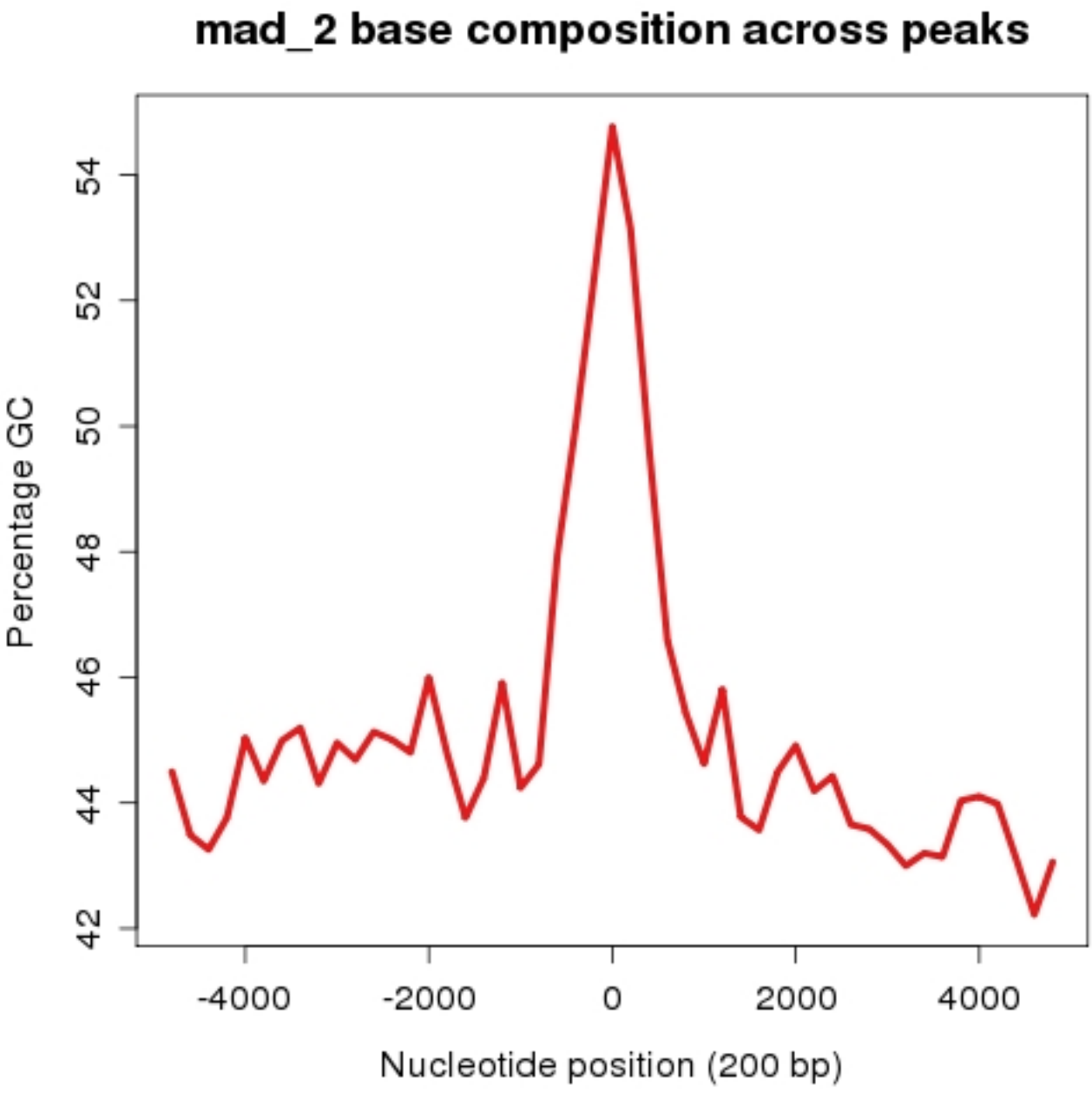
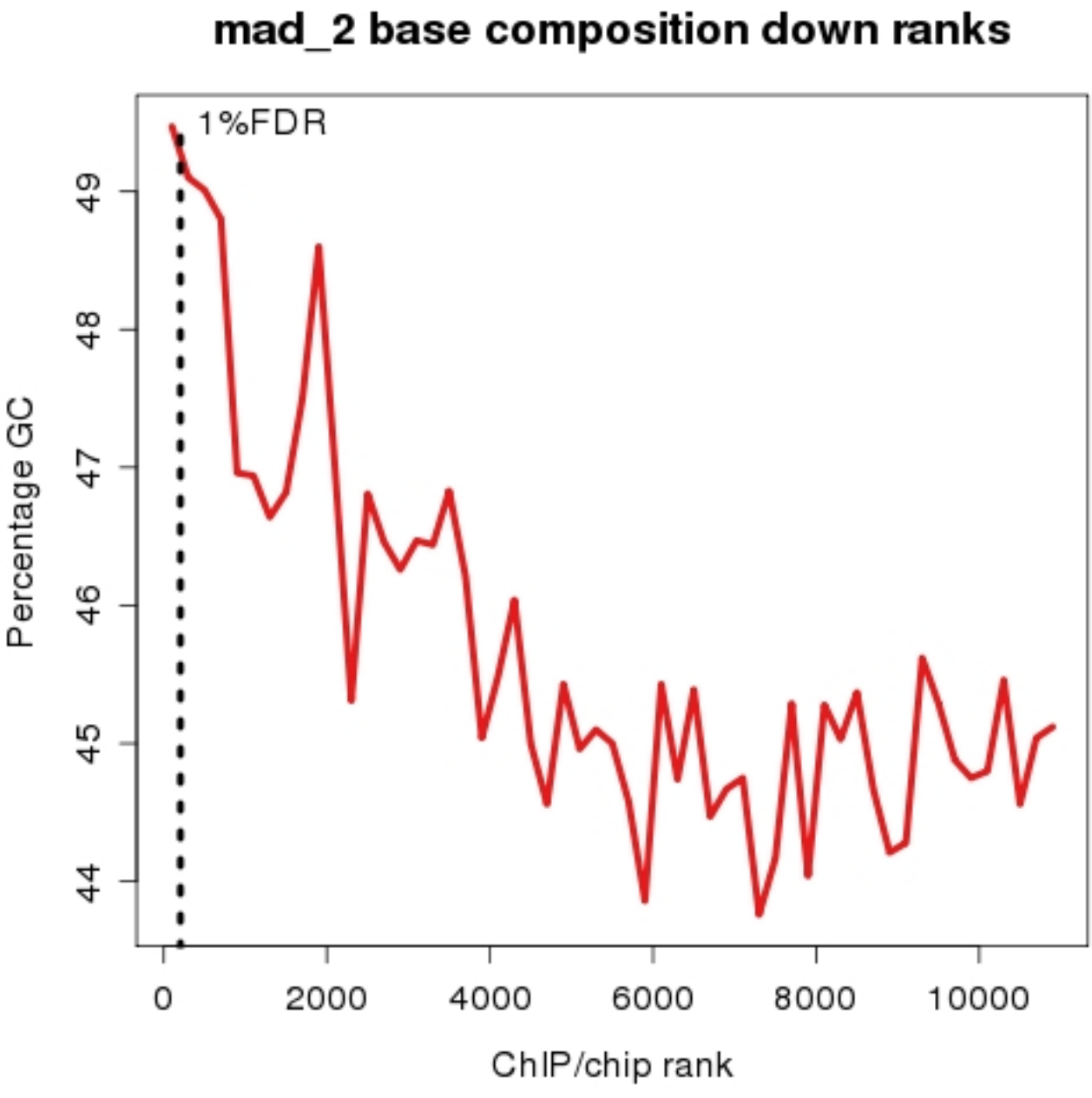
