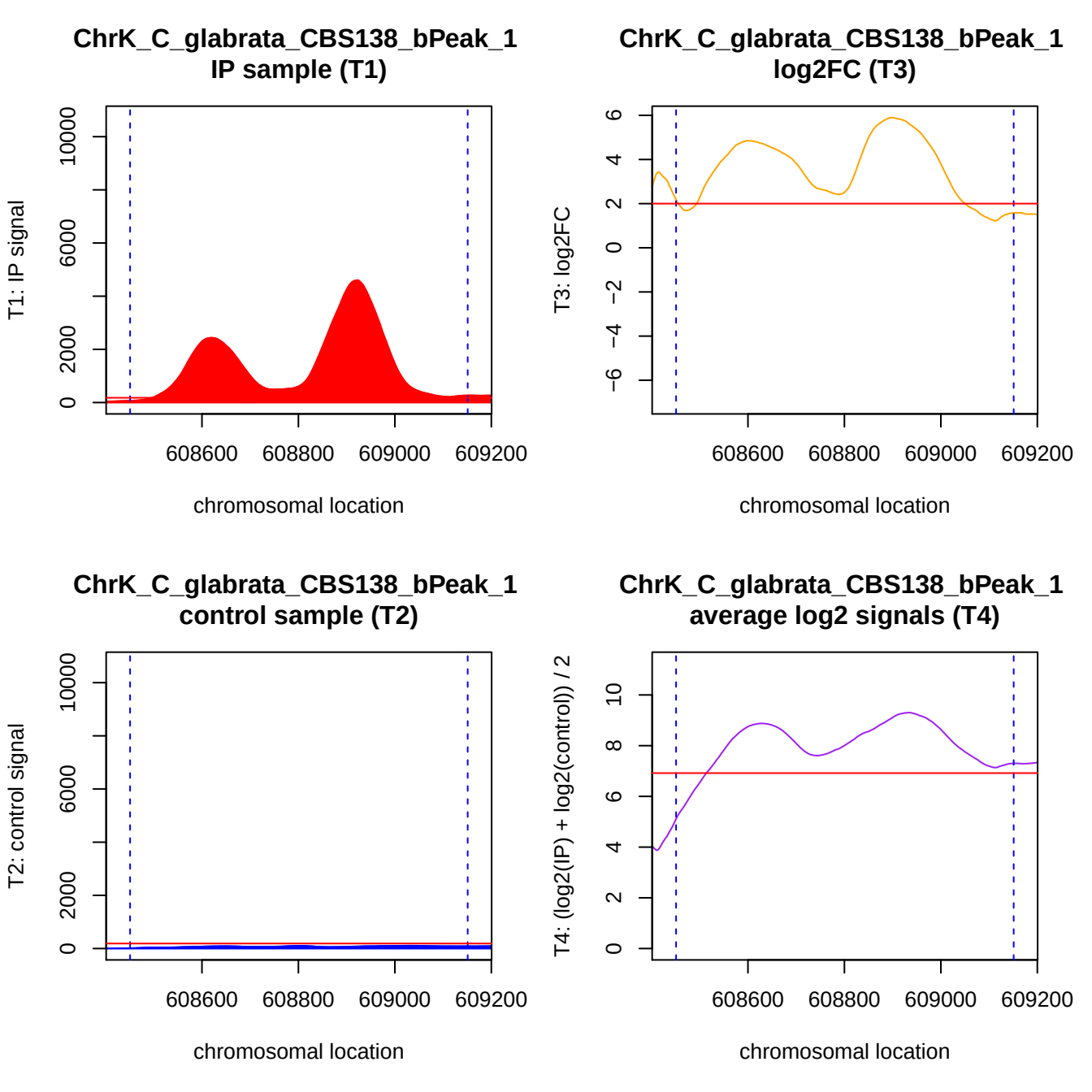
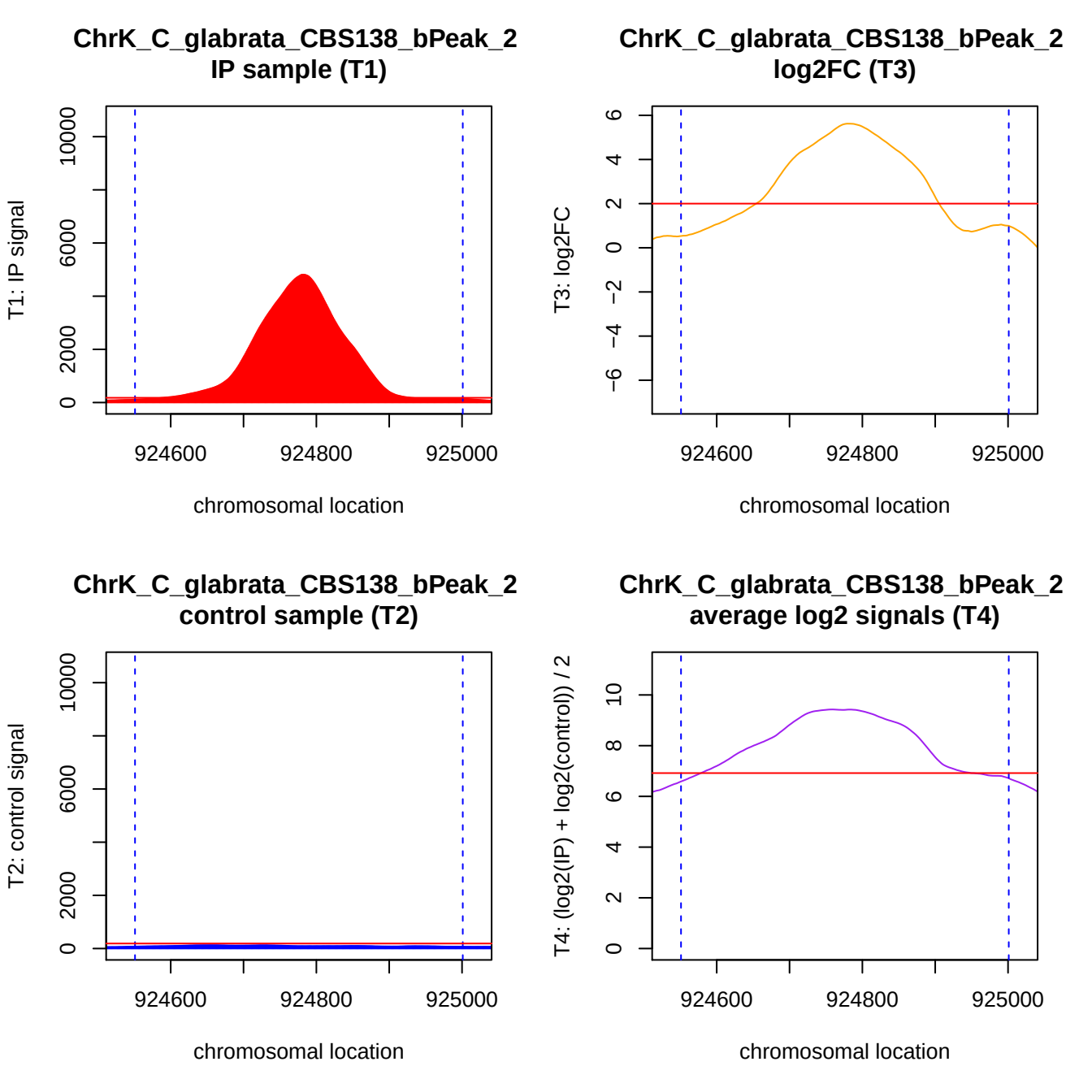
