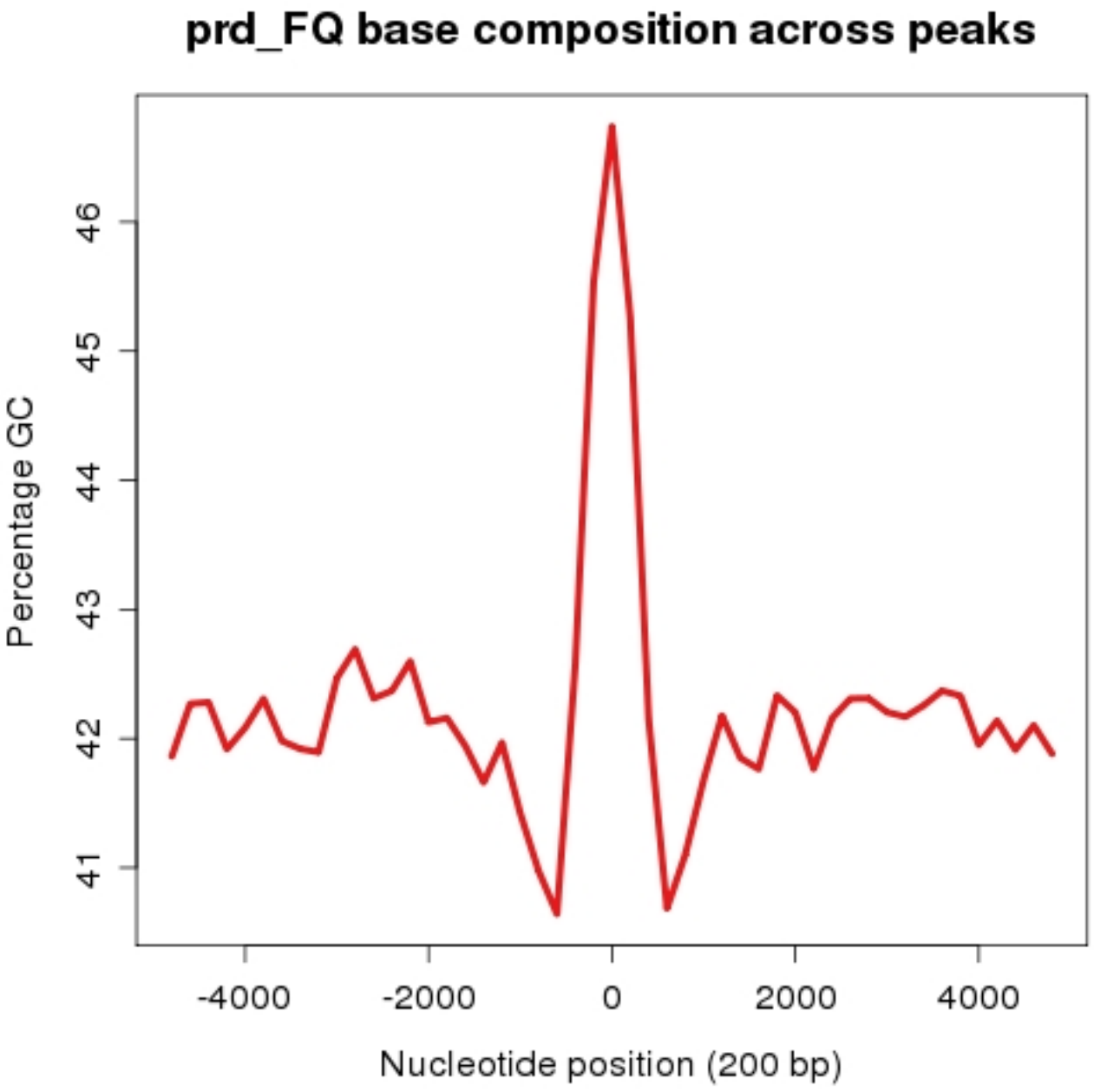
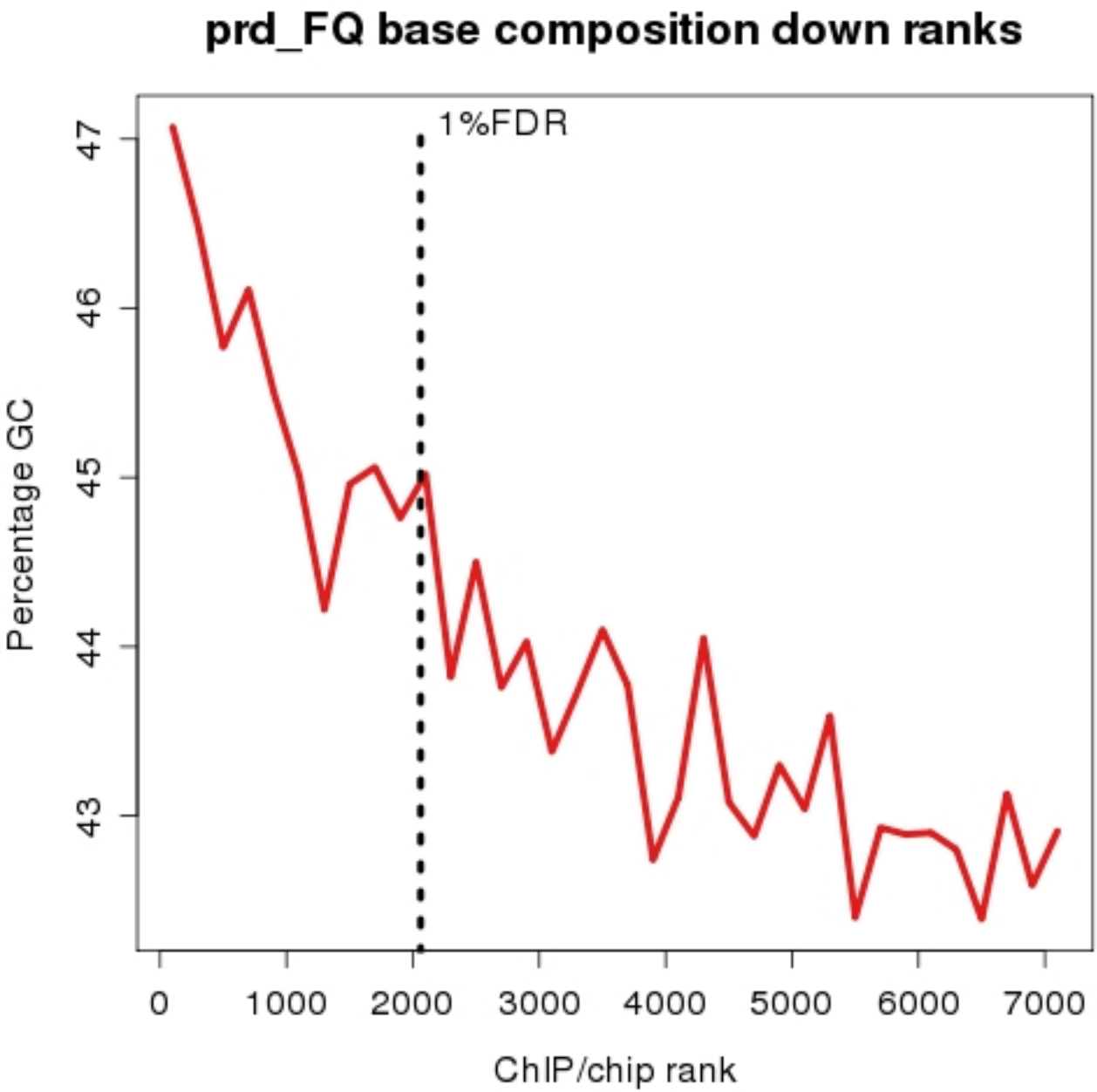
