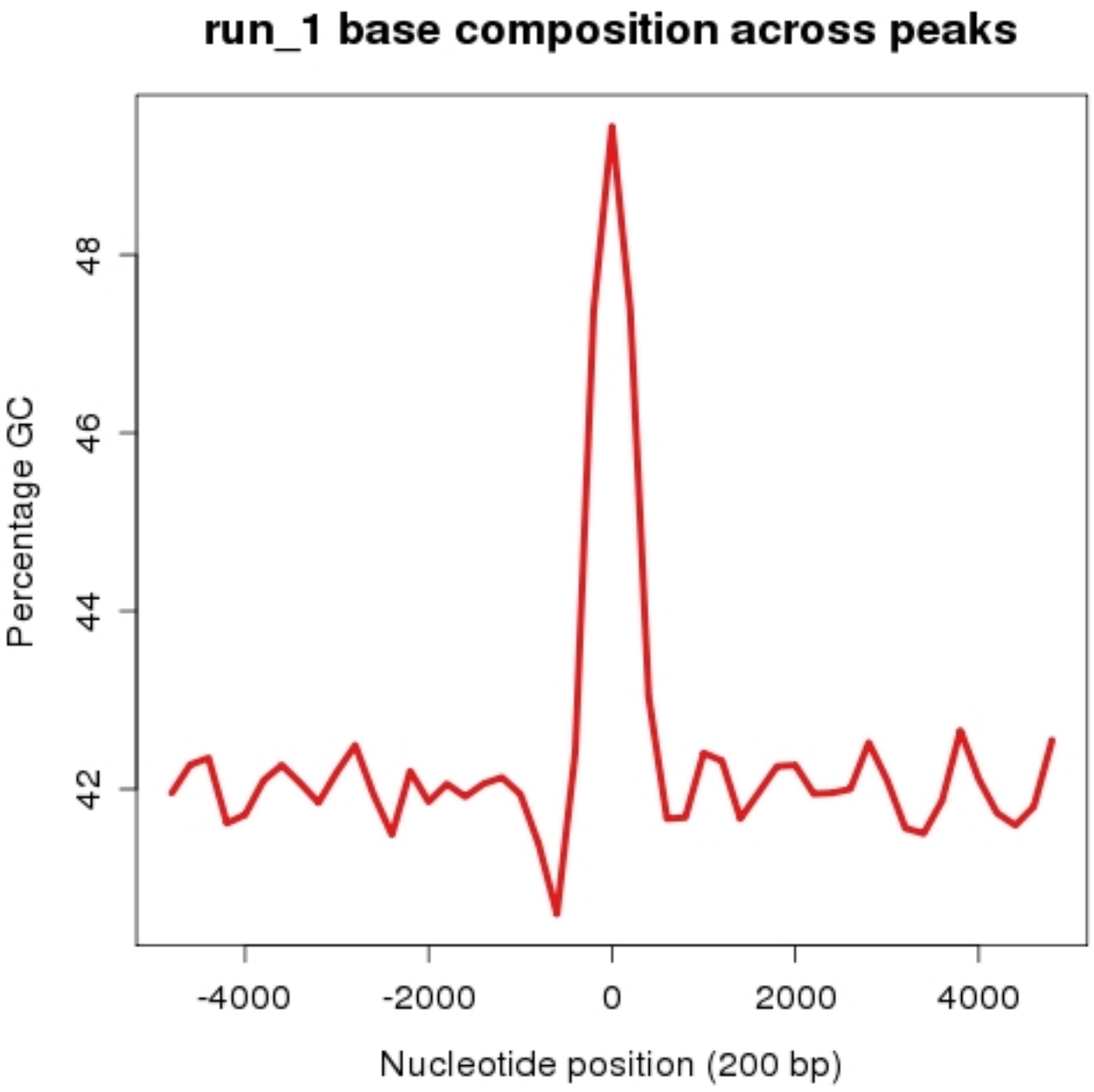
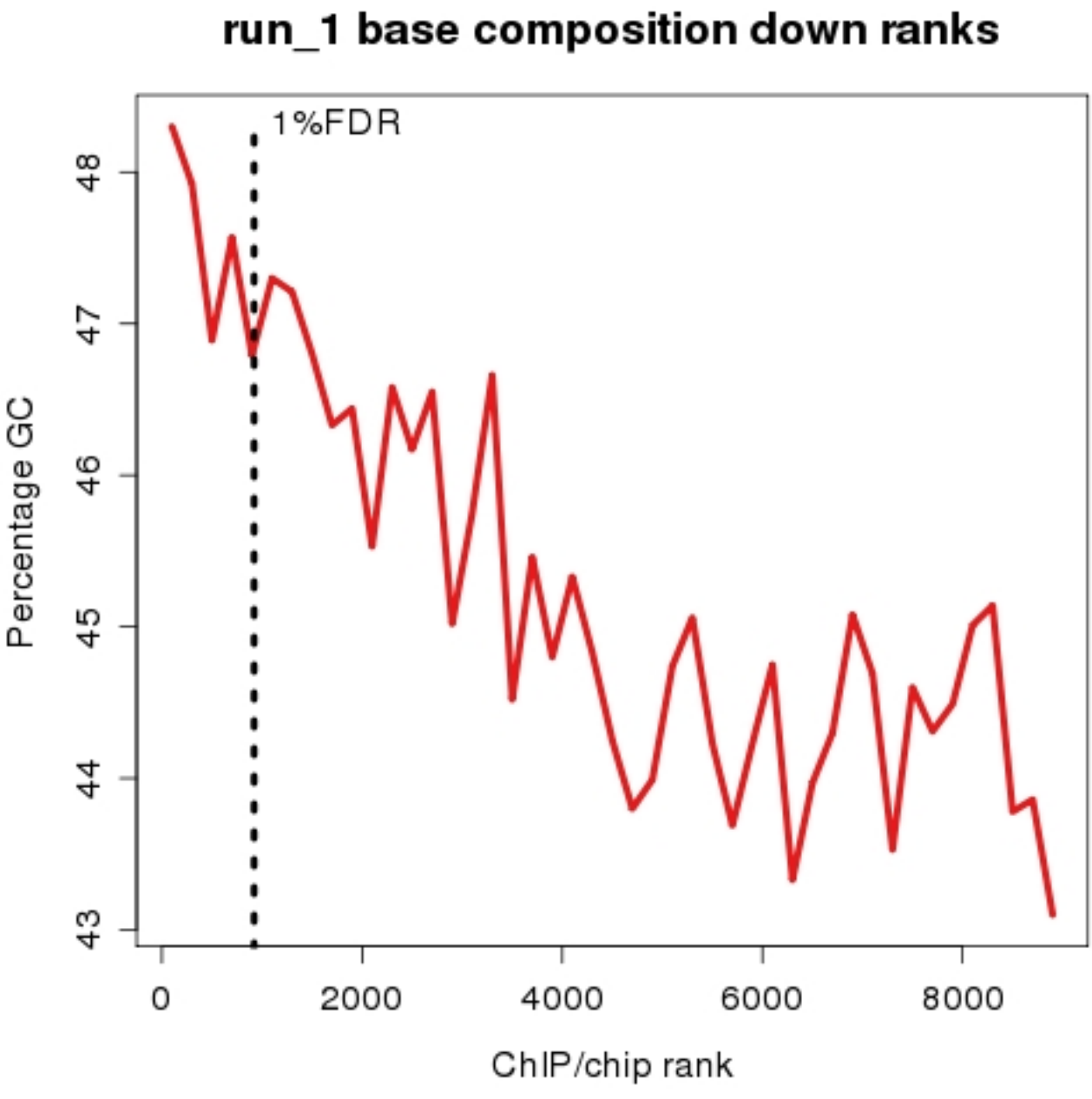