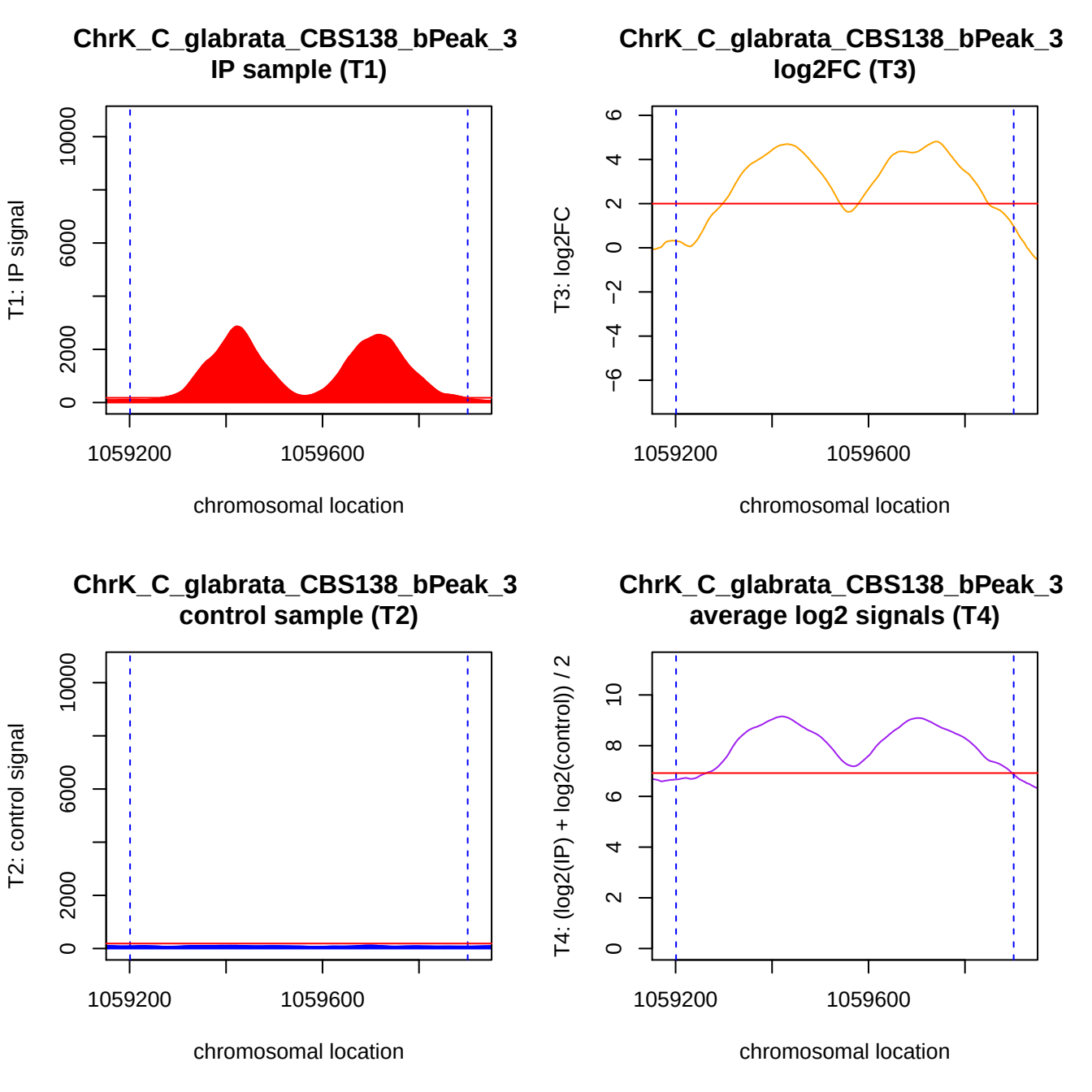