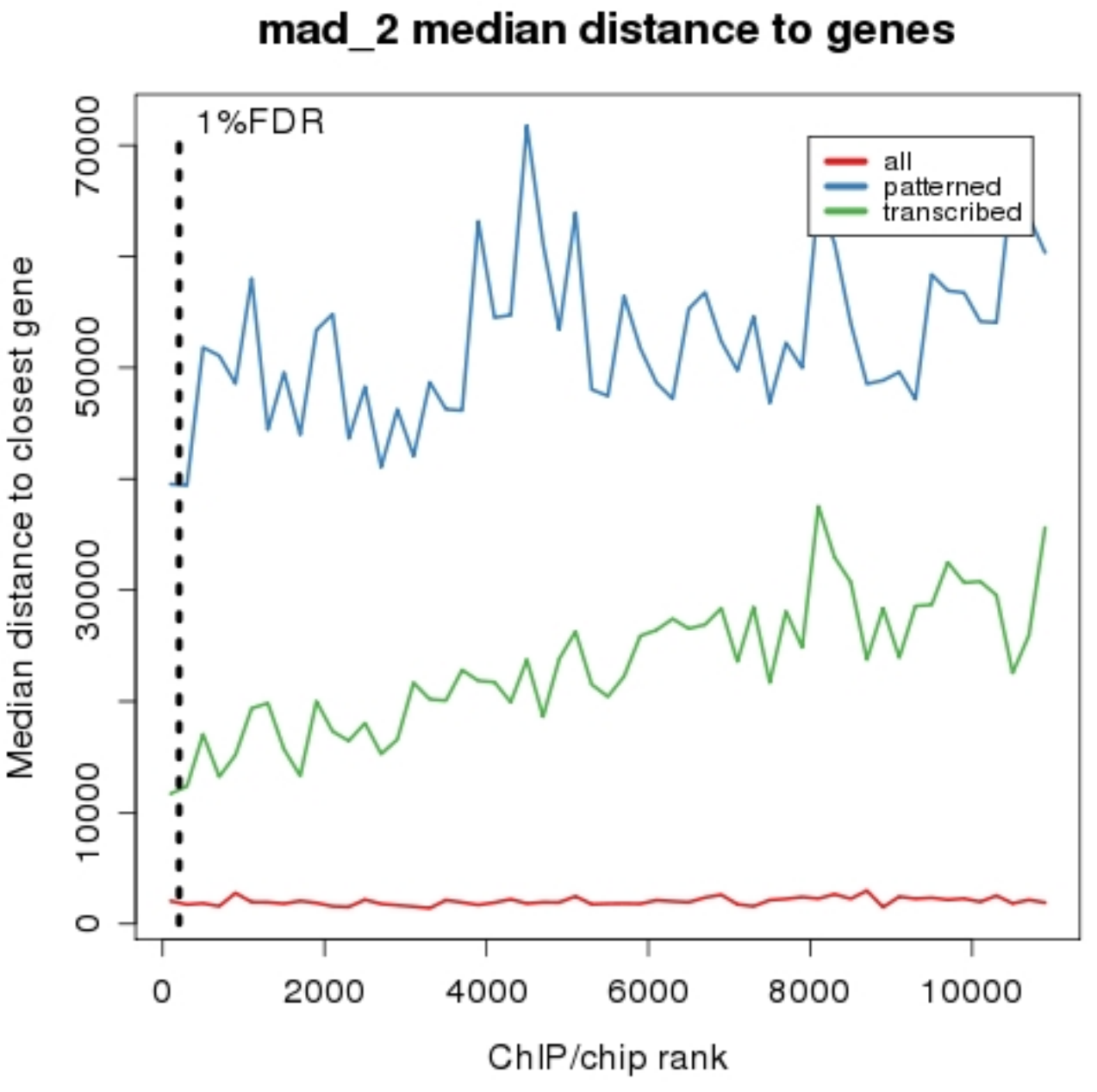
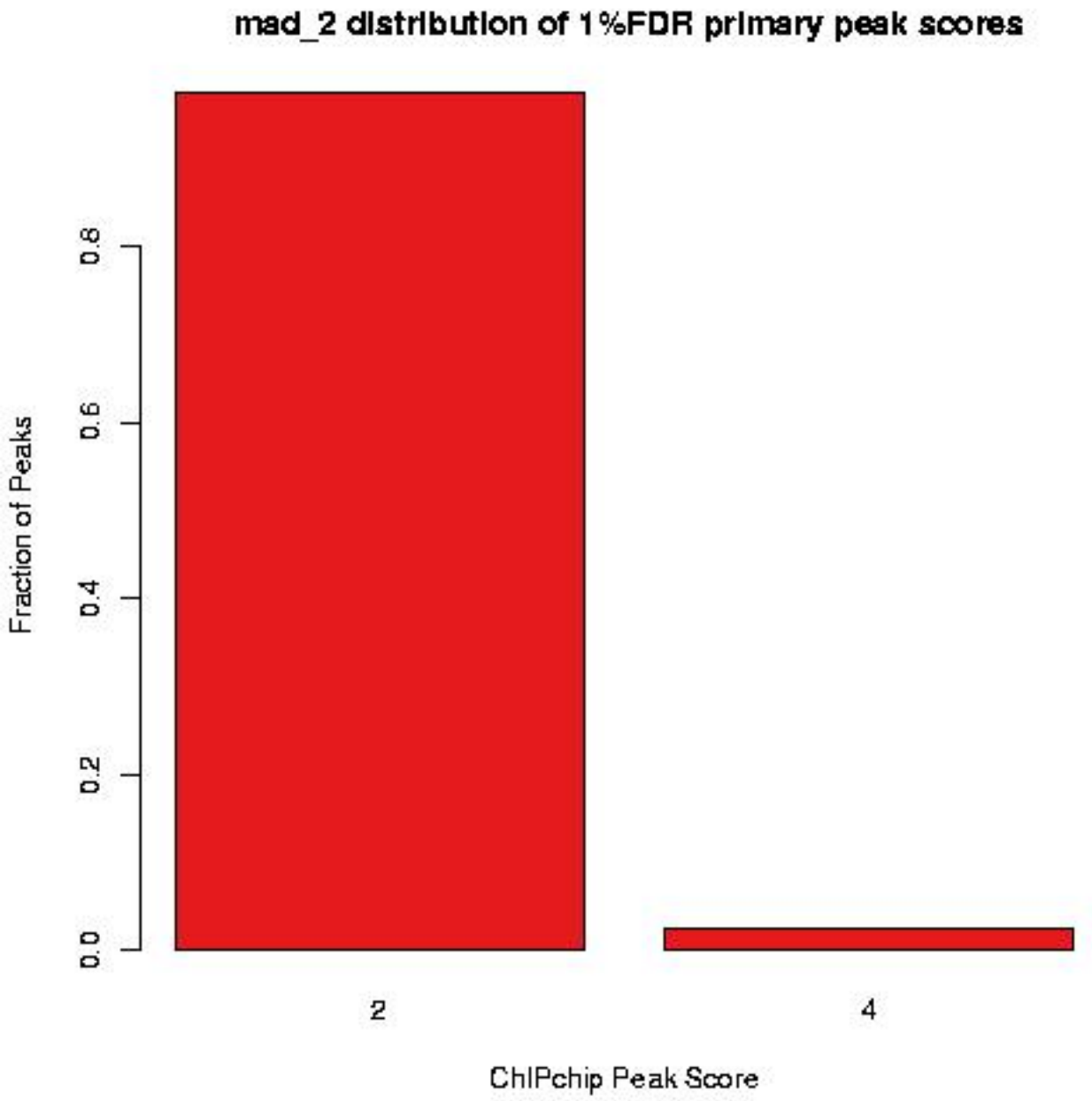
