Fig. S1

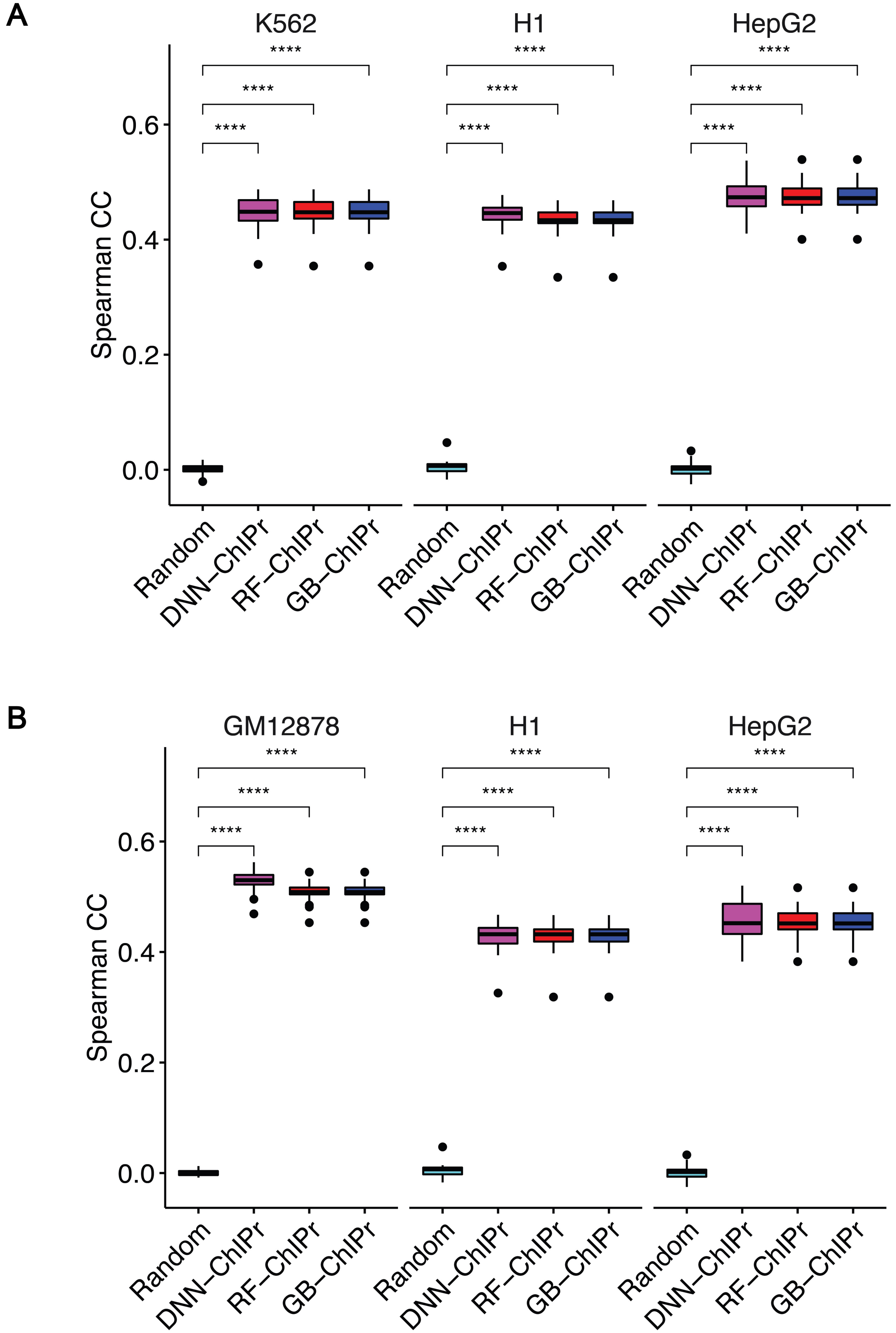

A
K562
H1
HepG2
****
****
****
Spearman CC
0.6
0.4
0.2
0.0
Random
DNN–ChIPr
RF–ChIPr
GB–ChIPr
B
GM12878
H1
HepG2
****
****
****
Spearman CC
0.6
0.4
0.2
0.0
Random
DNN–ChIPr
RF–ChIPr
GB–ChIPr