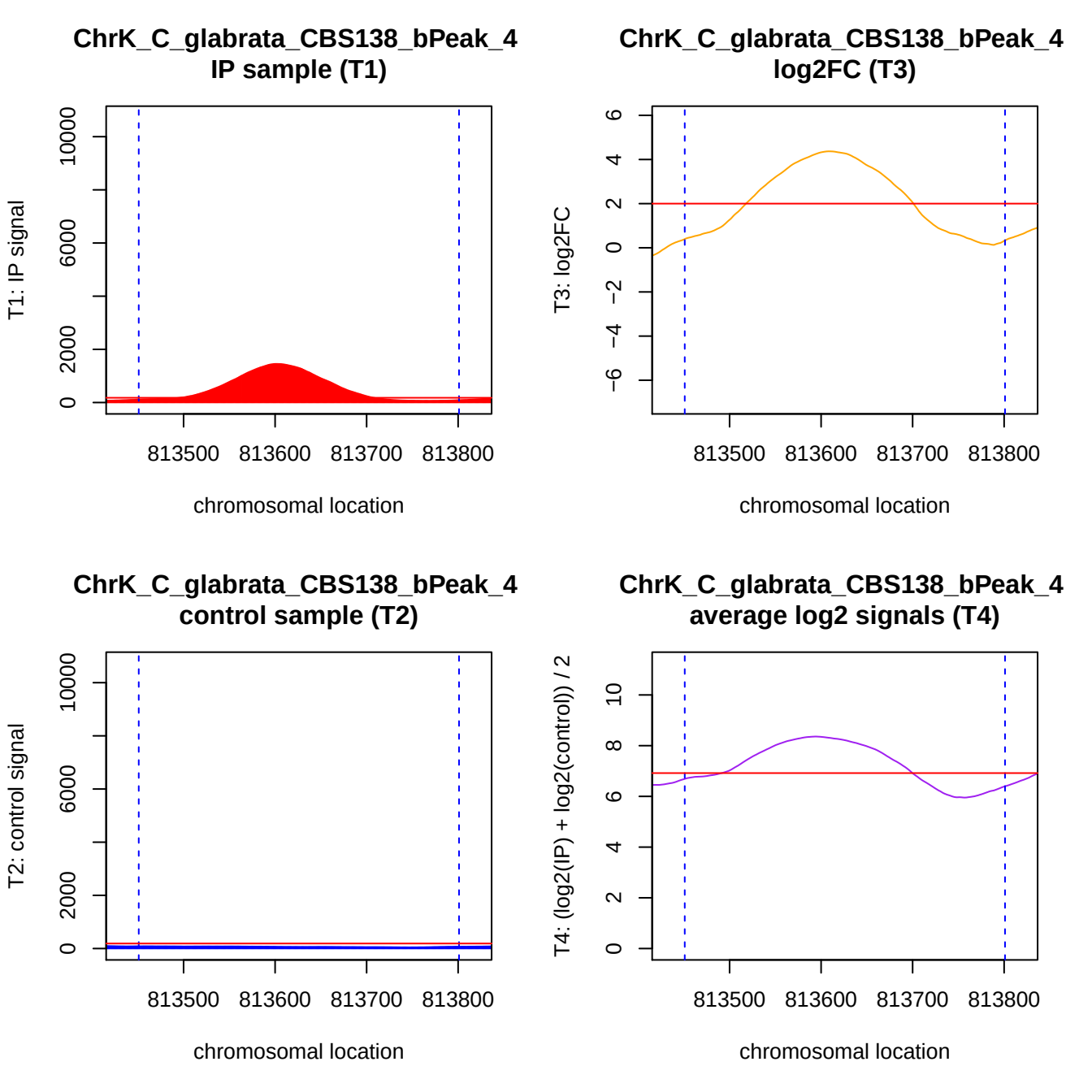
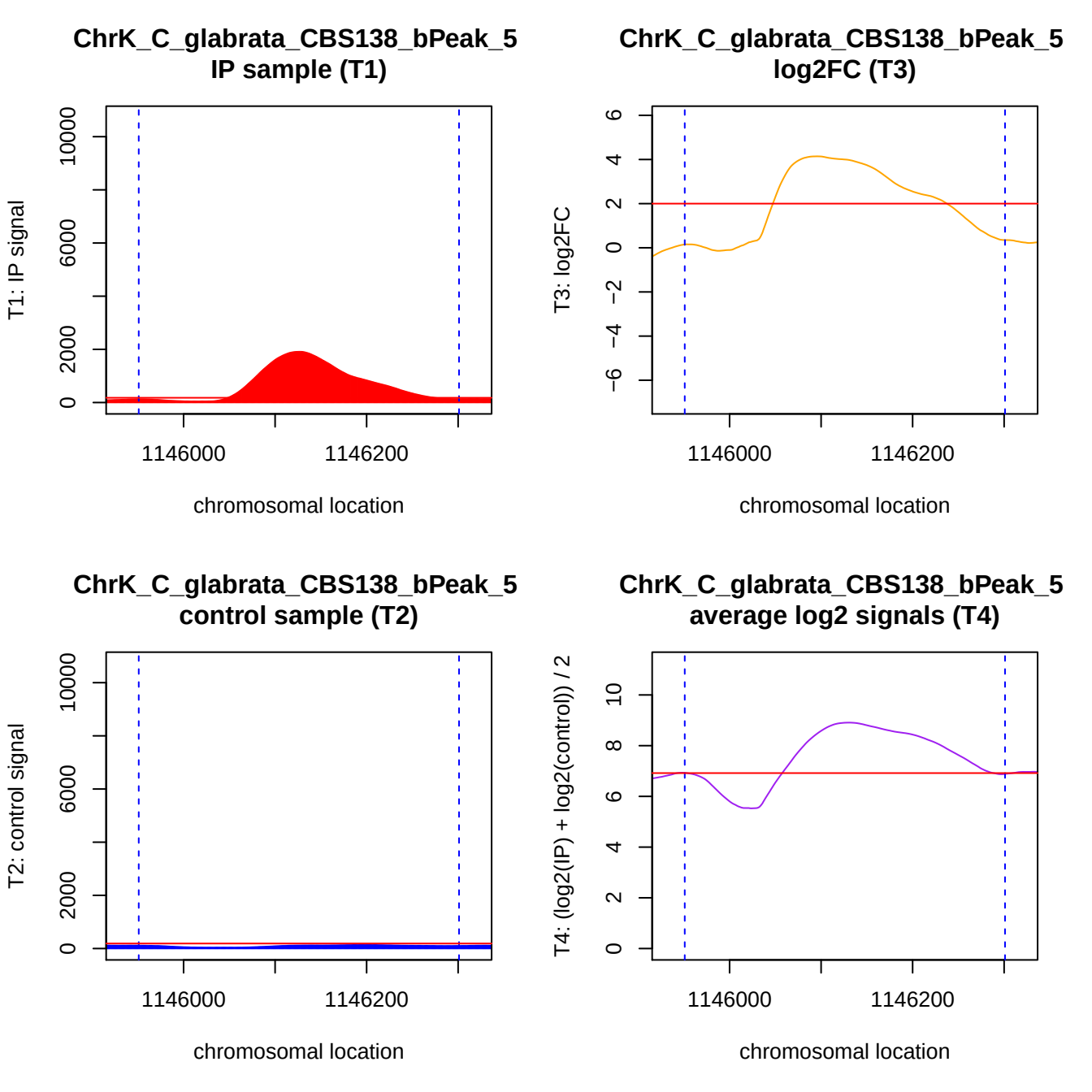