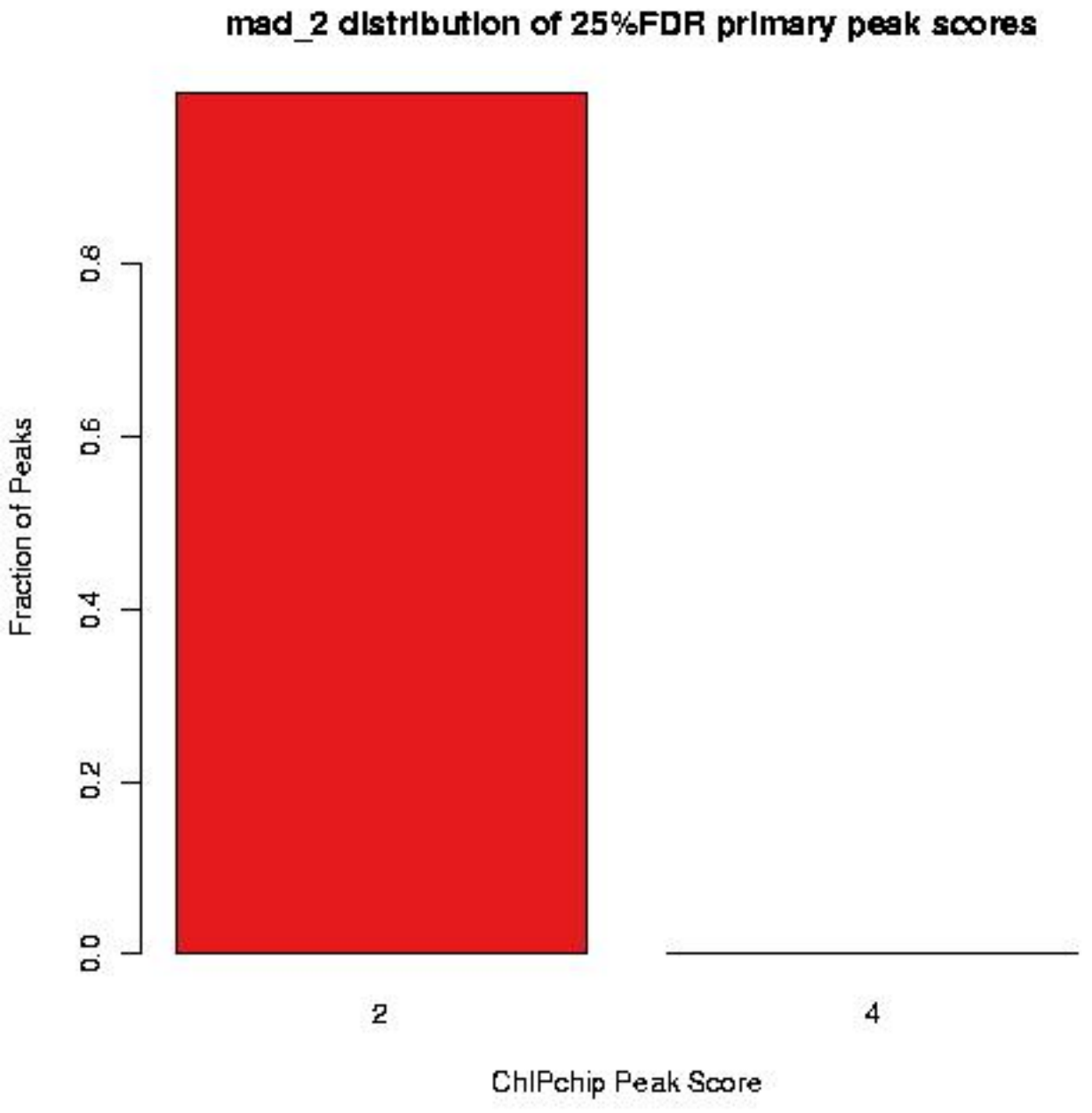
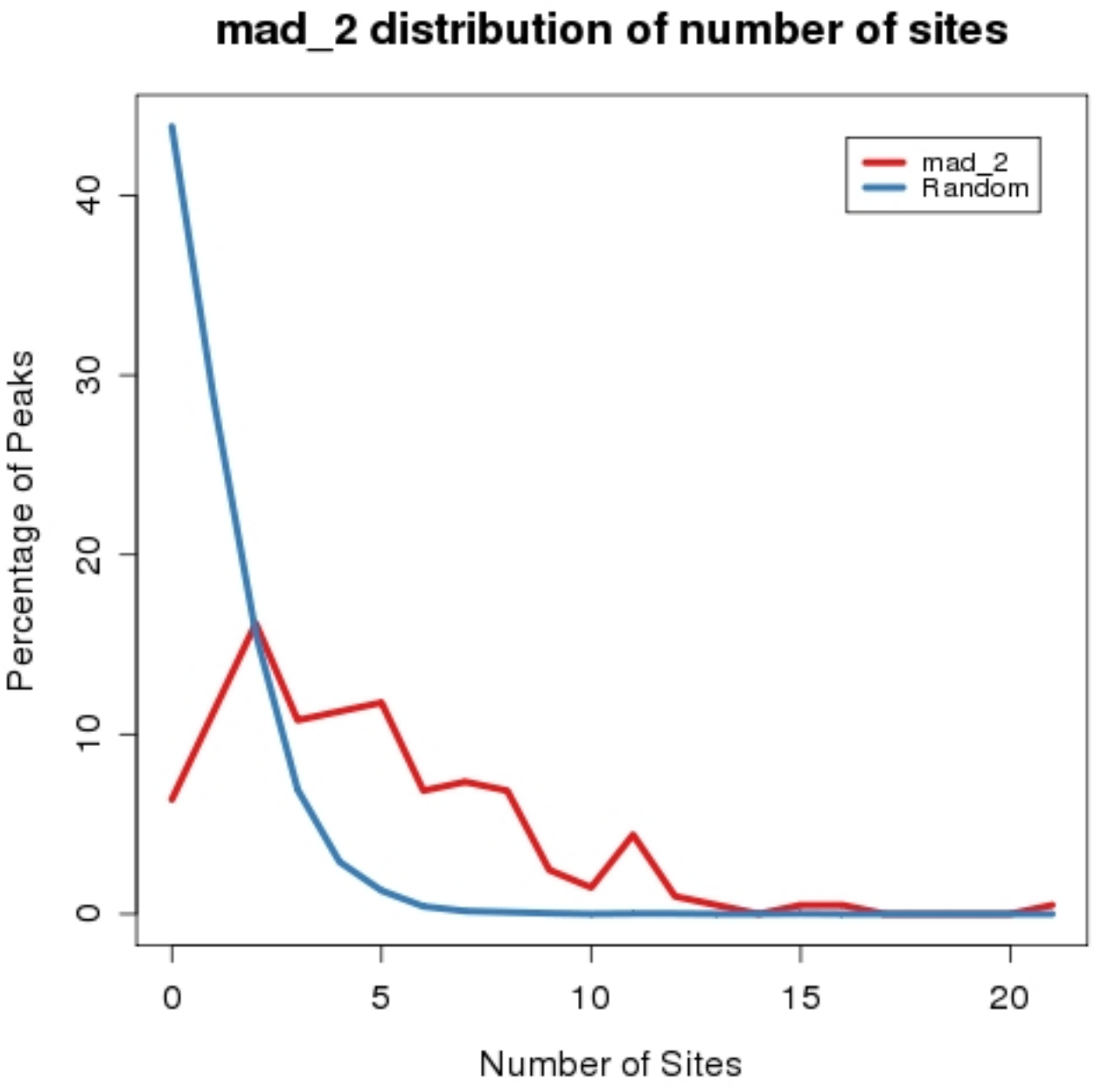