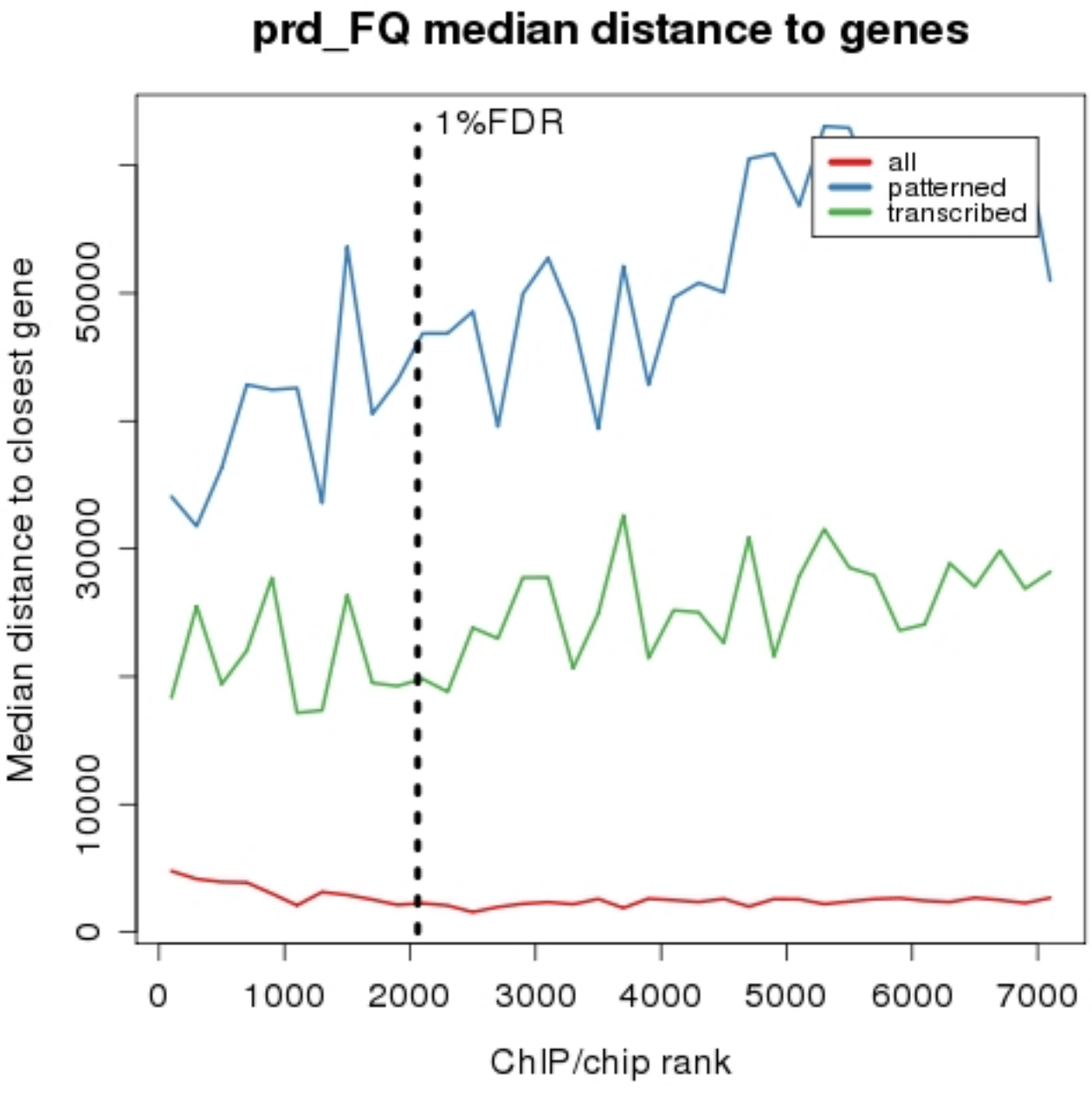
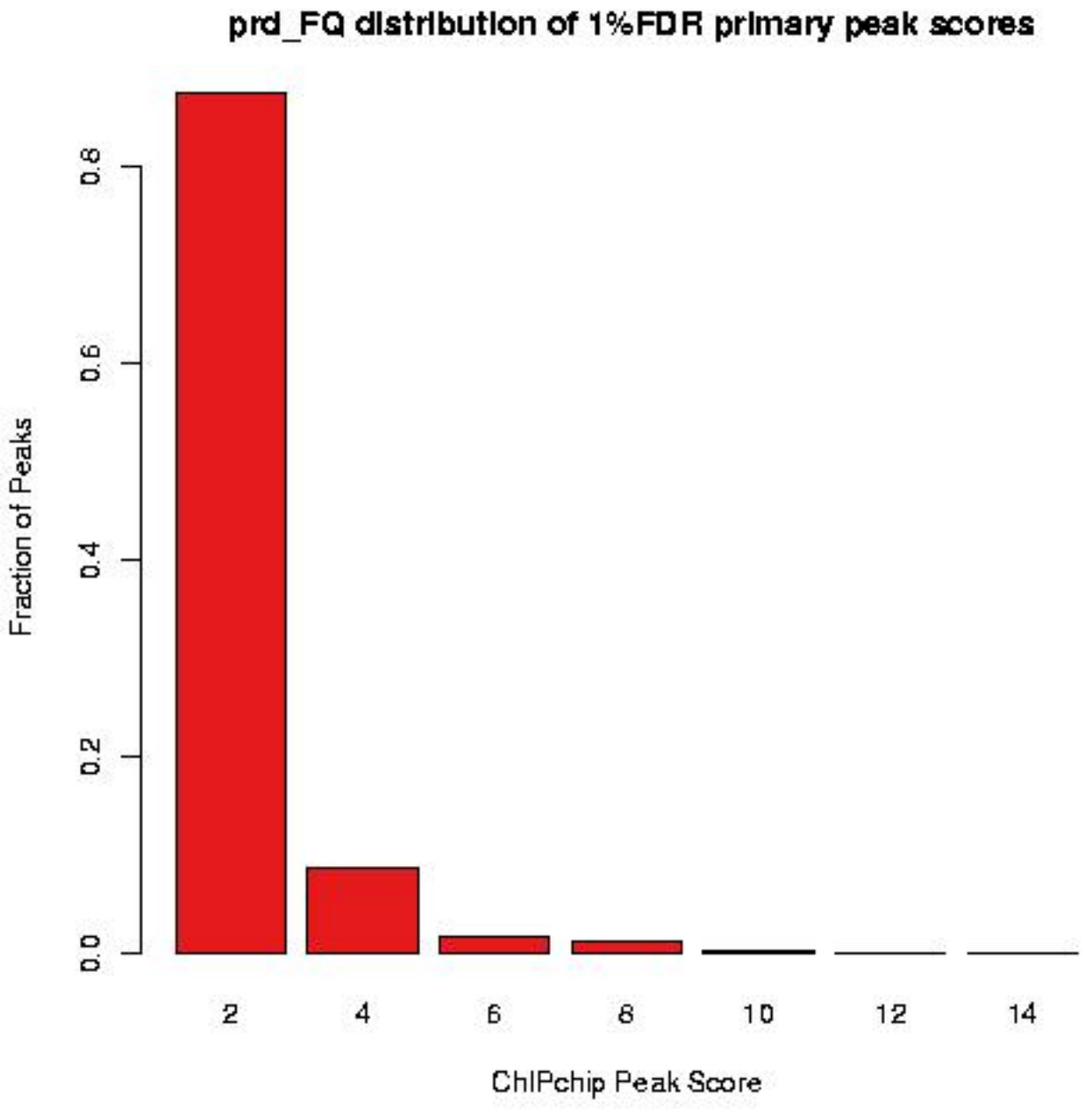
