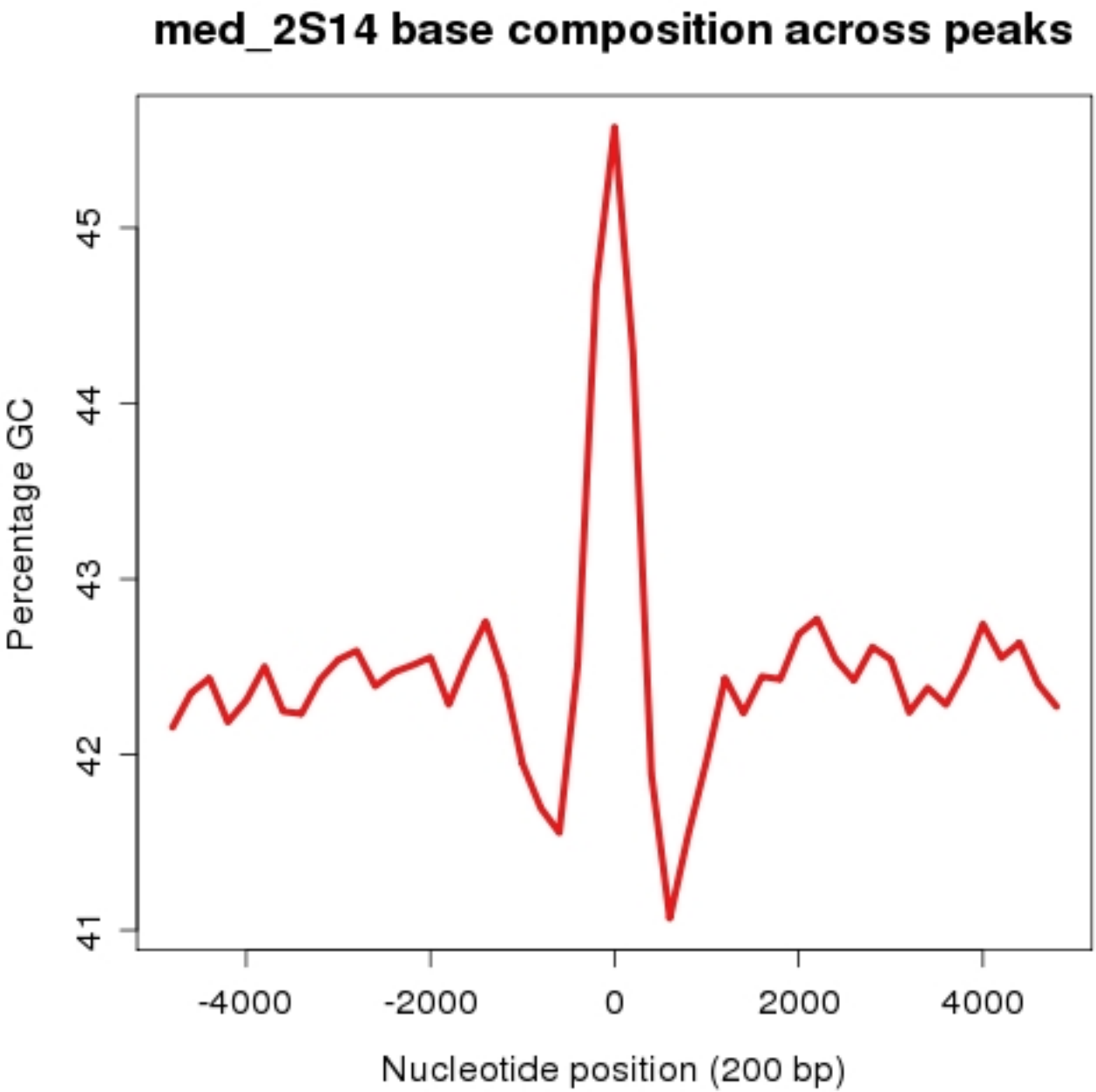
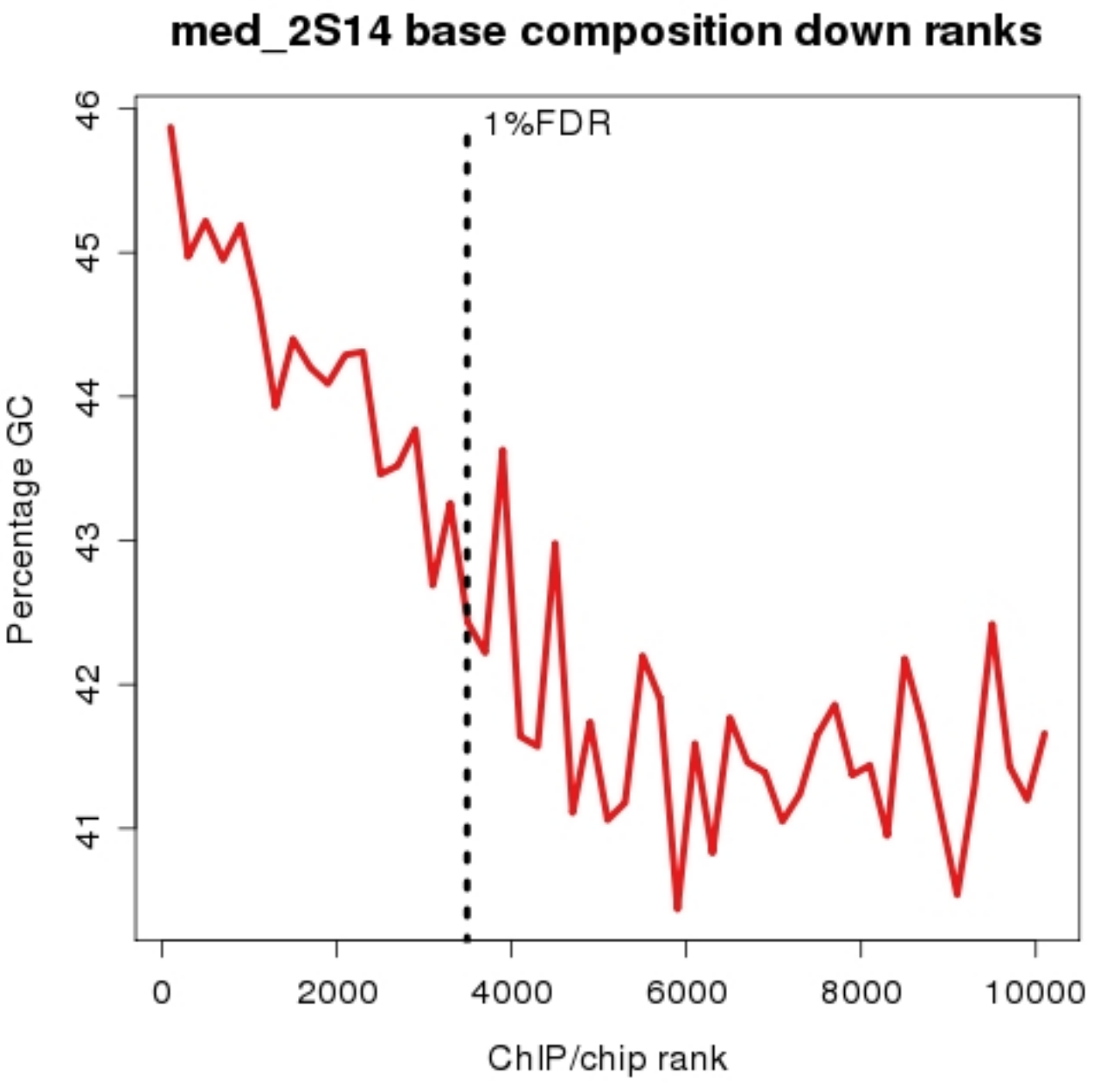
