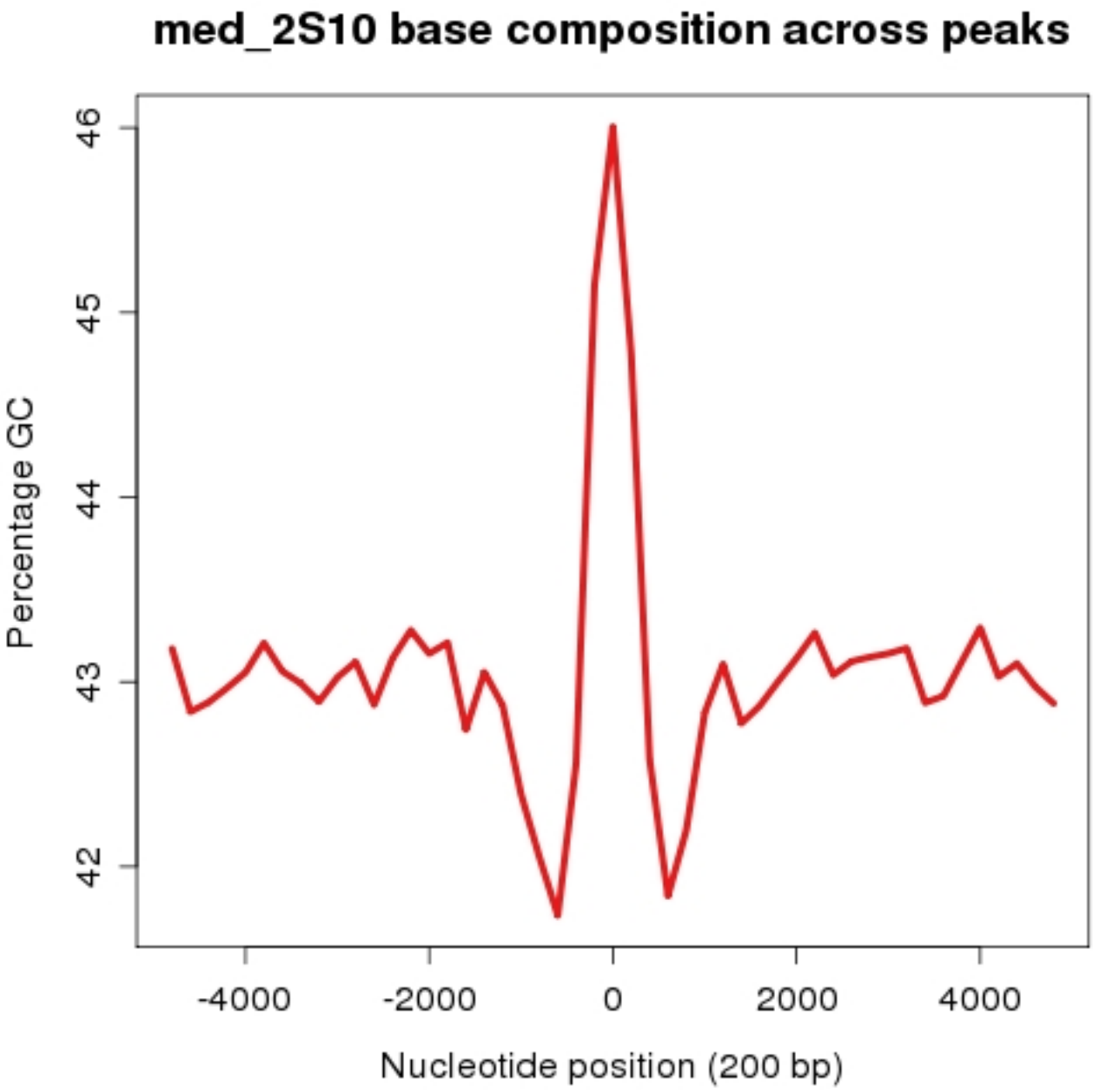
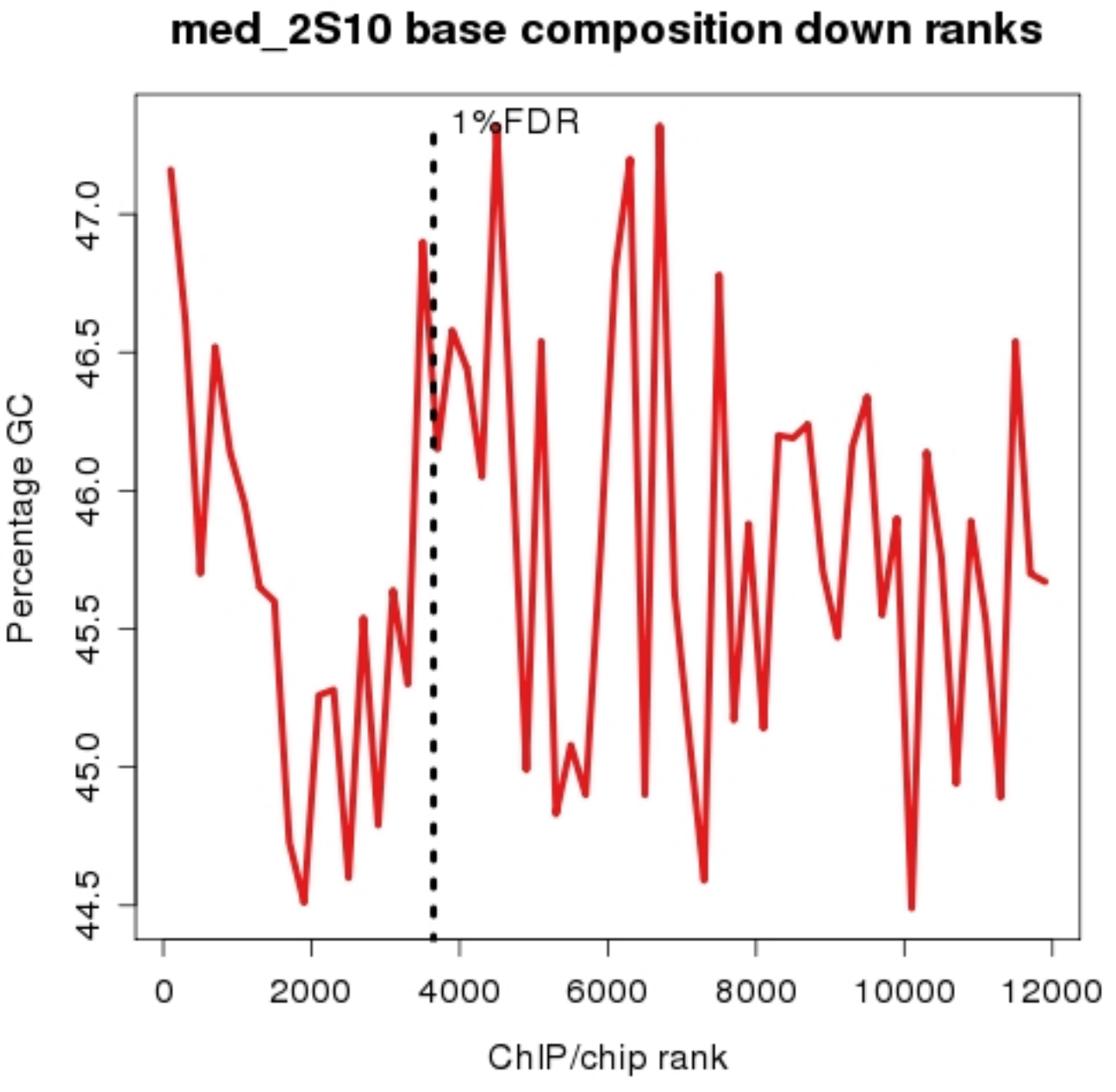
