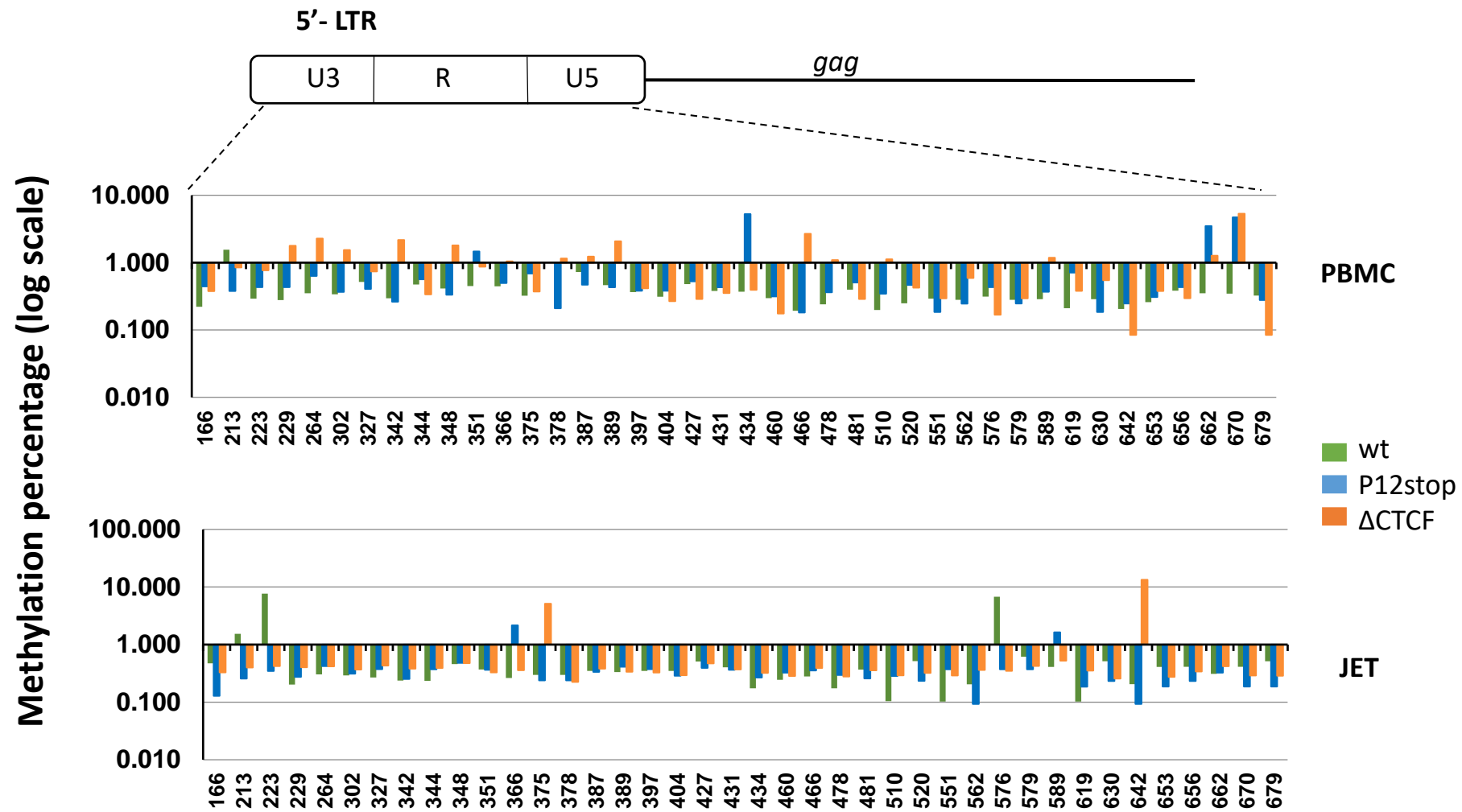
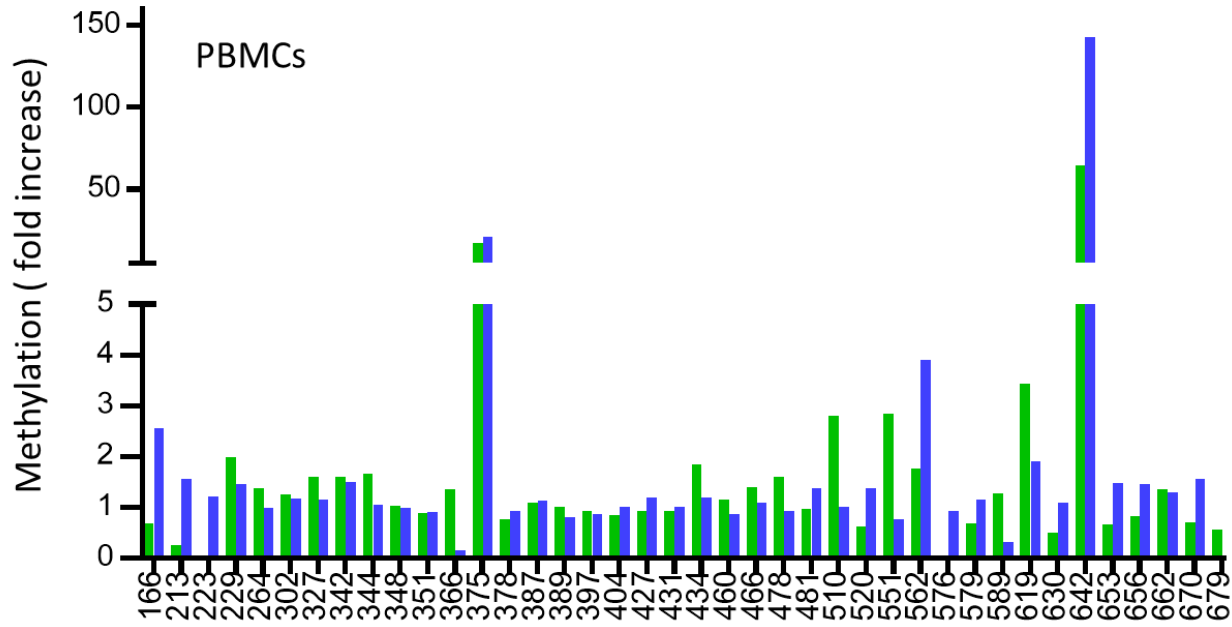
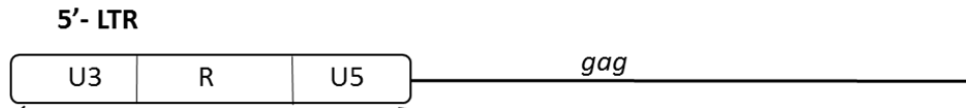