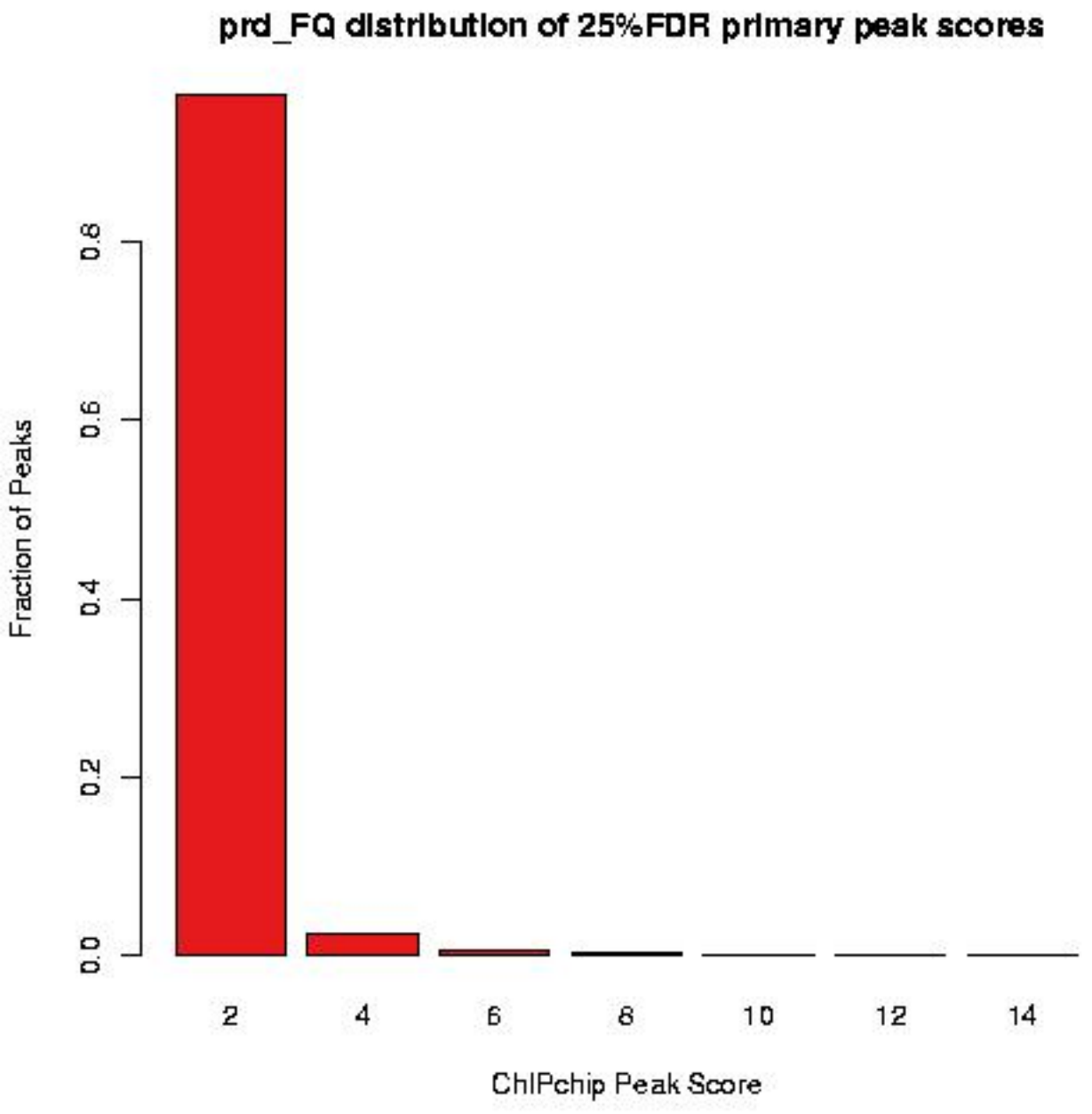
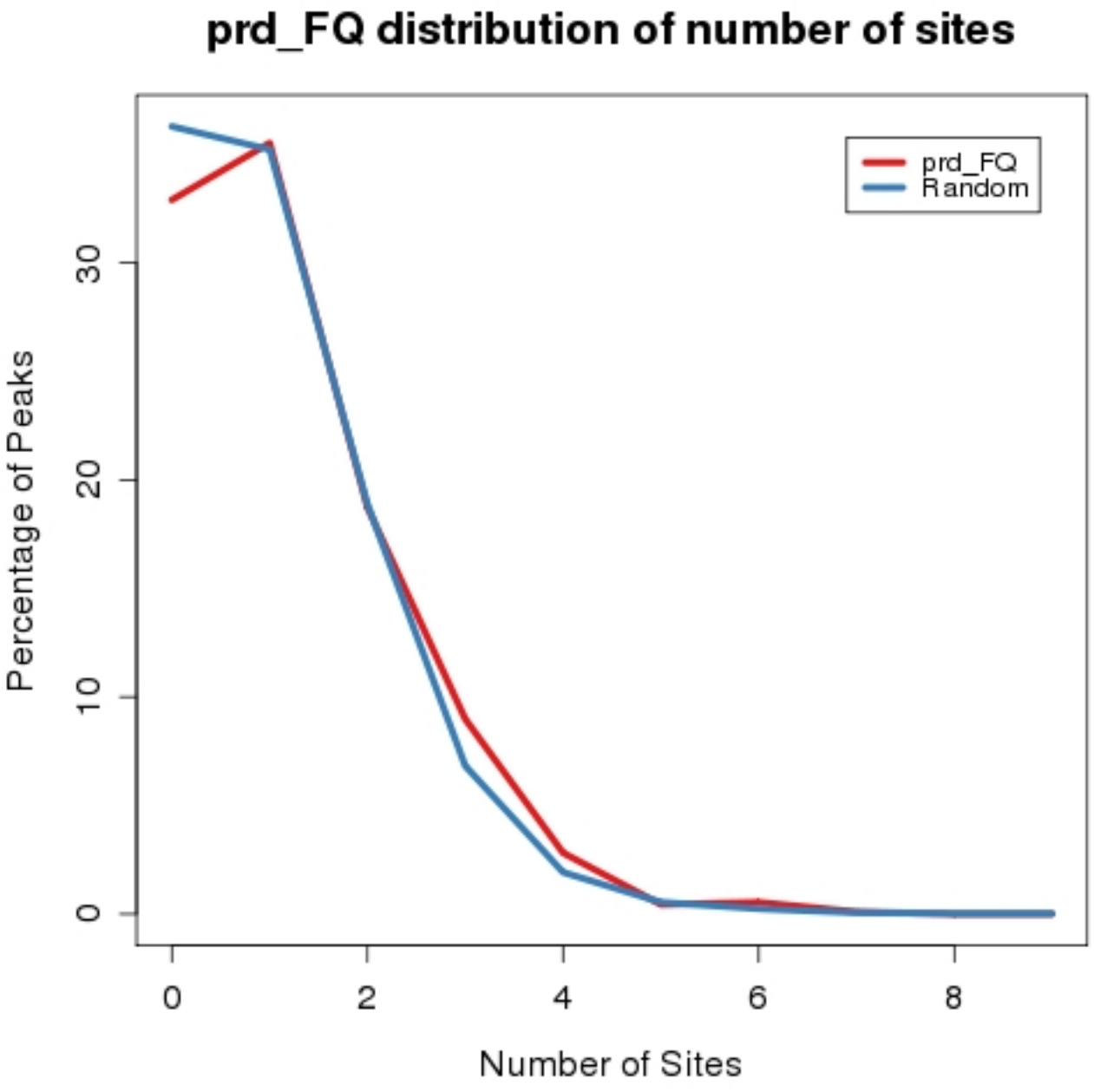

