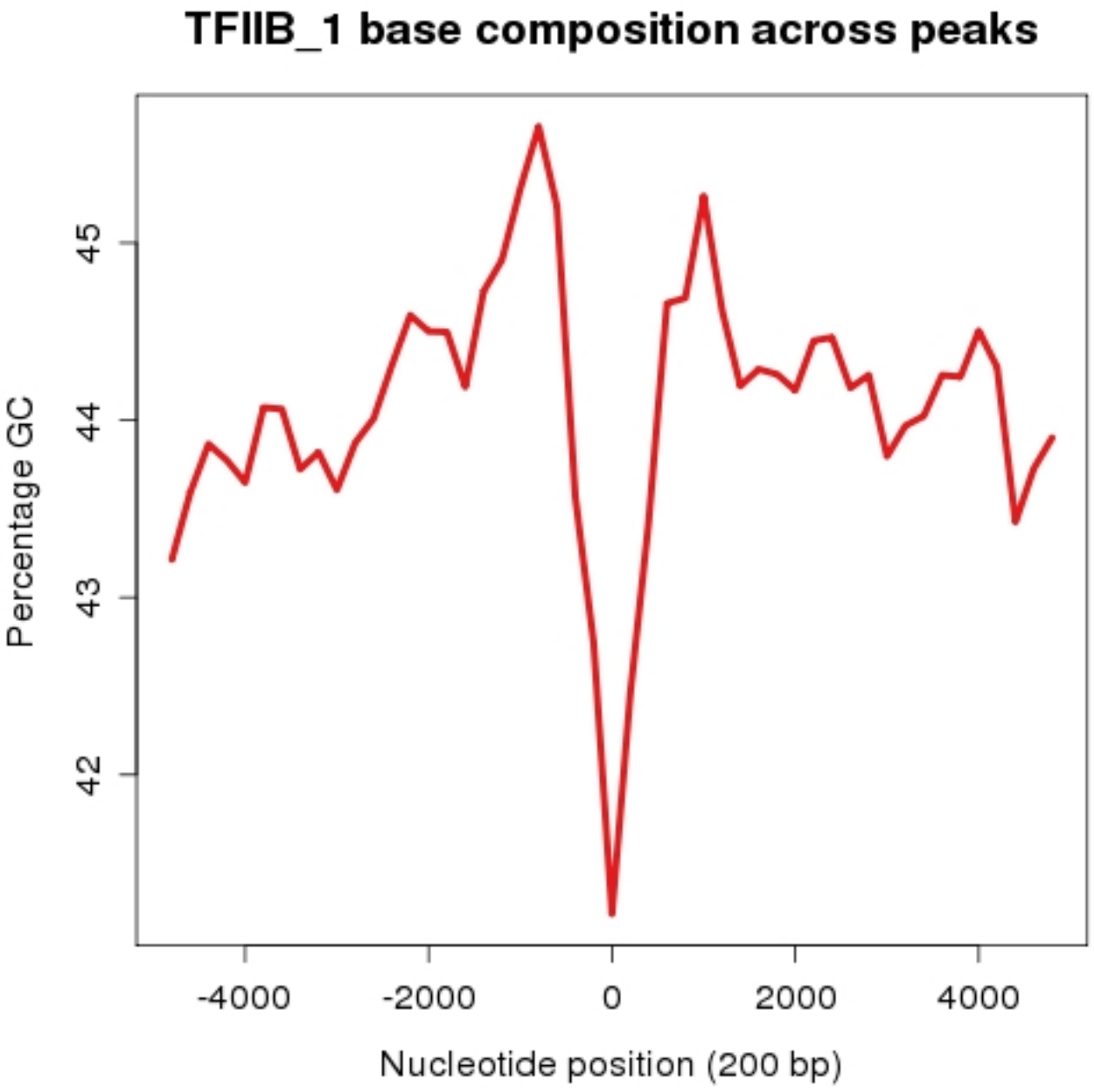