mad_2 base composition across peaks
Percentage GC
42
44
46
48
50
52
54
-4000
-2000
0
2000
4000
Nucleotide position (200 bp)

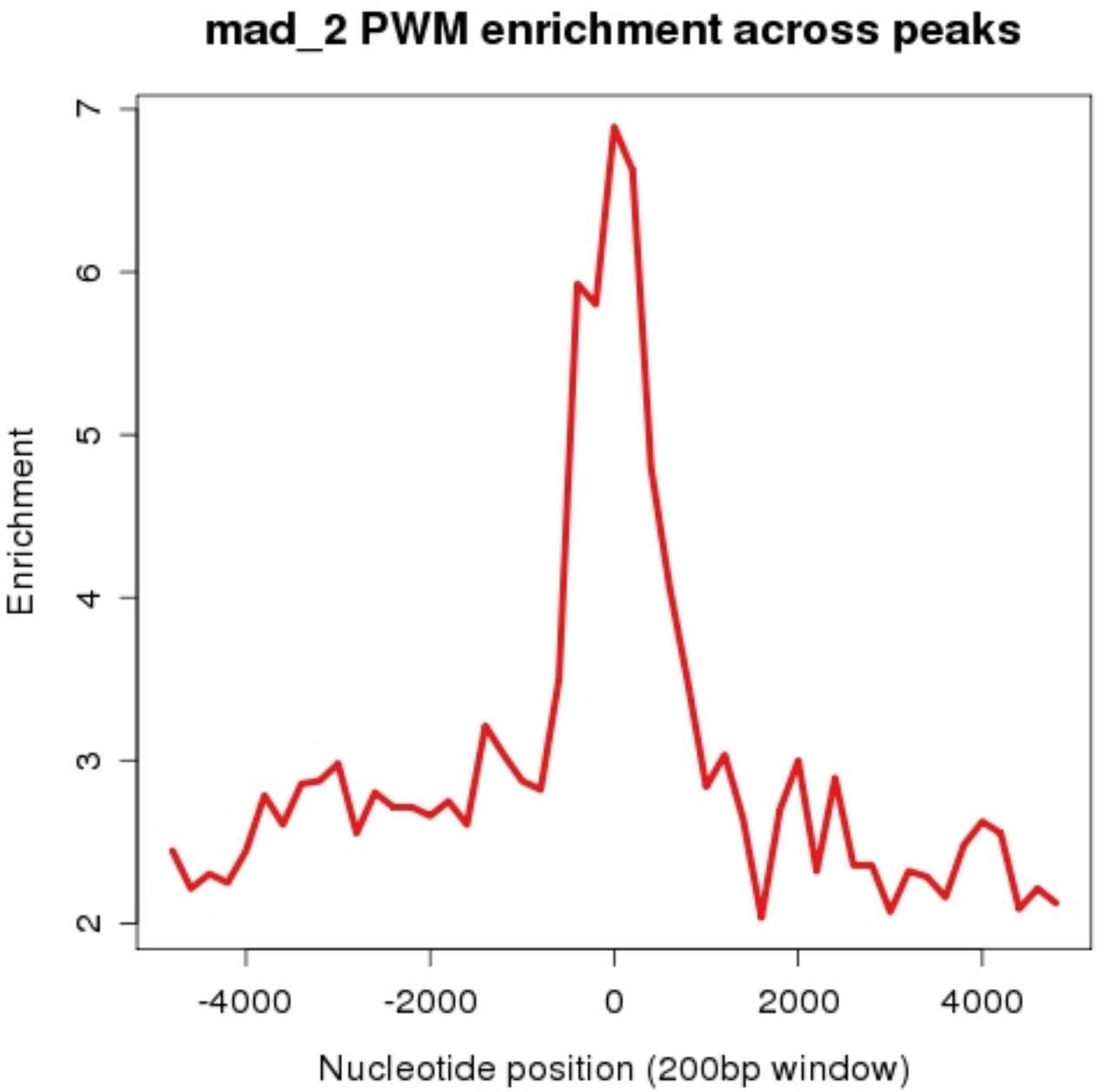

mad_2 base composition down ranks
1%FDR
Percentage GC
44
45
46
47
48
49
0
2000
4000
6000
8000
10000
ChIP/chip rank