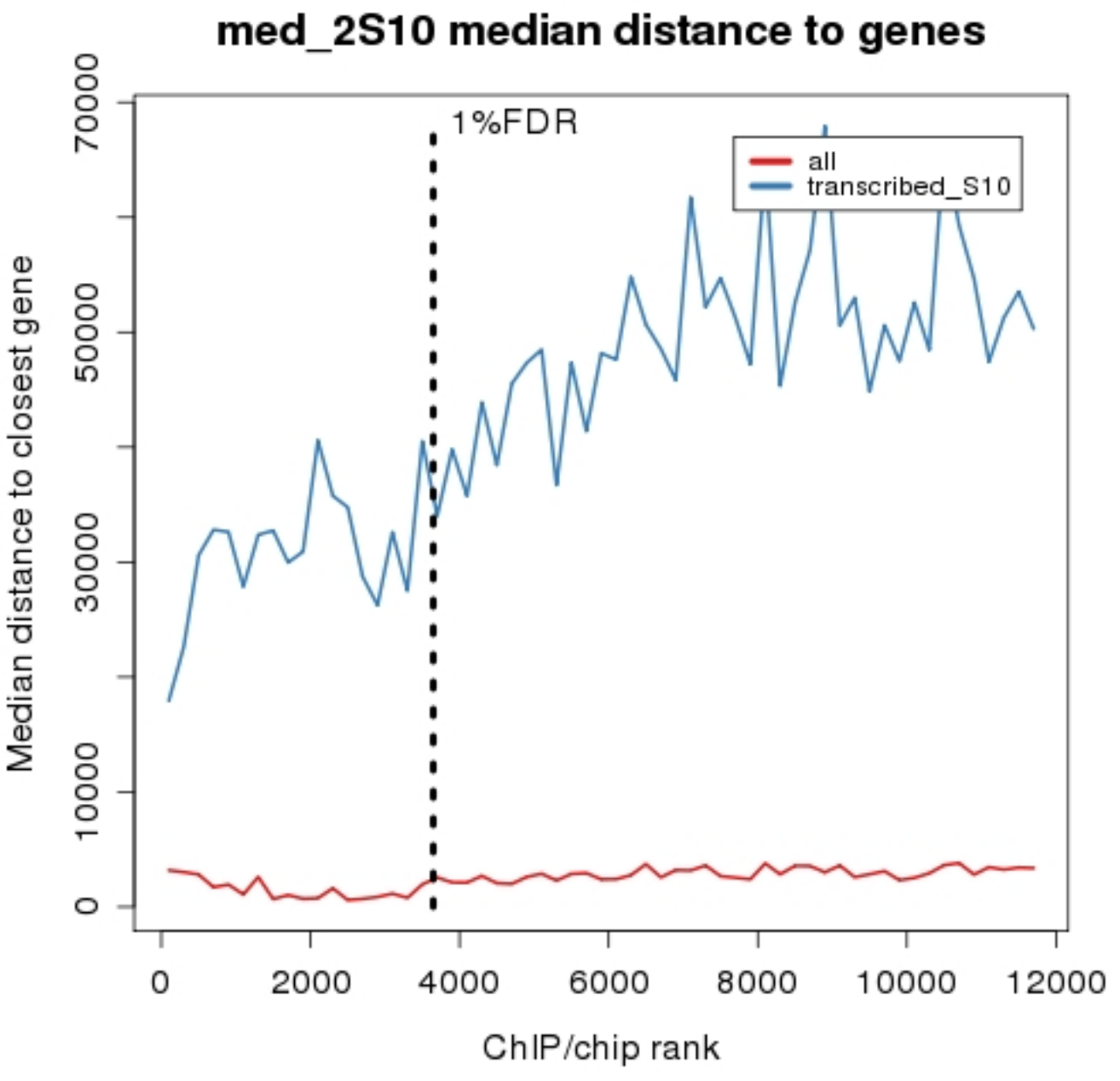
