Expanded View Figures

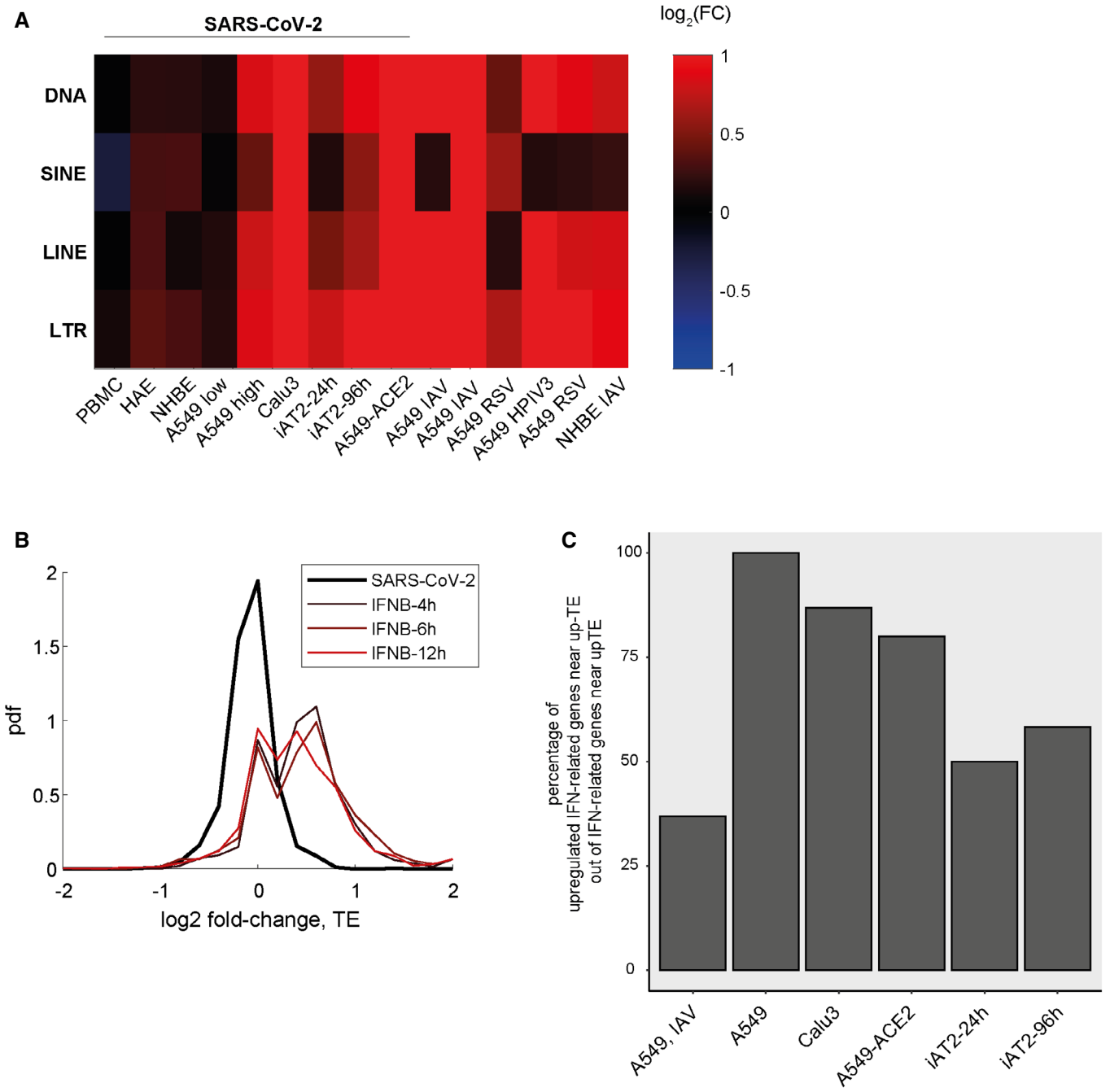

Figure EV1. Impaired TE activation in response to SARS-CoV-2 infection.

A The 95-percentile of TE subfamilies log2 fold-changes in response to IFNB treatment, and to SARS-CoV-2 and IAV infection in different cellular systems by class.

B The distribution of log2 fold-changes of TE subfamilies in response to SARS-CoV-2 infection and IFNB treatment at different times in NHBE cells.

C The percentage of upregulated IFN-related genes located near TEs that are upregulated following SARS-CoV-2 and IAV infections among all IFN-related genes located near upregulated TEs.

Figure EV2. Upregulation of TEs with bivalent epigenetic signature contributes to gene expression response to SARS-CoV-2 infection.

A Percentage of TEs with the bivalent signature of H3K9me3 and H3K36me3 marks.

B Shown are UCSC tracks for the H3K9me3-H3K36me3 bivalently marked LINE copy L1PA13, which is upregulated following SARS-CoV-2 infection in A549 cells, but not in response to IAV infection. The TE is located near the IFN-related gene IFNE which is also upregulated in these cells in response to SARS-CoV-2 infection.