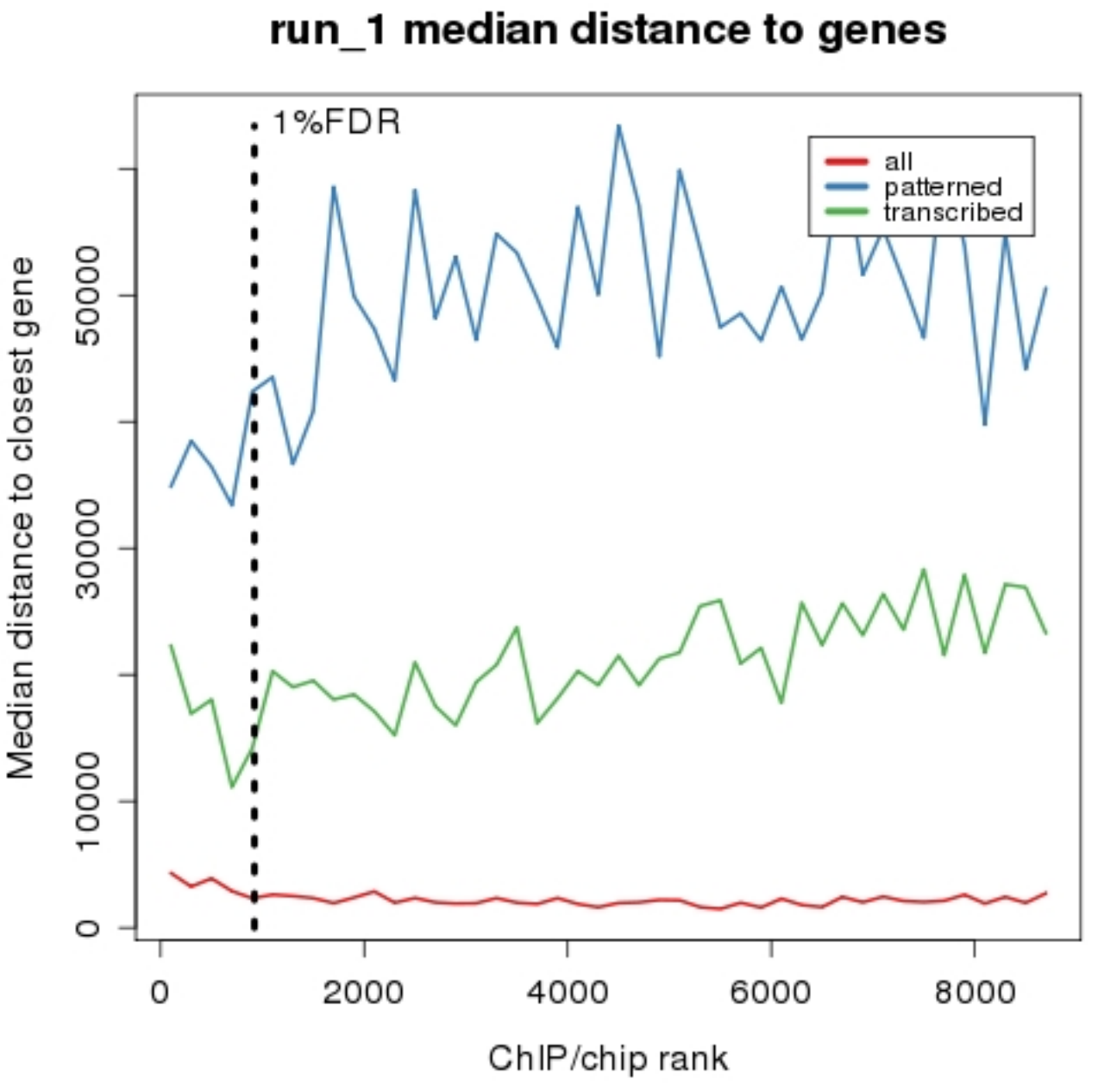
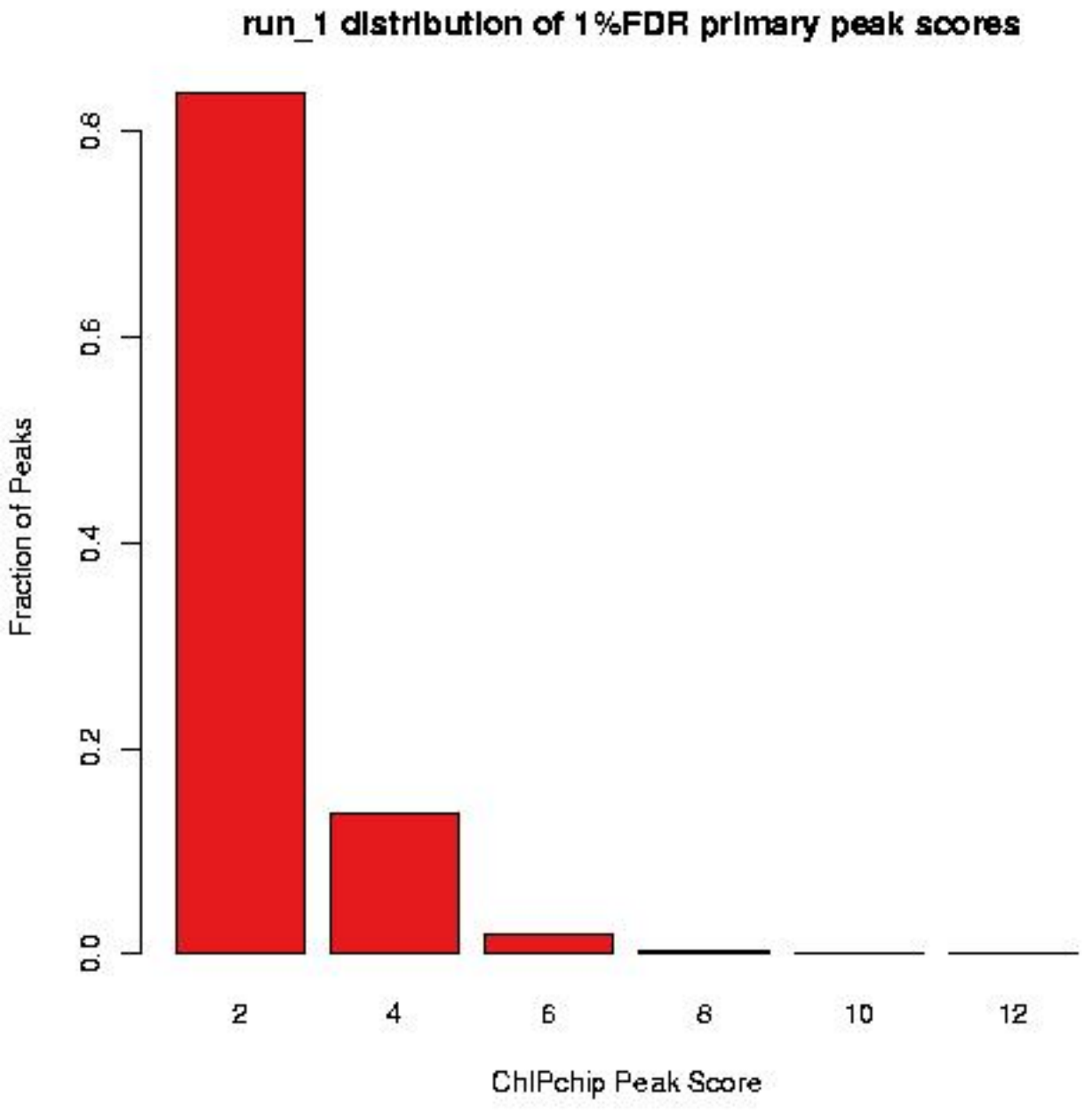