Fig. S2

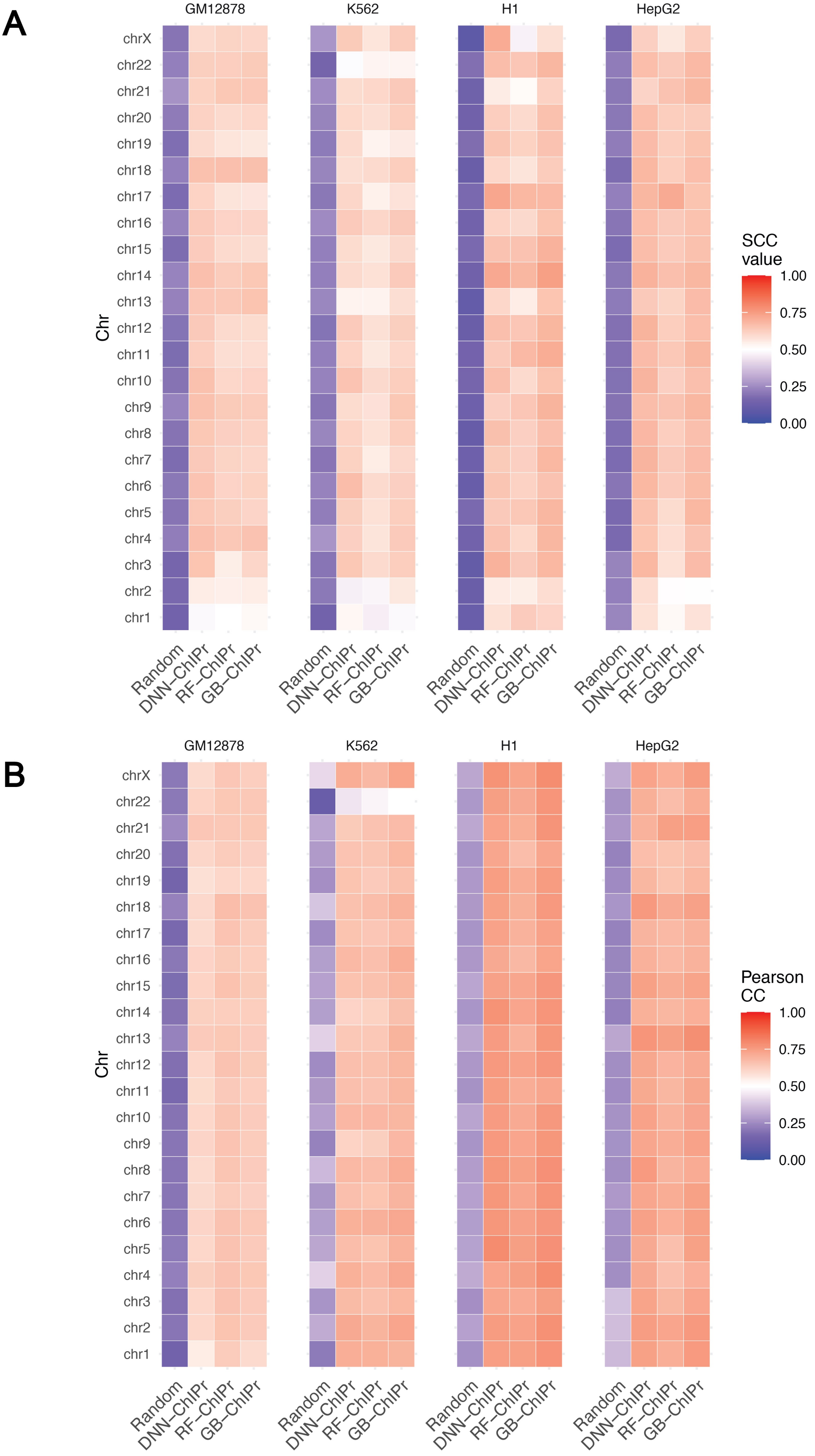

A
GM12878
K562
H1
HepG2
Chr
chrX
chr22
chr21
chr20
chr19
chr18
chr17
chr16
chr15
chr14
chr13
chr12
chr11
chr10
chr9
chr8
chr7
chr6
chr5
chr4
chr3
chr2
chr1
Random
DNN–ChIPr
RF–ChIPr
GB–ChIPr
SCC value
1.00
0.75
0.50
0.25
0.00
B
GM12878
K562
H1
HepG2
Chr
Random
DNN–ChIPr
RF–ChIPr
GB–ChIPr
Pearson CC
1.00
0.75
0.50
0.25
0.00

Fig. S3

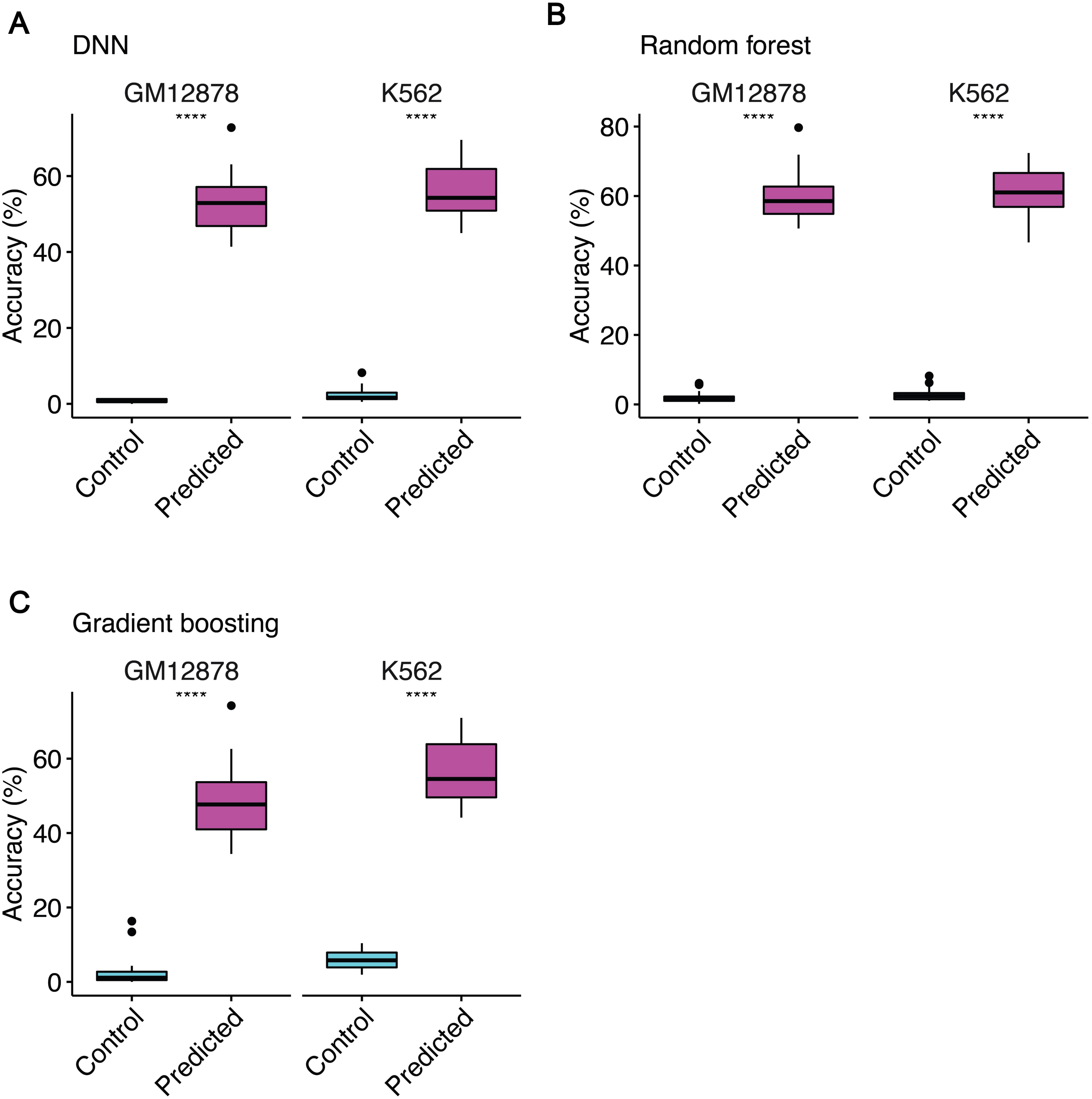

A
DNN
GM12878
K562
****
****
Accuracy (%)
0
20
40
60
Control
Predicted
Control
Predicted
B
Random forest
GM12878
K562
****
****
Accuracy (%)
0
20
40
60
80
Control
Predicted
Control
Predicted
C
Gradient boosting
GM12878
K562
****
****
Accuracy (%)
0
20
40
60
Control
Predicted
Control
Predicted