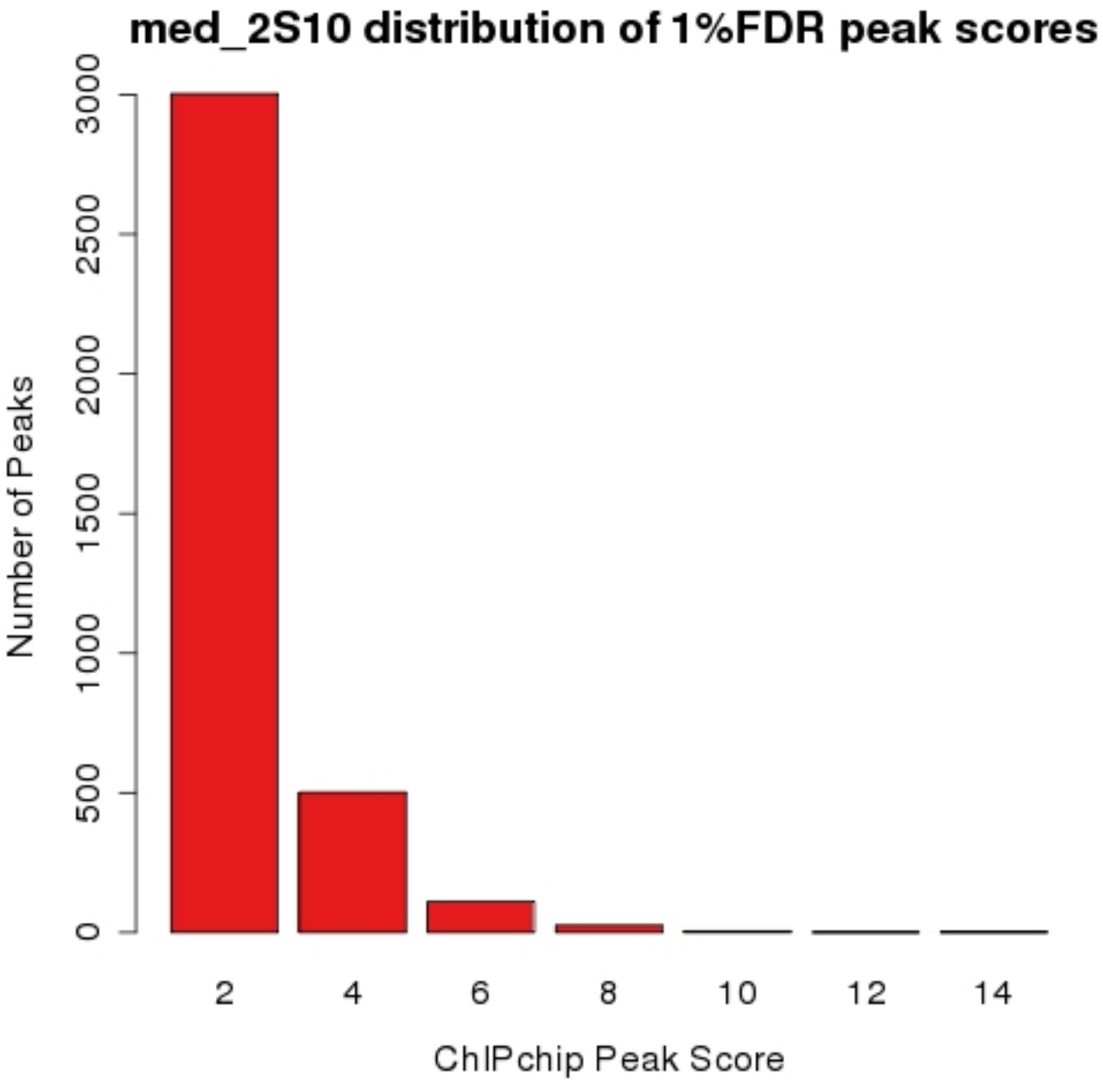
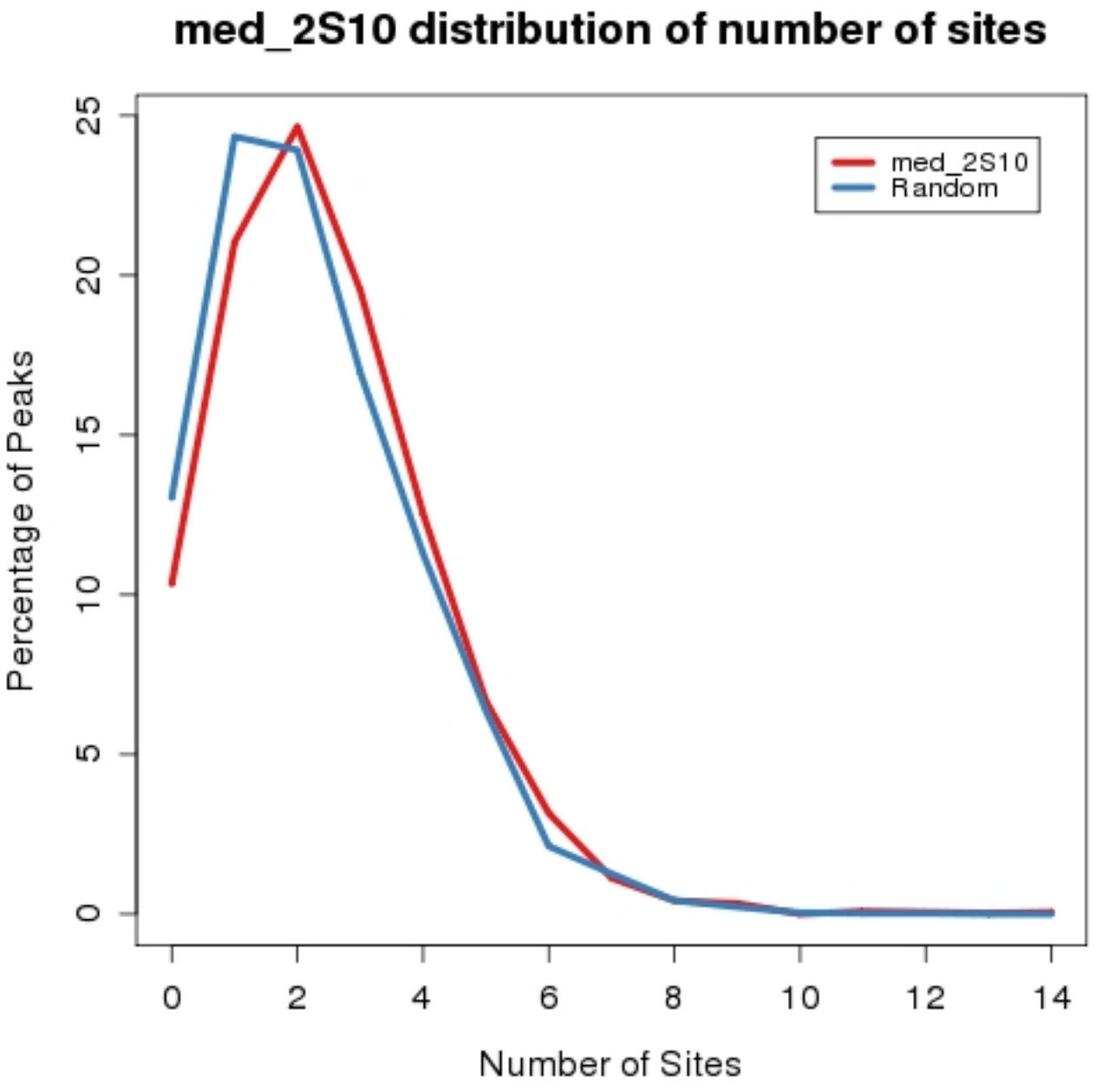