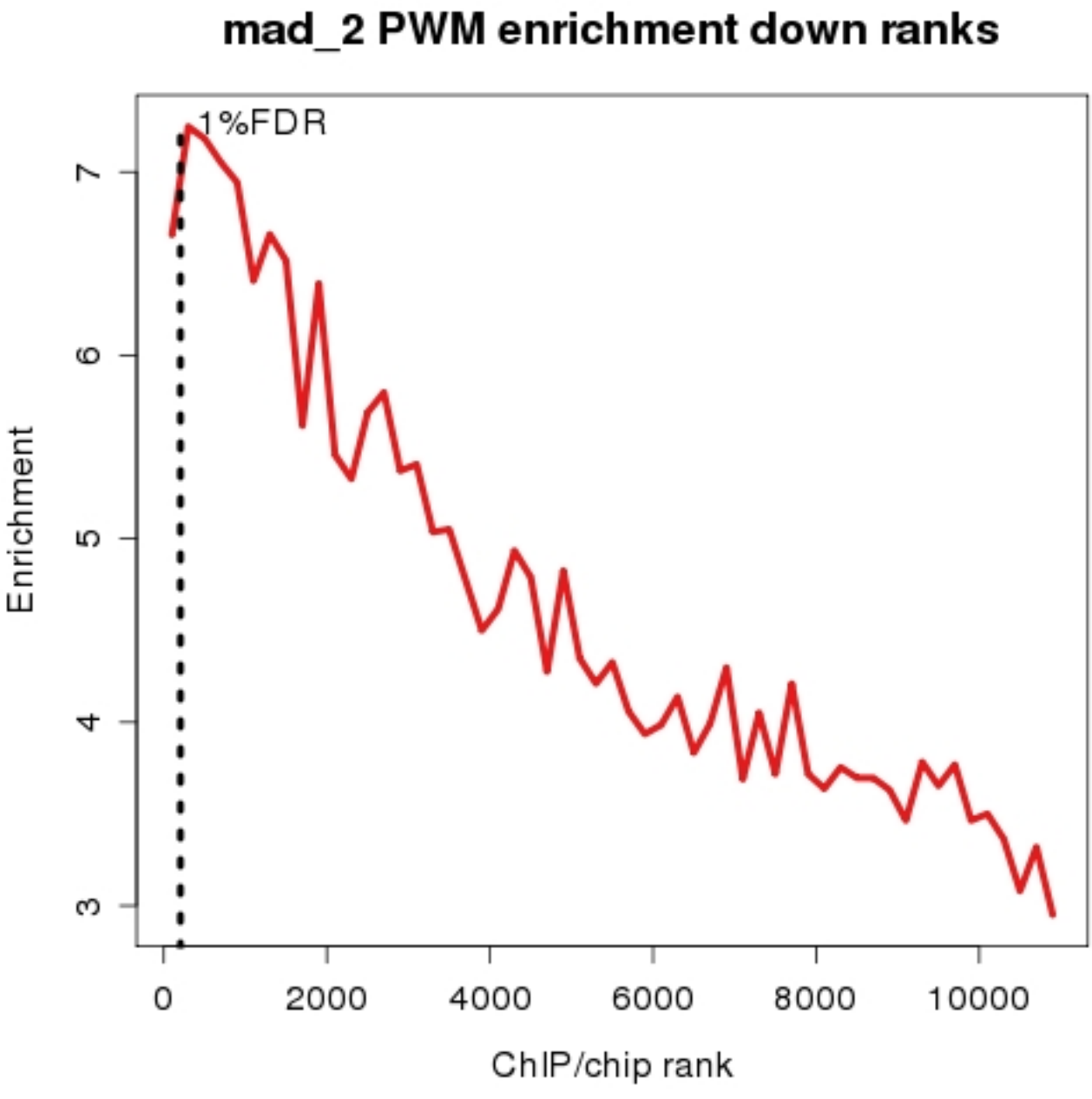

mad_2 median distance to genes
1%FDR
all
patterned
transcribed
Median distance to closest gene
0
10000
30000
50000
70000
0
2000
4000
6000
8000
10000
ChIP/chip rank