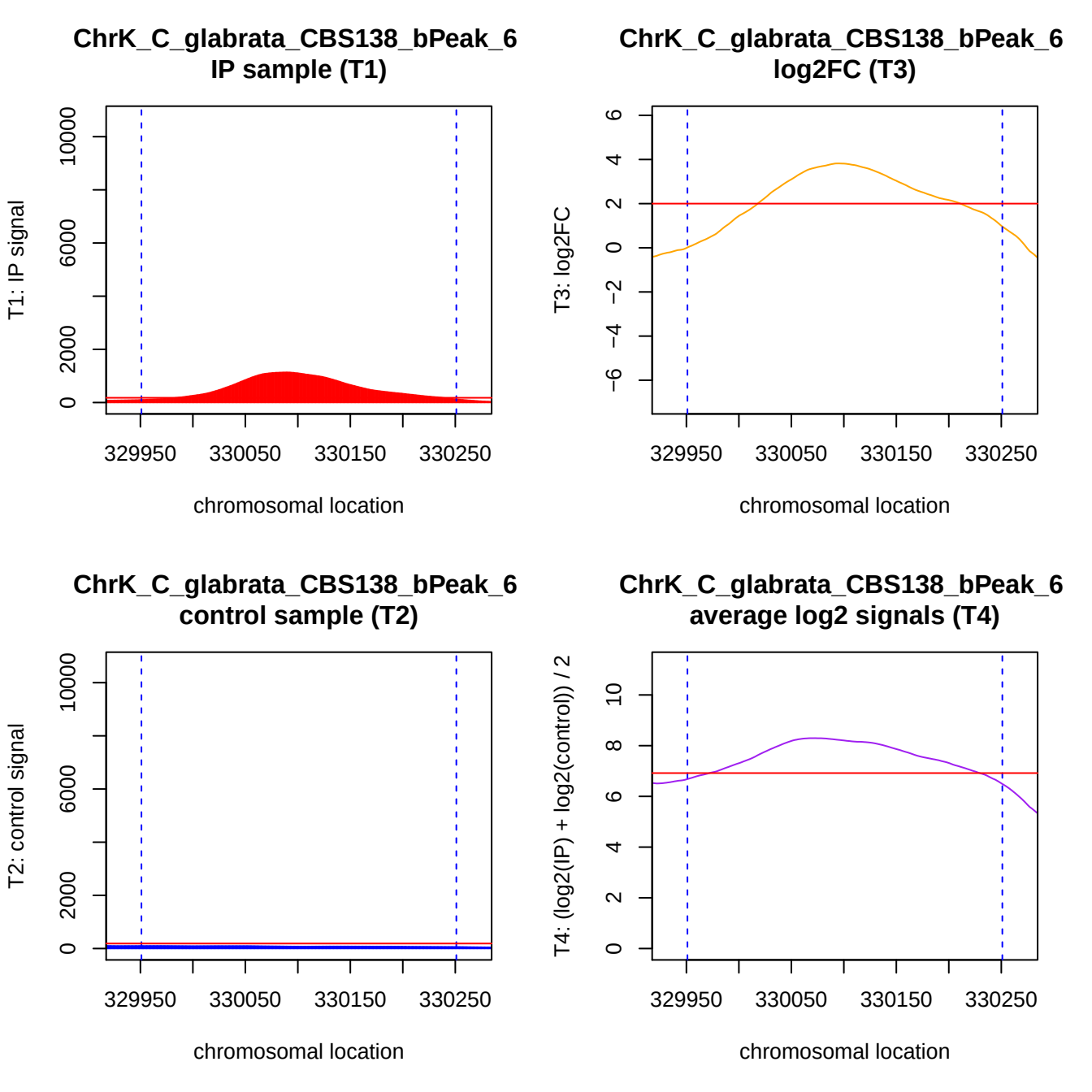