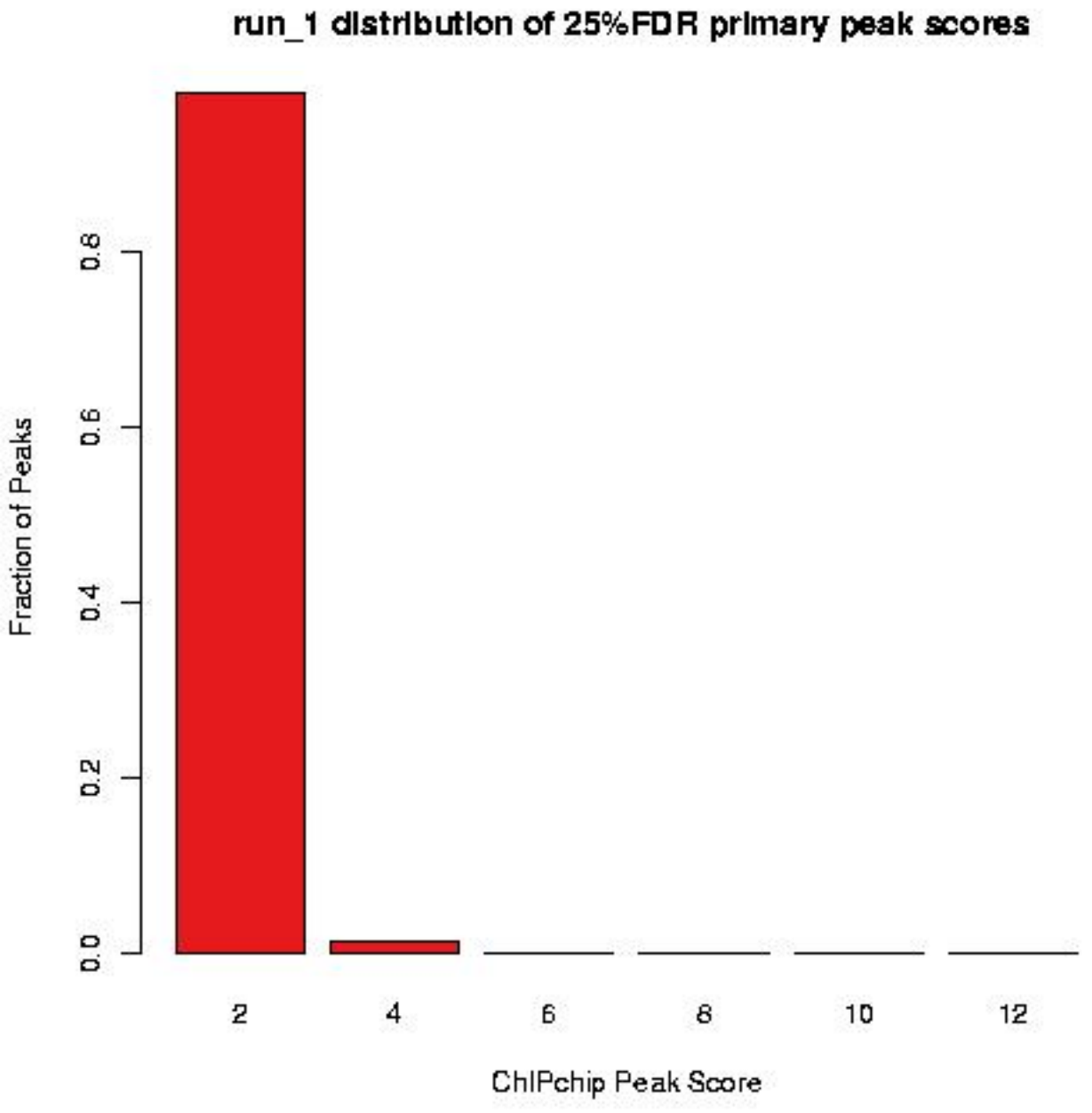
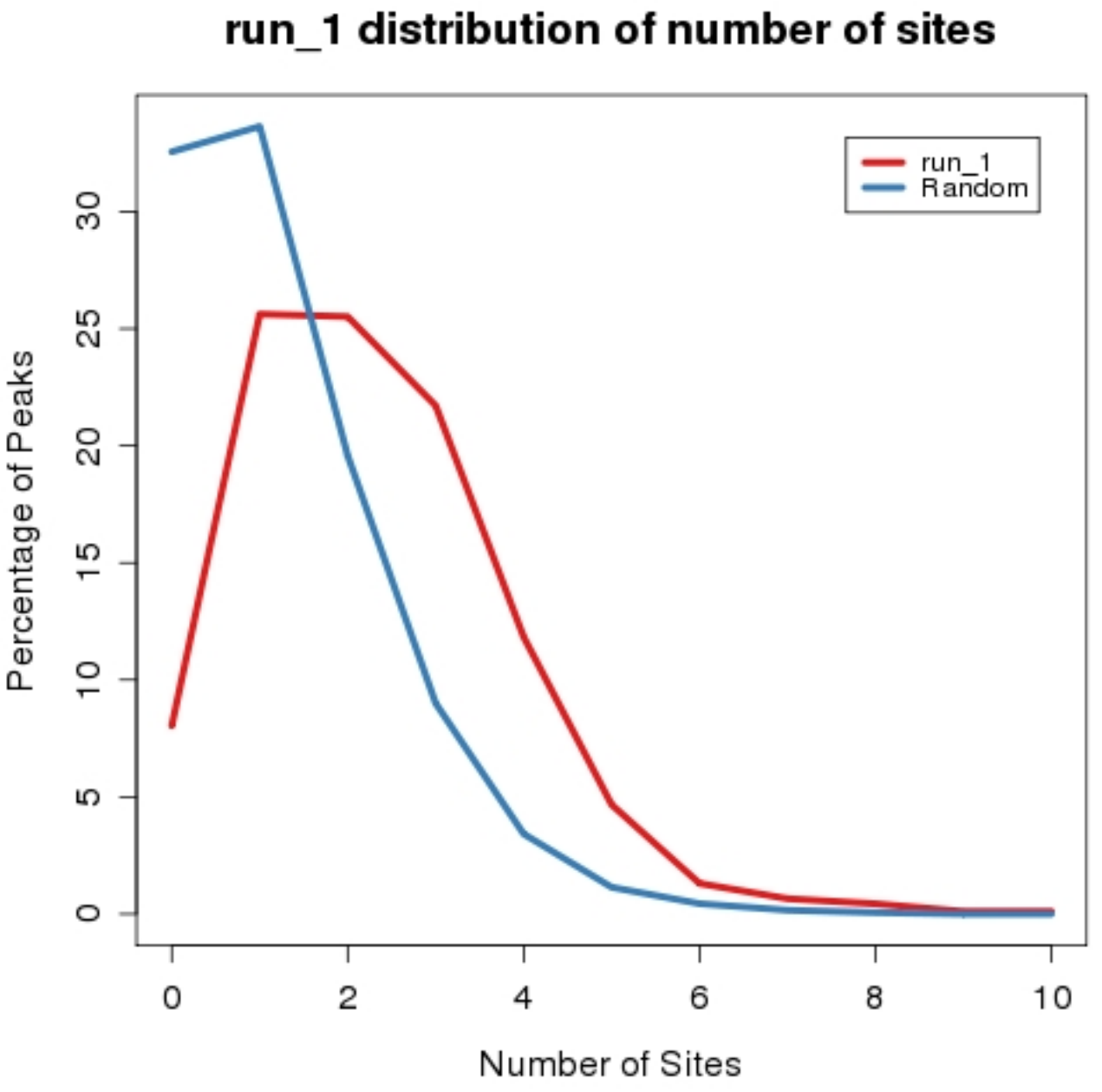