Fig. S4

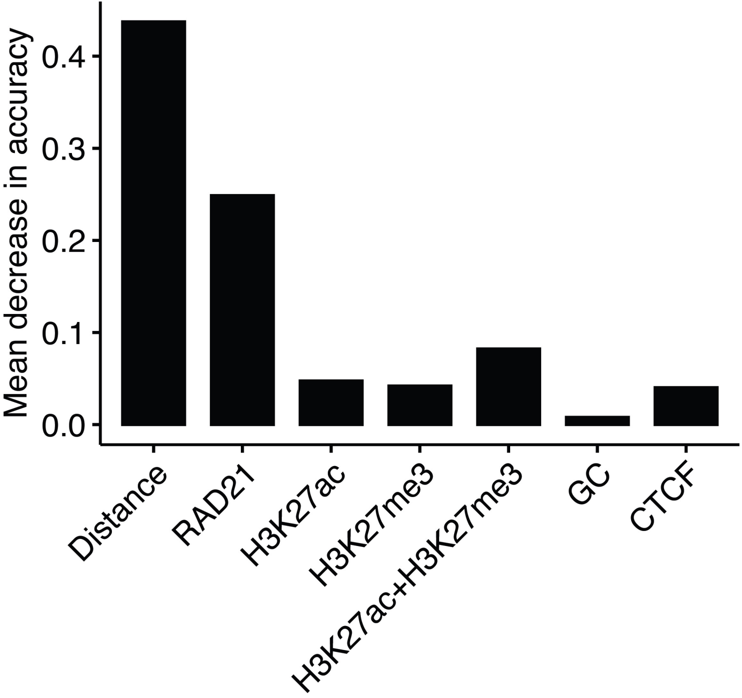

Mean decrease in accuracy
0.0
0.1
0.2
0.3
0.4
Distance
RAD21
H3K27ac
H3K27me3
H3K27ac+H3K27me3
GC
CTCF

Fig. S5

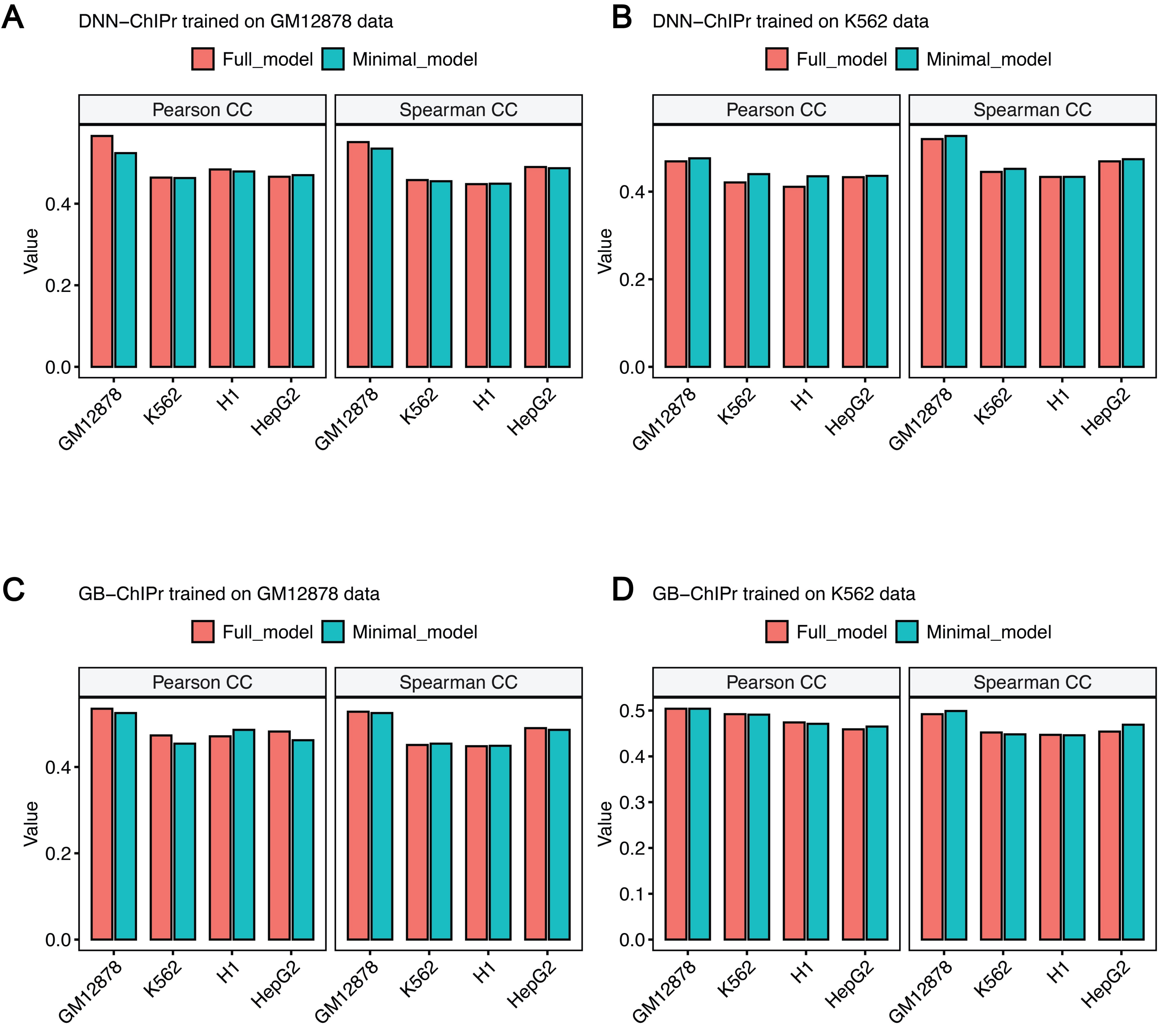

A
DNN−ChIPr trained on GM12878 data
B
DNN−ChIPr trained on K562 data
C
GB−ChIPr trained on GM12878 data
D
GB−ChIPr trained on K562 data
Full_model
Minimal_model
Pearson CC
Spearman CC
Value
0.0
0.1
0.2
0.3
0.4
0.5
GM12878
K562
H1
HepG2