ChrK_C_glabrata_CBS138_bPeak_1
IP sample (T1)
T1: IP signal
0
2000
6000
10000
608600
608800
609000
609200
chromosomal location
ChrK_C_glabrata_CBS138_bPeak_1
log2FC (T3)
T3: log2FC
−6
−4
−2
0
2
4
6
608600
608800
609000
609200
chromosomal location
ChrK_C_glabrata_CBS138_bPeak_1
control sample (T2)
T2: control signal
0
2000
6000
10000
608600
608800
609000
609200
chromosomal location
ChrK_C_glabrata_CBS138_bPeak_1
average log2 signals (T4)
T4: (log2(IP) + log2(control)) / 2
0
2
4
6
8
10
608600
608800
609000
609200
chromosomal location

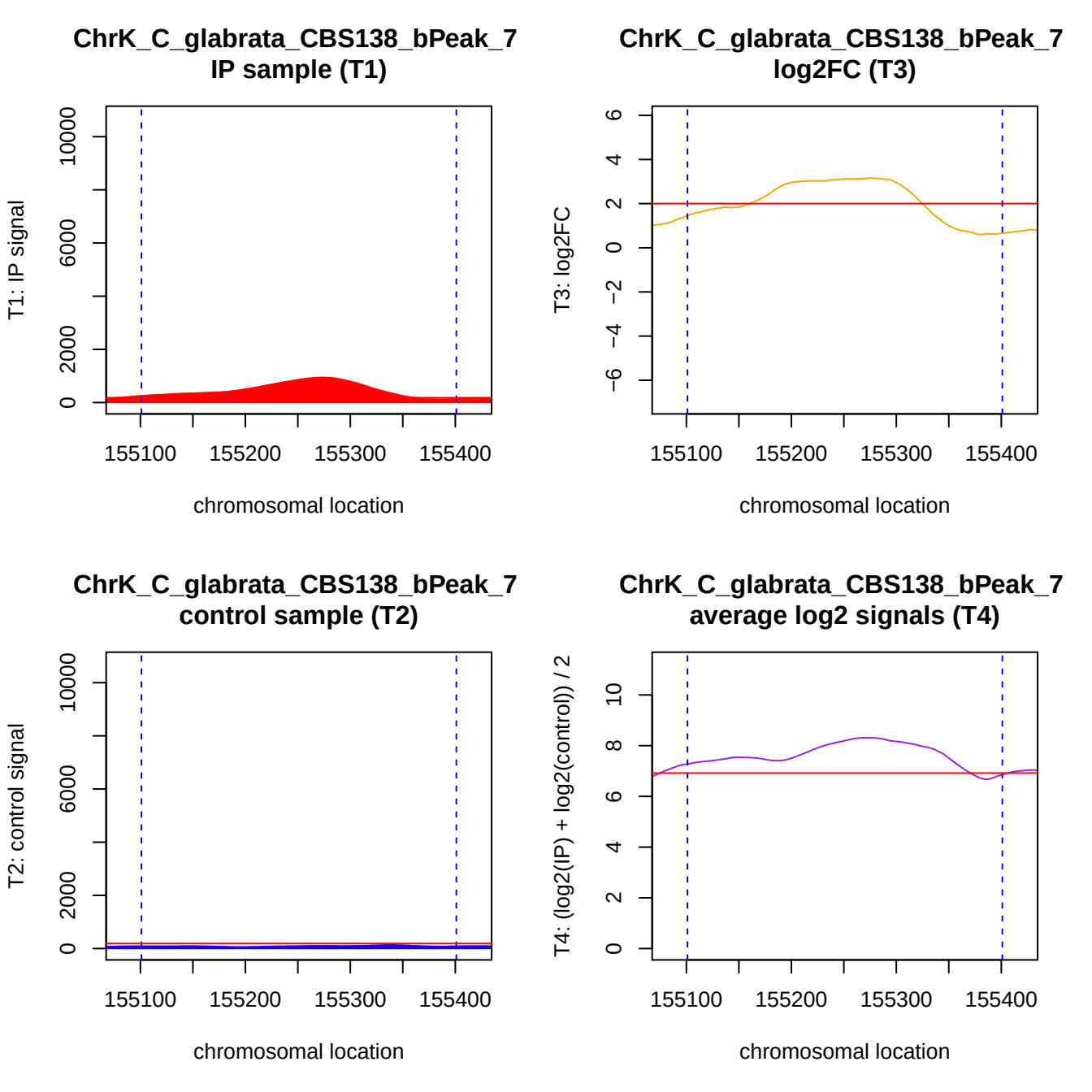

ChrK_C_glabrata_CBS138_bPeak_2
IP sample (T1)
T1: IP signal
0
2000
6000
10000
924600
924800
925000
chromosomal location
ChrK_C_glabrata_CBS138_bPeak_2
log2FC (T3)
T3: log2FC
−6
−4
−2
0
2
4
6
924600
924800
925000
chromosomal location
ChrK_C_glabrata_CBS138_bPeak_2
control sample (T2)
T2: control signal
0
2000
6000
10000
924600
924800
925000
chromosomal location
ChrK_C_glabrata_CBS138_bPeak_2
average log2 signals (T4)
T4: (log2(IP) + log2(control)) / 2
0
2
4
6
8
10
924600
924800
925000
chromosomal location

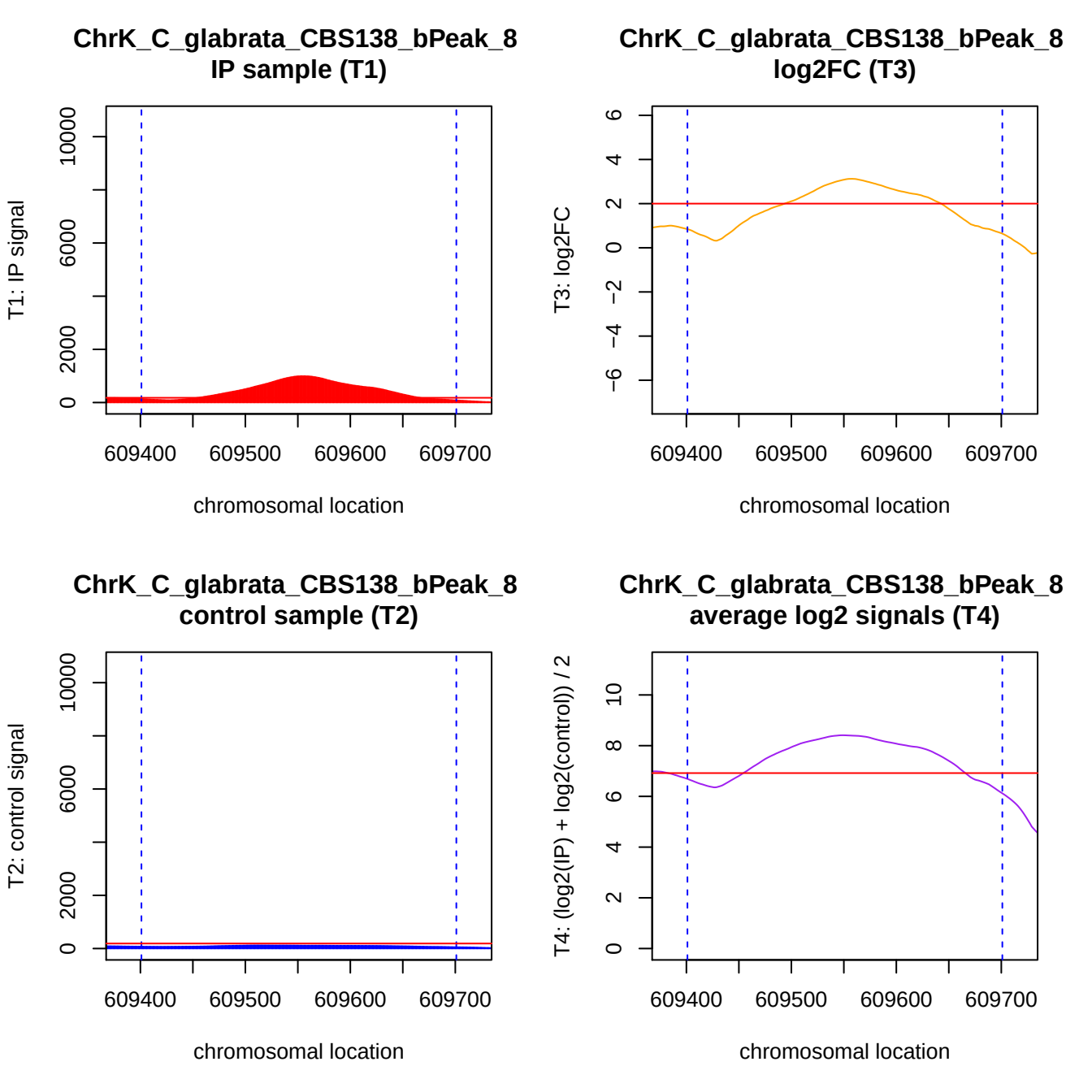

ChrK_C_glabrata_CBS138_bPeak_3
IP sample (T1)
T1: IP signal
0
2000
6000
10000
1059200
1059600
chromosomal location
ChrK_C_glabrata_CBS138_bPeak_3
log2FC (T3)
T3: log2FC
−6
−4
−2
0
2
4
6
1059200
1059600
chromosomal location
ChrK_C_glabrata_CBS138_bPeak_3
control sample (T2)
T2: control signal
0
2000
6000
10000
1059200
1059600
chromosomal location
ChrK_C_glabrata_CBS138_bPeak_3
average log2 signals (T4)
T4: (log2(IP) + log2(control)) / 2
0
2
4
6
8
10
1059200
1059600
chromosomal location

