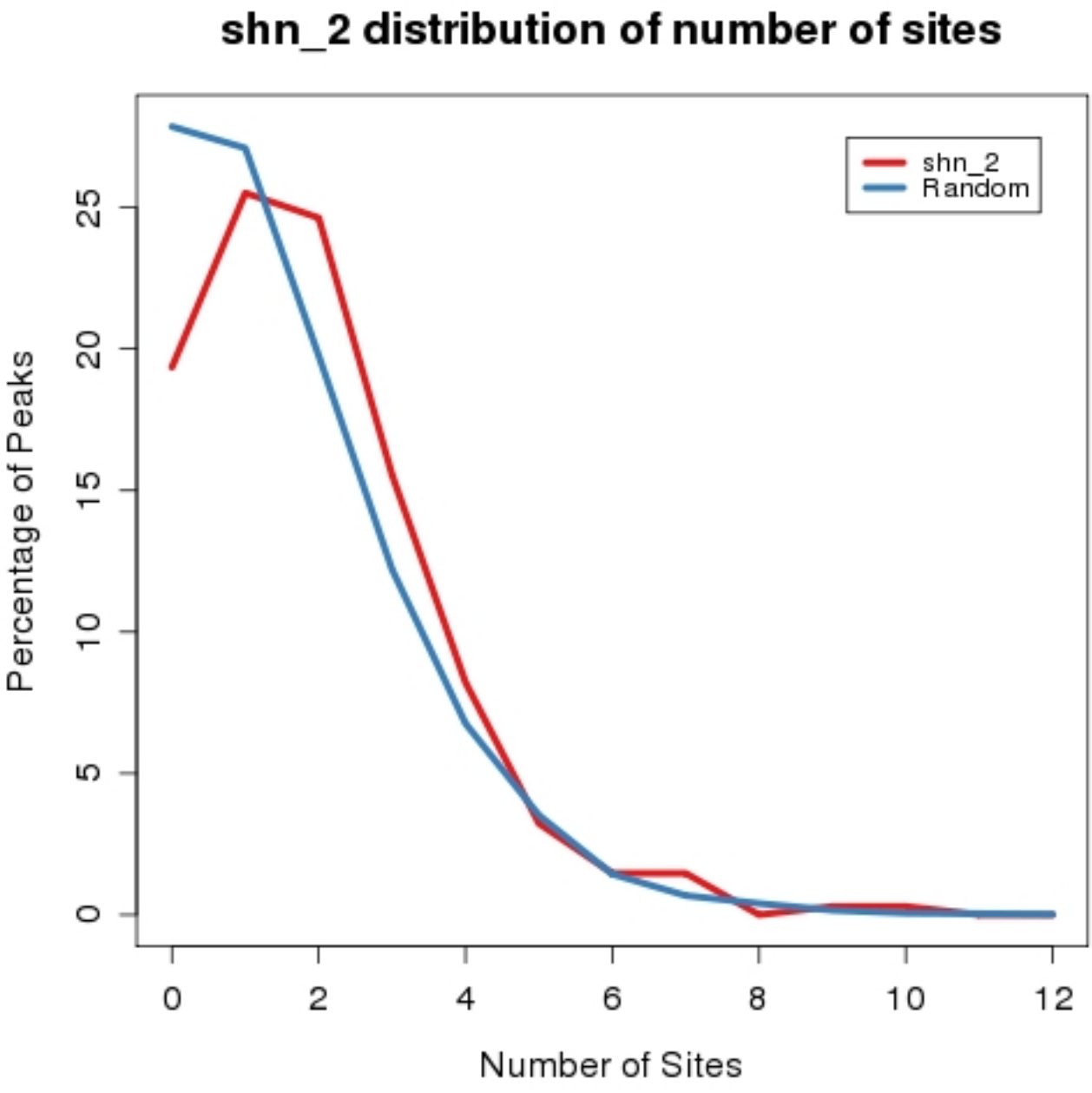

shn_2 distribution of 1%FDR peak scores
Number of Peaks
0
50
100
150
2
4
6
8
10
12
14
ChIPchip Peak Score

figure not available


shn_2 distribution of number of sites