prd_FQ base composition across peaks
Percentage GC
41
42
43
44
45
46
-4000
-2000
0
2000
4000
Nucleotide position (200 bp)

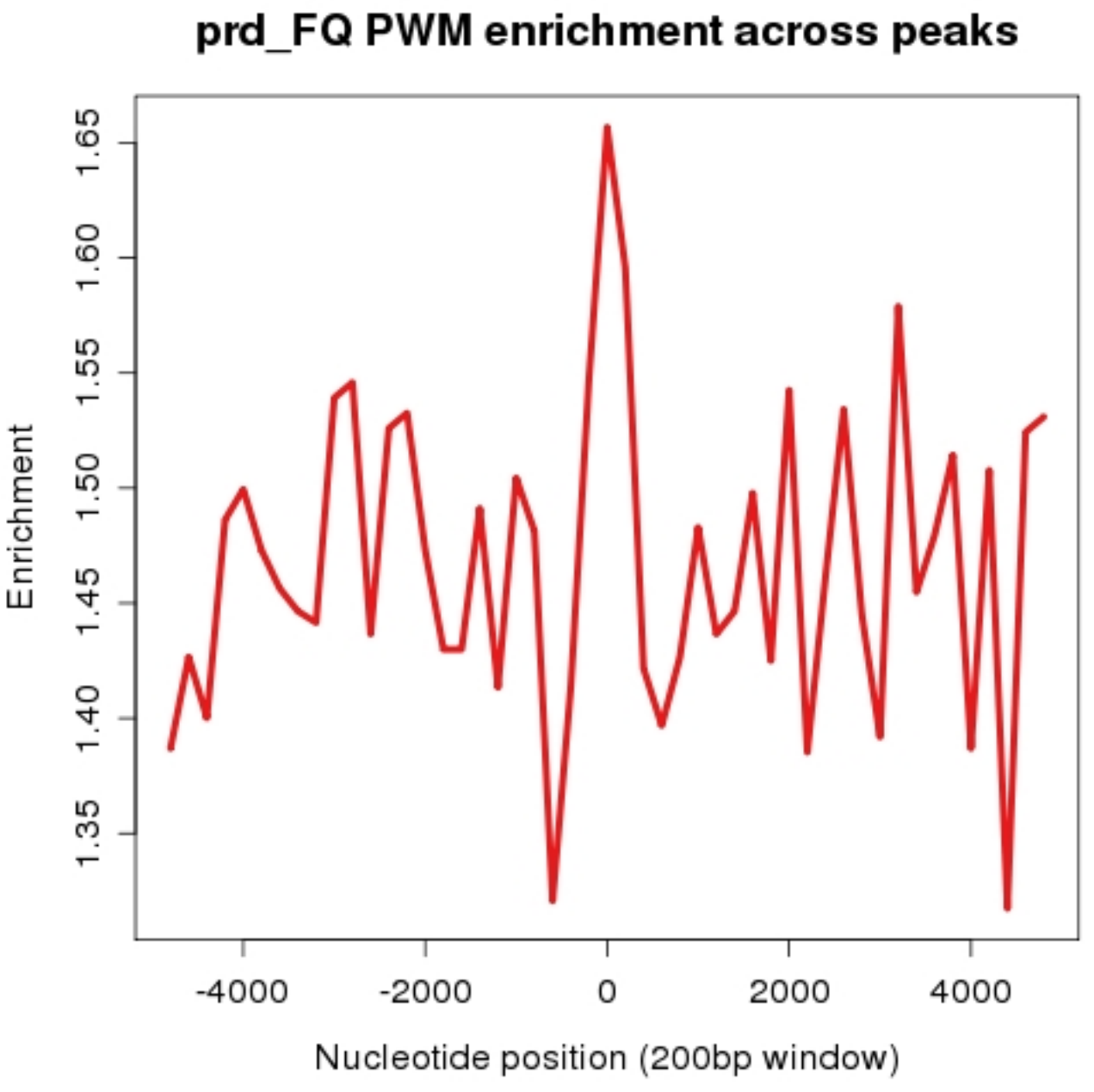

prd_FQ base composition down ranks
1%FDR
Percentage GC
43
44
45
46
47
0
1000
2000
3000
4000
5000
6000
7000
ChIP/chip rank