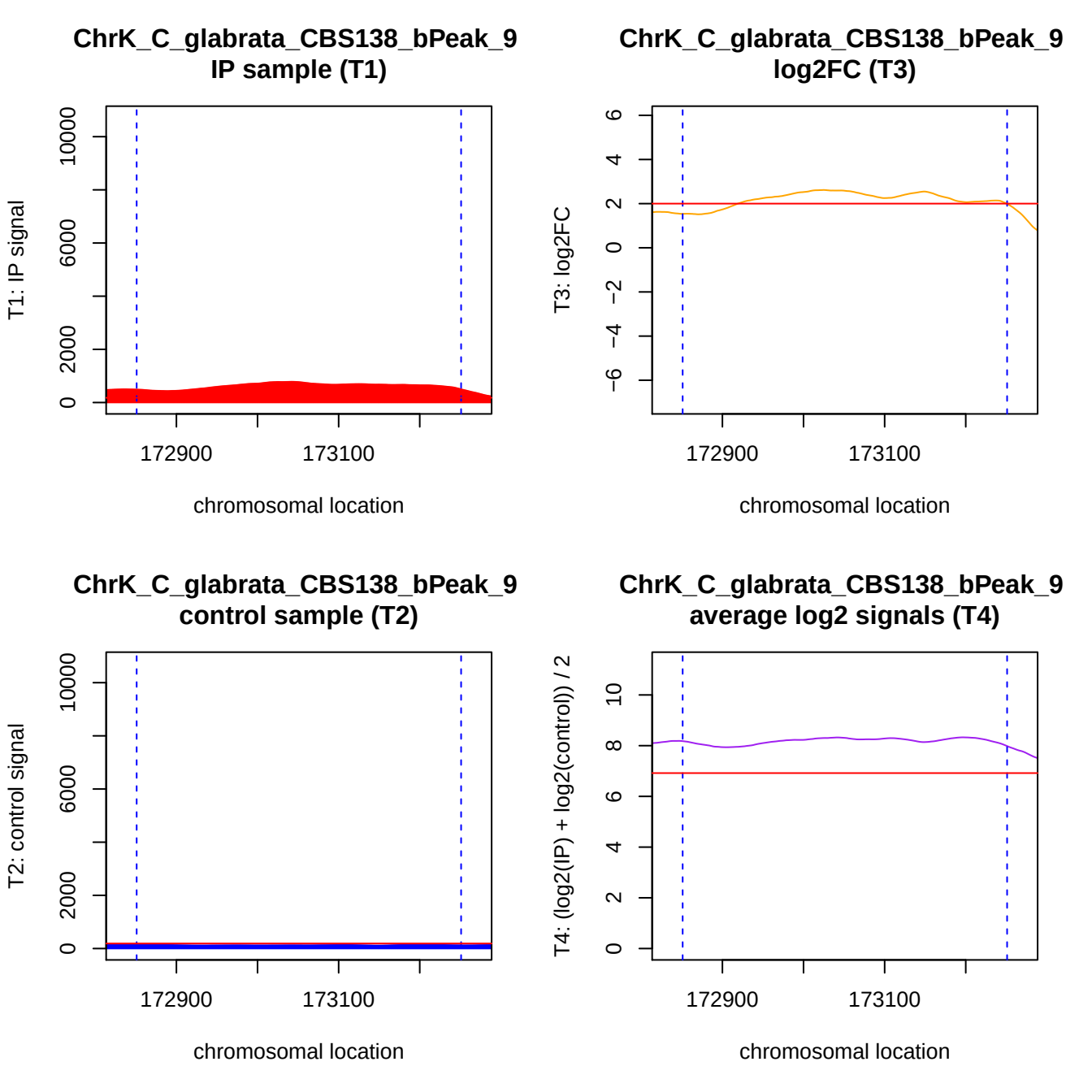

ChrK_C_glabrata_CBS138_bPeak_4
IP sample (T1)
T1: IP signal
0
2000
6000
10000
813500
813600
813700
813800
chromosomal location
ChrK_C_glabrata_CBS138_bPeak_4
log2FC (T3)
T3: log2FC
−6
−4
−2
0
2
4
6
813500
813600
813700
813800
chromosomal location
ChrK_C_glabrata_CBS138_bPeak_4
control sample (T2)
T2: control signal
0
2000
6000
10000
813500
813600
813700
813800
chromosomal location
ChrK_C_glabrata_CBS138_bPeak_4
average log2 signals (T4)
T4: (log2(IP) + log2(control)) / 2
0
2
4
6
8
10
813500
813600
813700
813800
chromosomal location

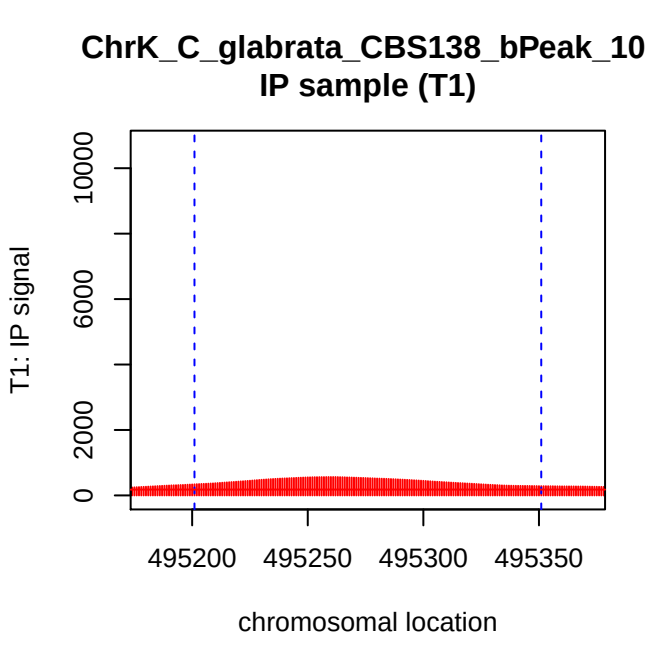

ChrK_C_glabrata_CBS138_bPeak_5
IP sample (T1)
T1: IP signal
0
2000
6000
10000
1146000
1146200
chromosomal location
ChrK_C_glabrata_CBS138_bPeak_5
log2FC (T3)
T3: log2FC
−6
−4
−2
0
2
4
6
1146000
1146200
chromosomal location
ChrK_C_glabrata_CBS138_bPeak_5
control sample (T2)
T2: control signal
0
2000
6000
10000
1146000
1146200
chromosomal location
ChrK_C_glabrata_CBS138_bPeak_5
average log2 signals (T4)
T4: (log2(IP) + log2(control)) / 2
0
2
4
6
8
10
1146000
1146200
chromosomal location