S5A Fig. Methylation in 5' LTR region (Sense strand)



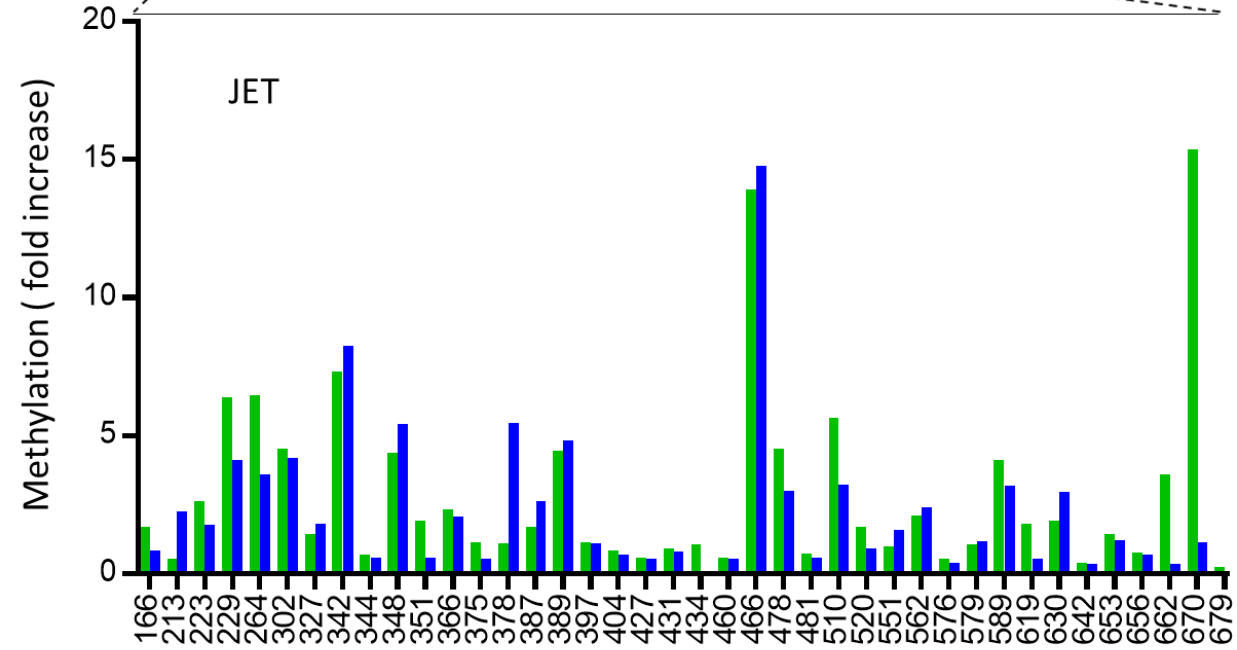
