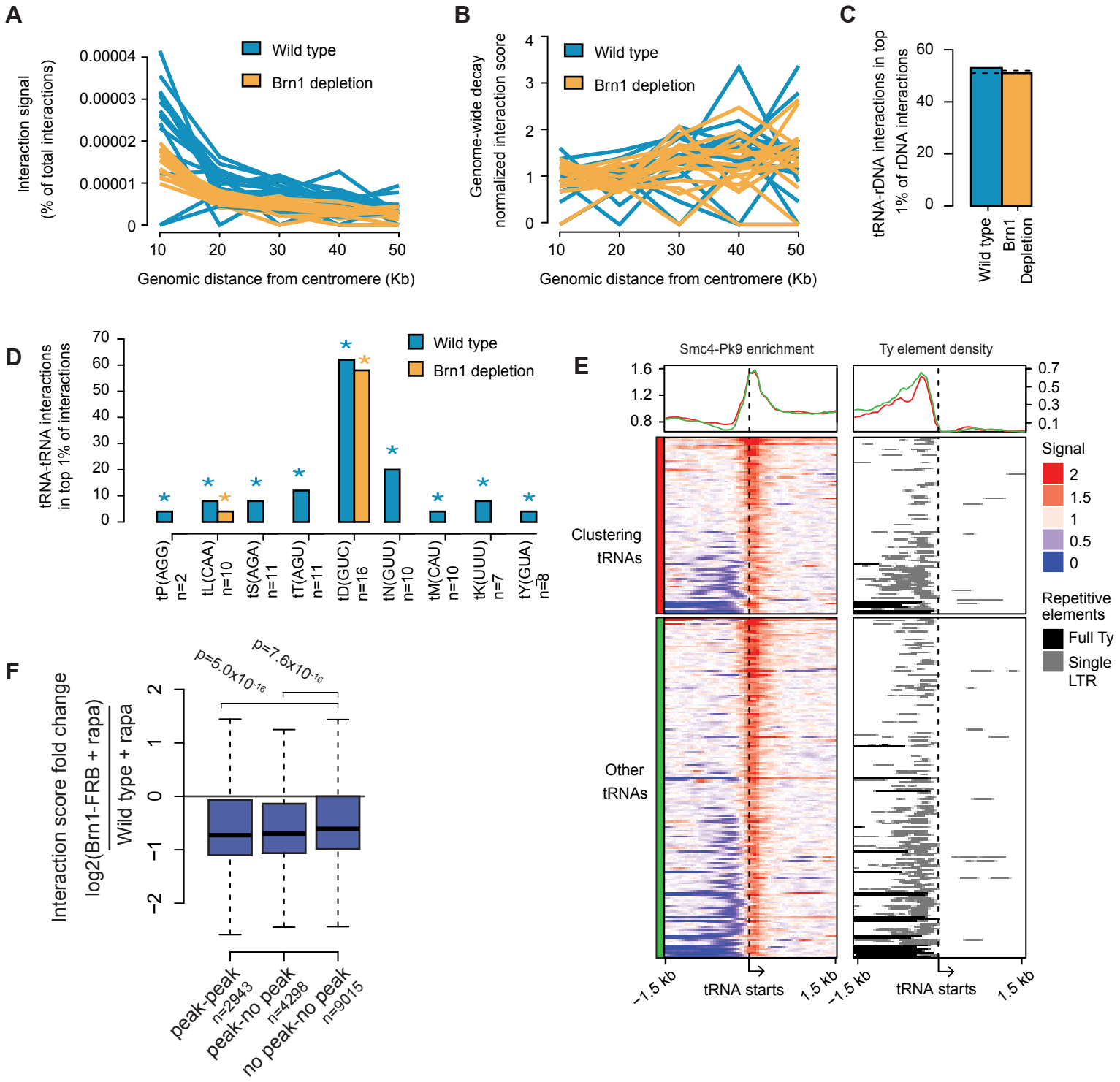
Figure S2


A
Interaction signal
(% of total interactions)
0.00004
0.00003
0.00002
0.00001
0
Wild type
Brn1 depletion
10
20
30
40
50
Genomic distance from centromere (Kb)
B
Genome-wide decay
normalized interaction score
4
3
2
1
0
Wild type
Brn1 depletion
10
20
30
40
50
Genomic distance from centromere (Kb)
C
tRNA-rDNA interactions in top
1% of rDNA interactions
60
40
20
0
Wild type
Brn1
Depletion
D
tRNA-tRNA interactions
in top 1% of interactions
70
60
50
40
30
20
10
0
Wild type
Brn1 depletion
tP(AGG)
n=2
tL(CAA)
n=10
tS(AGA)
n=11
tT(AGU)
n=11
tD(GUC)
n=16
tN(GUU)
n=10
tM(CAU)
n=10
tK(UUU)
n=7
tY(GUA)
n=8
E
Smc4-Pk9 enrichment
Ty element density
1.6
1.2
0.8
0.7
0.5
0.3
0.1
Signal
2
1.5
1
0.5
0
Repetitive
elements
Full Ty
Single
LTR
Clustering
tRNAs
Other
tRNAs
−1.5 kb
tRNA starts
1.5 kb
−1.5 kb
tRNA starts
1.5 kb
F
Interaction score fold change
log2(Brn1-FRB + rapa)
Wild type + rapa
2
1
0
−1
−2
p=5.0x10-16
p=7.6x10-16
peak-peak
n=2943
peak-no peak
n=4298
no peak-no peak
n=9015