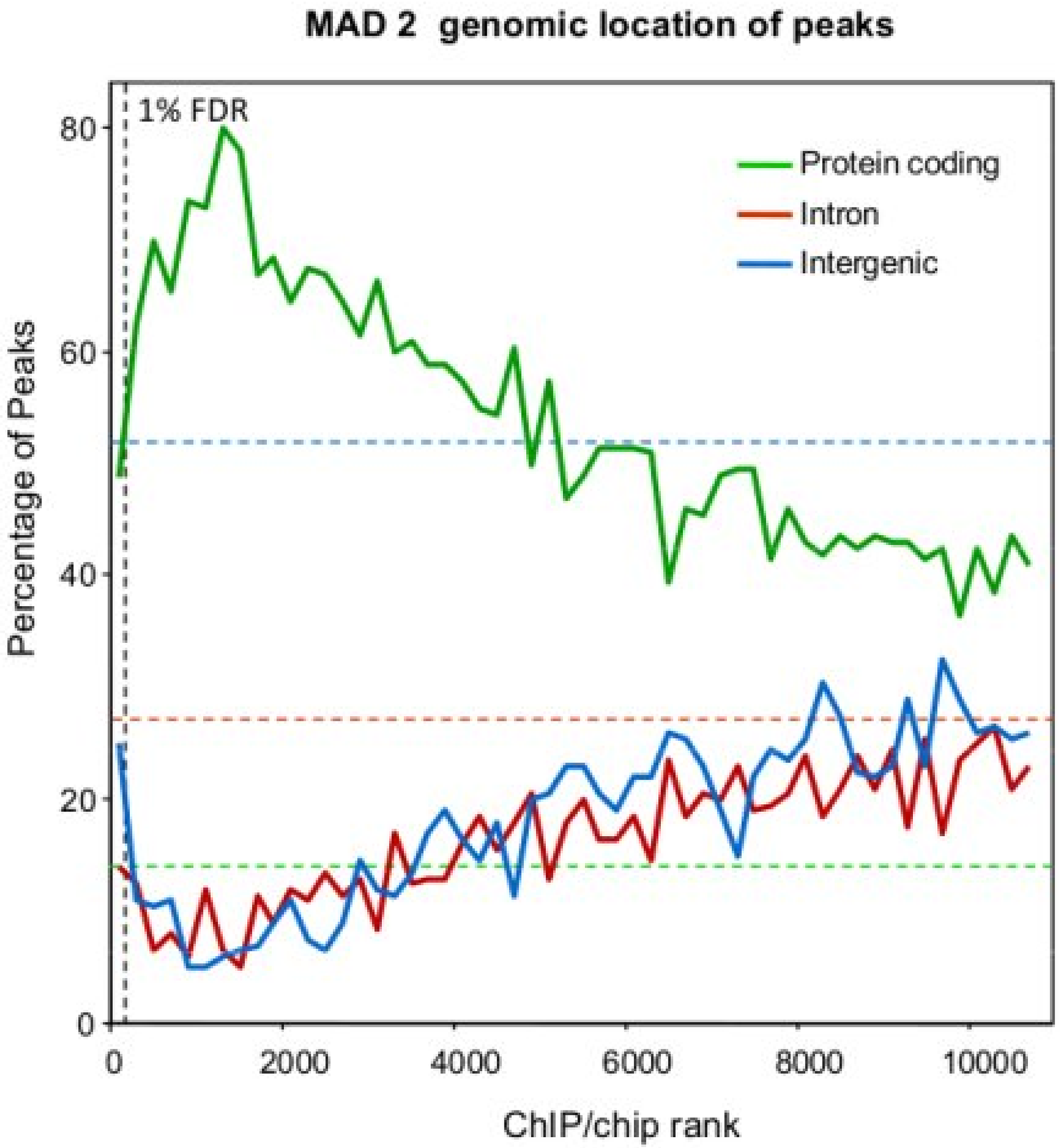

mad_2 distribution of 1%FDR primary peak scores
Fraction of Peaks
0.0
0.2
0.4
0.6
0.8
2
4
ChIPchip Peak Score

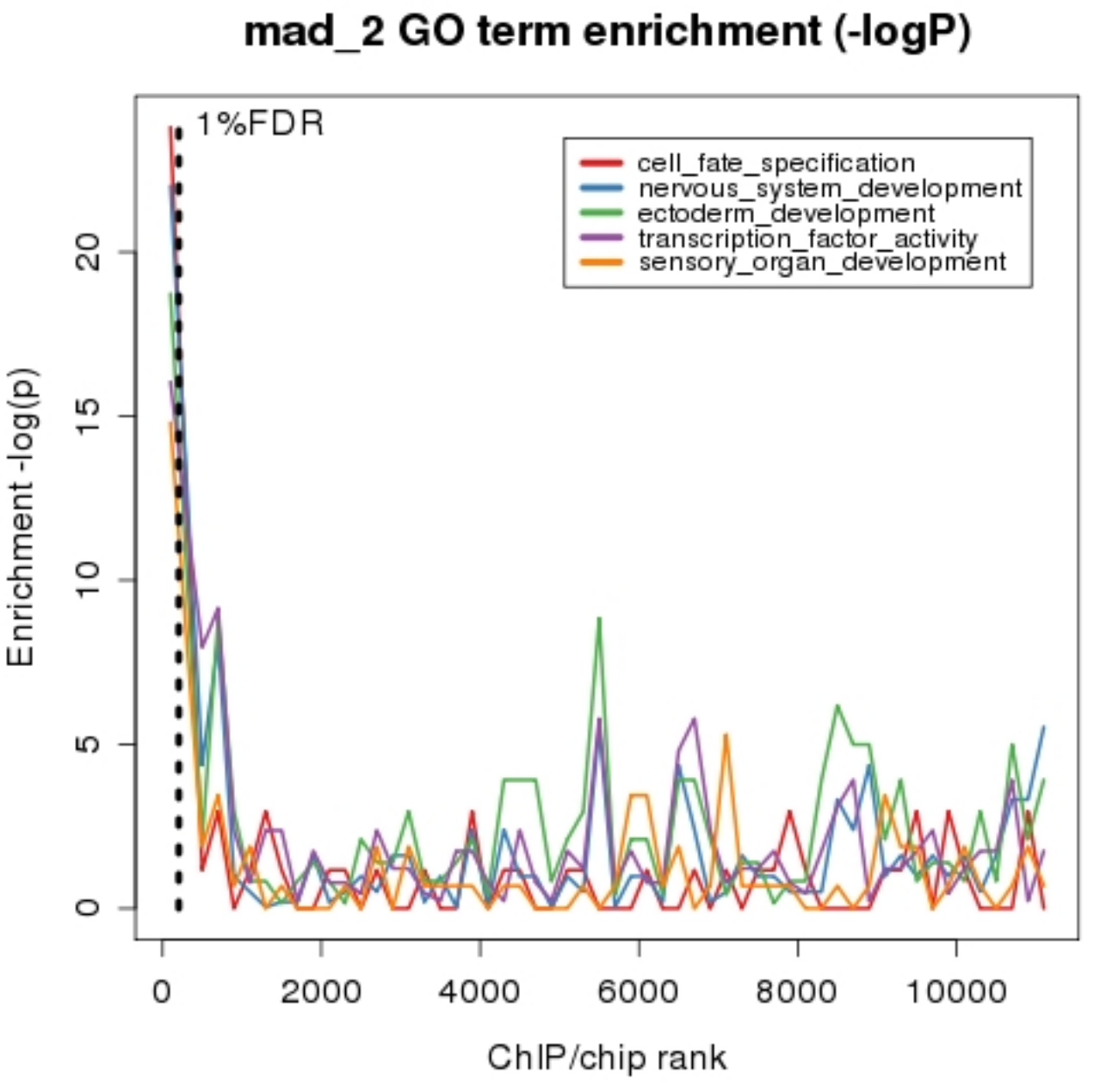

mad_2 distribution of 25%FDR primary peak scores
Fraction of Peaks
0.0
0.2
0.4
0.6
0.8
2
4
ChIPchip Peak Score

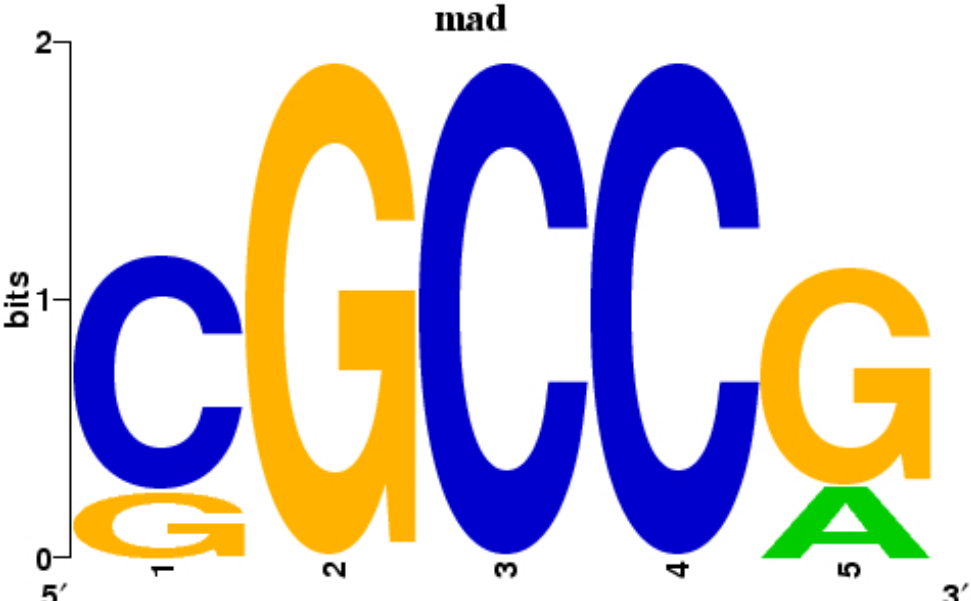

mad_2 distribution of number of sites
mad_2
Random
Percentage of Peaks
0
10
20
30
40
0
5
10
15
20
Number of Sites