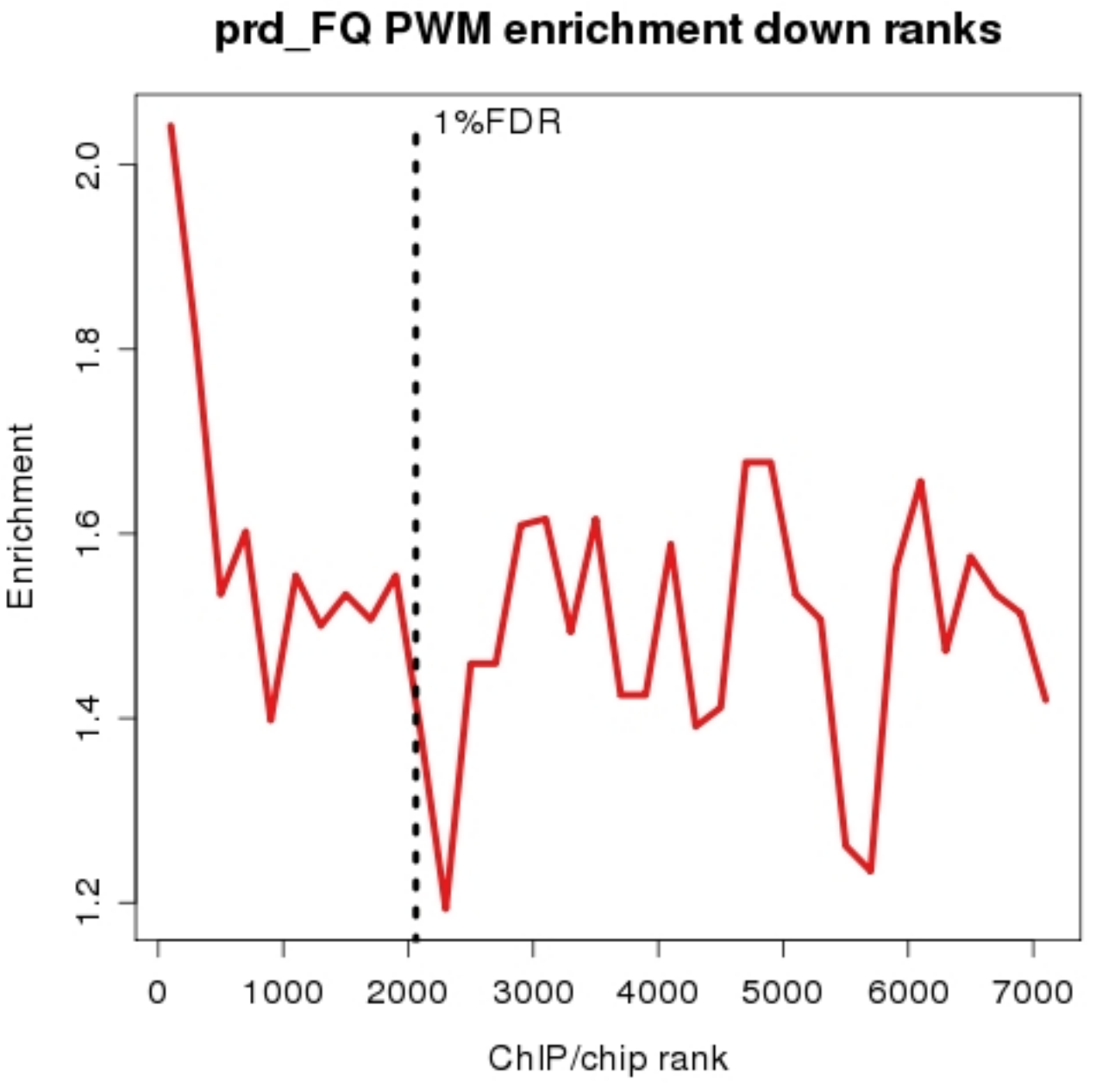

prd_FQ median distance to genes
1%FDR
all
patterned
transcribed
Median distance to closest gene
0
10000
30000
50000
0
1000
2000
3000
4000
5000
6000
7000
ChIP/chip rank