C Same as (B) for the LINE copy L1M3 and the TFPI2 gene.

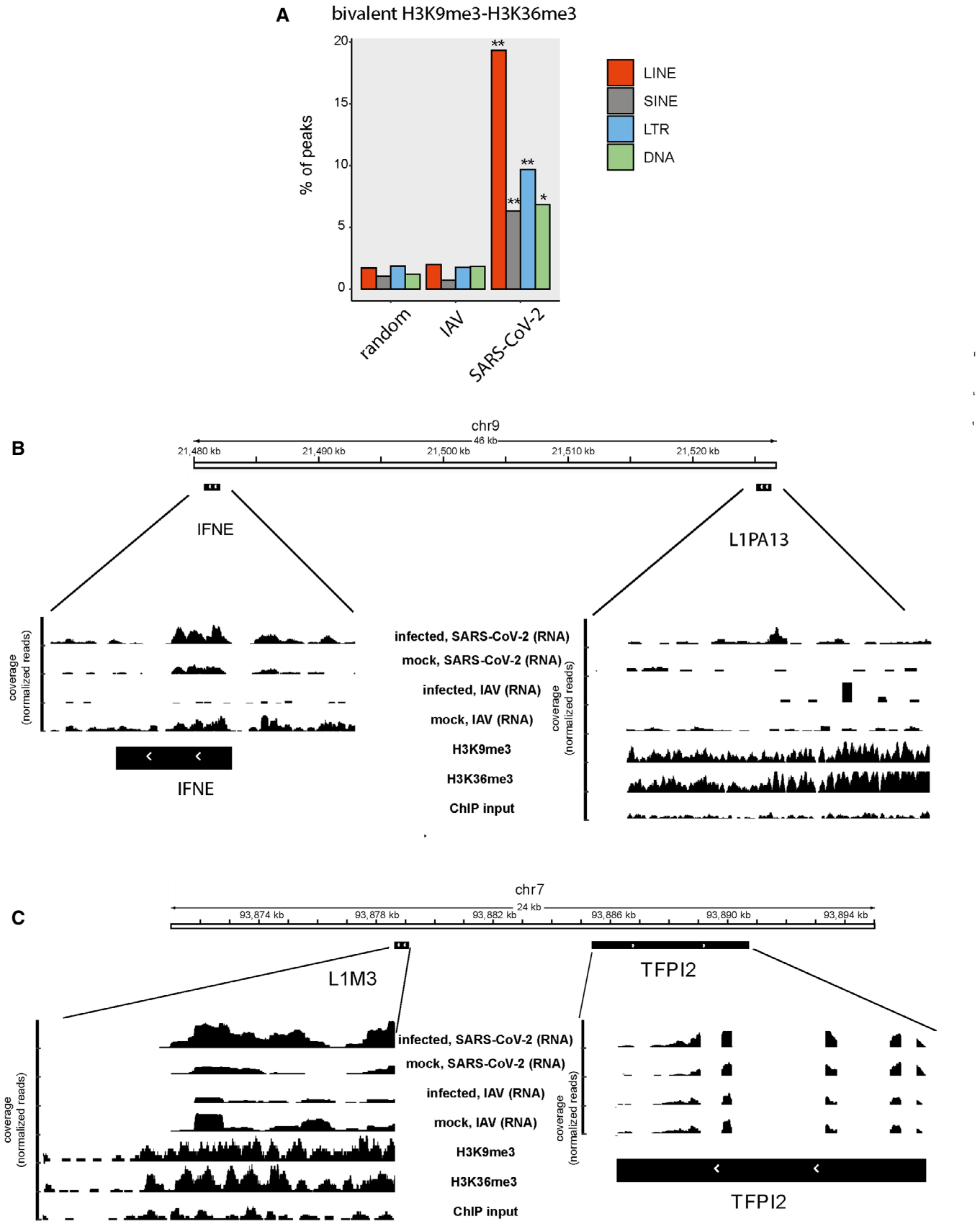
A
bivalent H3K9me3-H3K36me3
% of peaks
20
15
10
5
0
**
**
**
*
random
IAV
SARS-CoV-2
LINE
SINE
LTR
DNA
B
chr9
46 kb
21,480 kb
21,490 kb
21,500 kb
21,510 kb
21,520 kb
IFNE
L1PA13
coverage (normalized reads)
infected, SARS-CoV-2 (RNA)
mock, SARS-CoV-2 (RNA)
infected, IAV (RNA)
mock, IAV (RNA)
H3K9me3
H3K36me3
ChIP input
IFNE
C
chr7
24 kb
93,874 kb
93,878 kb
93,882 kb
93,886 kb
93,890 kb
93,894 kb
L1M3
TFPI2
TFPI2

Figure EV2.