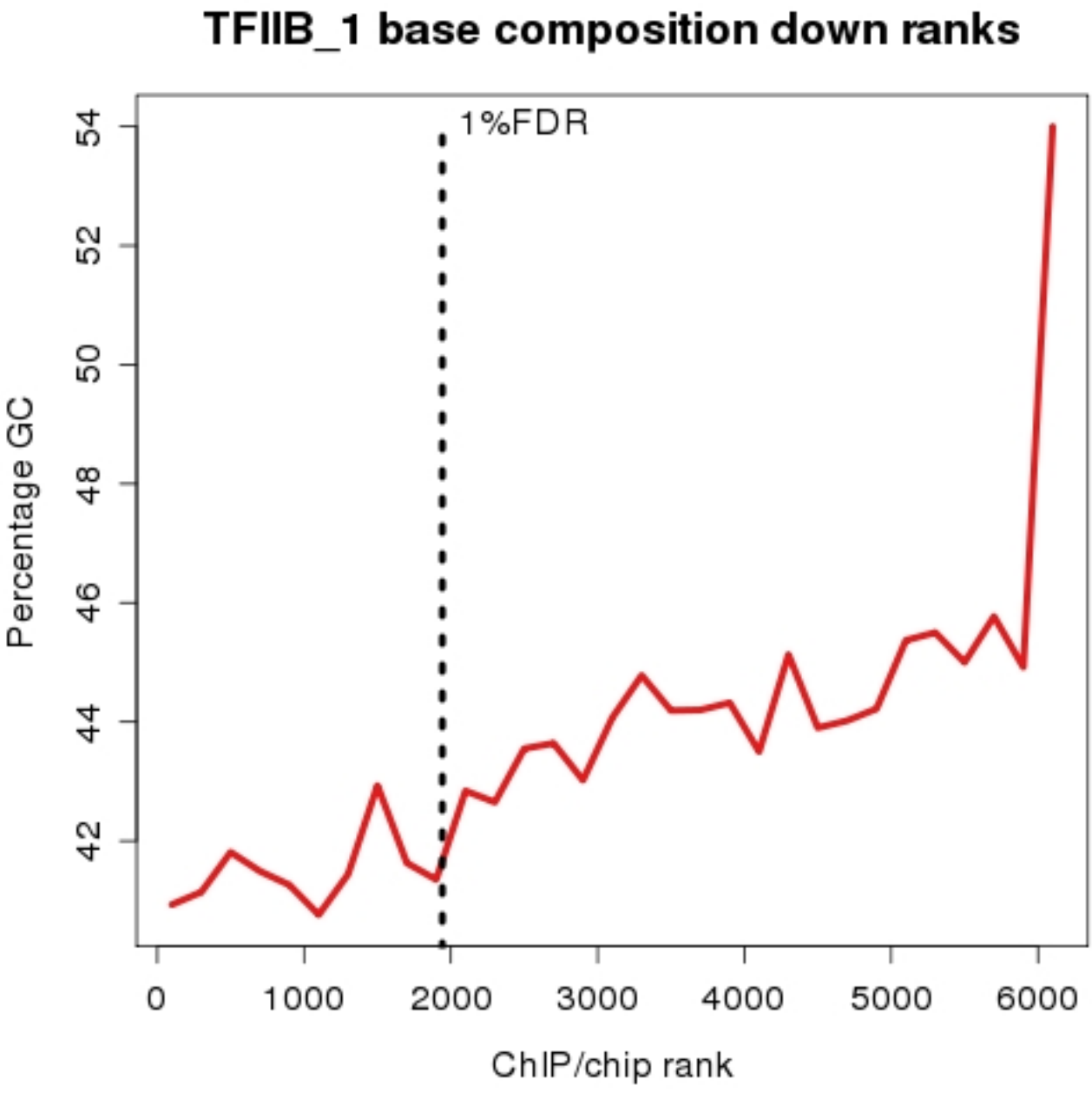