run_1 base composition across peaks
Percentage GC
42
44
46
48
-4000
-2000
0
2000
4000
Nucleotide position (200 bp)

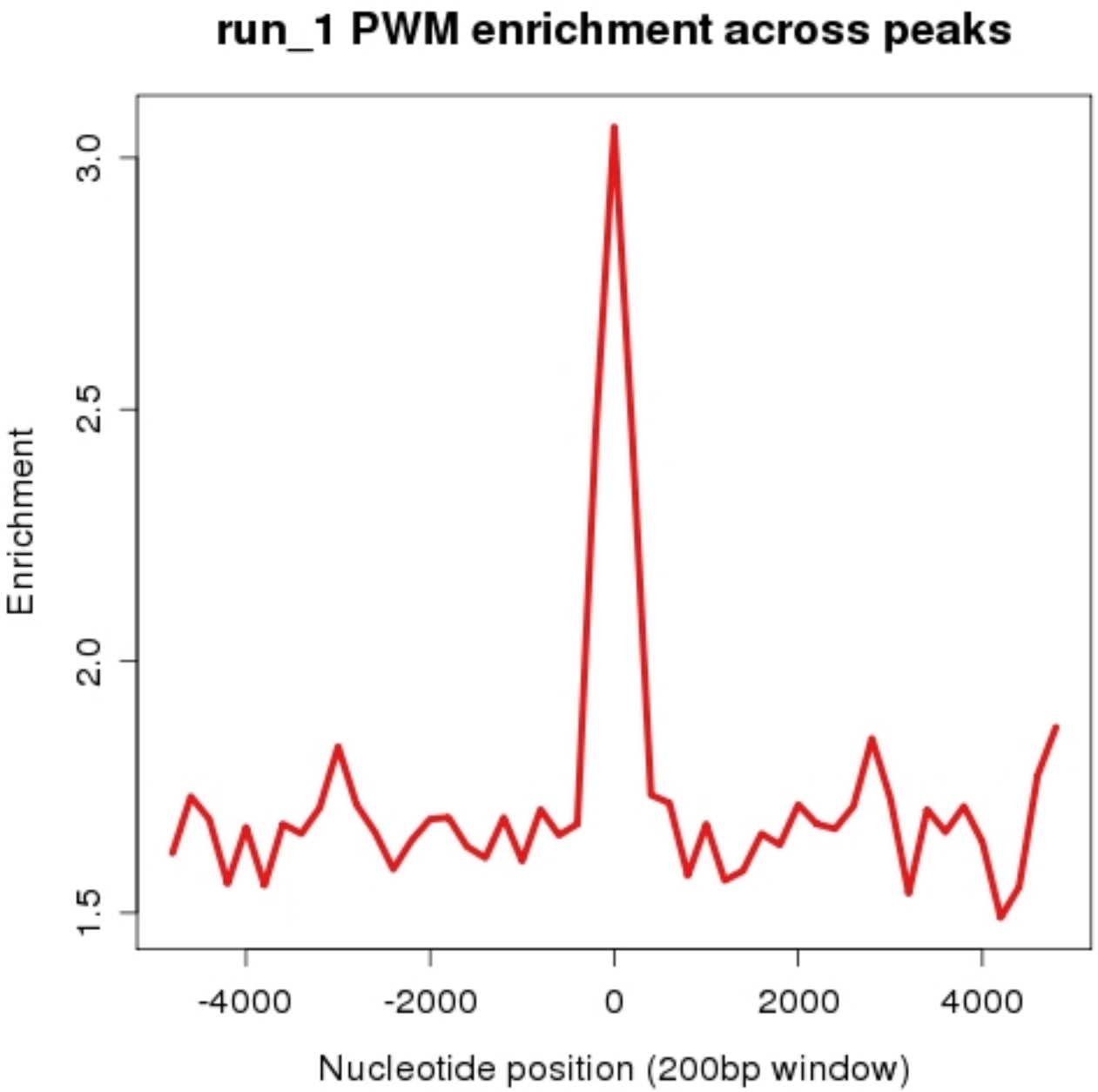

run_1 base composition down ranks
1%FDR
Percentage GC
43
44
45
46
47
48
0
2000
4000
6000
8000
ChIP/chip rank