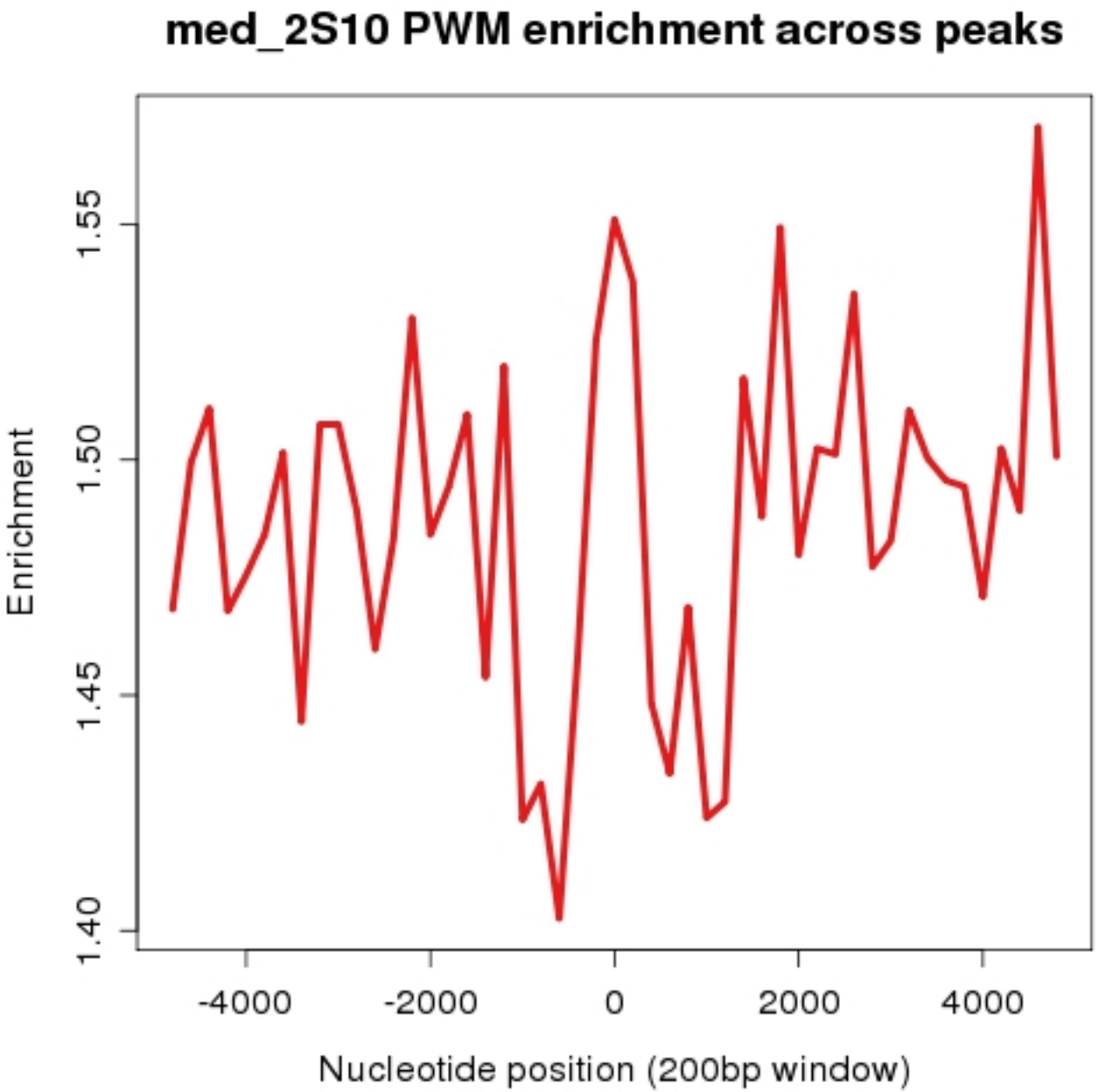