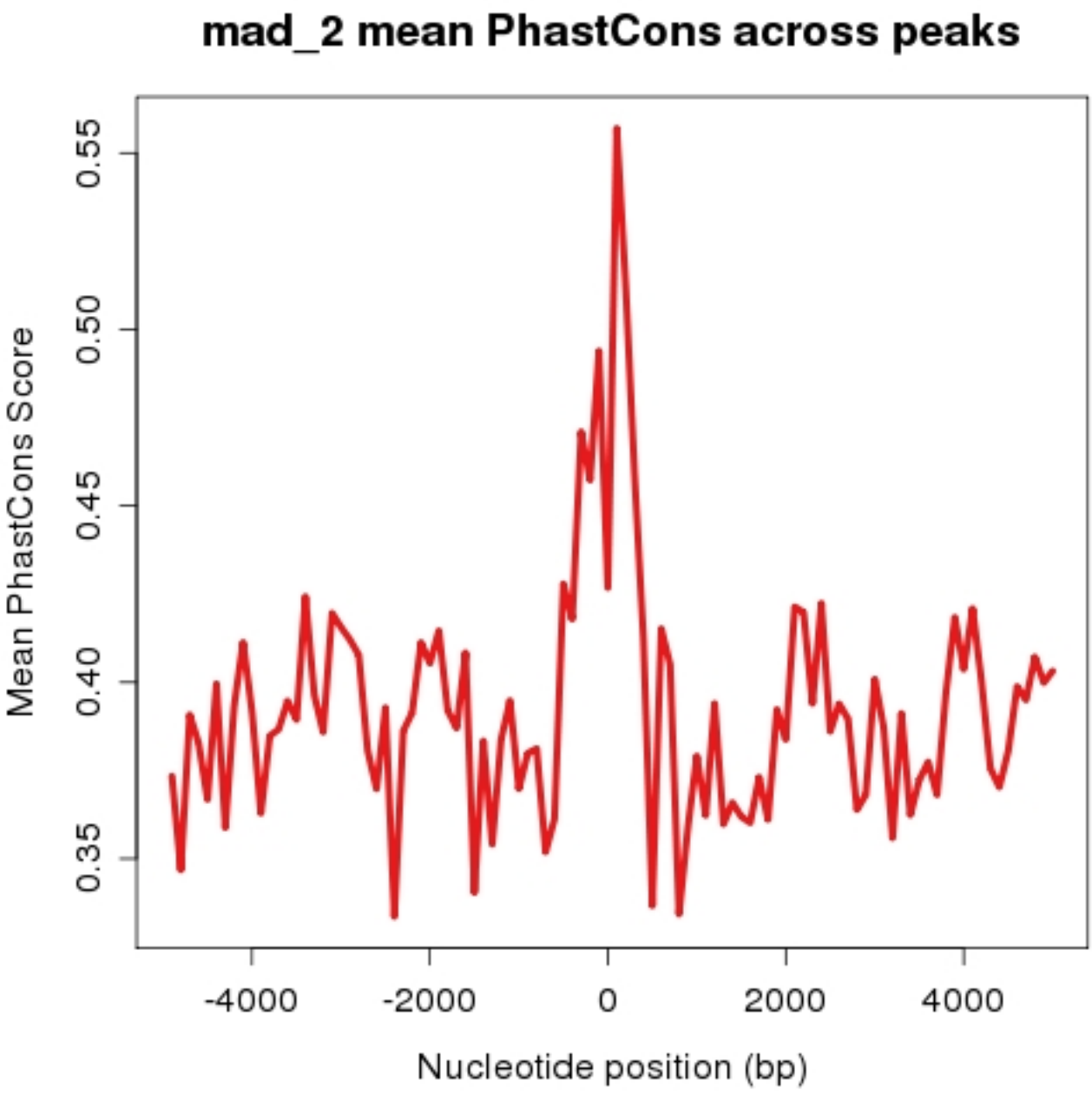

mad_2 PWM enrichment across peaks
Enrichment
2
3
4
5
6
7
-4000
-2000
0
2000
4000
Nucleotide position (200bp window)