shn_2
Random
Percentage of Peaks
0
5
10
15
20
25
0
2
4
6
8
10
12
Number of Sites

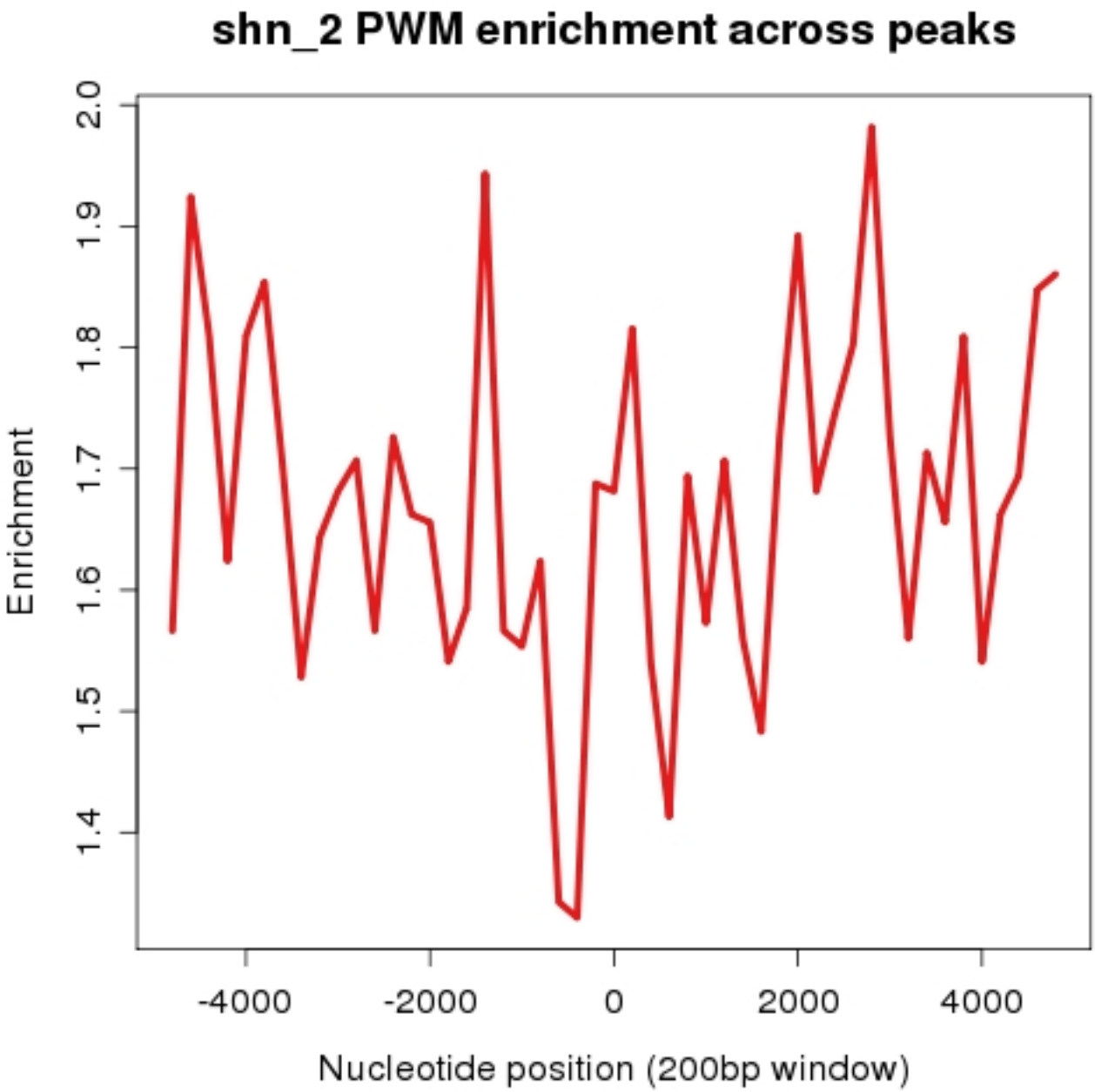
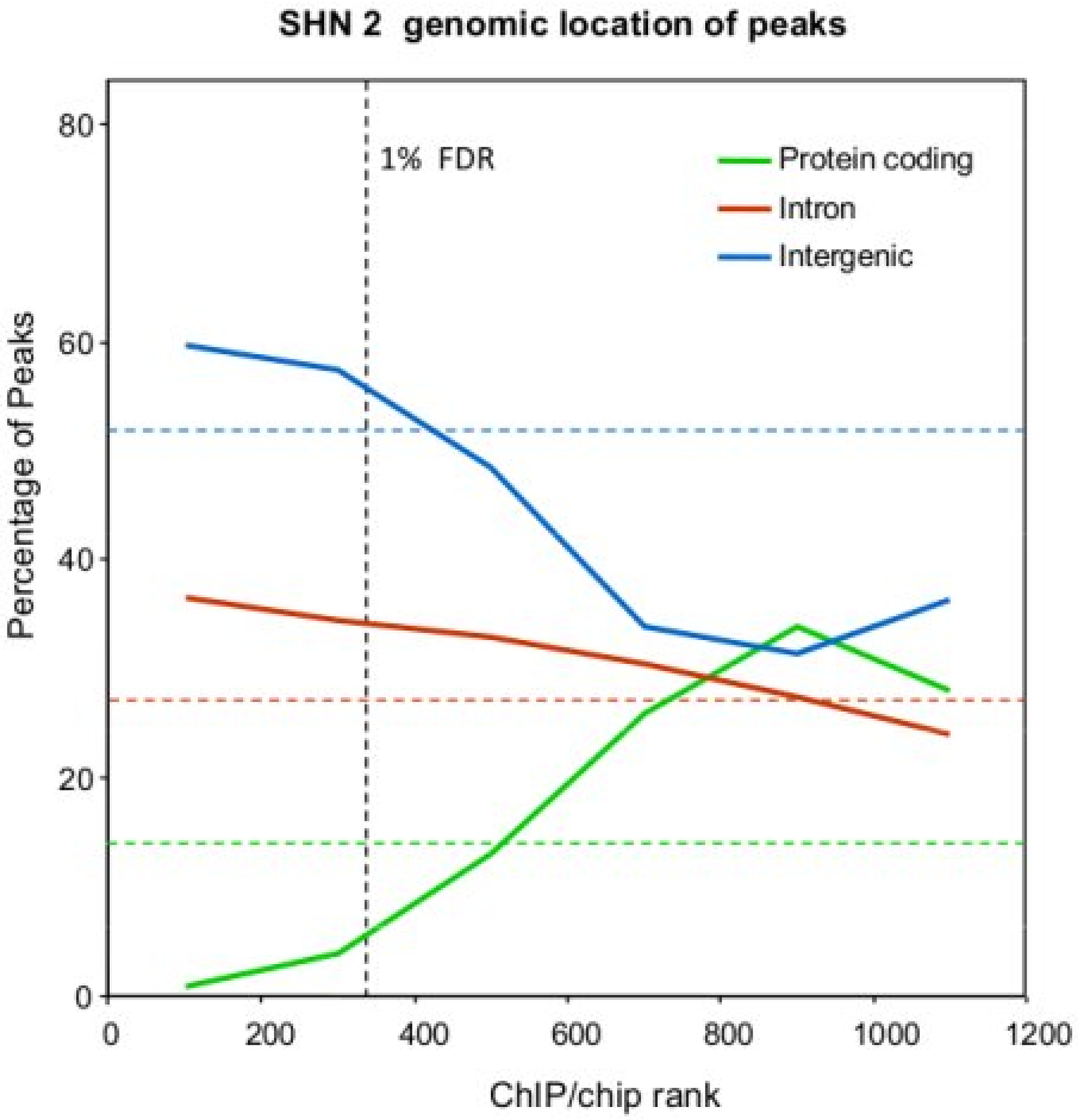
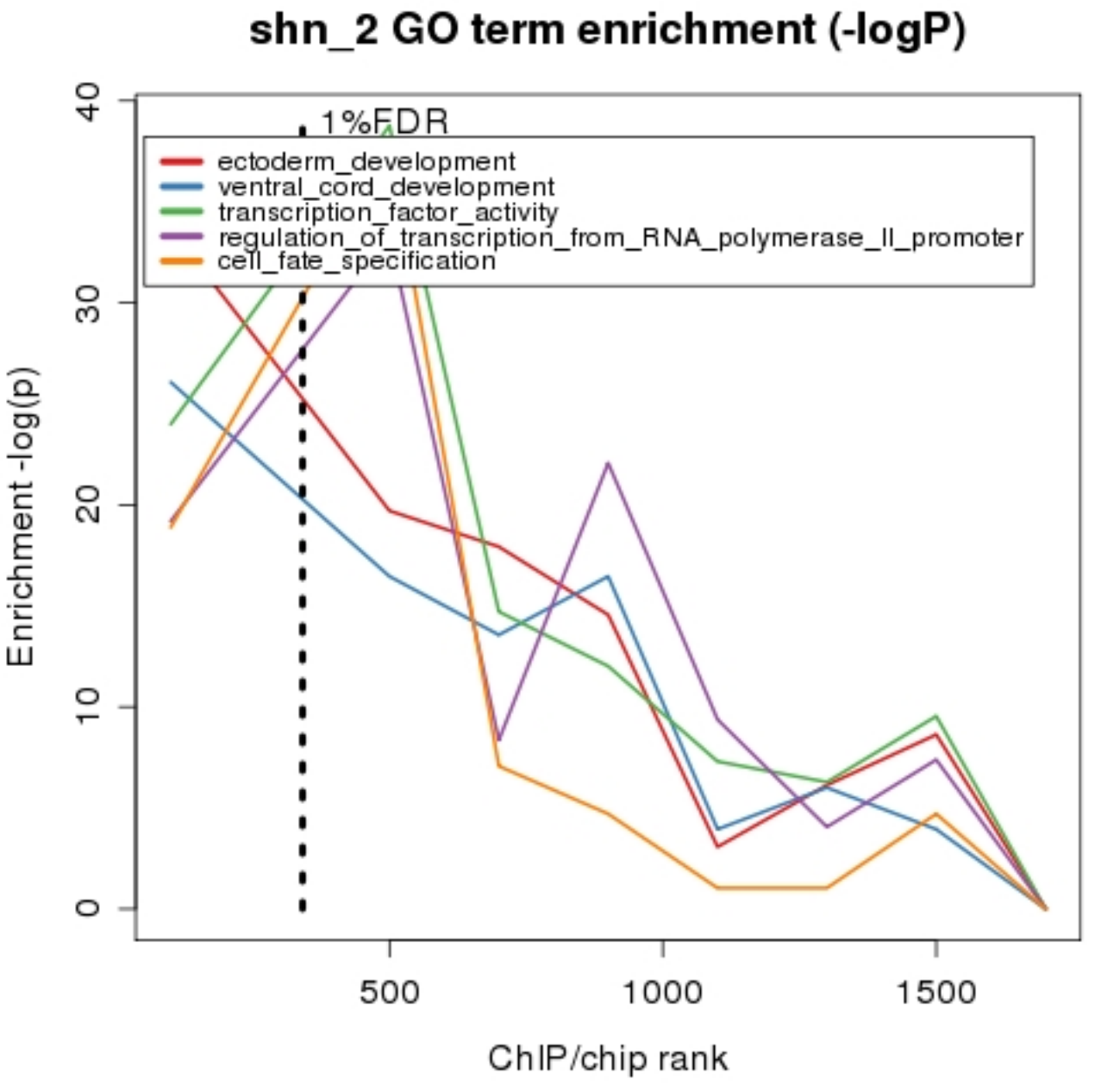