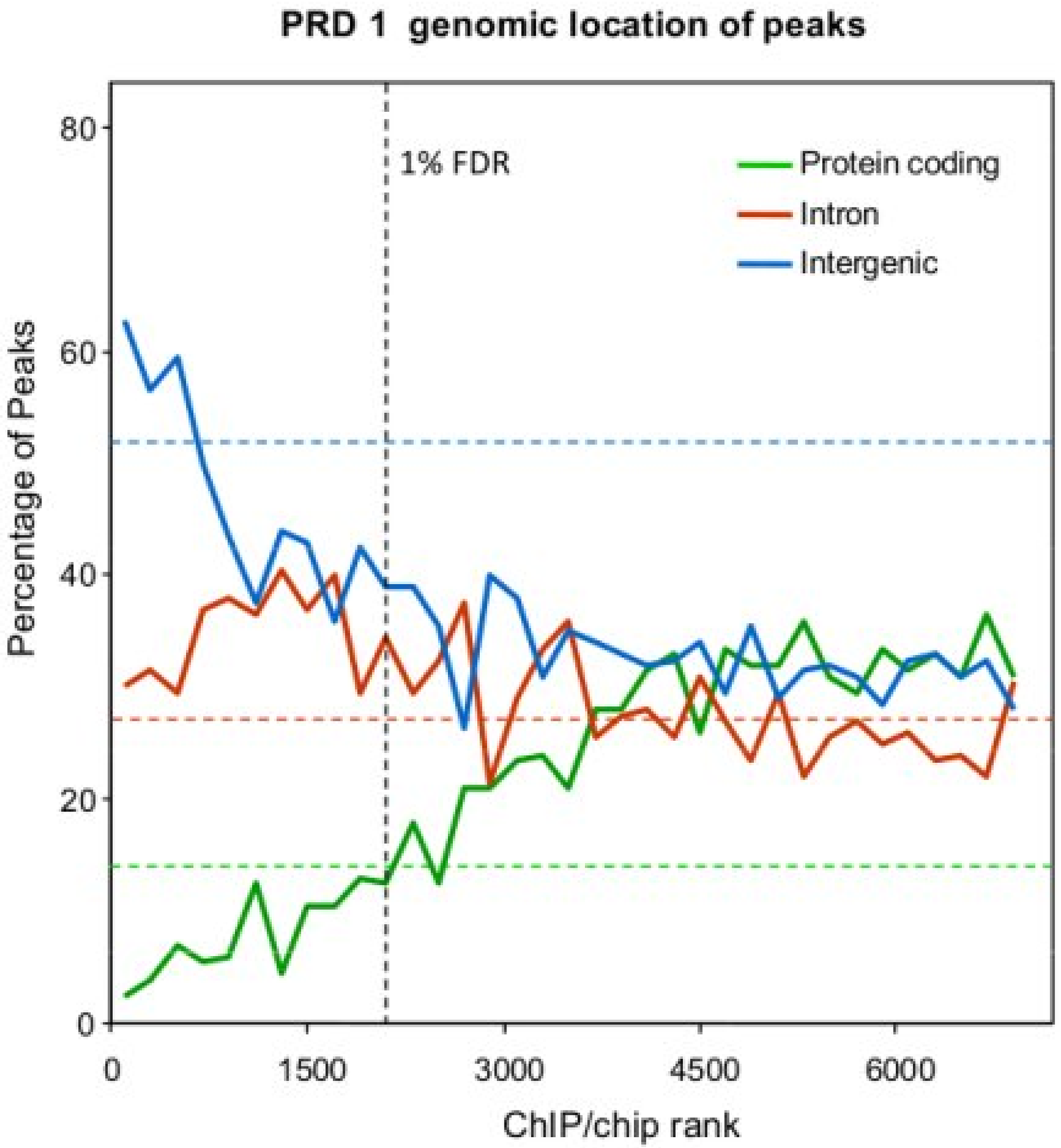

prd_FQ distribution of 1%FDR primary peak scores
Fraction of Peaks
0.0
0.2
0.4
0.6
0.8
2
4
6
8
10
12
14
ChIPchip Peak Score

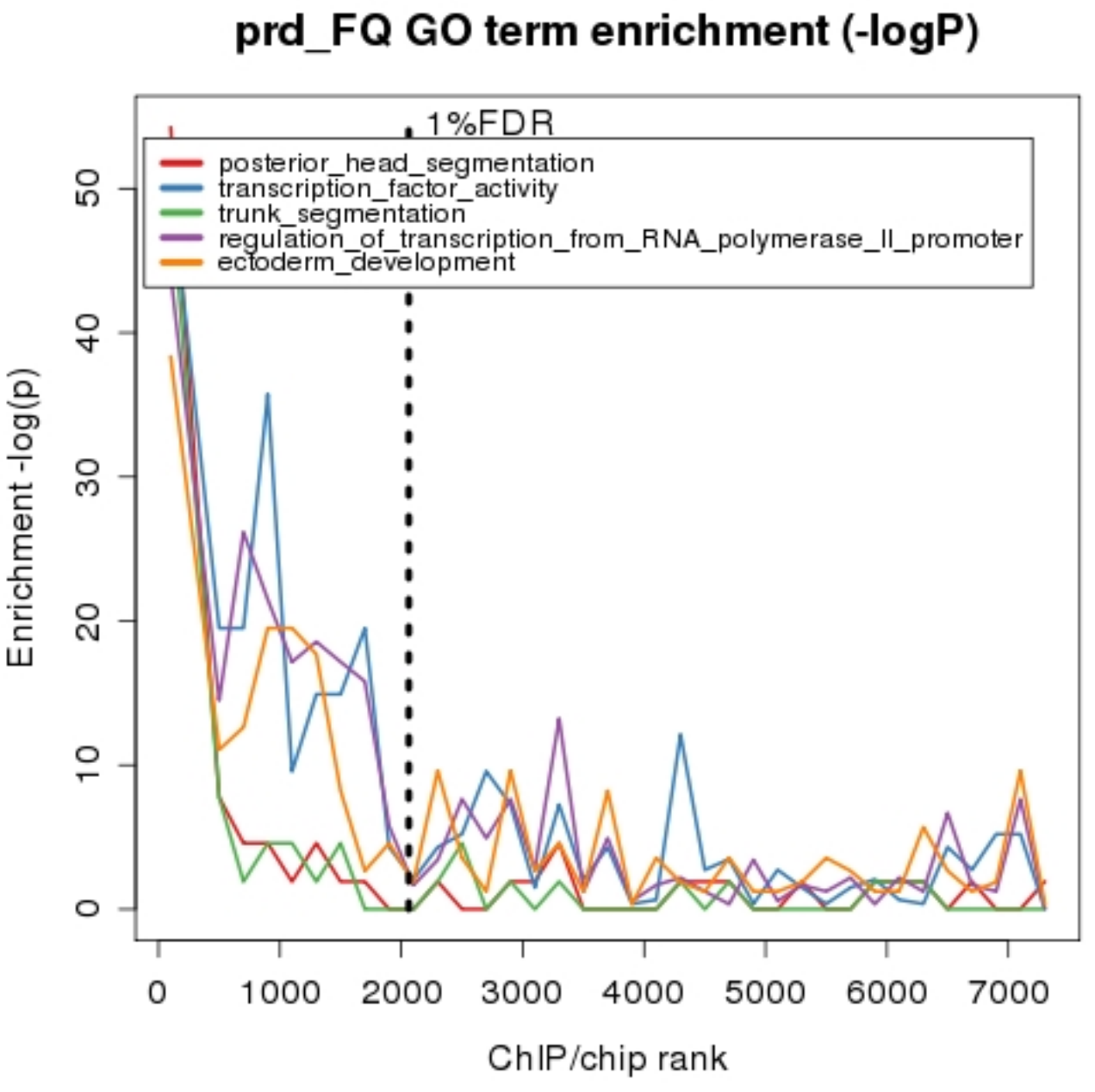

prd_FQ distribution of 25%FDR primary peak scores
Fraction of Peaks
0.0
0.2
0.4
0.6
0.8
2
4
6
8
10
12
14
ChIPchip Peak Score

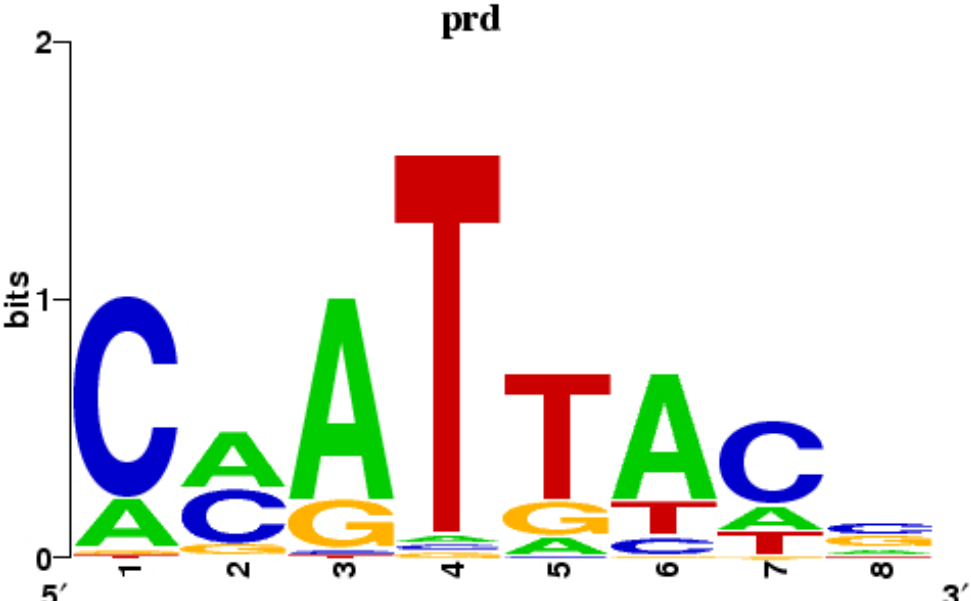

prd_FQ distribution of number of sites
prd_FQ
Random
Percentage of Peaks
0
10
20
30
0
2
4
6
8
Number of Sites