med_2S10 base composition across peaks
Percentage GC
42
43
44
45
46
-4000
-2000
0
2000
4000
Nucleotide position (200 bp)

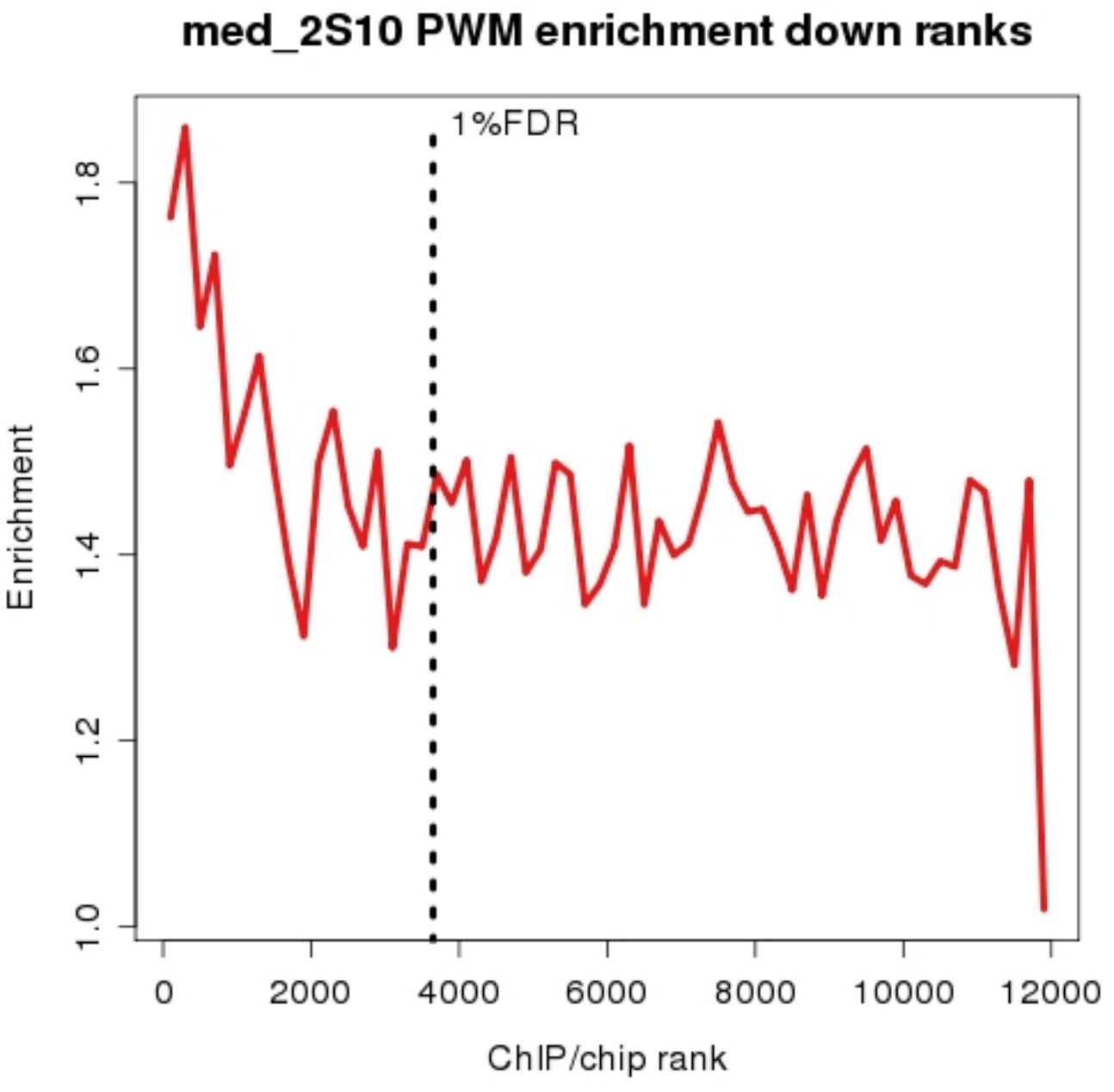

med_2S10 base composition down ranks
1%FDR
Percentage GC
44.5
45.0
45.5
46.0
46.5
47.0
0
2000
4000
6000
8000
10000
12000
ChIP/chip rank