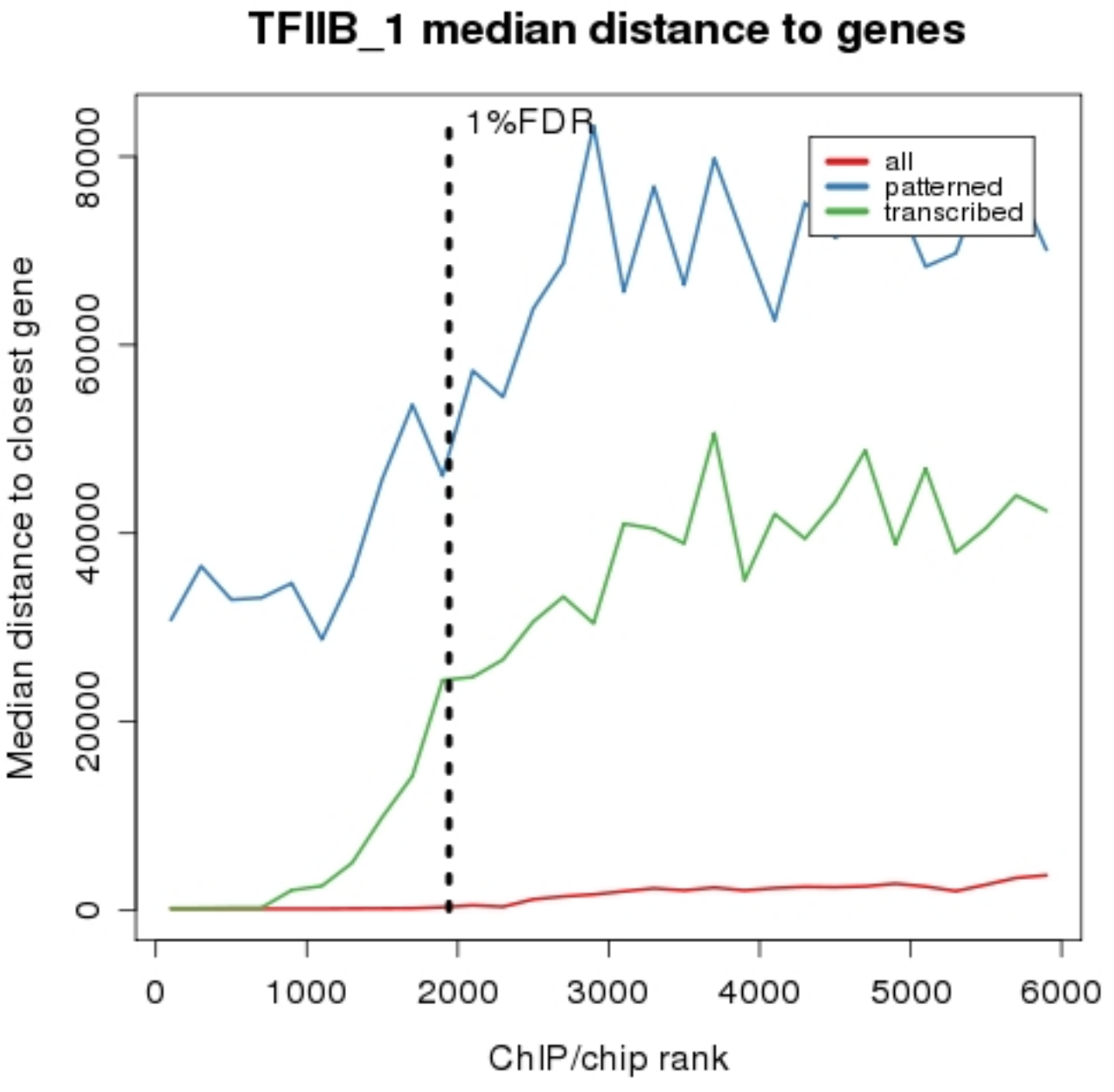