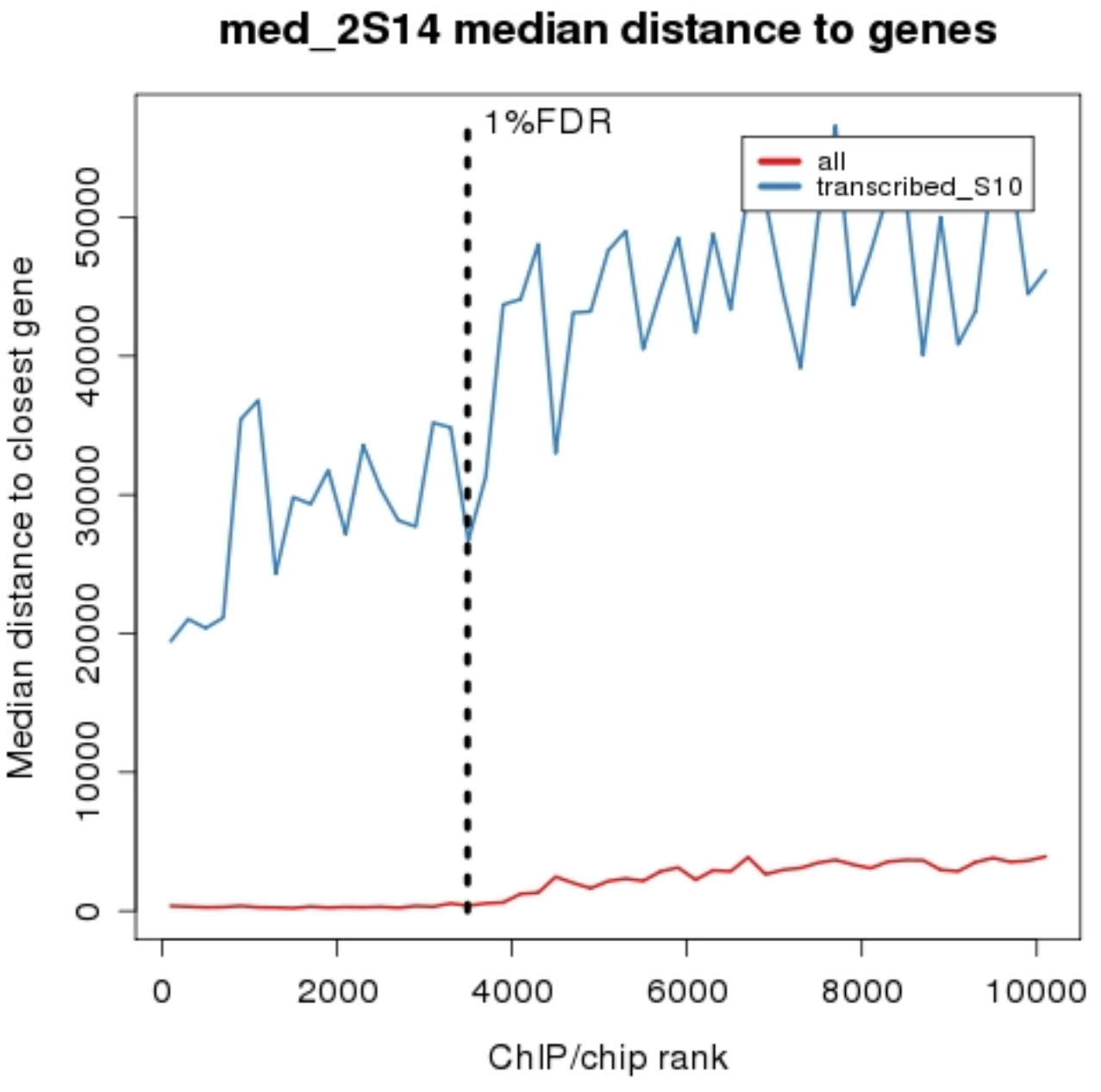