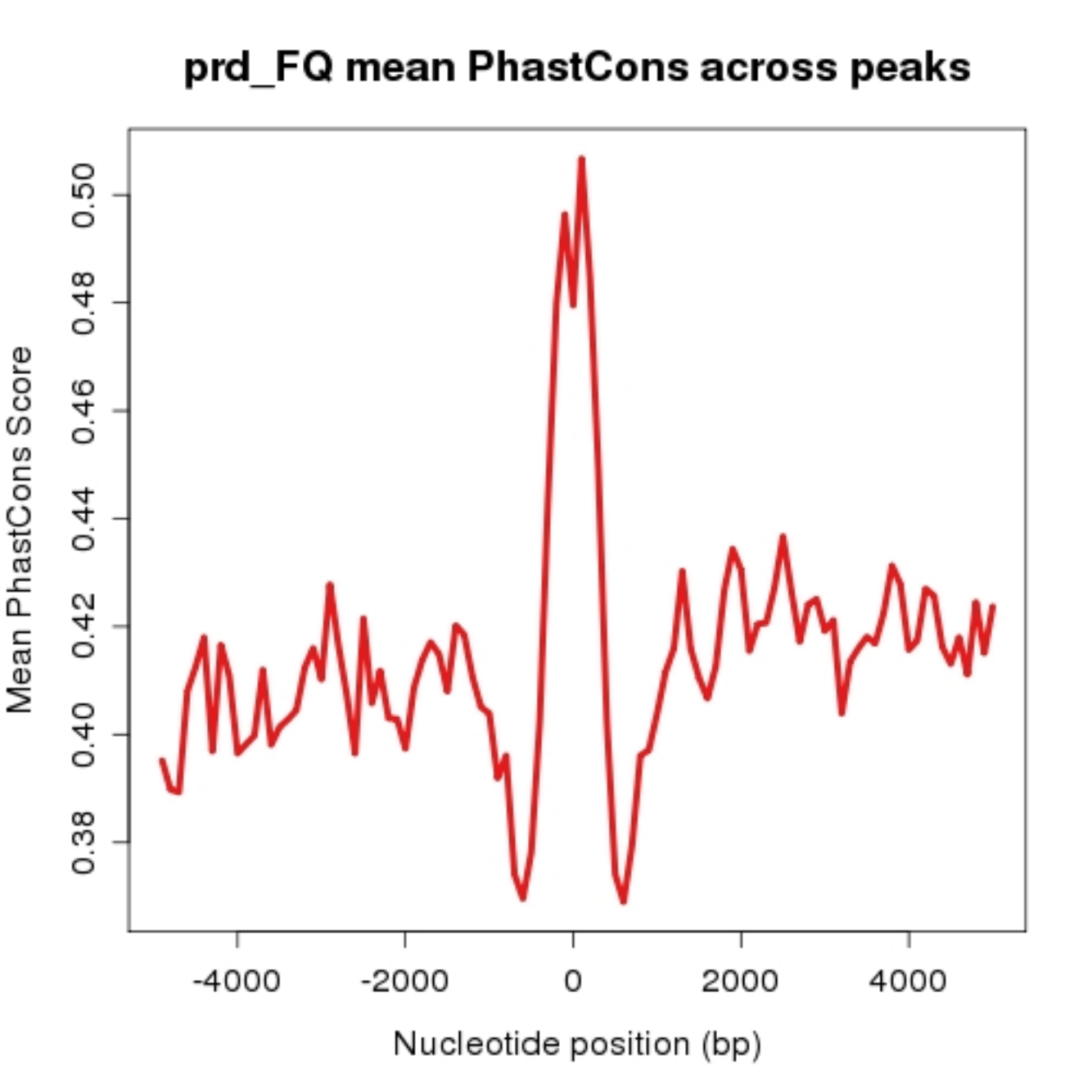

prd_FQ PWM enrichment across peaks
Enrichment
1.35
1.40
1.45
1.50
1.55
1.60
1.65
-4000
-2000
0
2000
4000
Nucleotide position (200bp window)