Fig. S6

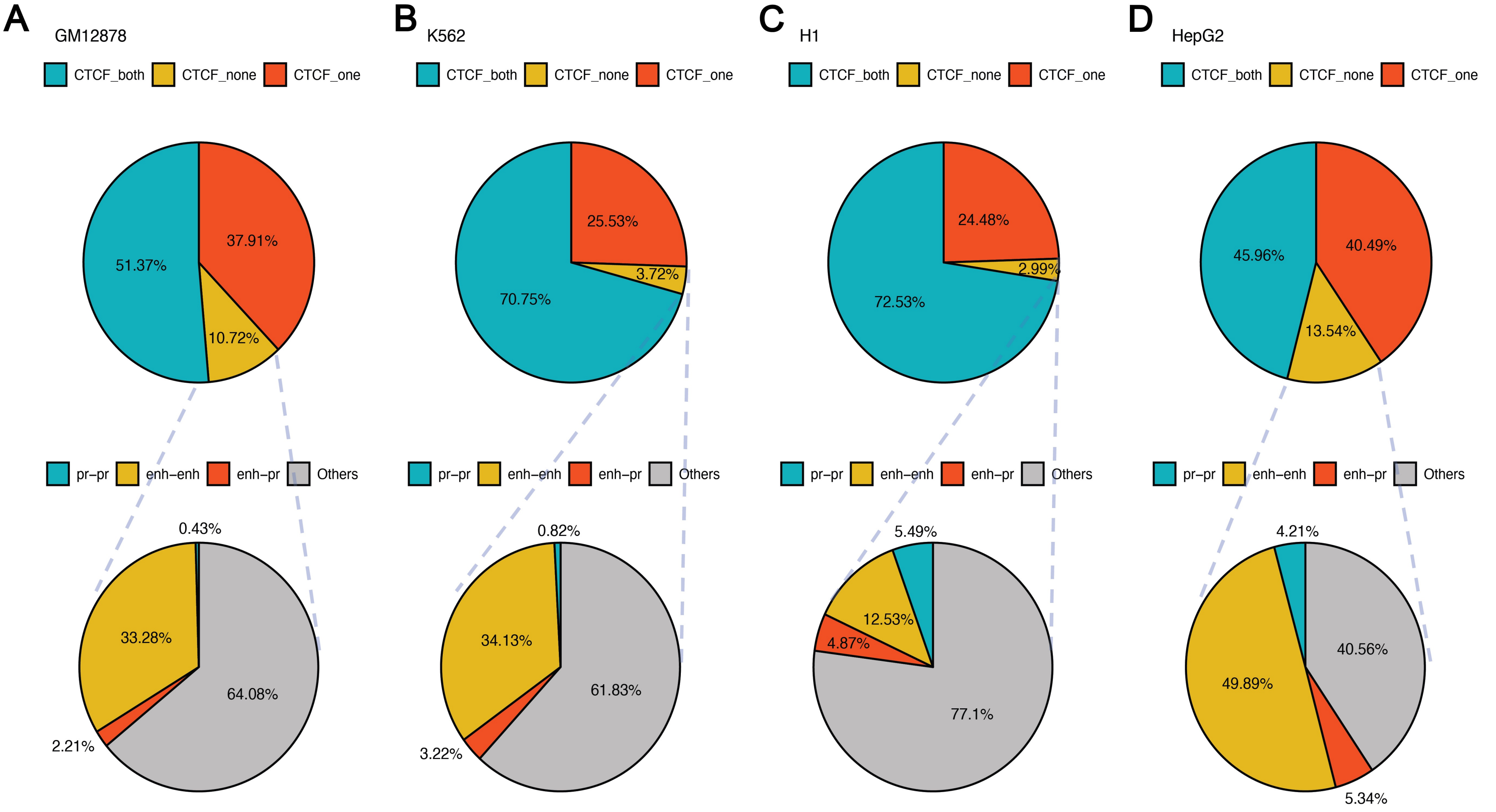

A
GM12878
CTCF_both
CTCF_none
CTCF_one
51.37%
37.91%
10.72%
pr−pr
enh−enh
enh−pr
Others
0.43%
33.28%
64.08%
2.21%
B
K562
CTCF_both
CTCF_none
CTCF_one
25.53%
3.72%
70.75%
pr−pr
enh−enh
enh−pr
Others
0.82%
34.13%
61.83%
3.22%
C
H1
CTCF_both
CTCF_none
CTCF_one
24.48%
2.99%
72.53%
pr−pr
enh−enh
enh−pr
Others
5.49%
12.53%
4.87%
77.1%
D
HepG2
CTCF_both
CTCF_none
CTCF_one
45.96%
40.49%
13.54%
pr−pr
enh−enh
enh−pr
Others
4.21%
40.56%
49.89%
5.34%