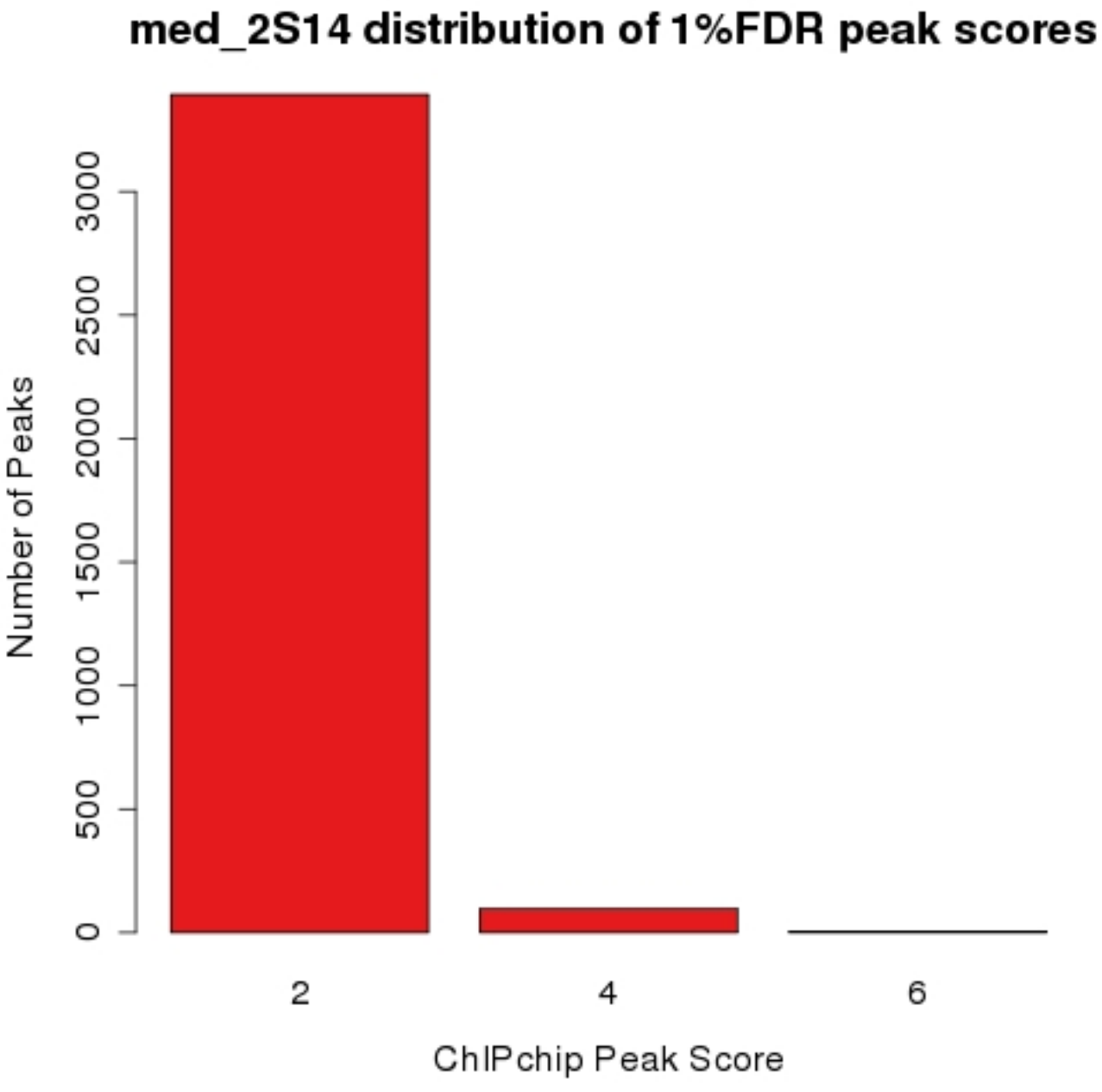
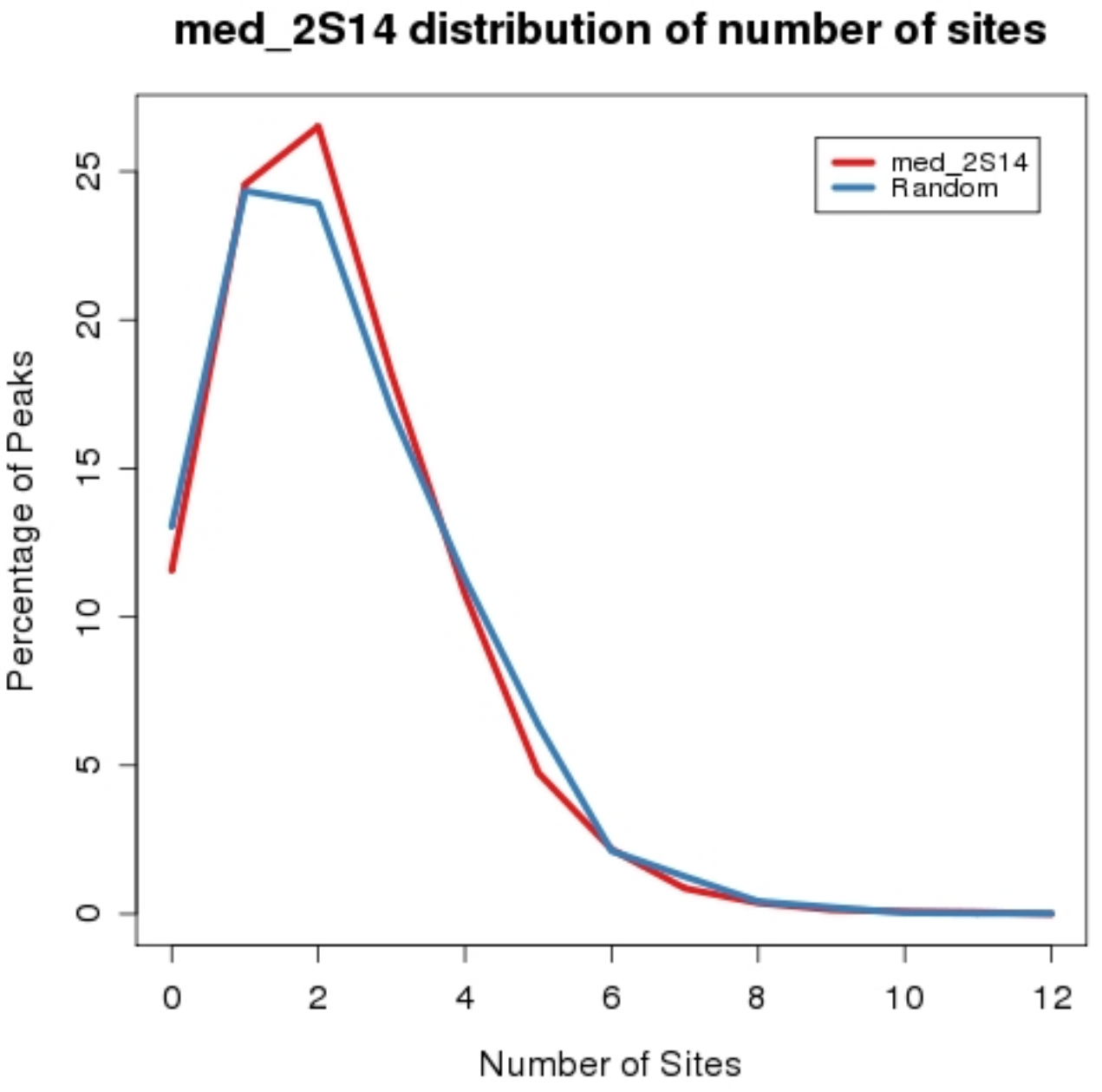