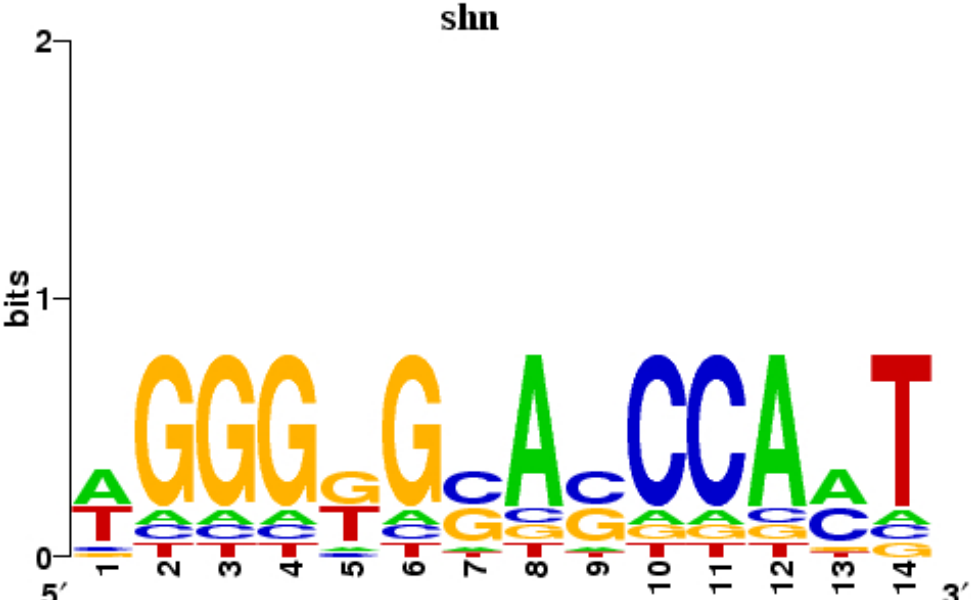
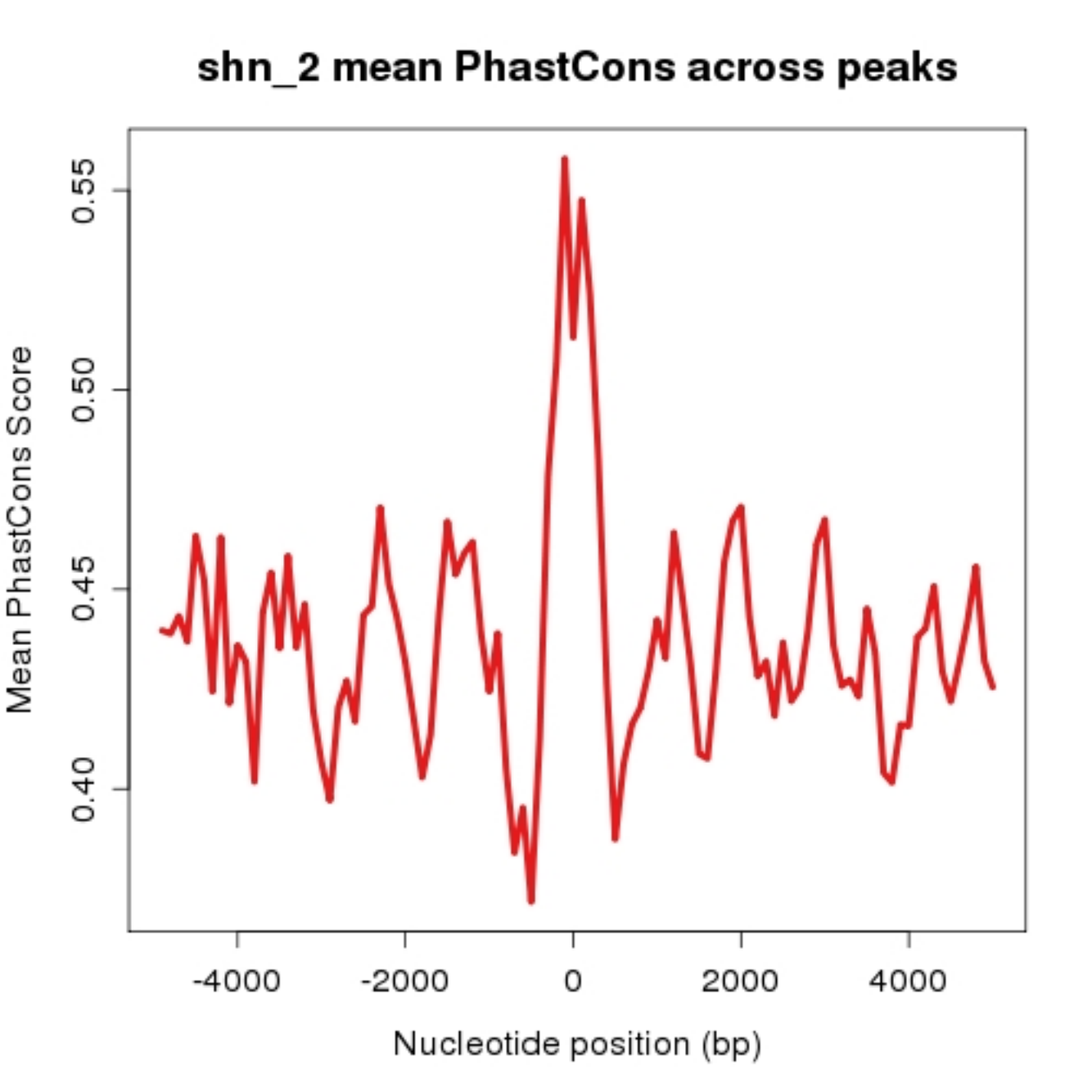

shn_2 PWM enrichment across peaks
Enrichment
2.0
1.9
1.8
1.7
1.6
1.5
1.4
-4000
-2000
0
2000
4000