Fig. S7

H1 cell line

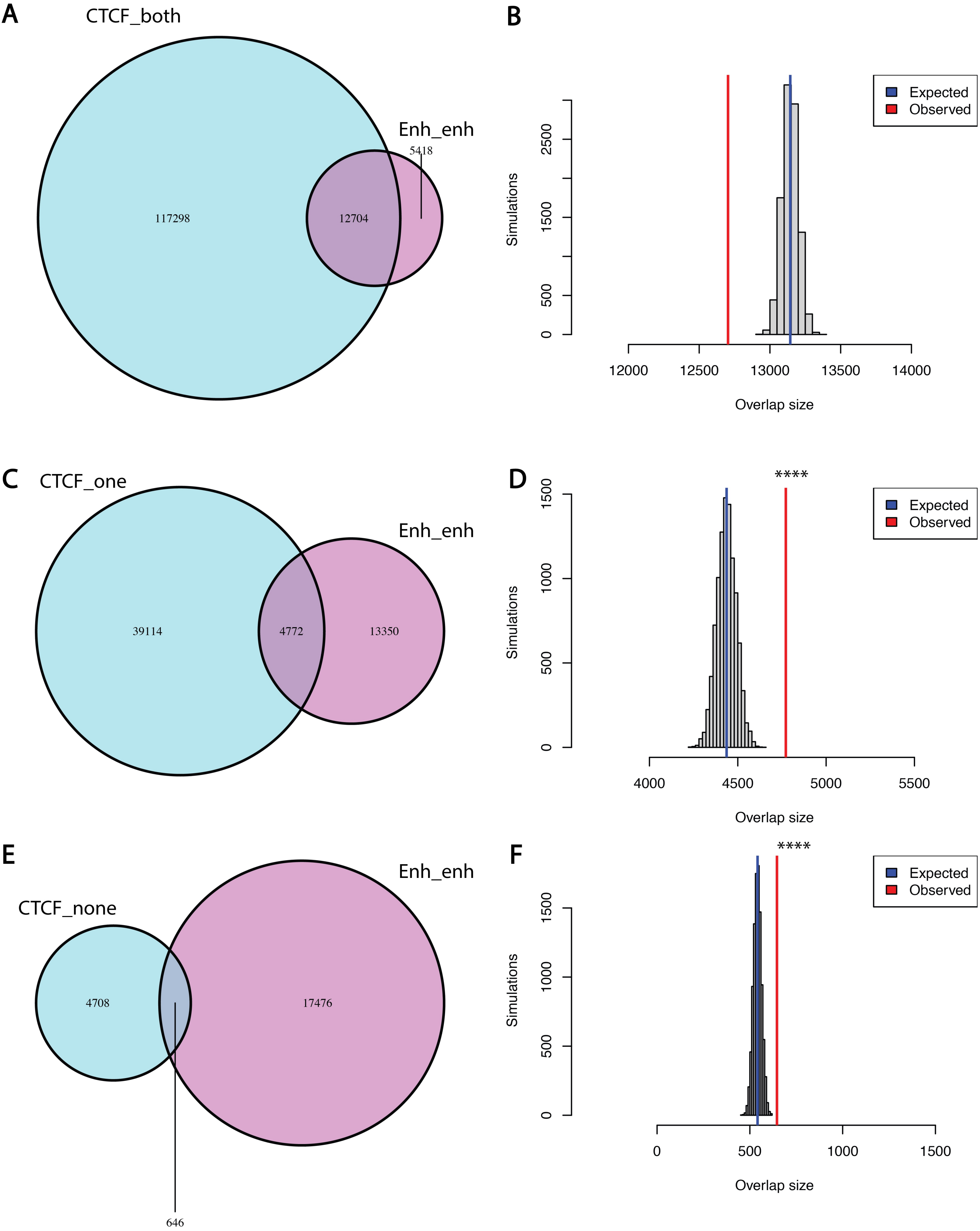


Fig. S8

HepG2 cell line

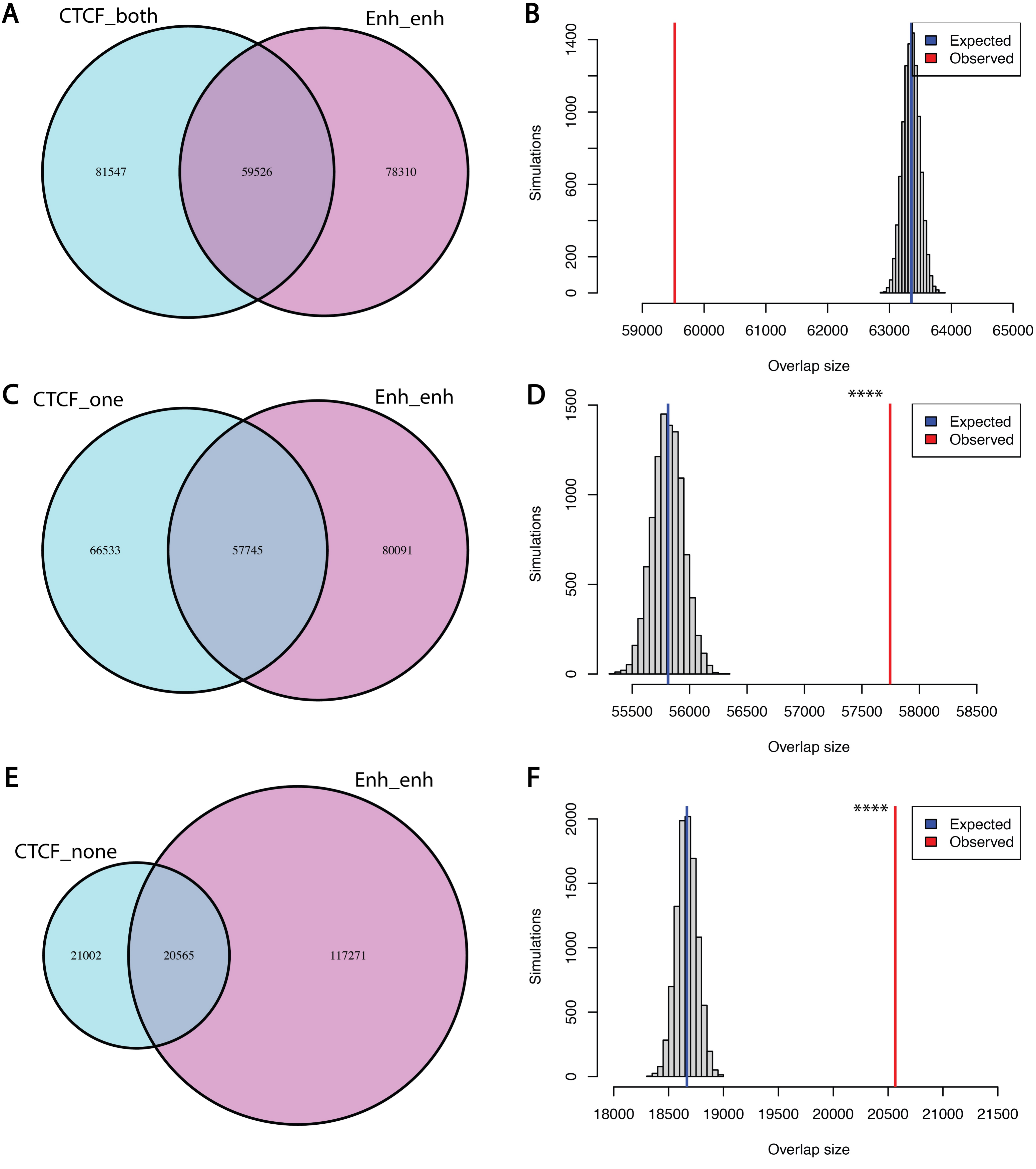


Fig. S9

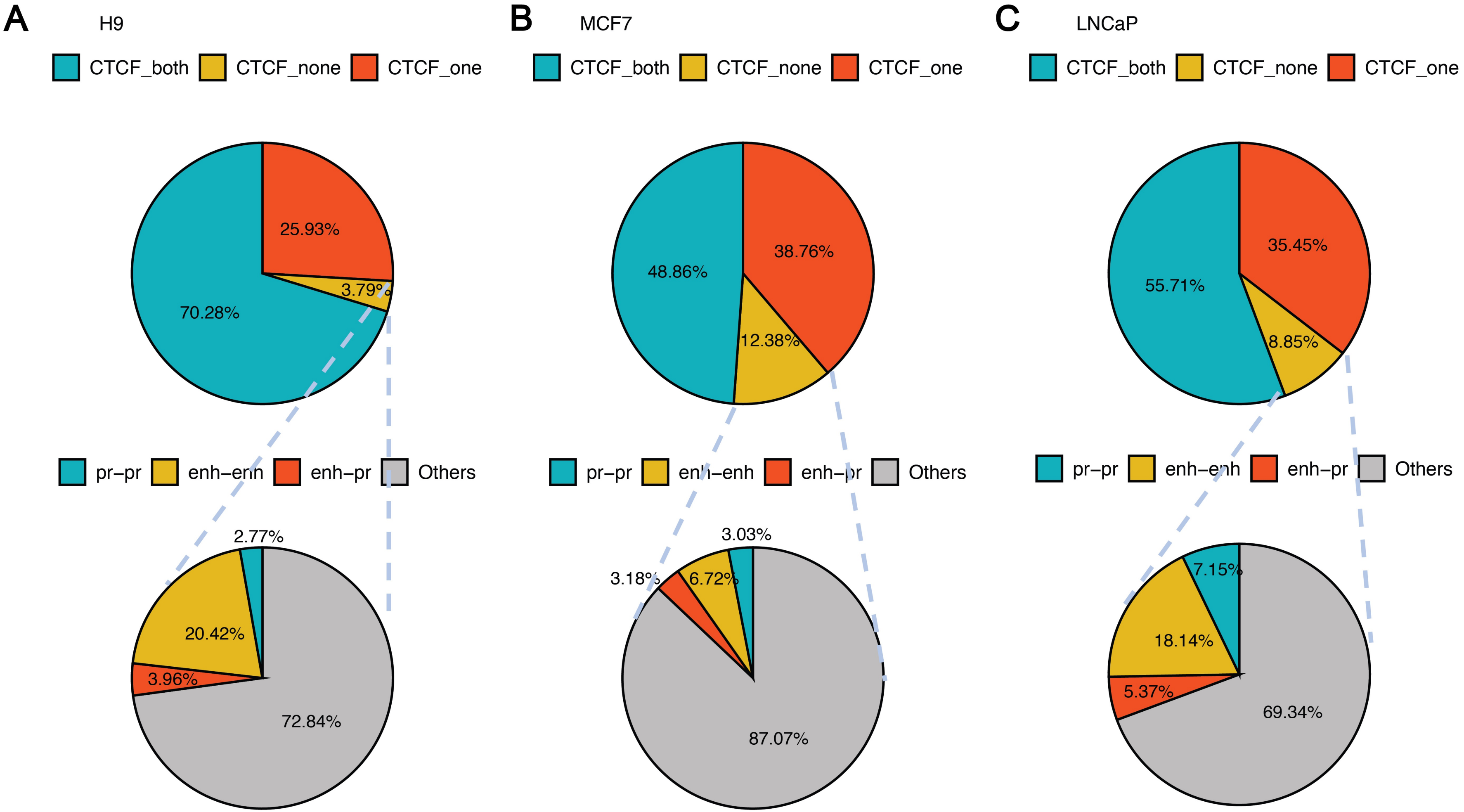

A
H9
CTCF_both
CTCF_none
CTCF_one
25.93%
3.79%
70.28%
pr–pr
enh–enh
enh–pr
Others
2.77%
20.42%
3.96%
72.84%
B
MCF7
CTCF_both
CTCF_none
CTCF_one
38.76%
48.86%
12.38%
pr–pr
enh–enh
enh–pr
Others
3.03%
3.18%
6.72%
87.07%
C
LNCaP
CTCF_both
CTCF_none
CTCF_one
35.45%
55.71%
8.85%
pr–pr
enh–enh
enh–pr
Others
7.15%
18.14%
5.37%
69.34%