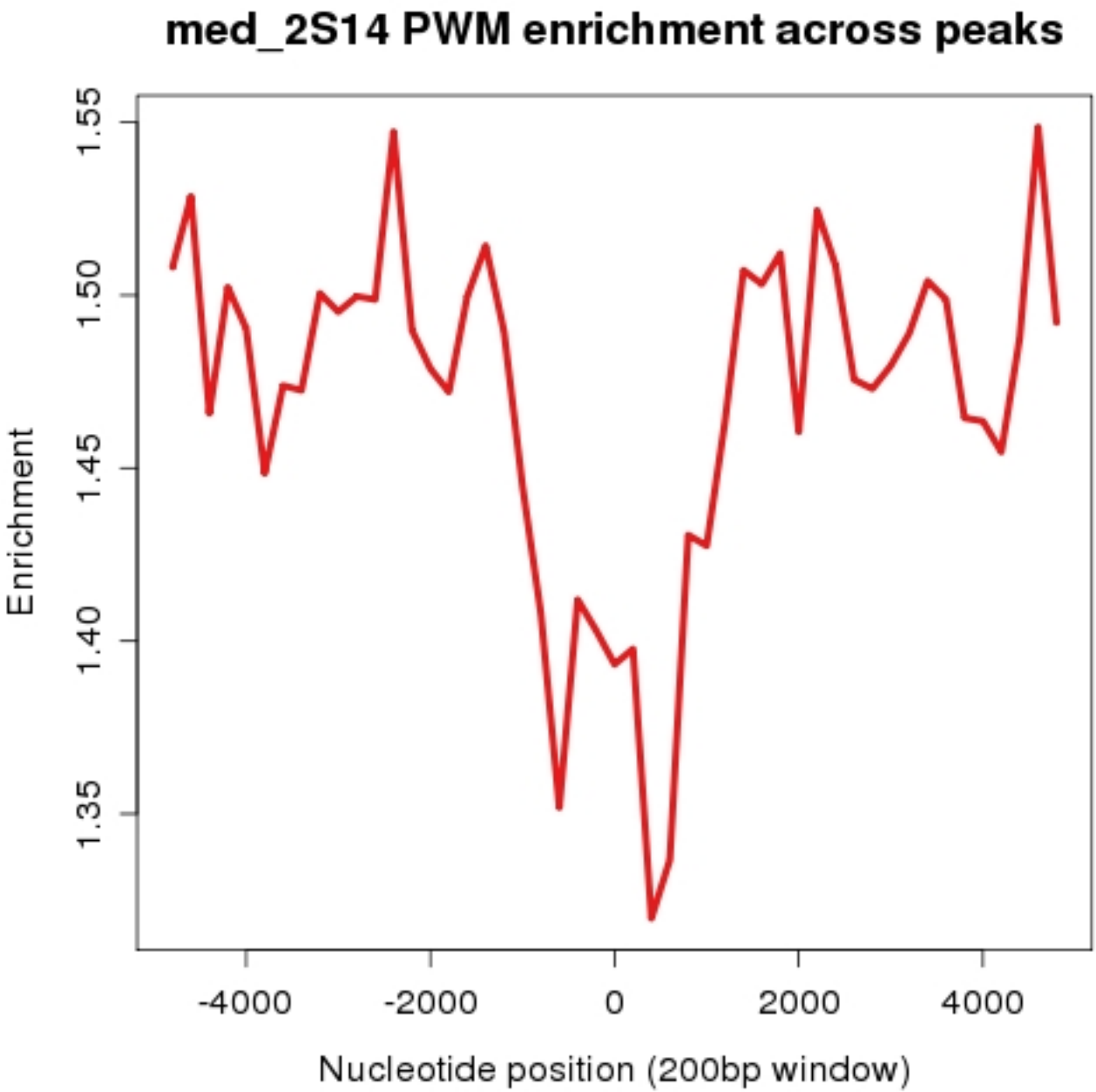