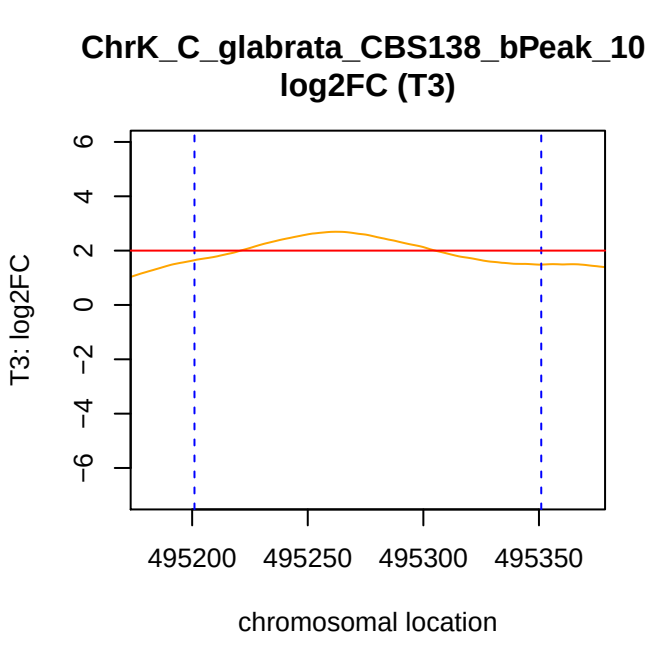

ChrK_C_glabrata_CBS138_bPeak_6
IP sample (T1)
T1: IP signal
0
2000
6000
10000
329950
330050
330150
330250
chromosomal location
ChrK_C_glabrata_CBS138_bPeak_6
log2FC (T3)
T3: log2FC
−6
−4
−2
0
2
4
6
329950
330050
330150
330250
chromosomal location
ChrK_C_glabrata_CBS138_bPeak_6
control sample (T2)
T2: control signal
0
2000
6000
10000
329950
330050
330150
330250
chromosomal location
ChrK_C_glabrata_CBS138_bPeak_6
average log2 signals (T4)
T4: (log2(IP) + log2(control)) / 2
0
2
4
6
8
10
329950
330050
330150
330250
chromosomal location

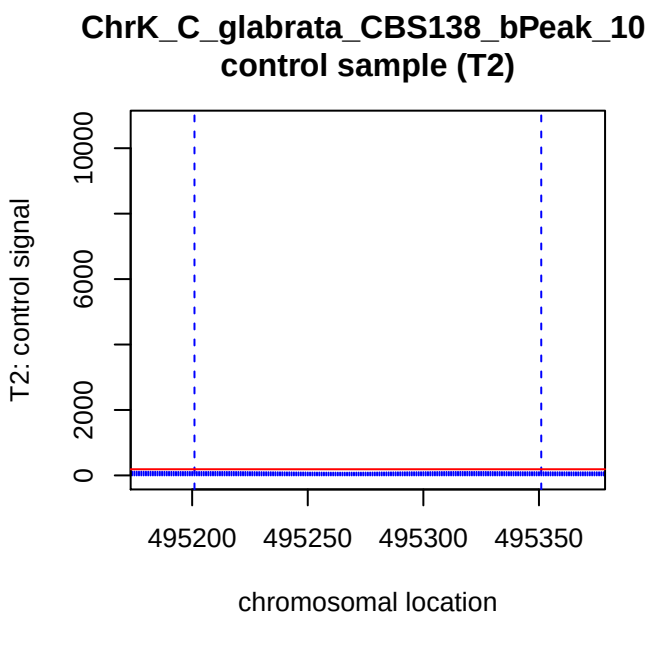

ChrK_C_glabrata_CBS138_bPeak_7
IP sample (T1)
T1: IP signal
0
2000
6000
10000
155100
155200
155300
155400
chromosomal location
ChrK_C_glabrata_CBS138_bPeak_7
log2FC (T3)
T3: log2FC
−6
−4
−2
0
2
4
6
155100
155200
155300
155400
chromosomal location
ChrK_C_glabrata_CBS138_bPeak_7
control sample (T2)
T2: control signal
0
2000
6000
10000
155100
155200
155300
155400
chromosomal location
ChrK_C_glabrata_CBS138_bPeak_7
average log2 signals (T4)
T4: (log2(IP) + log2(control)) / 2
0
2
4
6
8
10
155100
155200
155300
155400
chromosomal location

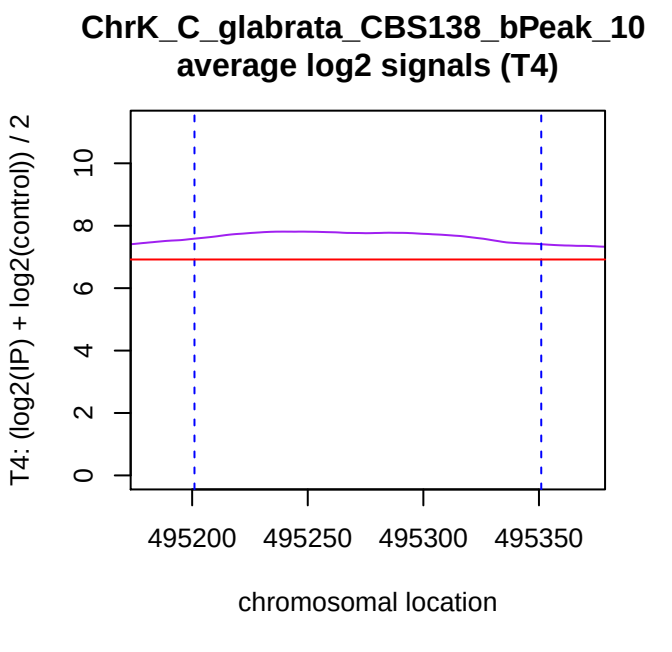

ChrK_C_glabrata_CBS138_bPeak_8
IP sample (T1)
T1: IP signal
0
2000
6000
10000
609400
609500
609600
609700
chromosomal location
ChrK_C_glabrata_CBS138_bPeak_8
log2FC (T3)
T3: log2FC
−6
−4
−2
0
2
4
6
609400
609500
609600
609700
chromosomal location
ChrK_C_glabrata_CBS138_bPeak_8
control sample (T2)
T2: control signal
0
2000
6000
10000
609400
609500
609600
609700
chromosomal location
ChrK_C_glabrata_CBS138_bPeak_8
average log2 signals (T4)
T4: (log2(IP) + log2(control)) / 2
0
2
4
6
8
10
609400
609500
609600
609700
chromosomal location