Fig. S10

H9 cell line

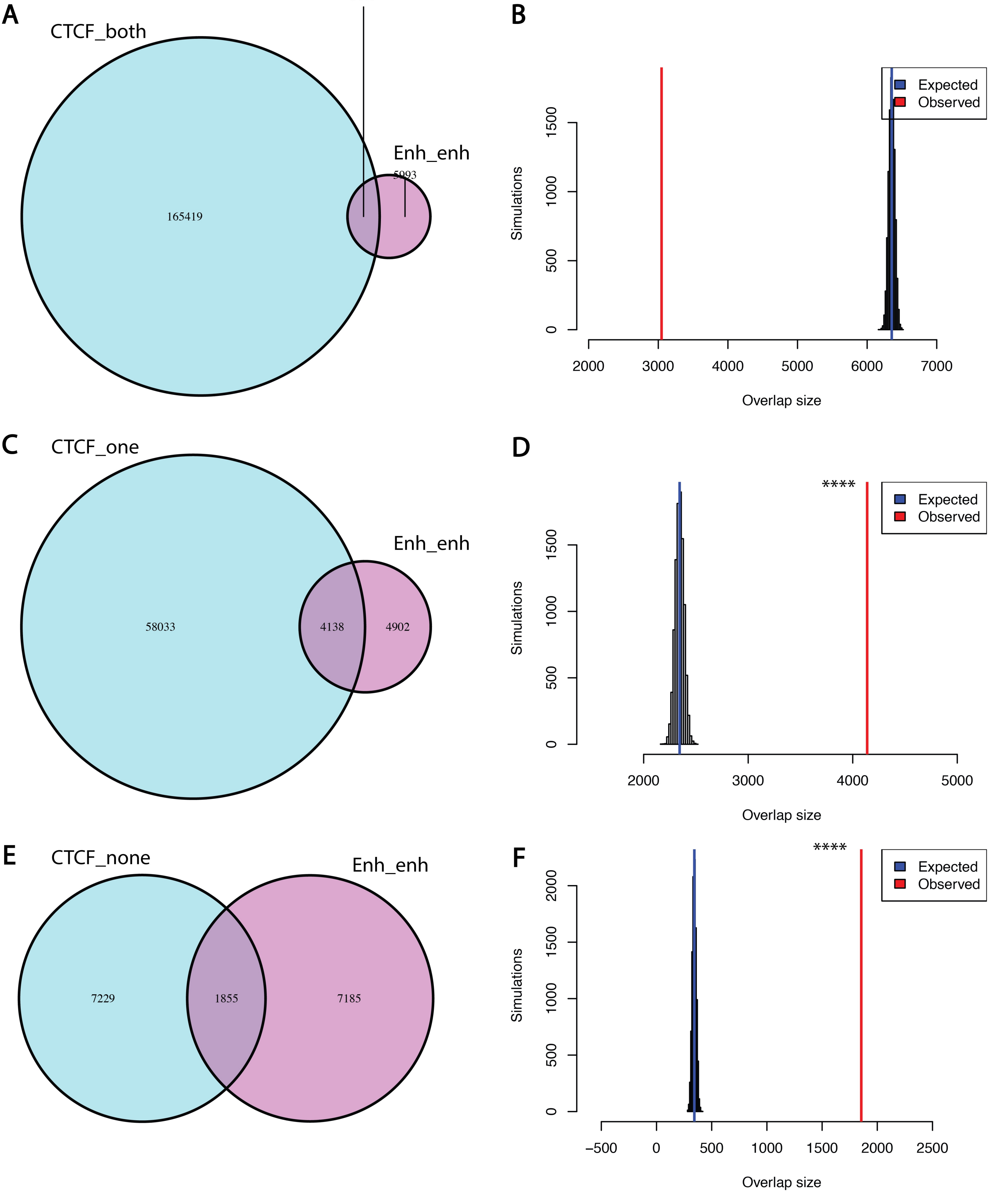


Fig. S11

MCF7 cell line

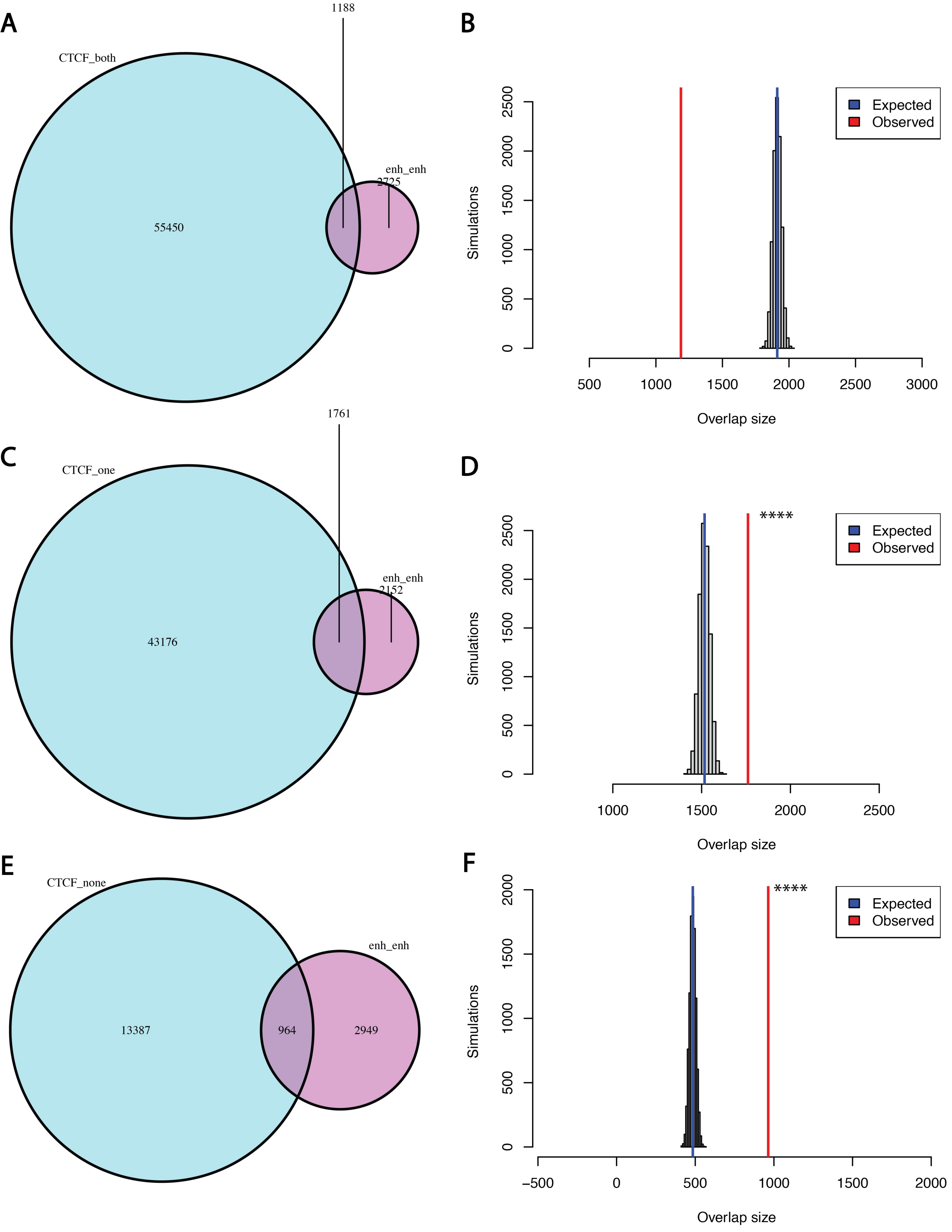


Fig. S12

LNCaP cell line

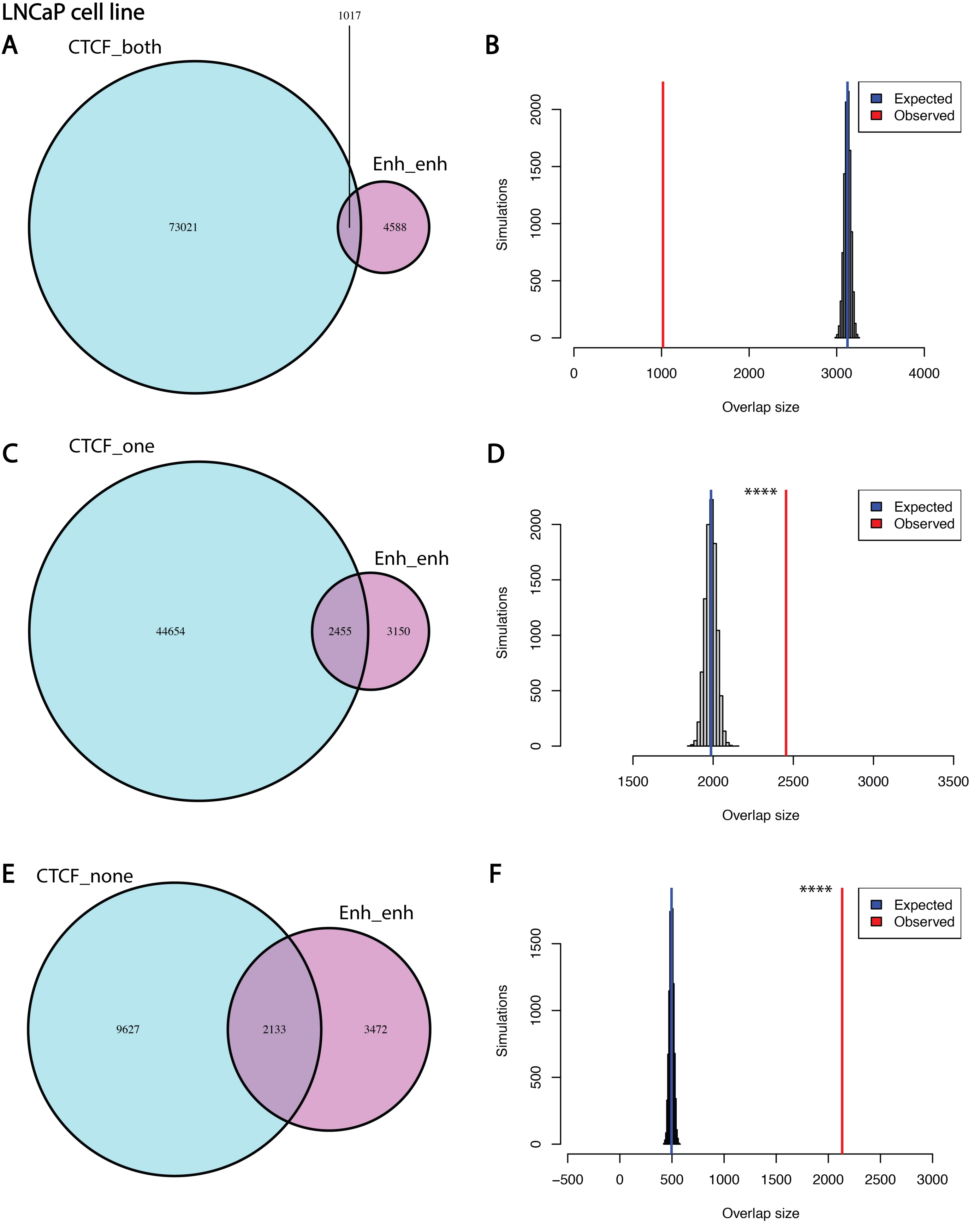


Fig. S13

BORIS(Zf)/K562-CTCFL-ChIP-Seq(GSE32465)/Homer

Match Rank: 1
Score: 0.91
Offset: -1
Orientation: reverse strand
Alignment: -CCACTAGRGGGC-------
GCCASCAGGGGGCGCYVNNG