med_2S14 base composition across peaks
Percentage GC
41
42
43
44
45
-4000
-2000
0
2000
4000
Nucleotide position (200 bp)

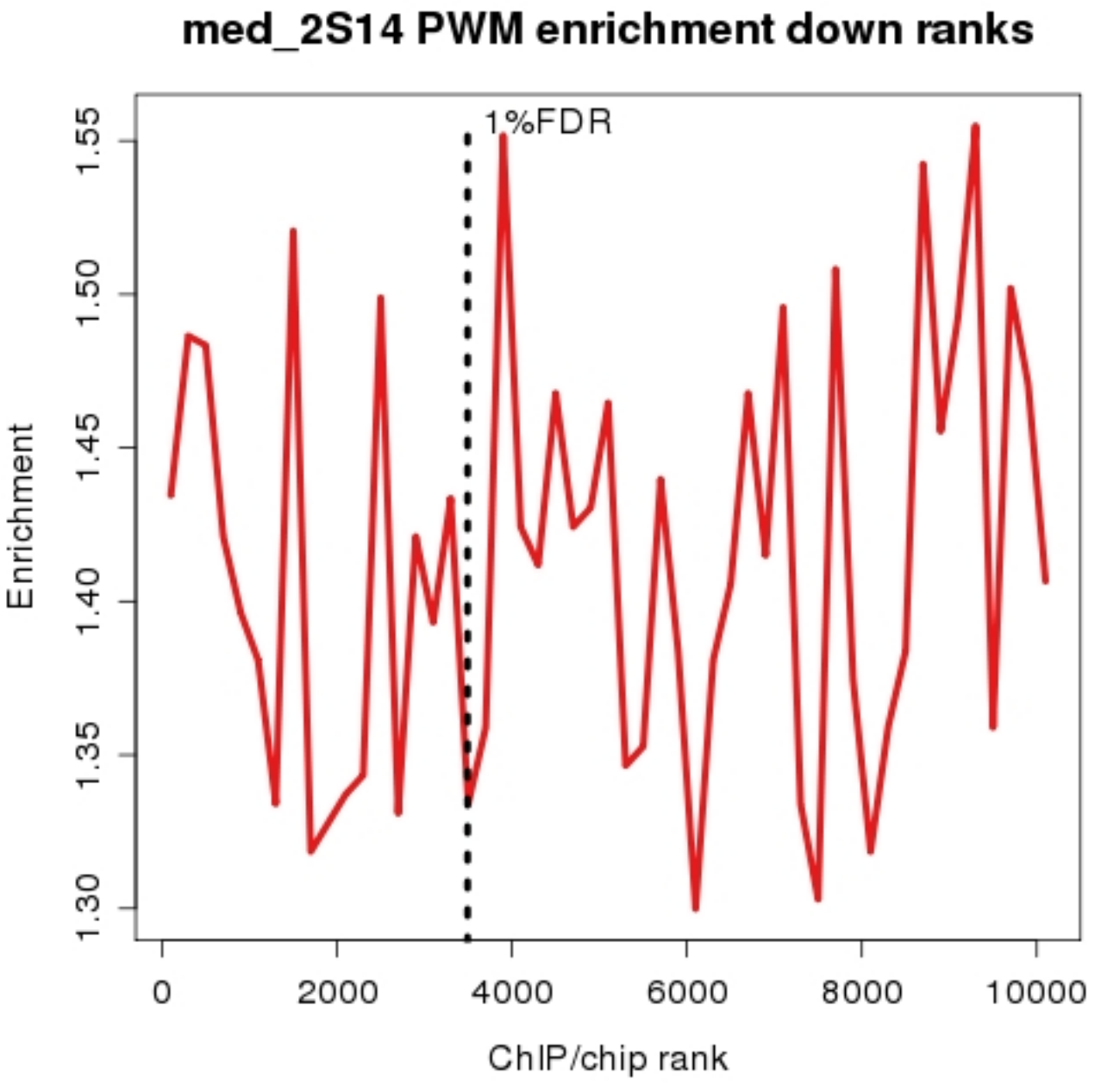

med_2S14 base composition down ranks
1%FDR
Percentage GC
46
45
44
43
42
41
0
2000
4000
6000
8000
10000
ChIP/chip rank