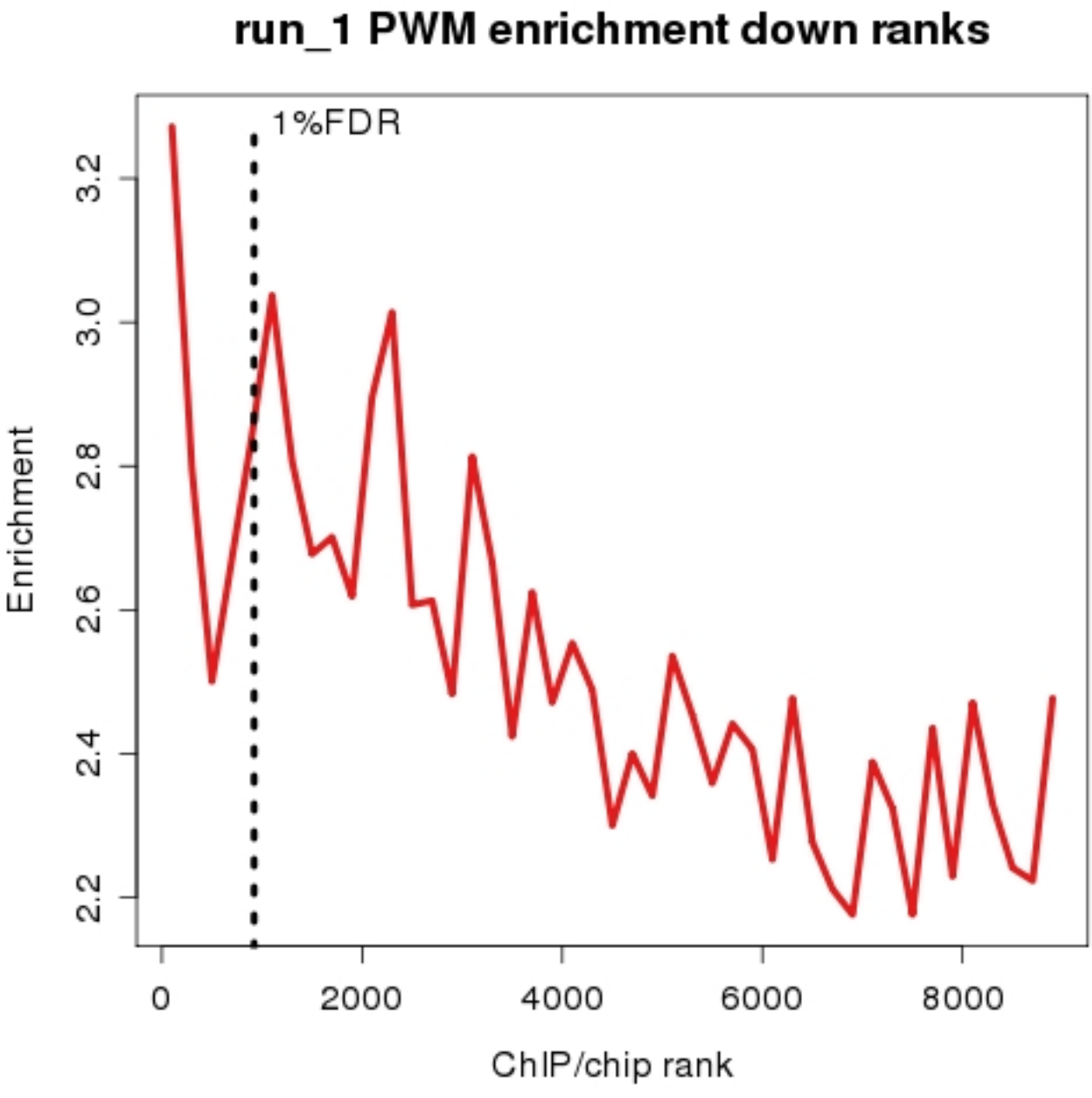

run_1 median distance to genes
1%FDR
all
patterned
transcribed
Median distance to closest gene
0
10000
30000
50000
0
2000
4000
6000
8000
ChIP/chip rank