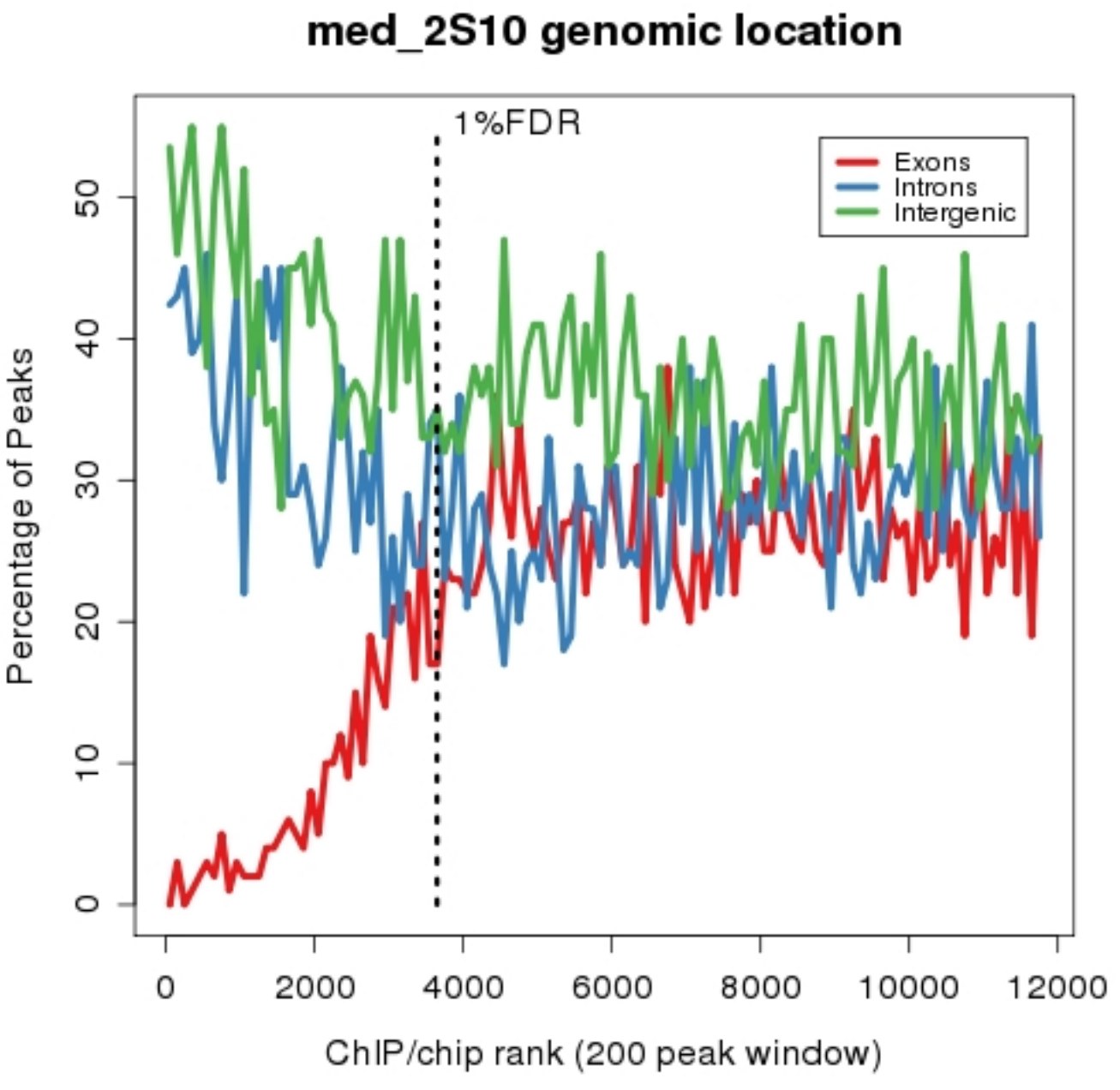

med_2S10 median distance to genes
1%FDR
all
transcribed_S10
Median distance to closest gene
0
10000
30000
50000
70000
0
2000
4000
6000
8000
10000
12000
ChIP/chip rank