Figure EV3. TE families that are induced by SARS-CoV-2 in A549 cells have a unique epigenetic profile.

A–D Percentage of TEs with peaks of H3K36me3 (A), H3K79me2 (B), H3K27ac (C), and H3K27me3 (D) on SARS-CoV-2-induced TEs, IAV induced TEs and on all expressed TEs outside genes. Shown are DNA families (first column), LTR families (second column) and LINE and SINE families (third column). Asterisks mark significance level of the difference compared with all expressed TE outside genes: one asterisk marks FDR-adjusted P-value < 0.05 and two asterisks mark $P < 0.001$, requiring at least a twofold difference in Fisher's exact test.

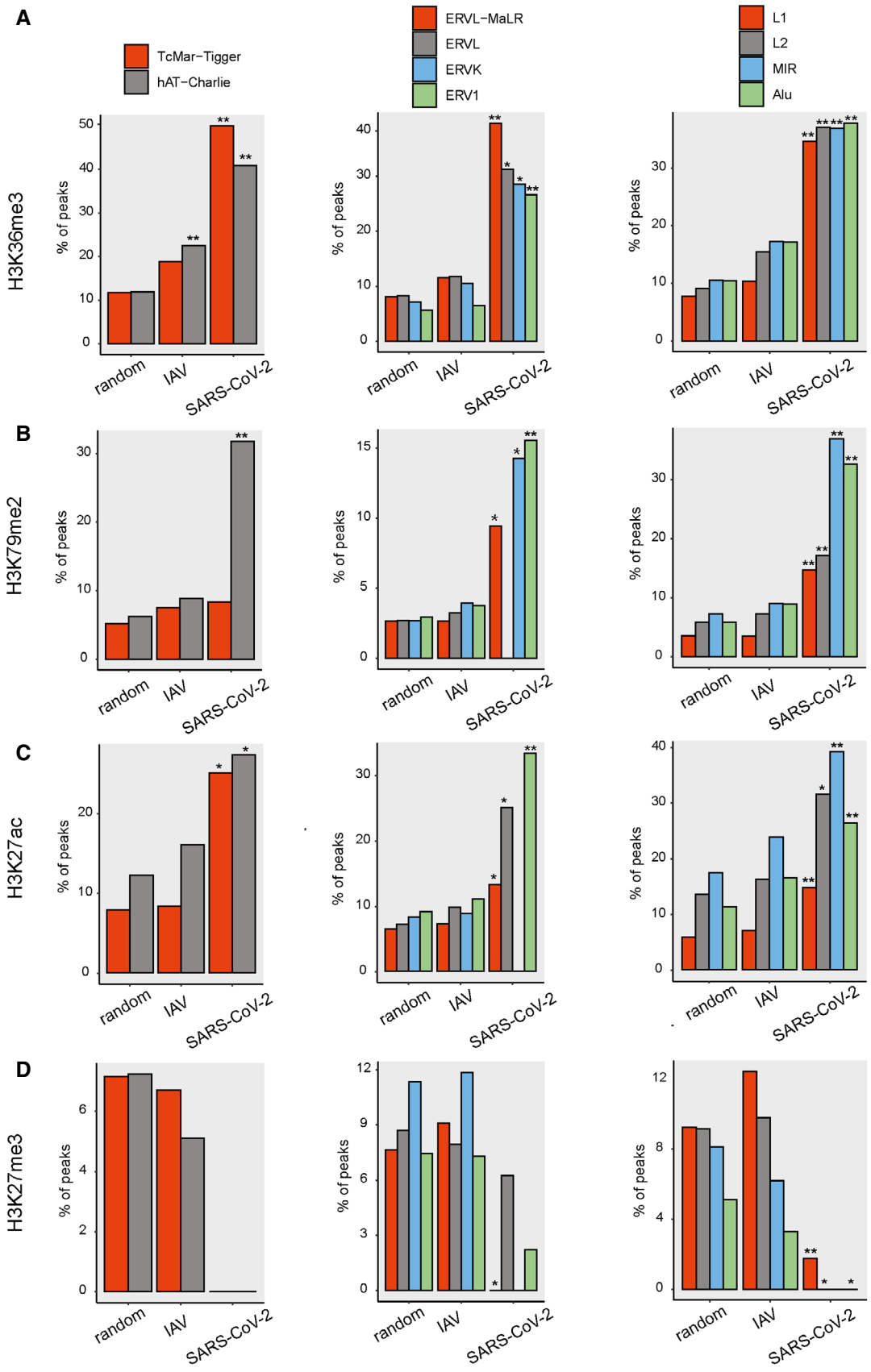
A
B
C
D
H3K36me3
H3K79me2
H3K27ac
H3K27me3
TcMar−Tigger
hAT−Charlie
ERVL−MaLR
ERVL
ERVK
ERV1
L1
L2
MIR
Alu
% of peaks
random
IAV
SARS-CoV-2

Figure EV3.