CTCF/MA0139.1/Jaspar

Match Rank: 2
Score: 0.90
Offset: -3
Orientation: forward strand
Alignment: ---CCACTAGRGGGC----
TGGCCACCAGGGGGCGCTA

CTCF(Zf)/CD4+-CTCF-ChIP-Seq(Barski_et_al.)/Homer

Match Rank: 3
Score: 0.90
Offset: -3
Orientation: reverse strand
Alignment: ---CCACTAGRGGGC-----
TGGCCACCAGGTGGCACTNT

PB0076.1_Sp4_1/Jaspar

Match Rank: 4
Score: 0.60
Offset: 1
Orientation: reverse strand
Alignment: CCACTAGRGGGC------
-NNNAAGGGGGCGGGNNN

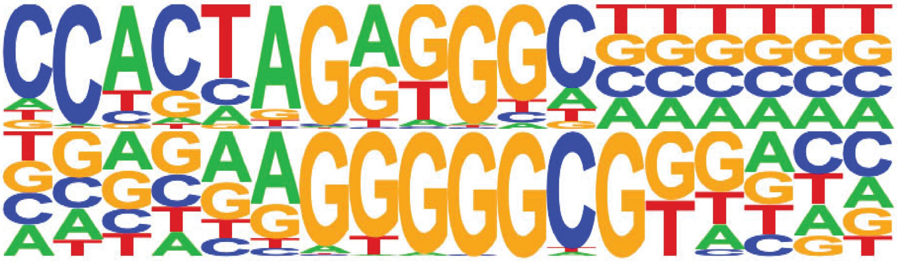
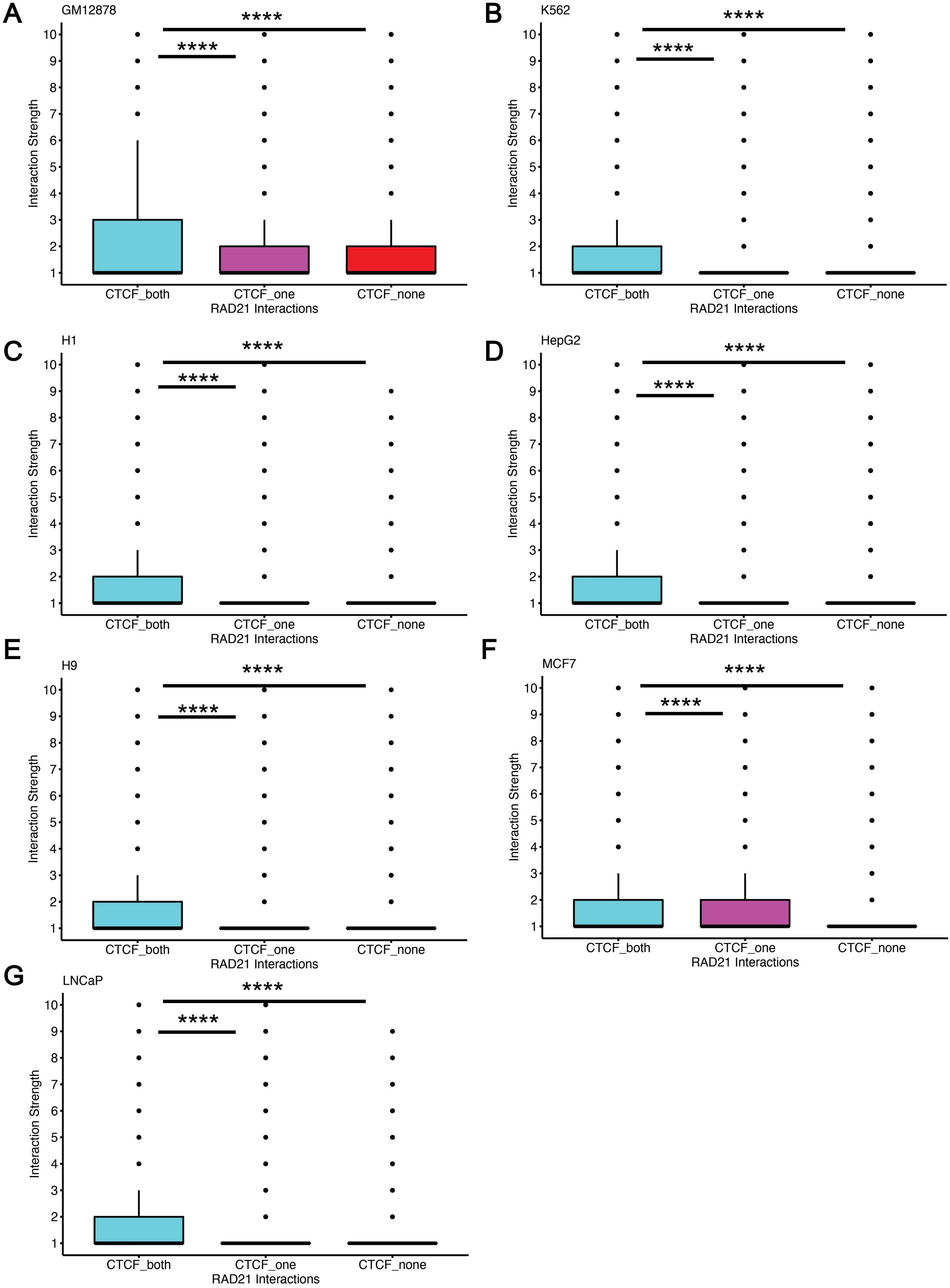


Fig. S14


A
GM12878
B
K562
C
H1
D
HepG2
E
H9
F
MCF7
G
LNCaP
****
****
Interaction Strength
1
2
3
4
5
6
7
8
9
10
CTCF_both
CTCF_one
CTCF_none
RAD21 Interactions