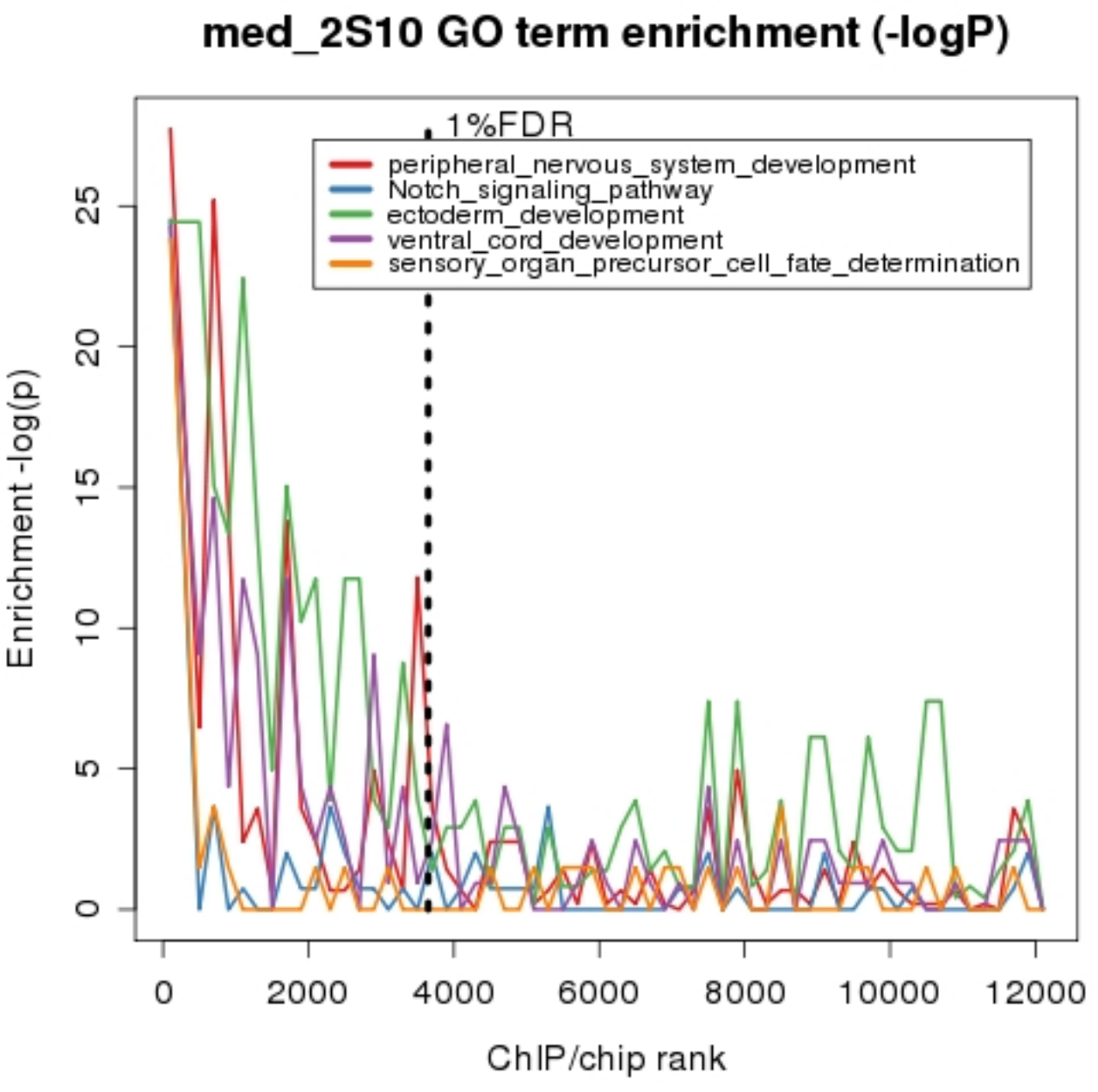

med_2S10 distribution of 1%FDR peak scores
Number of Peaks
0
500
1000
1500
2000
2500
3000
2
4
6
8
10
12
14
ChIPchip Peak Score

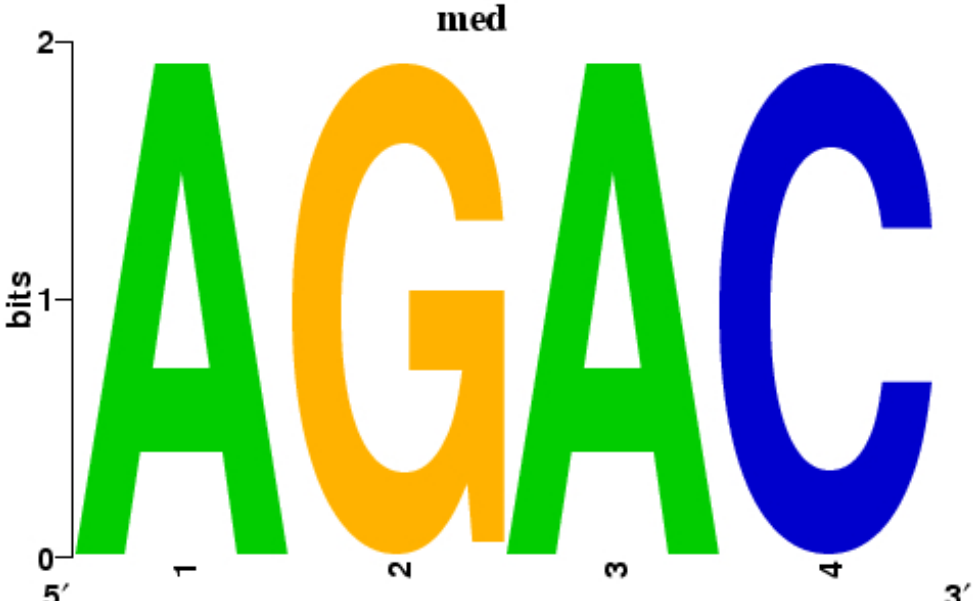

med_2S10 distribution of number of sites
med_2S10
Random
Percentage of Peaks
0
5
10
15
20
25
0
2
4
6
8
10
12
14
Number of Sites