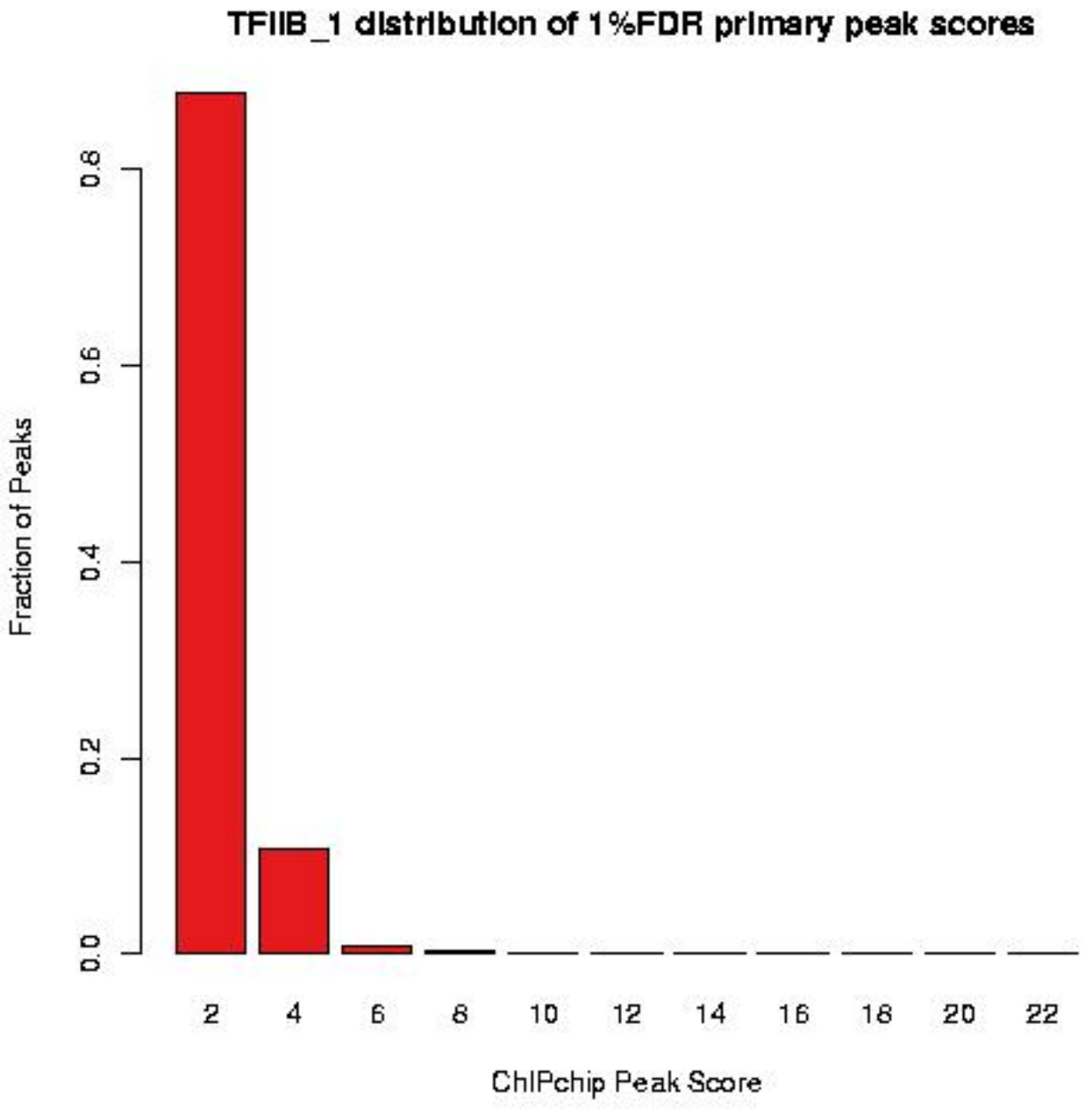