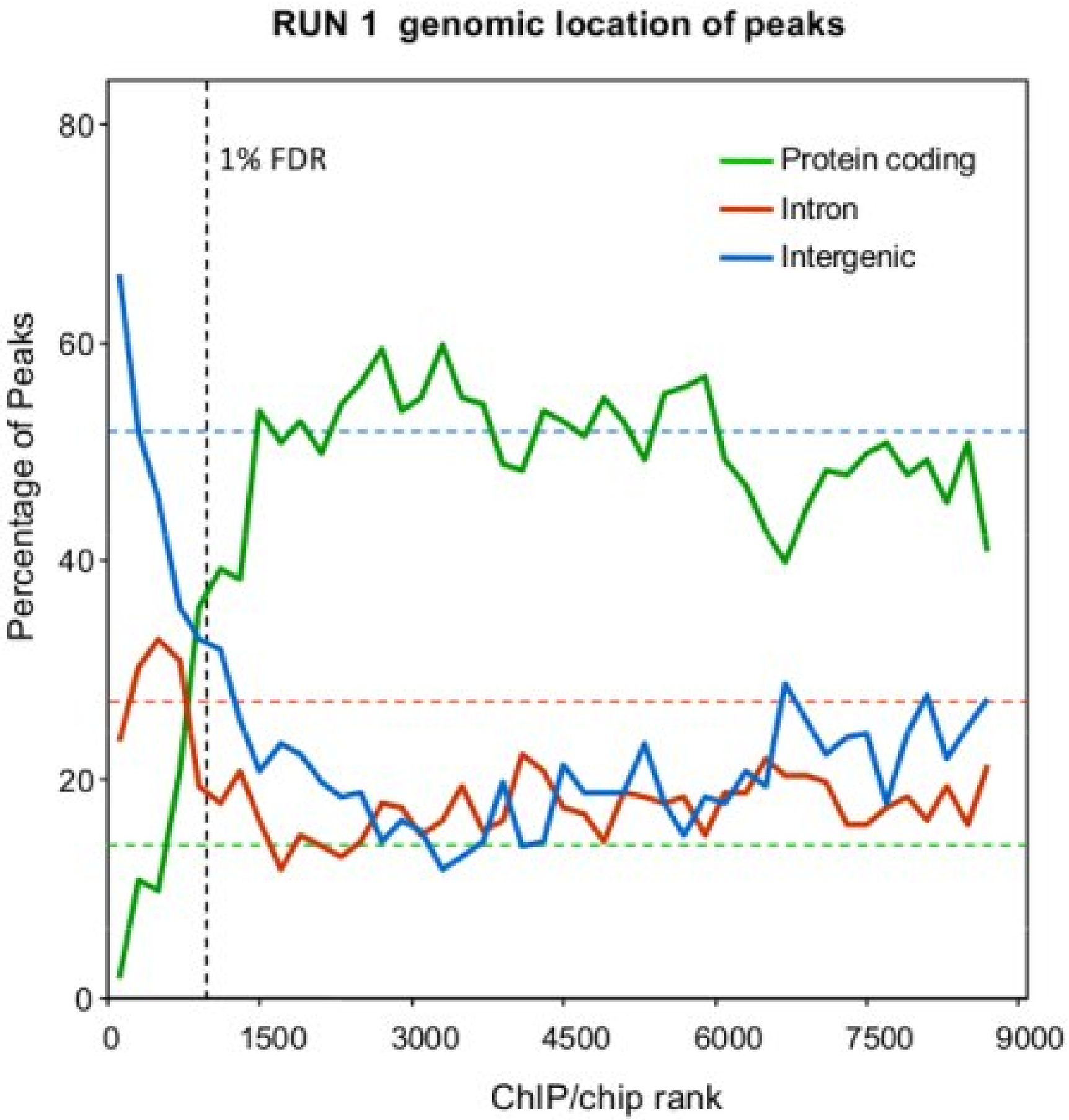

run_1 distribution of 1%FDR primary peak scores
Fraction of Peaks
0.0
0.2
0.4
0.6
0.8
2
4
6
8
10
12
ChIPchip Peak Score

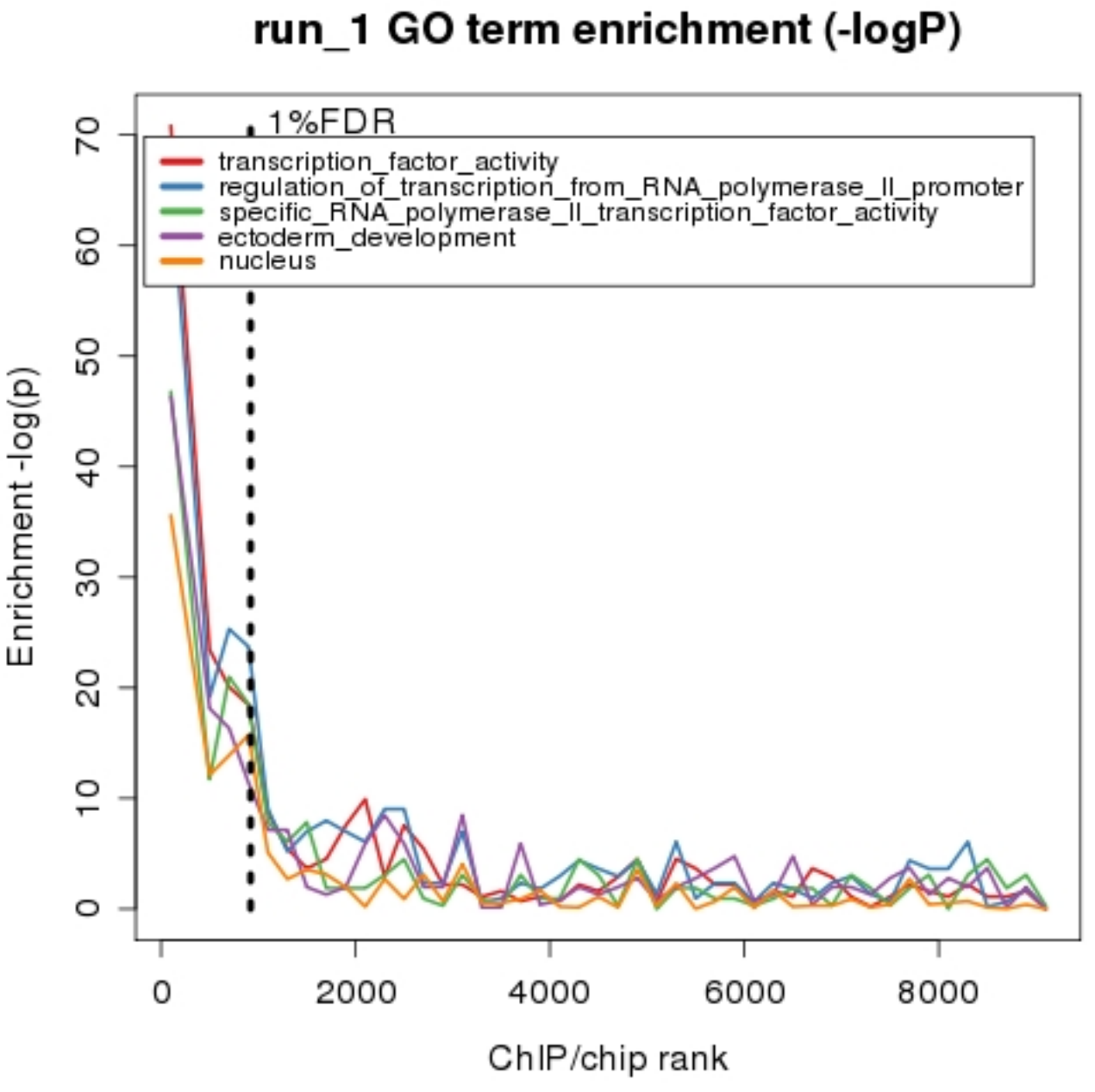

run_1 distribution of 25%FDR primary peak scores
Fraction of Peaks
0.0
0.2
0.4
0.6
0.8
2
4
6
8
10
12
ChIPchip Peak Score

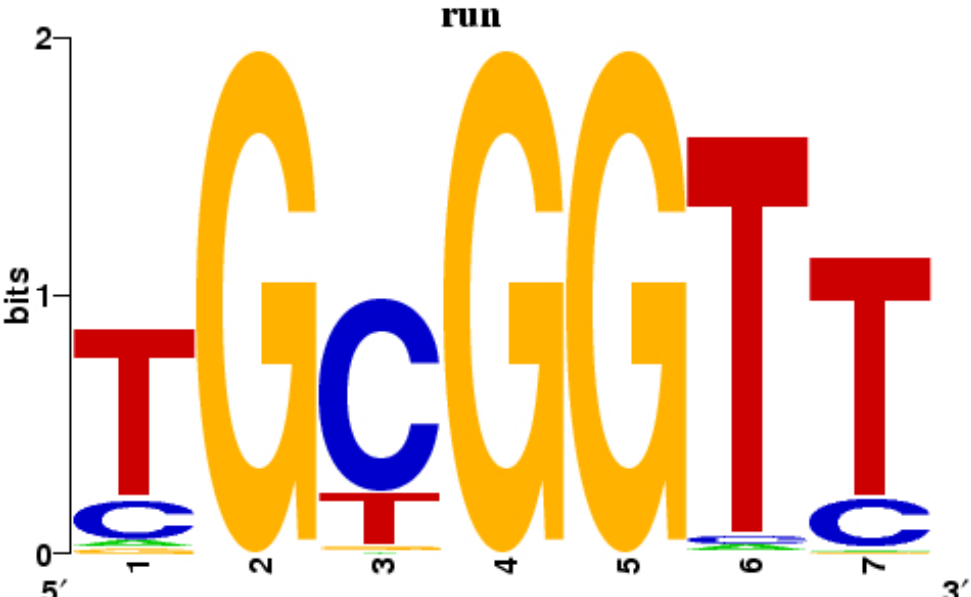

run_1 distribution of number of sites
run_1
Random
Percentage of Peaks
0
5
10
15
20
25
30
0
2
4
6
8
10
Number of Sites