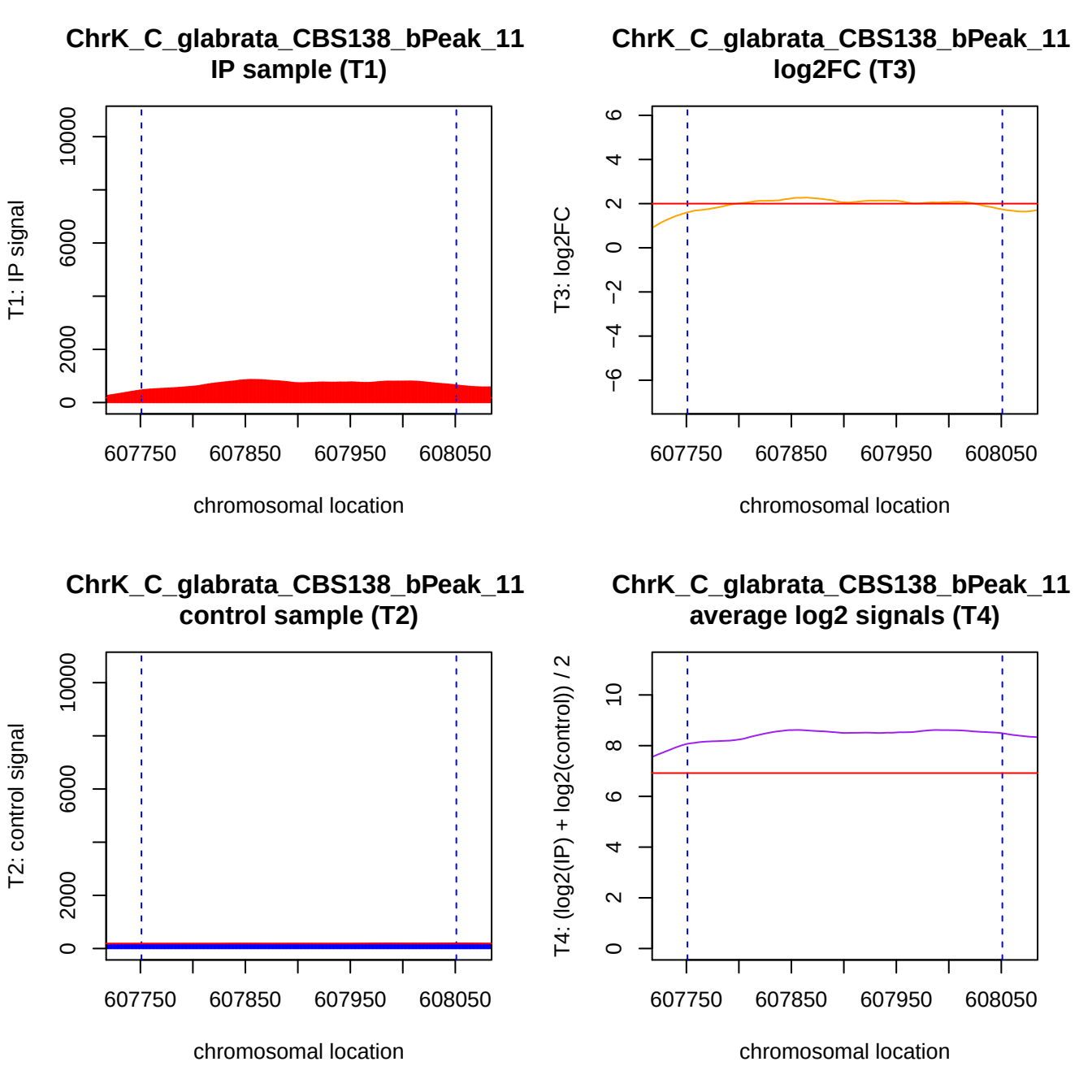

ChrK_C_glabrata_CBS138_bPeak_9
IP sample (T1)
T1: IP signal
0
2000
6000
10000
172900
173100
chromosomal location
ChrK_C_glabrata_CBS138_bPeak_9
log2FC (T3)
T3: log2FC
−6
−4
−2
0
2
4
6
172900
173100
chromosomal location
ChrK_C_glabrata_CBS138_bPeak_9
control sample (T2)
T2: control signal
0
2000
6000
10000
172900
173100
chromosomal location
ChrK_C_glabrata_CBS138_bPeak_9
average log2 signals (T4)
T4: (log2(IP) + log2(control)) / 2
0
2
4
6
8
10
172900
173100
chromosomal location


ChrK_C_glabrata_CBS138_bPeak_10
IP sample (T1)
T1: IP signal
0
2000
6000
10000
495200
495250
495300
495350
chromosomal location


ChrK_C_glabrata_CBS138_bPeak_10
log2FC (T3)
T3: log2FC
−6
−4
−2
0
2
4
6
495200
495250
495300
495350
chromosomal location


ChrK_C_glabrata_CBS138_bPeak_10
control sample (T2)
T2: control signal
0
2000
6000
10000
495200
495250
495300
495350
chromosomal location


ChrK_C_glabrata_CBS138_bPeak_10
average log2 signals (T4)
T4: (log2(IP) + log2(control)) / 2
0
2
4
6
8
10
495200
495250
495300
495350
chromosomal location


ChrK_C_glabrata_CBS138_bPeak_11
IP sample (T1)
T1: IP signal
0
2000
6000
10000
607750
607850
607950
608050
chromosomal location
ChrK_C_glabrata_CBS138_bPeak_11
log2FC (T3)
T3: log2FC
−6
−4
−2
0
2
4
6
607750
607850
607950
608050
chromosomal location
ChrK_C_glabrata_CBS138_bPeak_11
control sample (T2)
T2: control signal
0
2000
6000
10000
607750
607850
607950
608050
chromosomal location
ChrK_C_glabrata_CBS138_bPeak_11
average log2 signals (T4)
T4: (log2(IP) + log2(control)) / 2
0
2
4
6
8
10
607750
607850
607950
608050
chromosomal location