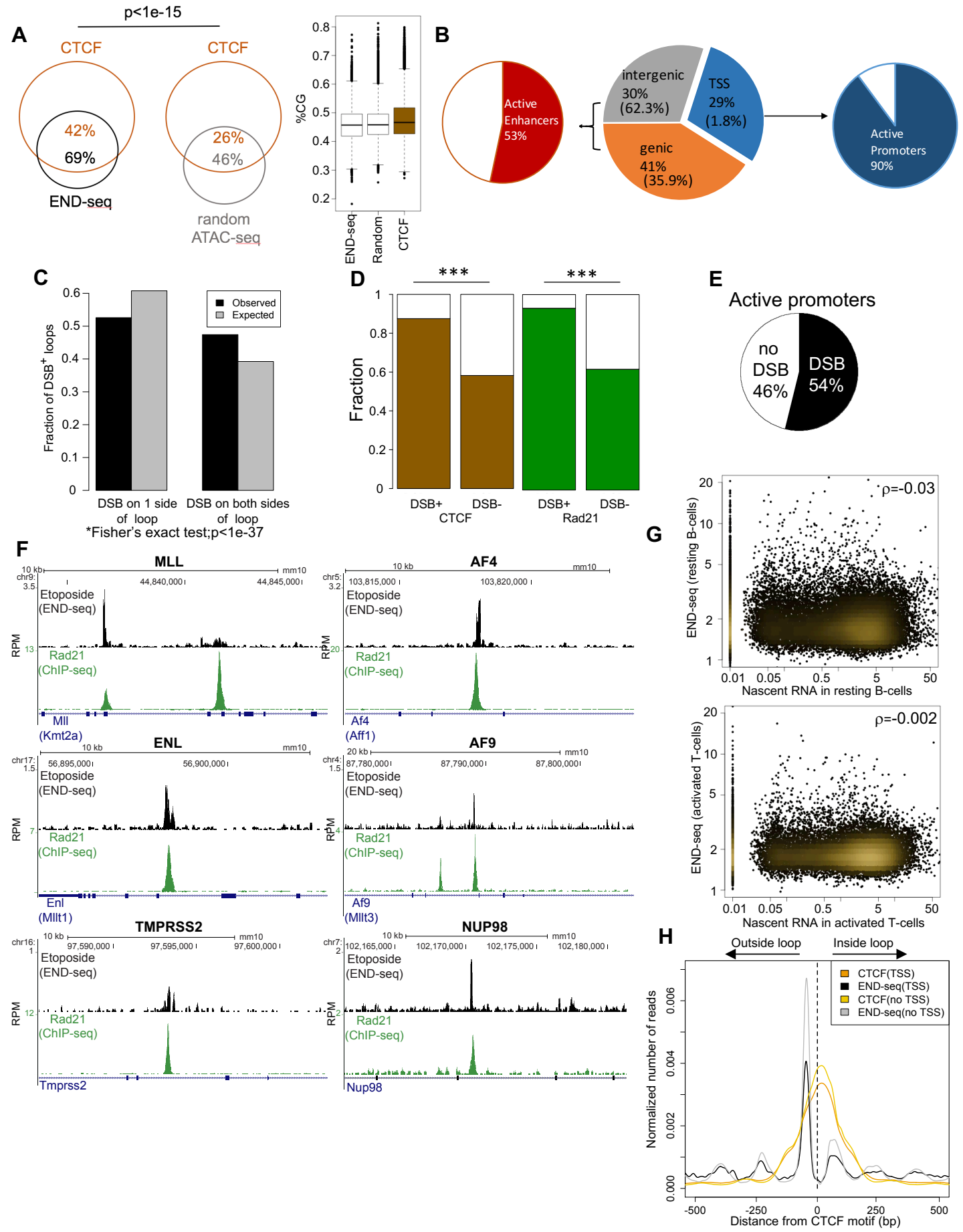
A
p<1e-15
CTCF
42%
69%
END-seq
CTCF
26%
46%
random
ATAC-seq
%CG
END-seq
Random
CTCF
B
Active
Enhancers
53%
intergenic
30%
(62.3%)
TSS
29%
(1.8%)
genic
41%
(35.9%)
Active
Promoters
90%
C
Observed
Expected
Fraction of DSB+ loops
DSB on 1 side
of loop
DSB on both sides
of loop
*Fisher's exact test;p<1e-37
D
***
***
Fraction
DSB+
CTCF
DSB-
DSB+
Rad21
DSB-
E
Active promoters
no
DSB
46%
DSB
54%
F
MLL
AF4
ENL
AF9
TMPRSS2
NUP98
Etoposide
(END-seq)
Rad21
(ChIP-seq)
Mll
(Kmt2a)
Af4
(Aff1)
Enl
(Mllt1)
Af9
(Mllt3)
Tmprss2
Nup98
RPM
G
ρ=-0.03
END-seq (resting B-cells)
Nascent RNA in resting B-cells
ρ=-0.002
END-seq (activated T-cells)
Nascent RNA in activated T-cells
H
Outside loop
Inside loop
CTCF(TSS)
END-seq(TSS)
CTCF(no TSS)
END-seq(no TSS)
Normalized number of reads
Distance from CTCF motif (bp)

Figure S3