Nucleotide position (200bp window)

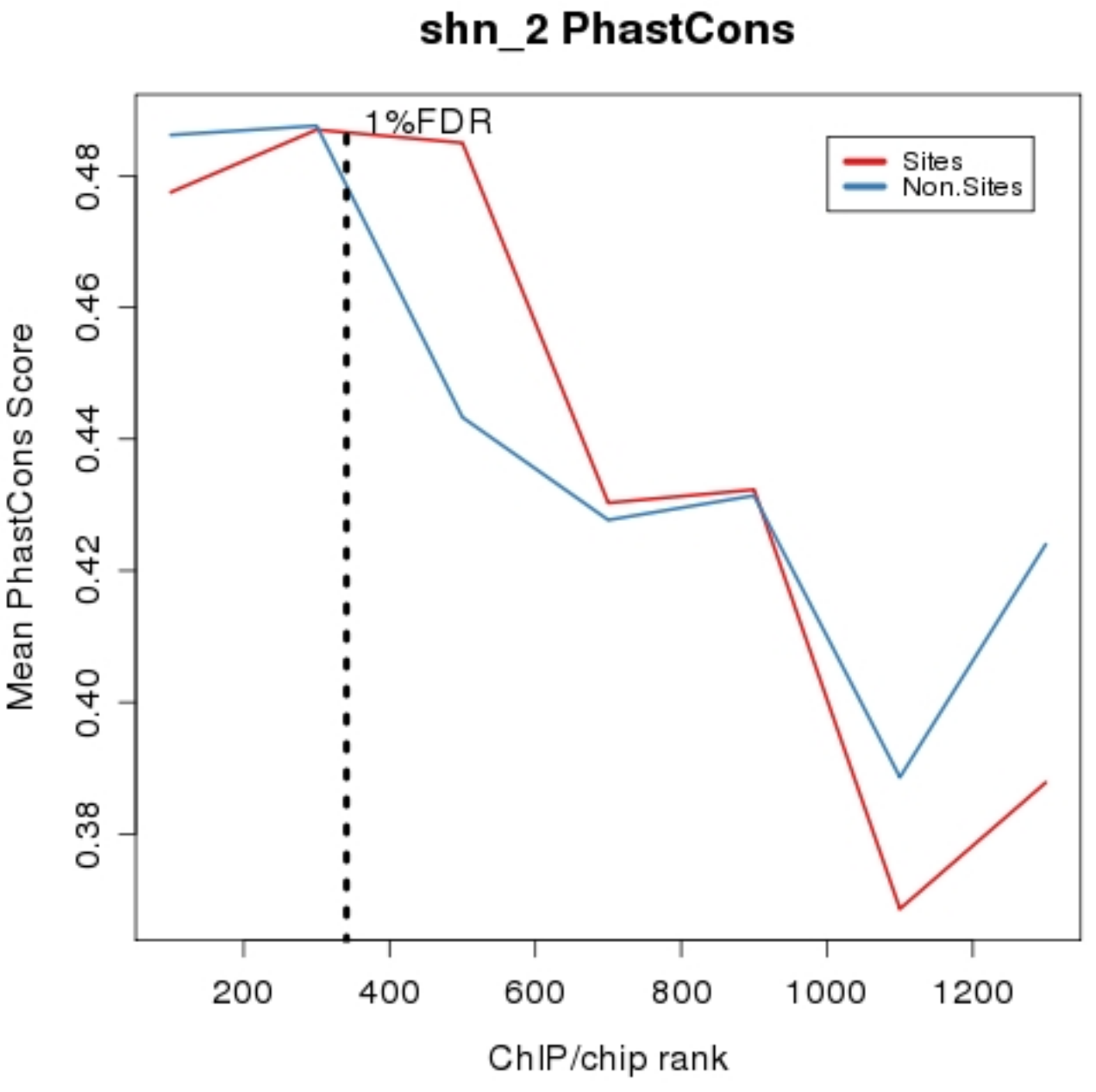
figure not available

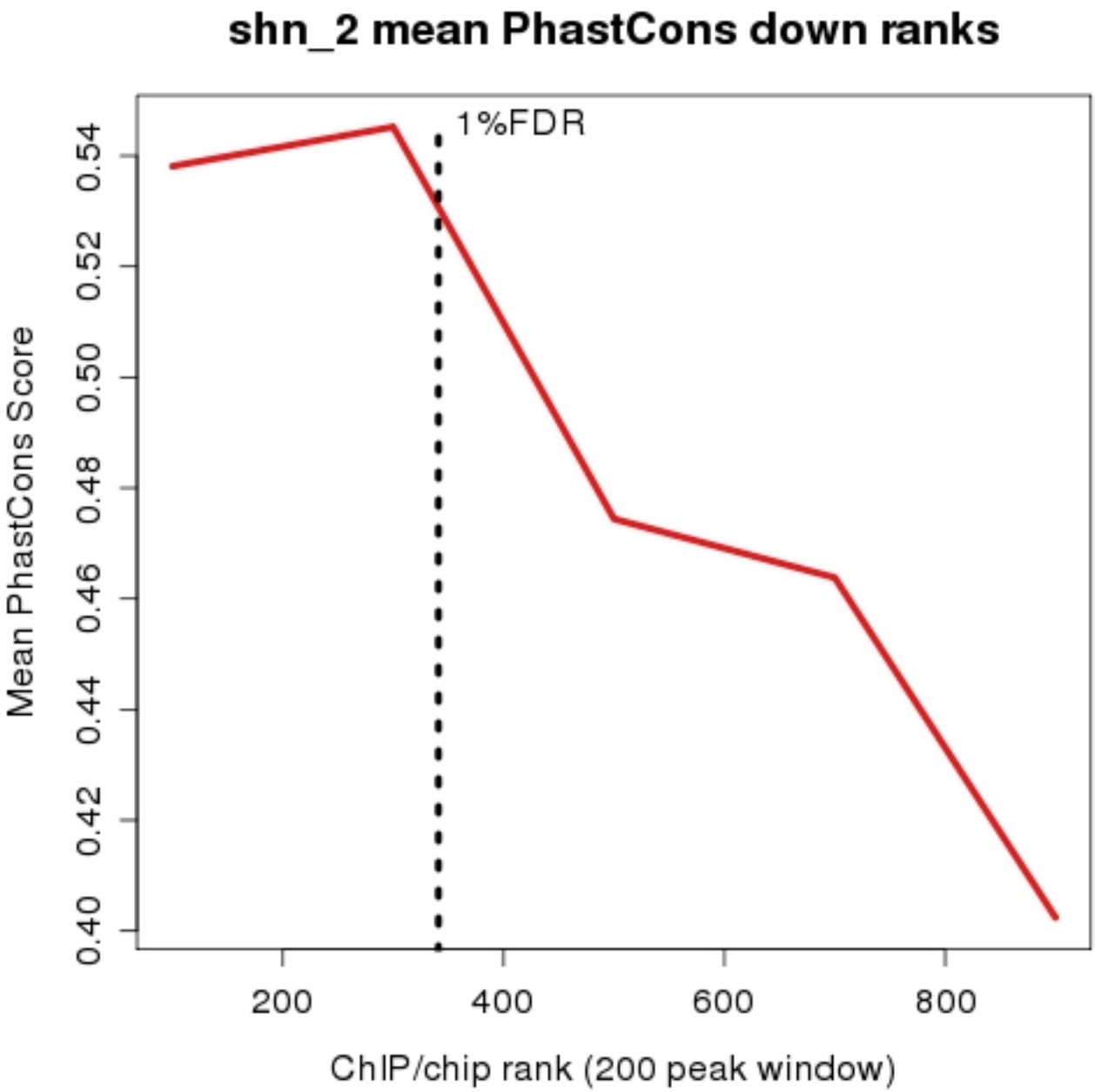

SHN 2 genomic location of peaks
1% FDR
Protein coding
Intron
Intergenic
Percentage of Peaks
0
20
40
60
80
0
200
400
600
800
1000
1200
ChIP/chip rank


shn_2 GO term enrichment (-logP)
1%FDR
ectoderm_development
ventral_cord_development
transcription_factor_activity
regulation_of_transcription_from_RNA_polymerase_II_promoter
cell_fate_specification
Enrichment -log(p)
0
10
20
30
40
500
1000
1500
ChIP/chip rank


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


shn_2 mean PhastCons across peaks
Mean PhastCons Score
0.40
0.45
0.50
0.55
-4000
-2000
0
2000
4000
Nucleotide position (bp)


shn_2 PhastCons
1%FDR
Sites
Non.Sites
Mean PhastCons Score
0.38
0.40
0.42
0.44
0.46
0.48
200
400
600
800
1000
1200
ChIP/chip rank


shn_2 mean PhastCons down ranks
1%FDR
Mean PhastCons Score
0.40
0.42
0.44
0.46
0.48
0.50
0.52
0.54
200
400
600
800
ChIP/chip rank (200 peak window)