TFIIB_1 base composition across peaks
Percentage GC
42
43
44
45
-4000
-2000
0
2000
4000
Nucleotide position (200 bp)


TFIIB_1 base composition down ranks
1%FDR
Percentage GC
42
44
46
48
50
52
54
0
1000
2000
3000
4000
5000
6000
ChIP/chip rank


TFIIB_1 median distance to genes
1%FDR
all
patterned
transcribed
Median distance to closest gene
0
20000
40000
60000
80000
0
1000
2000
3000
4000
5000
6000
ChIP/chip rank


TFIIB_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
14
16
18
20
22
ChIPchip Peak Score

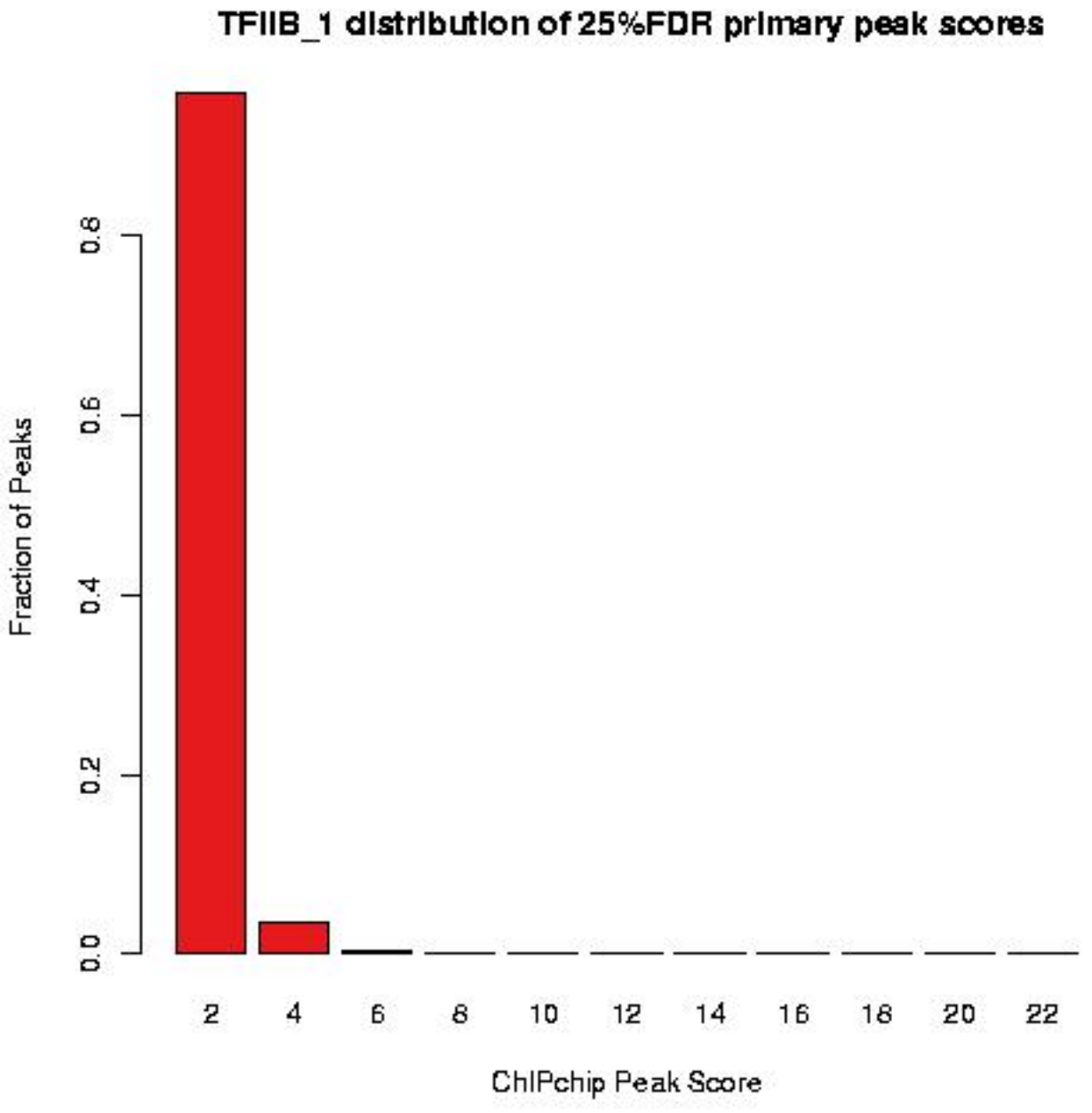

TFIIB_1 distribution of 25%FDR primary peak scores
Fraction of Peaks
0.0
0.2
0.4
0.6
0.8
2
4
6
8
10
12
14
16
18
20
22
ChIPchip Peak Score