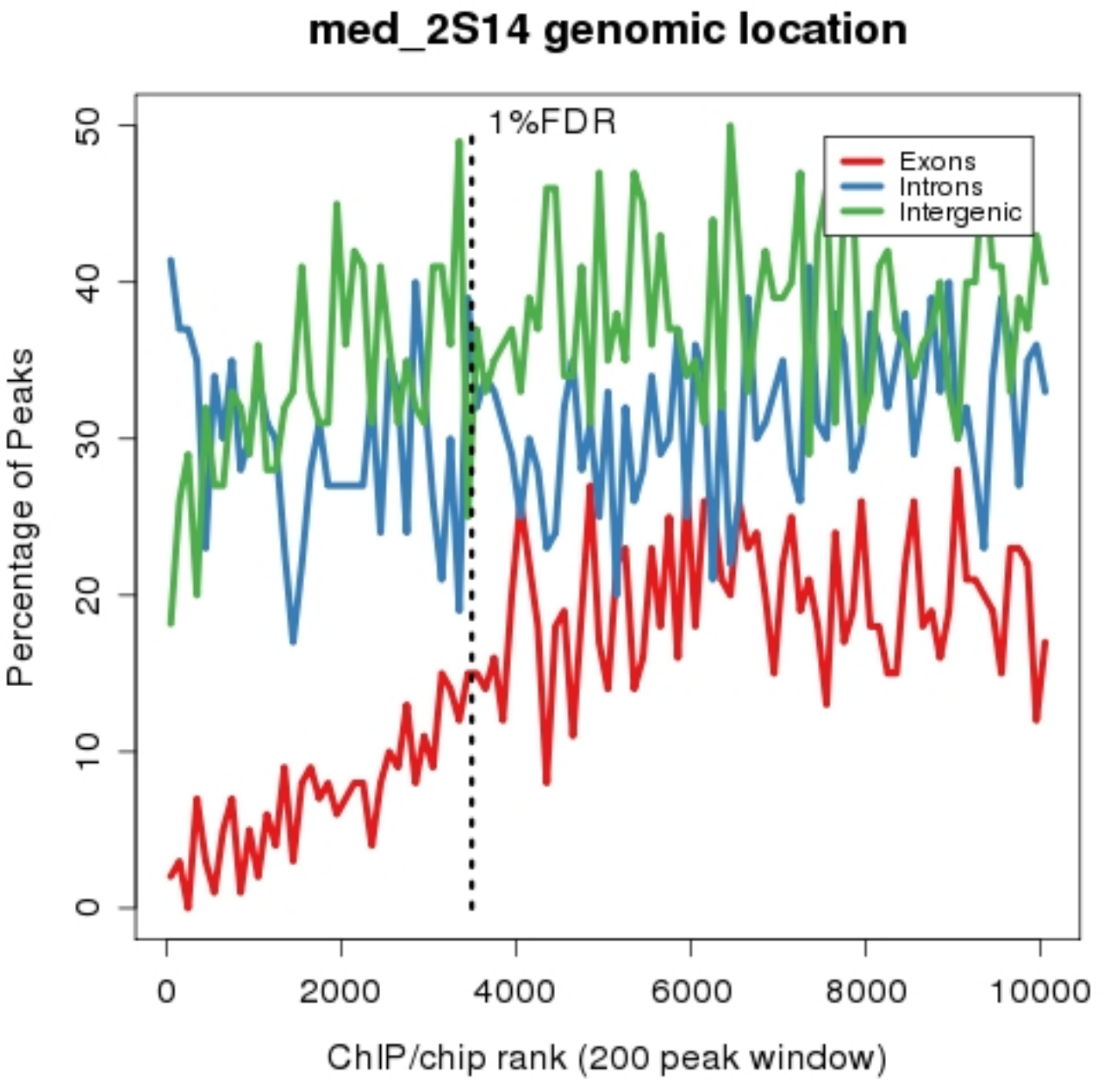

med_2S14 median distance to genes
1%FDR
all
transcribed_S10
Median distance to closest gene
0
10000
20000
30000
40000
50000
0
2000
4000
6000
8000
10000
ChIP/chip rank