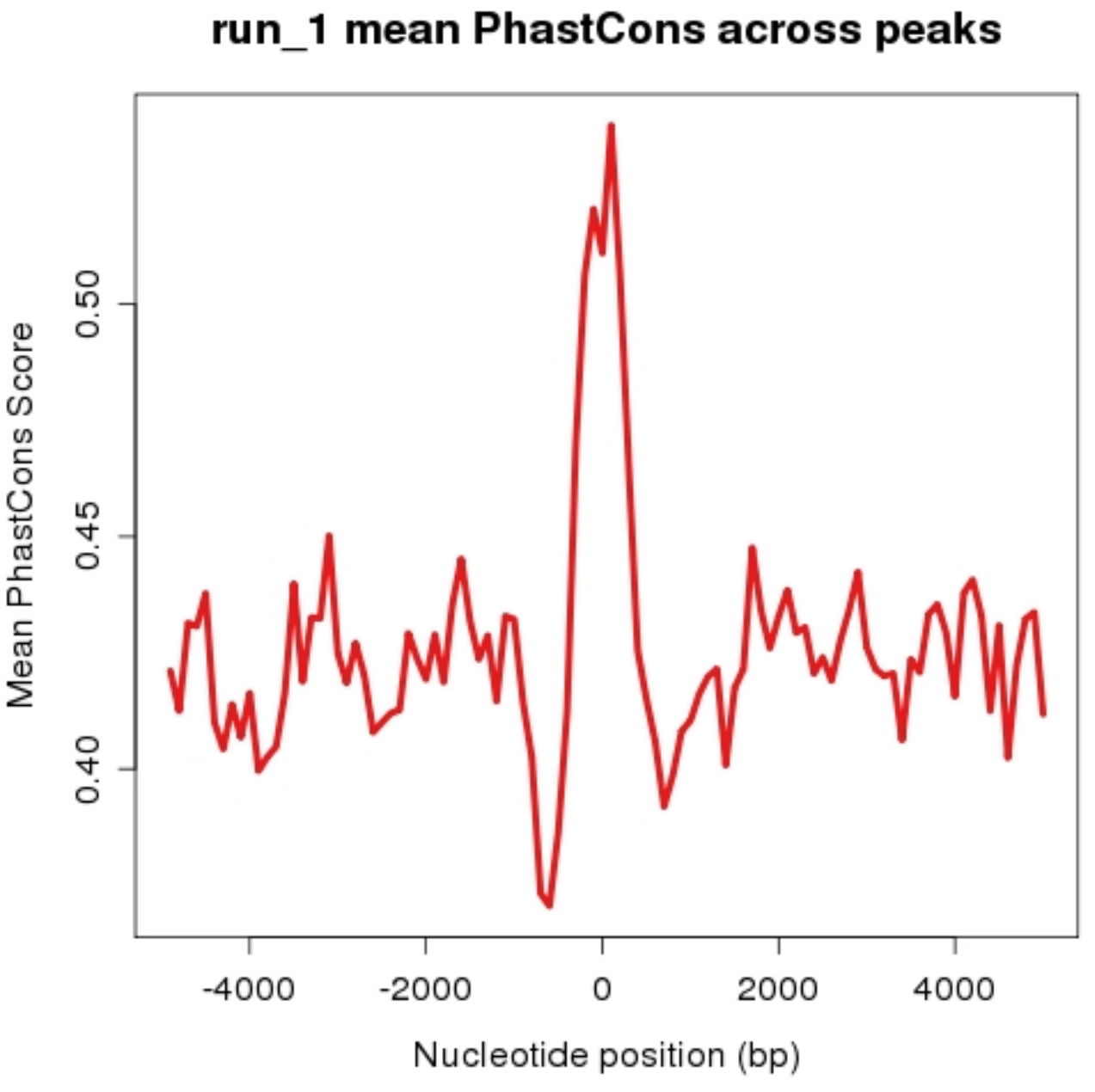

run_1 PWM enrichment across peaks
Enrichment
3.0
2.5
2.0
1.5
-4000
-2000
0
2000
4000
Nucleotide position (200bp window)