Image Not Applicable

No Matrix (PWM)
for this factor

Image Not Applicable

No Matrix (PWM)
for this factor

Image Not Applicable

No Matrix (PWM)
for this factor

figure not available

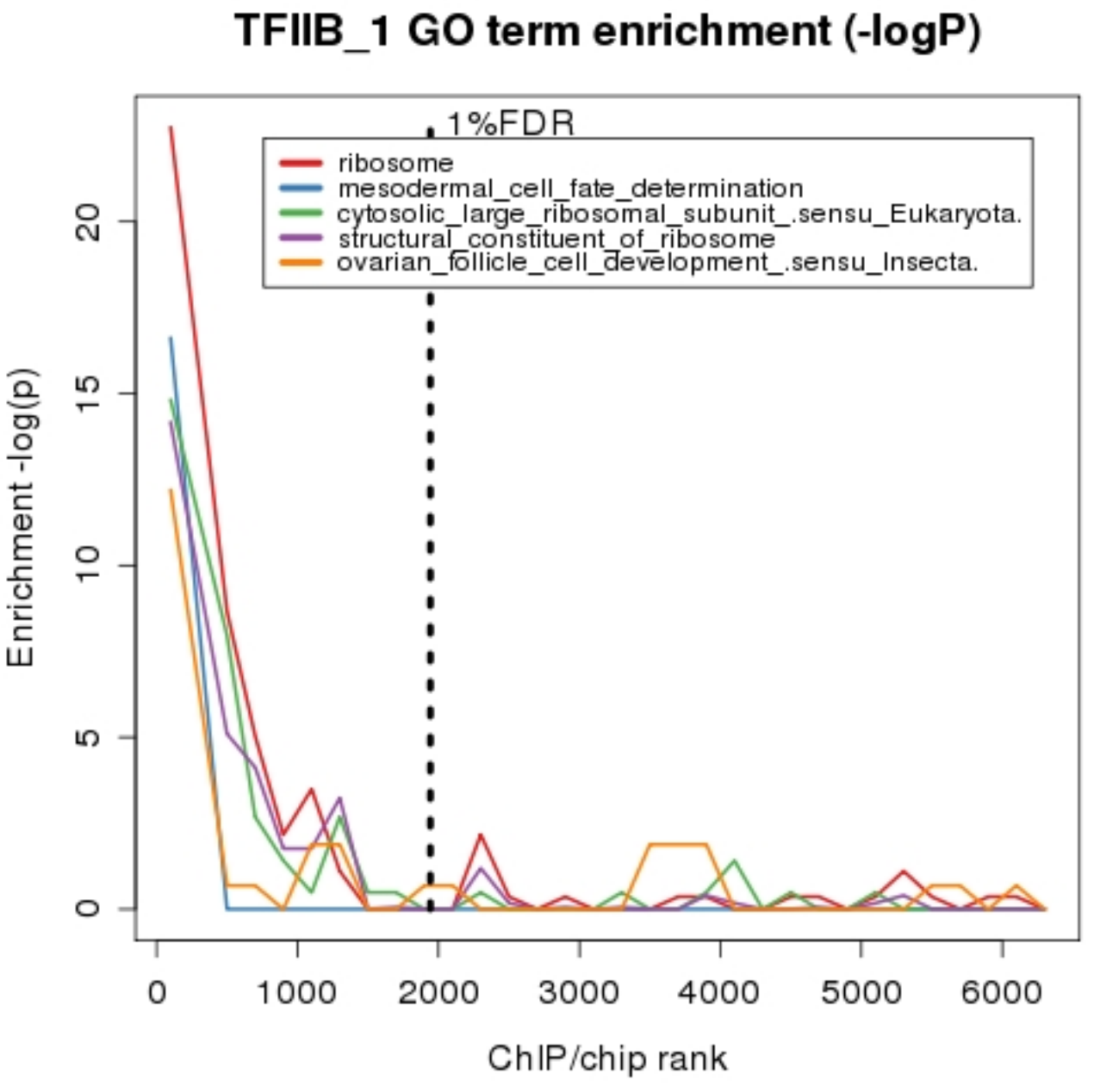
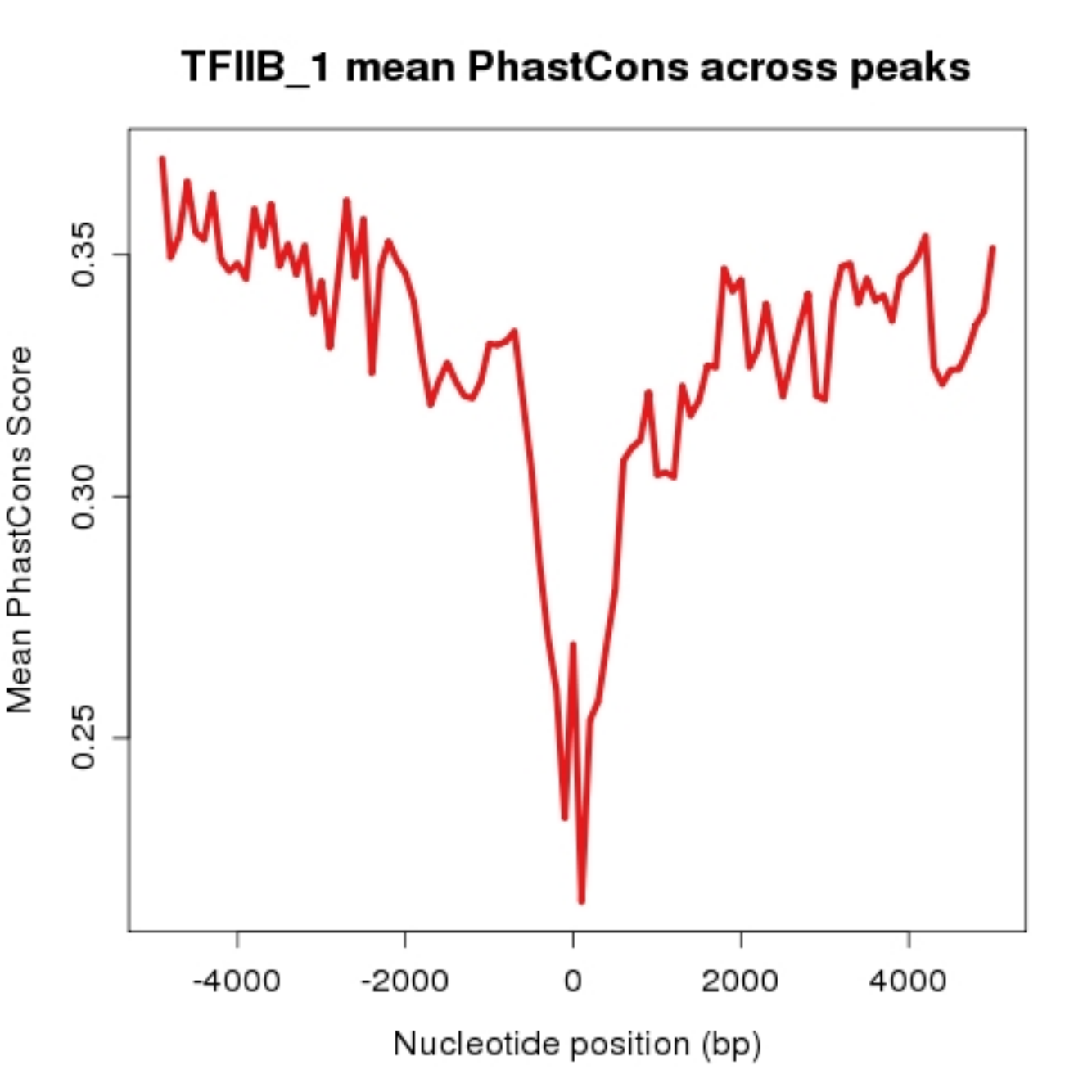
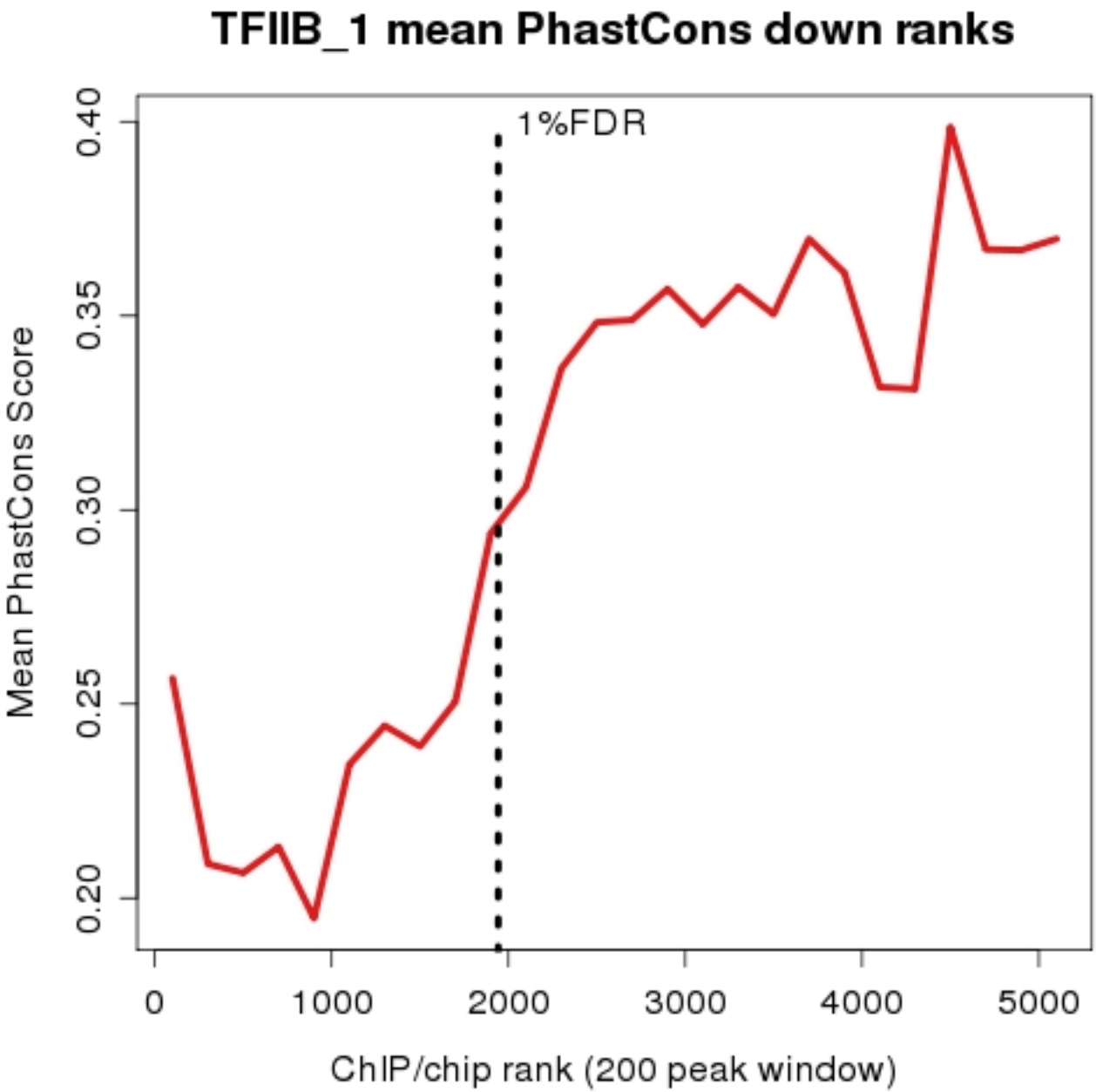

TFIIB_1 GO term enrichment (-logP)
1%FDR
ribosome
mesodermal_cell_fate_determination
cytosolic_large_ribosomal_subunit_.sensu_Eukaryota.
structural_constituent_of_ribosome
ovarian_follicle_cell_development_.sensu_Insecta.
Enrichment -log(p)
0
5
10
15
20
0
1000
2000
3000
4000
5000
6000
ChIP/chip rank

Image Not Applicable

No Matrix (PWM)
for this factor


TFIIB_1 mean PhastCons across peaks
Mean PhastCons Score
0.25
0.30
0.35
-4000
-2000
0
2000
4000
Nucleotide position (bp)


TFIIB_1 mean PhastCons down ranks
1%FDR
Mean PhastCons Score
0.20
0.25
0.30
0.35
0.40
0
1000
2000
3000
4000
5000
ChIP/chip rank (200 peak window)