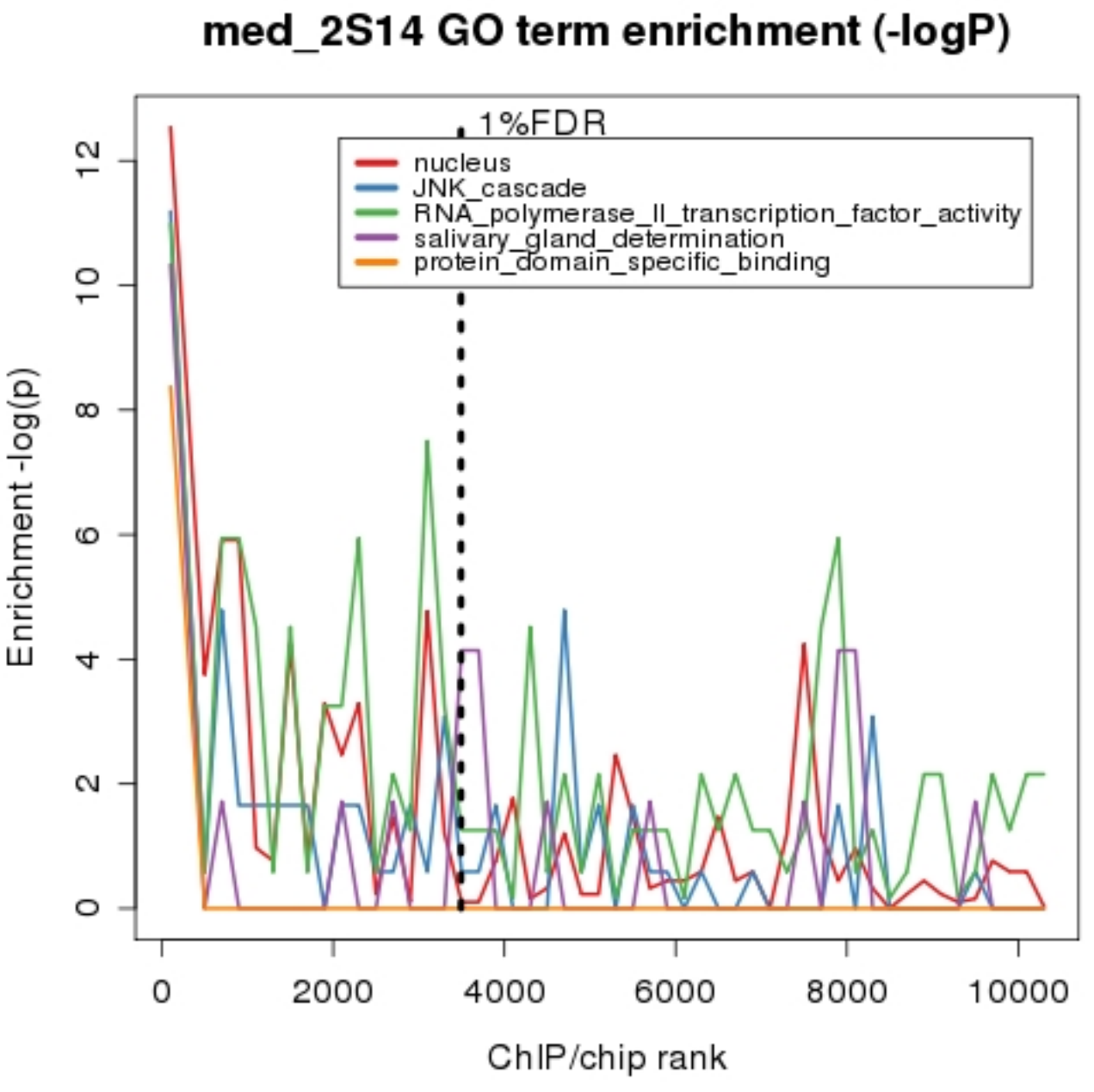

med_2S14 distribution of 1%FDR peak scores
Number of Peaks
0
500
1000
1500
2000
2500
3000
2
4
6
ChIPchip Peak Score

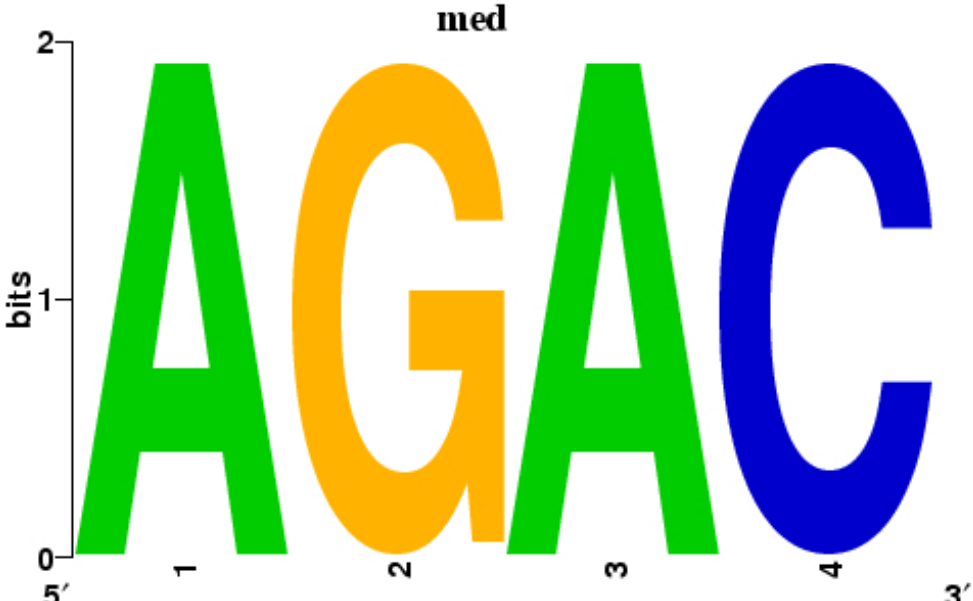

med_2S14 distribution of number of sites
med_2S14
Random
Percentage of Peaks
0
5
10
15
20
25
0
2
4
6
8
10
12
Number of Sites