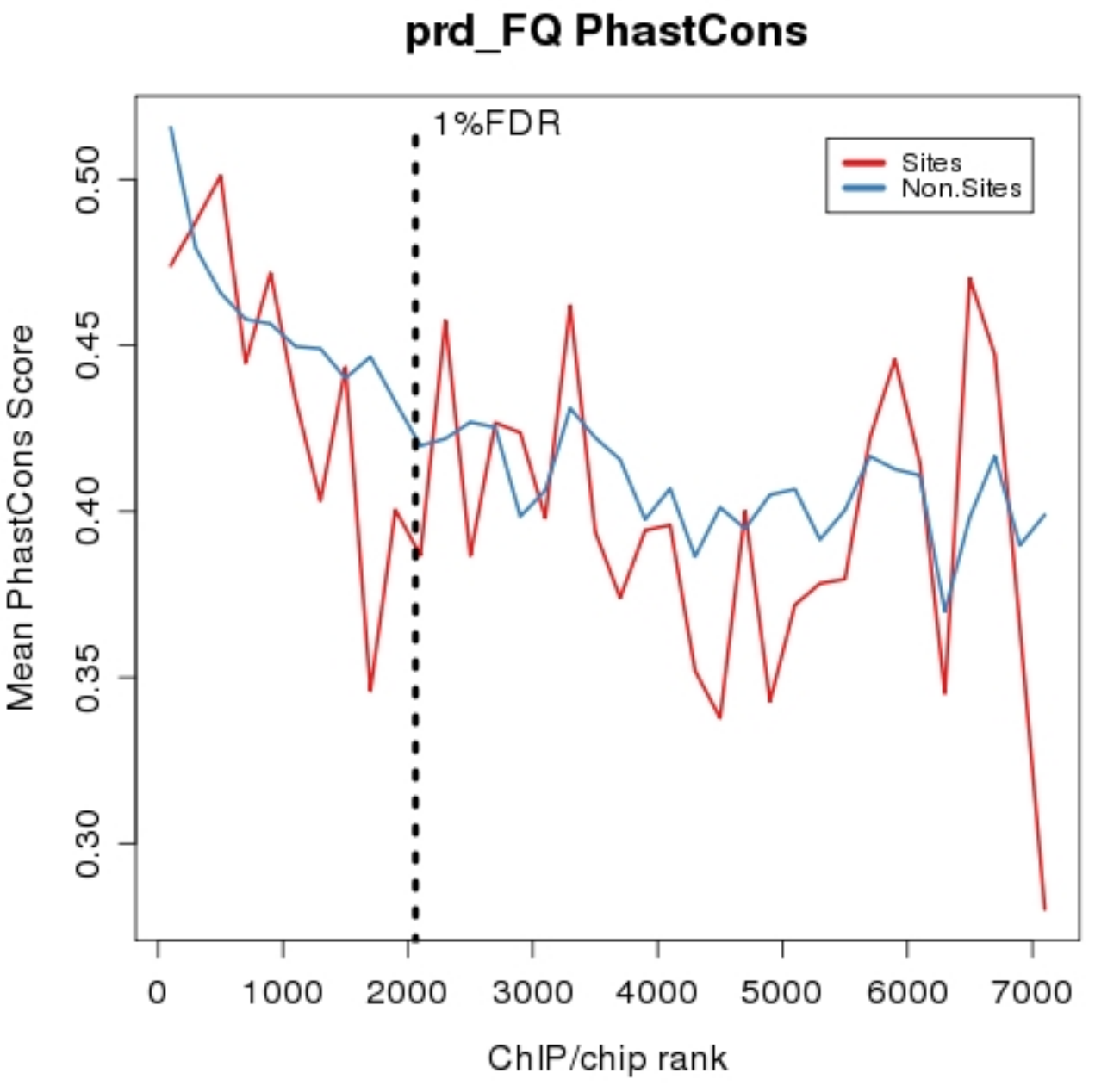

prd_FQ PWM enrichment down ranks
1%FDR
Enrichment
2.0
1.8
1.6
1.4
1.2
0
1000
2000
3000
4000
5000
6000
7000
ChIP/chip rank

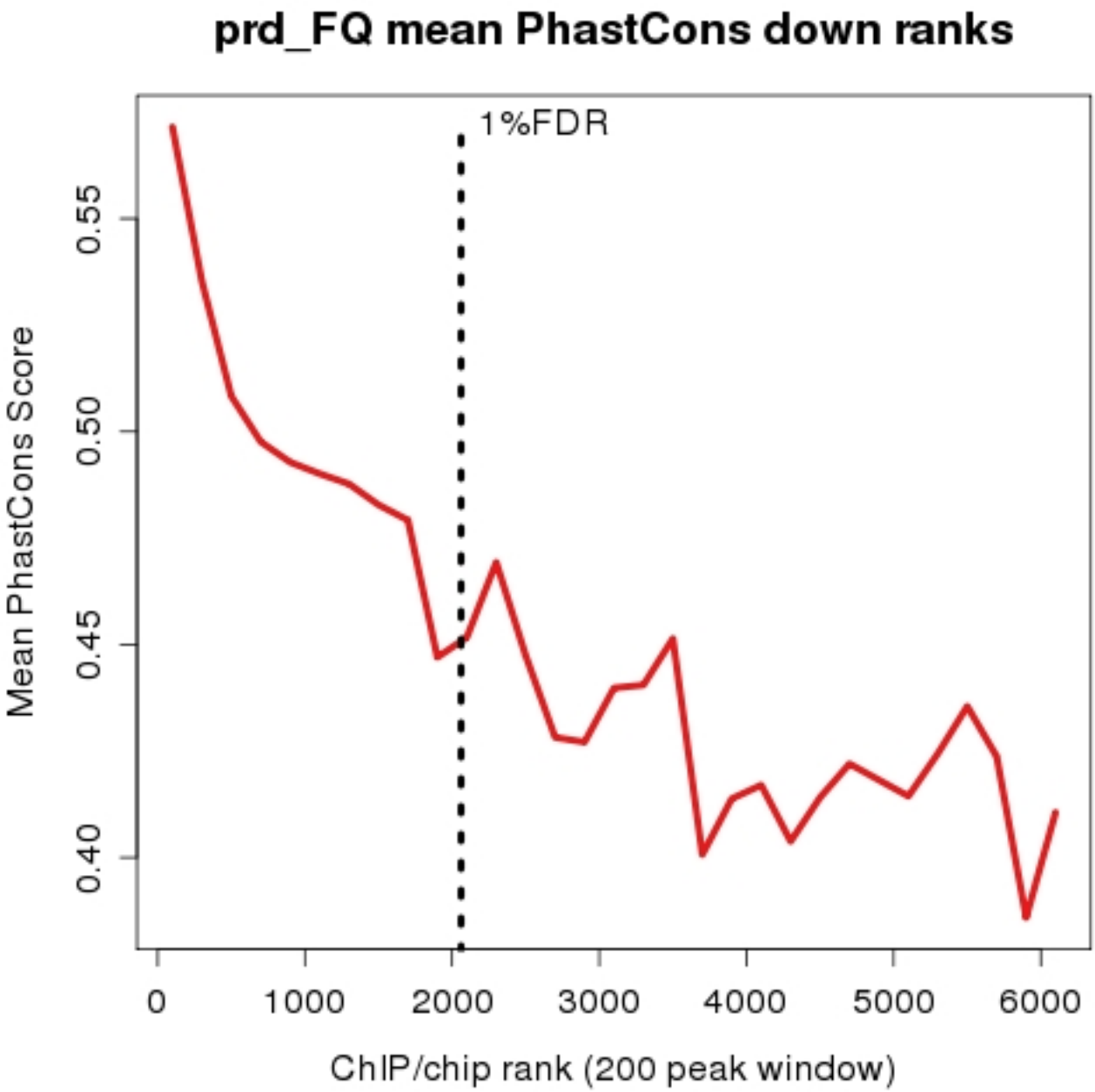

PRD 1 genomic location of peaks
1% FDR
Protein coding
Intron
Intergenic
Percentage of Peaks
0
20
40
60
80
0
1500
3000
4500
6000
ChIP/chip rank


prd_FQ GO term enrichment (-logP)
1%FDR
posterior_head_segmentation
transcription_factor_activity
trunk_segmentation
regulation_of_transcription_from_RNA_polymerase_II_promoter
ectoderm_development
Enrichment -log(p)
0
10
20
30
40
50
0
1000
2000
3000
4000
5000
6000
7000
ChIP/chip rank


prd
bits
2
1
0
1
2
3
4
5
6
7
8
5′
3′


prd_FQ mean PhastCons across peaks
Mean PhastCons Score
0.38
0.40
0.42
0.44
0.46
0.48
0.50
-4000
-2000
0
2000
4000
Nucleotide position (bp)


prd_FQ PhastCons
1%FDR
Sites
Non.Sites
Mean PhastCons Score
0.30
0.35
0.40
0.45
0.50
0
1000
2000
3000
4000
5000
6000
7000
ChIP/chip rank


prd_FQ 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)