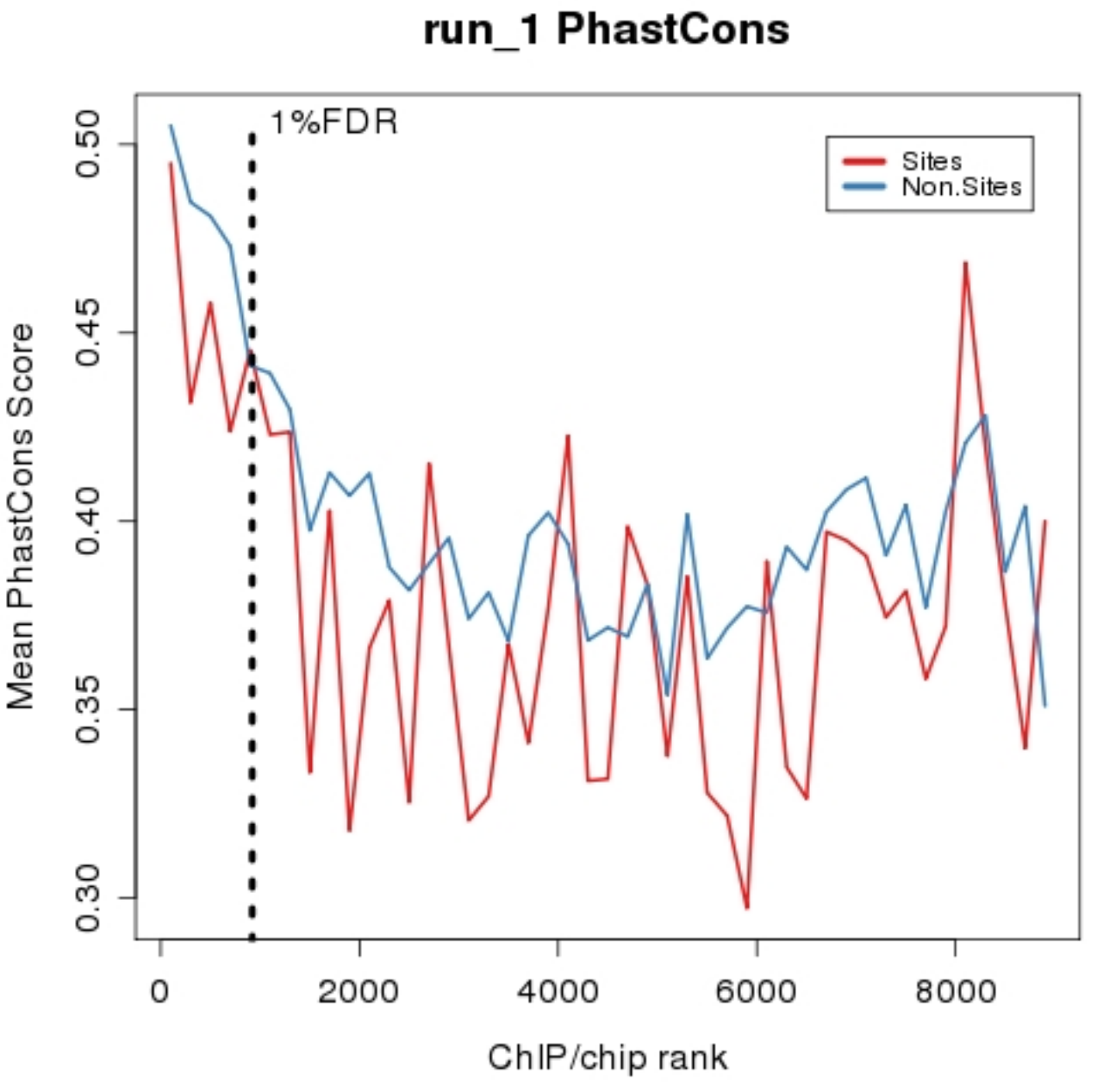

run_1 PWM enrichment down ranks
1%FDR
Enrichment
2.2
2.4
2.6
2.8
3.0
3.2
0
2000
4000
6000
8000
ChIP/chip rank

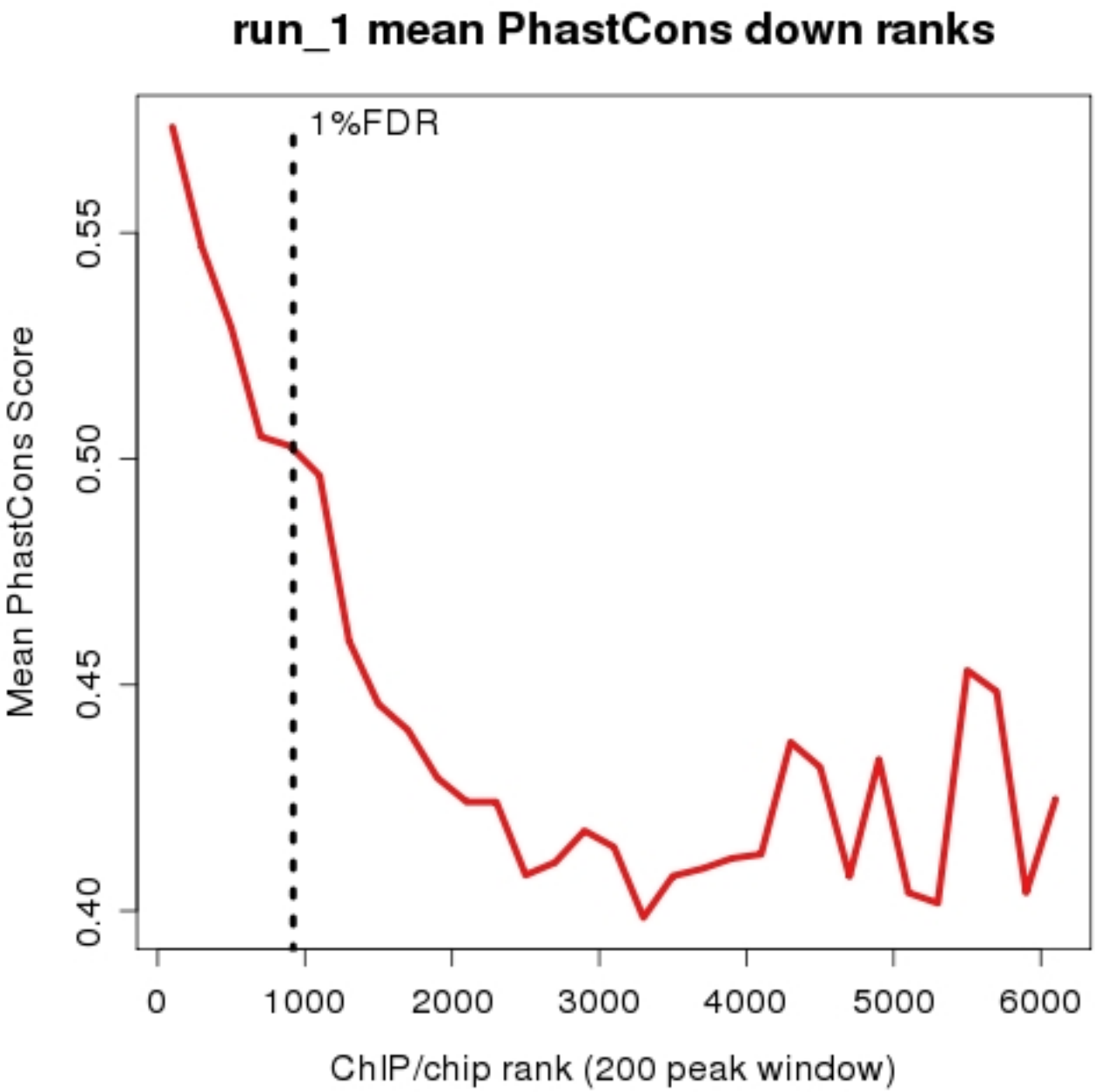

RUN 1 genomic location of peaks
1% FDR
Protein coding
Intron
Intergenic
Percentage of Peaks
0
20
40
60
80
0
1500
3000
4500
6000
7500
9000
ChIP/chip rank


run_1 GO term enrichment (-logP)
1%FDR
transcription_factor_activity
regulation_of_transcription_from_RNA_polymerase_II_promoter
specific_RNA_polymerase_II_transcription_factor_activity
ectoderm_development
nucleus
Enrichment -log(p)
0
10
20
30
40
50
60
70
0
2000
4000
6000
8000
ChIP/chip rank


run
bits
2
1
0
5′
1
2
3
4
5
6
7
3′


run_1 mean PhastCons across peaks
Mean PhastCons Score
0.40
0.45
0.50
-4000
-2000
0
2000
4000
Nucleotide position (bp)


run_1 PhastCons
1%FDR
Sites
Non.Sites
Mean PhastCons Score
0.30
0.35
0.40
0.45
0.50
0
2000
4000
6000
8000
ChIP/chip rank


run_1 mean PhastCons down ranks
1%FDR
Mean PhastCons Score
0.40
0.45
0.50
0.55
0
1000
2000
3000
4000
5000
6000
ChIP/chip rank (200 peak window)