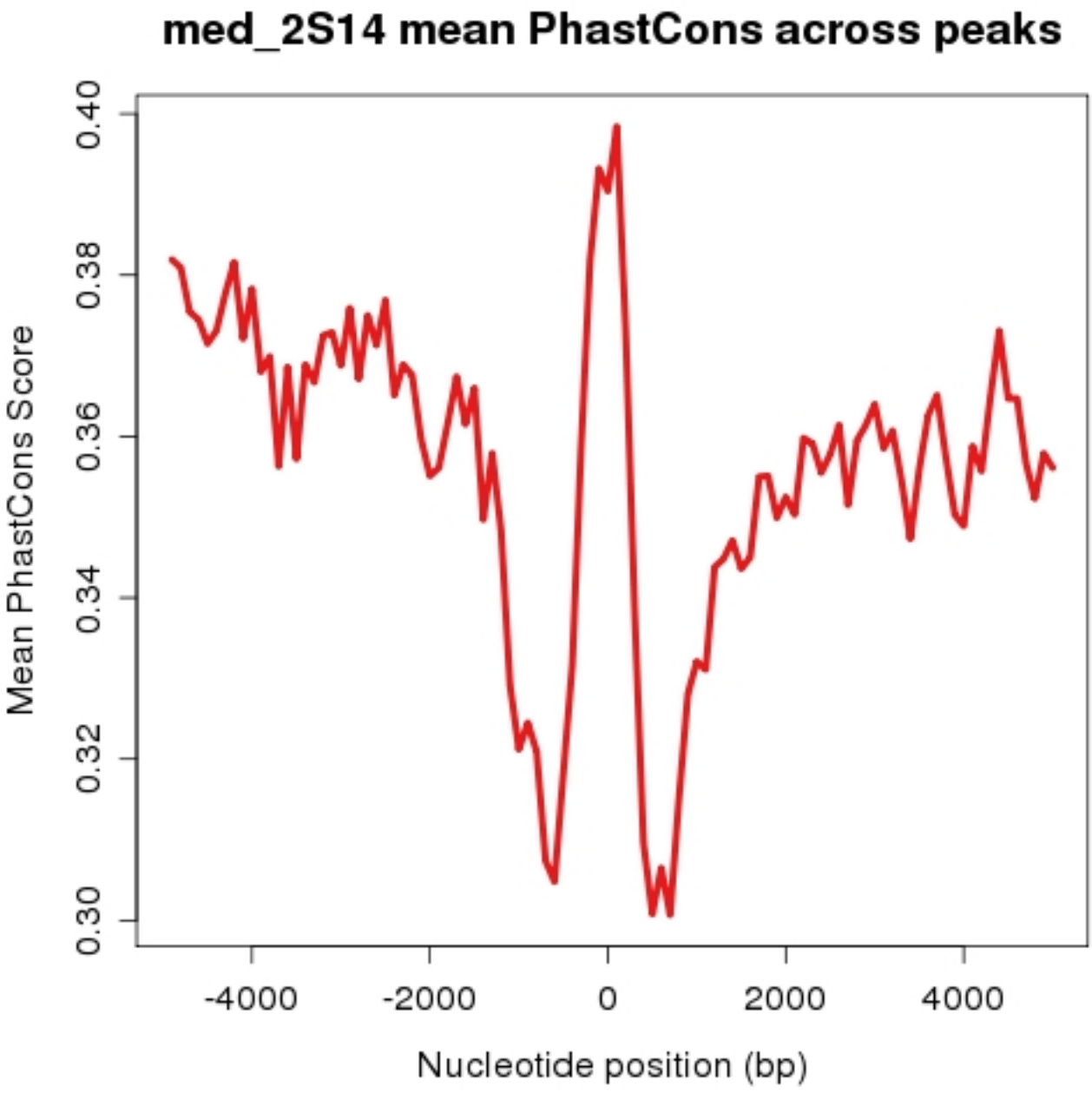

med_2S14 PWM enrichment across peaks
Enrichment
1.35
1.40
1.45
1.50
1.55
-4000
-2000
0
2000
4000
Nucleotide position (200bp window)


med_2S14 PWM enrichment down ranks
1%FDR
Enrichment
1.30
1.35
1.40
1.45
1.50
1.55
0
2000
4000
6000
8000
10000
ChIP/chip rank


med_2S14 genomic location
1%FDR
Exons
Introns
Intergenic
Percentage of Peaks
0
10
20
30
40
50
0
2000
4000
6000
8000
10000
ChIP/chip rank (200 peak window)


med_2S14 GO term enrichment (-logP)
1%FDR
nucleus
JNK_cascade
RNA_polymerase_II_transcription_factor_activity
salivary_gland_determination
protein_domain_specific_binding
Enrichment -log(p)
0
2
4
6
8
10
12
0
2000
4000
6000
8000
10000
ChIP/chip rank


med
bits
2
1
0
5′
1
2
3
4
3′


med_2S14 mean PhastCons across peaks
Mean PhastCons Score
0.30
0.32
0.34
0.36
0.38
0.40
-4000
-2000
0
2000
4000
Nucleotide position (bp)

insufficient in vitro binding data