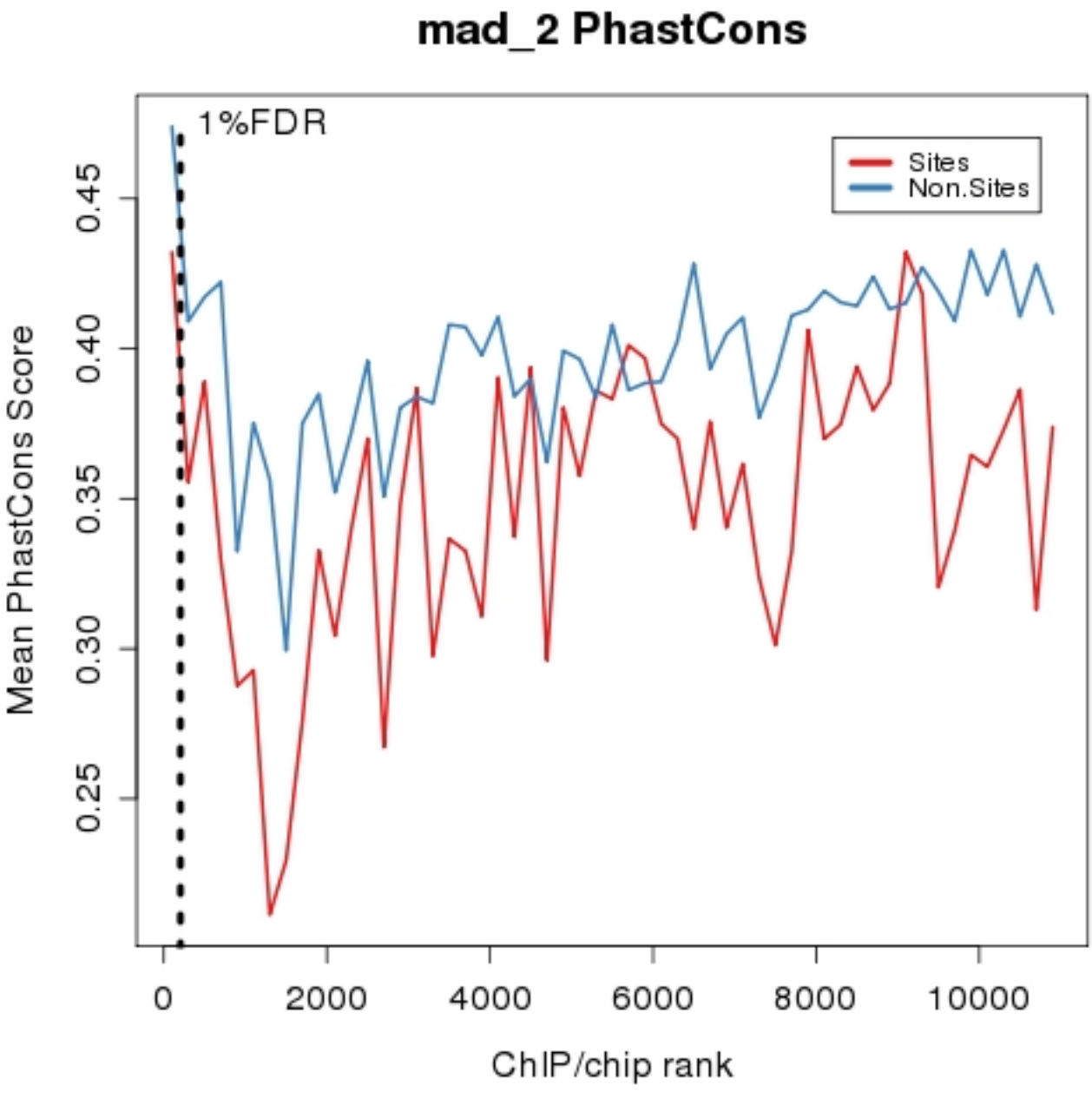

mad_2 PWM enrichment down ranks
1%FDR
Enrichment
3
4
5
6
7
0
2000
4000
6000
8000
10000
ChIP/chip rank

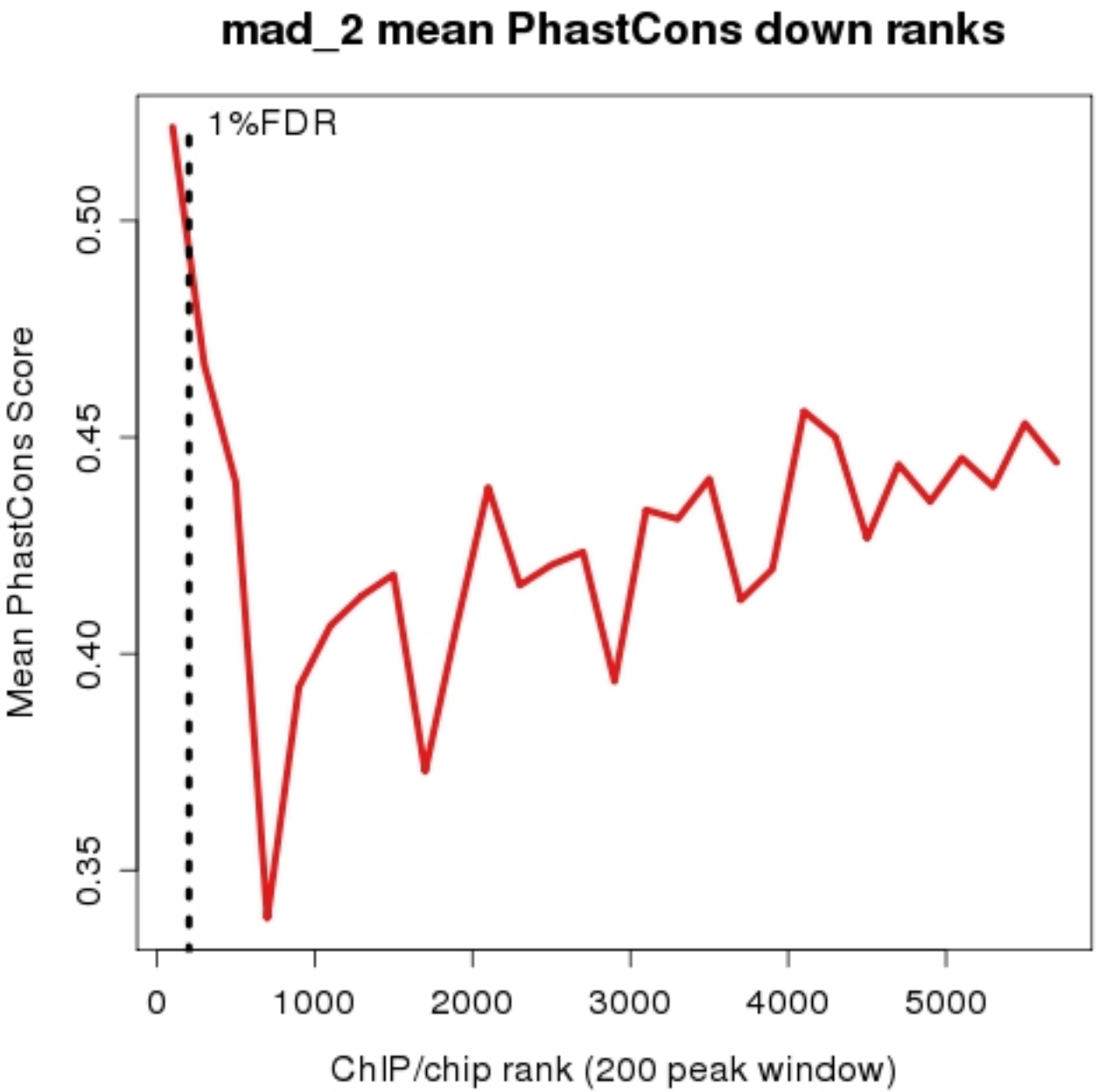

MAD 2 genomic location of peaks
1% FDR
Protein coding
Intron
Intergenic
Percentage of Peaks
0
20
40
60
80
0
2000
4000
6000
8000
10000
ChIP/chip rank


mad_2 GO term enrichment (-logP)
1%FDR
cell_fate_specification
nervous_system_development
ectoderm_development
transcription_factor_activity
sensory_organ_development
Enrichment -log(p)
0
5
10
15
20
0
2000
4000
6000
8000
10000
ChIP/chip rank


mad
bits
2
1
0
5′
1
2
3
4
5
3′


mad_2 mean PhastCons across peaks
Mean PhastCons Score
0.35
0.40
0.45
0.50
0.55
-4000
-2000
0
2000
4000
Nucleotide position (bp)


mad_2 PhastCons
1%FDR
Sites
Non.Sites
Mean PhastCons Score
0.25
0.30
0.35
0.40
0.45
0
2000
4000
6000
8000
10000
ChIP/chip rank


mad_2 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)