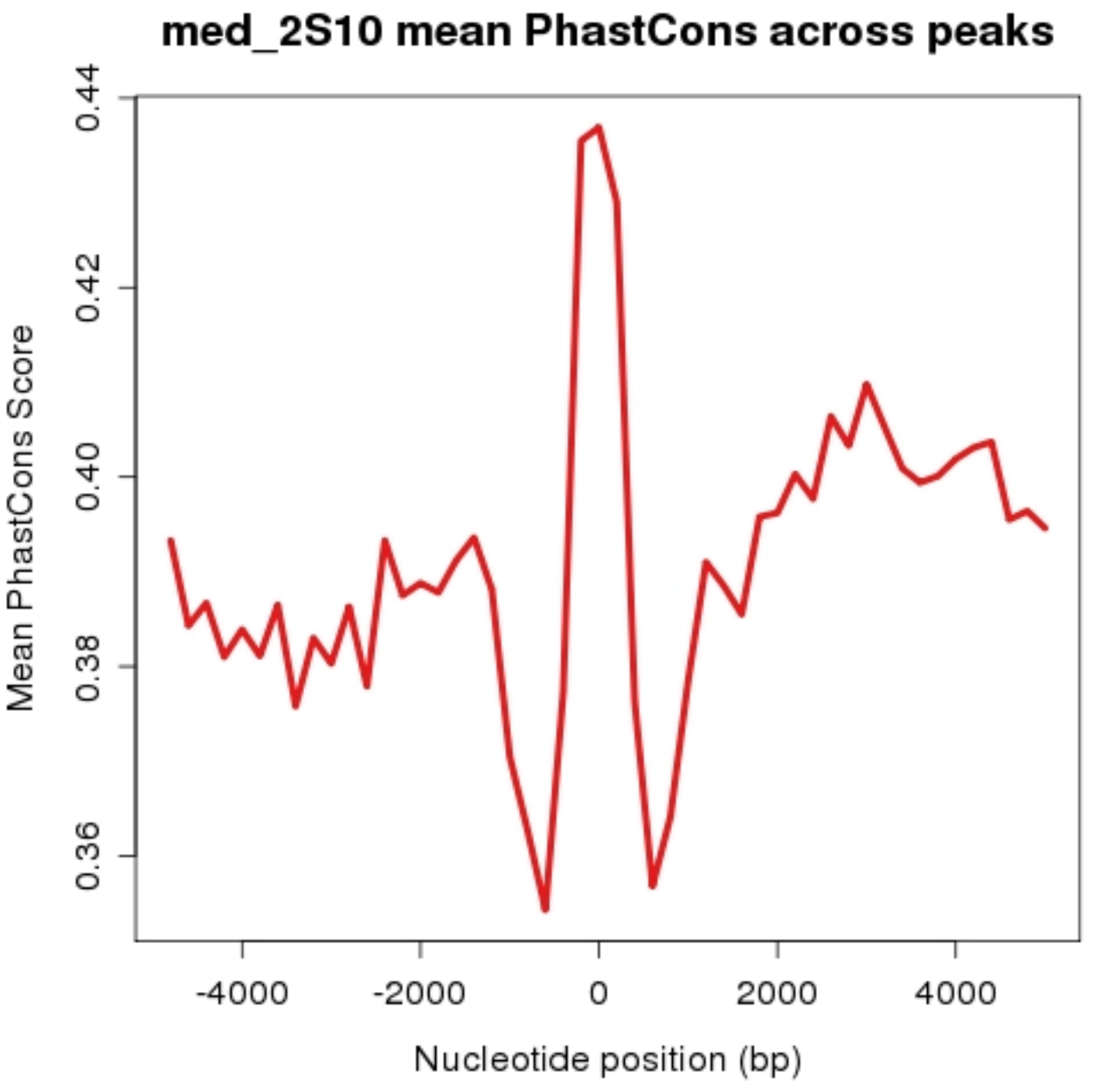

med_2S10 PWM enrichment across peaks
Enrichment
1.40
1.45
1.50
1.55
-4000
-2000
0
2000
4000
Nucleotide position (200bp window)


med_2S10 PWM enrichment down ranks
1%FDR
Enrichment
1.0
1.2
1.4
1.6
1.8
0
2000
4000
6000
8000
10000
12000
ChIP/chip rank


med_2S10 genomic location
1%FDR
Exons
Introns
Intergenic
Percentage of Peaks
0
10
20
30
40
50
0
2000
4000
6000
8000
10000
12000
ChIP/chip rank (200 peak window)


med_2S10 GO term enrichment (-logP)
1%FDR
peripheral_nervous_system_development
Notch_signaling_pathway
ectoderm_development
ventral_cord_development
sensory_organ_precursor_cell_fate_determination
Enrichment -log(p)
0
5
10
15
20
25
0
2000
4000
6000
8000
10000
12000
ChIP/chip rank


med
bits
2
1
0
5′
1
2
3
4
3′


med_2S10 mean PhastCons across peaks
Mean PhastCons Score
0.36
0.38
0.40
0.42
0.44
-4000
-2000
0
2000
4000
Nucleotide position (bp)

insufficient in vitro binding data