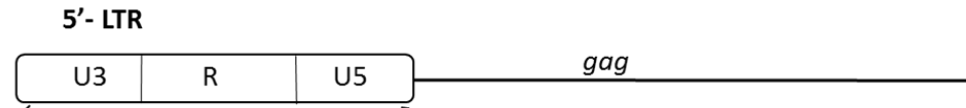
S5B and 5C Fig

B)



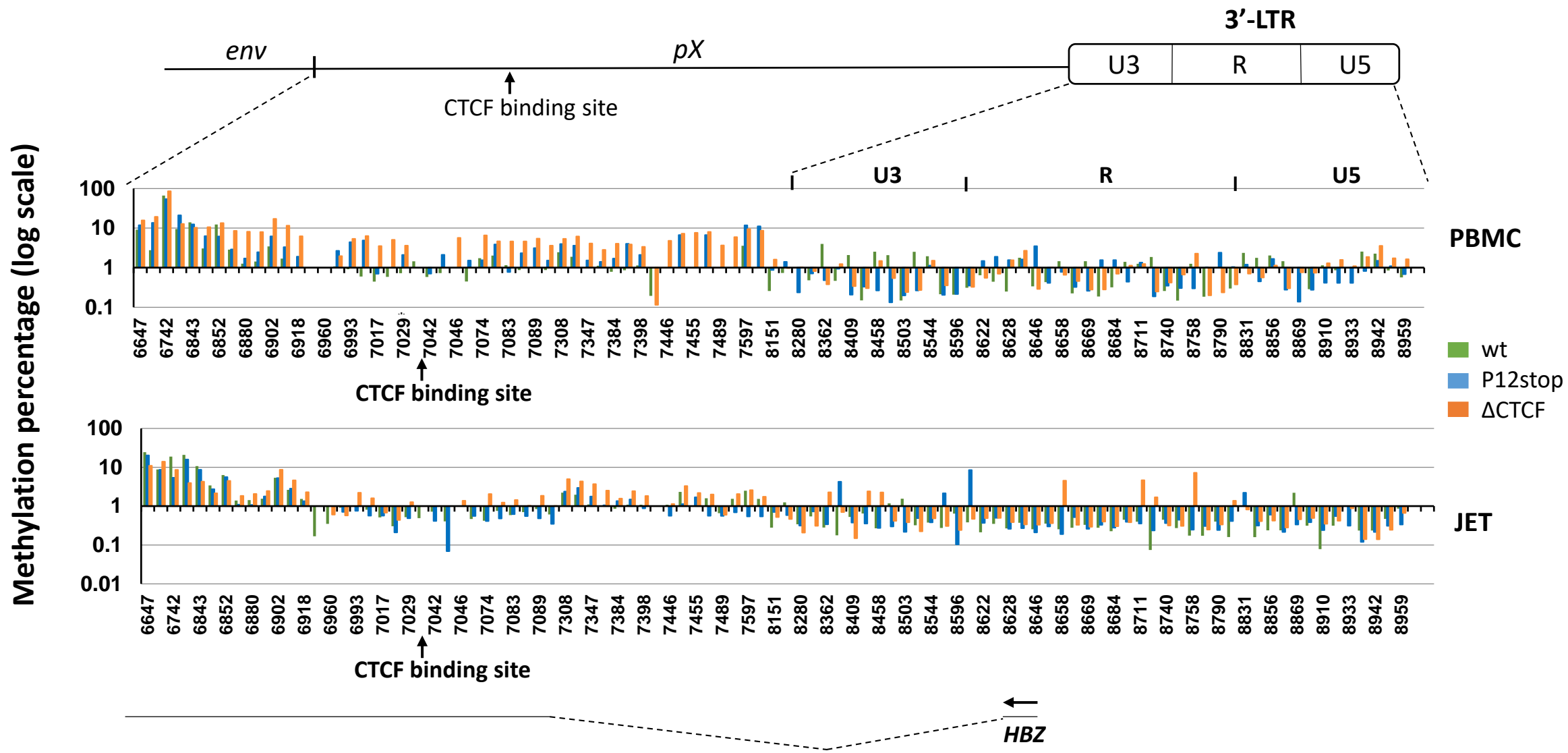
HTLV-1ΔCTCF vs HTLV-1 wt

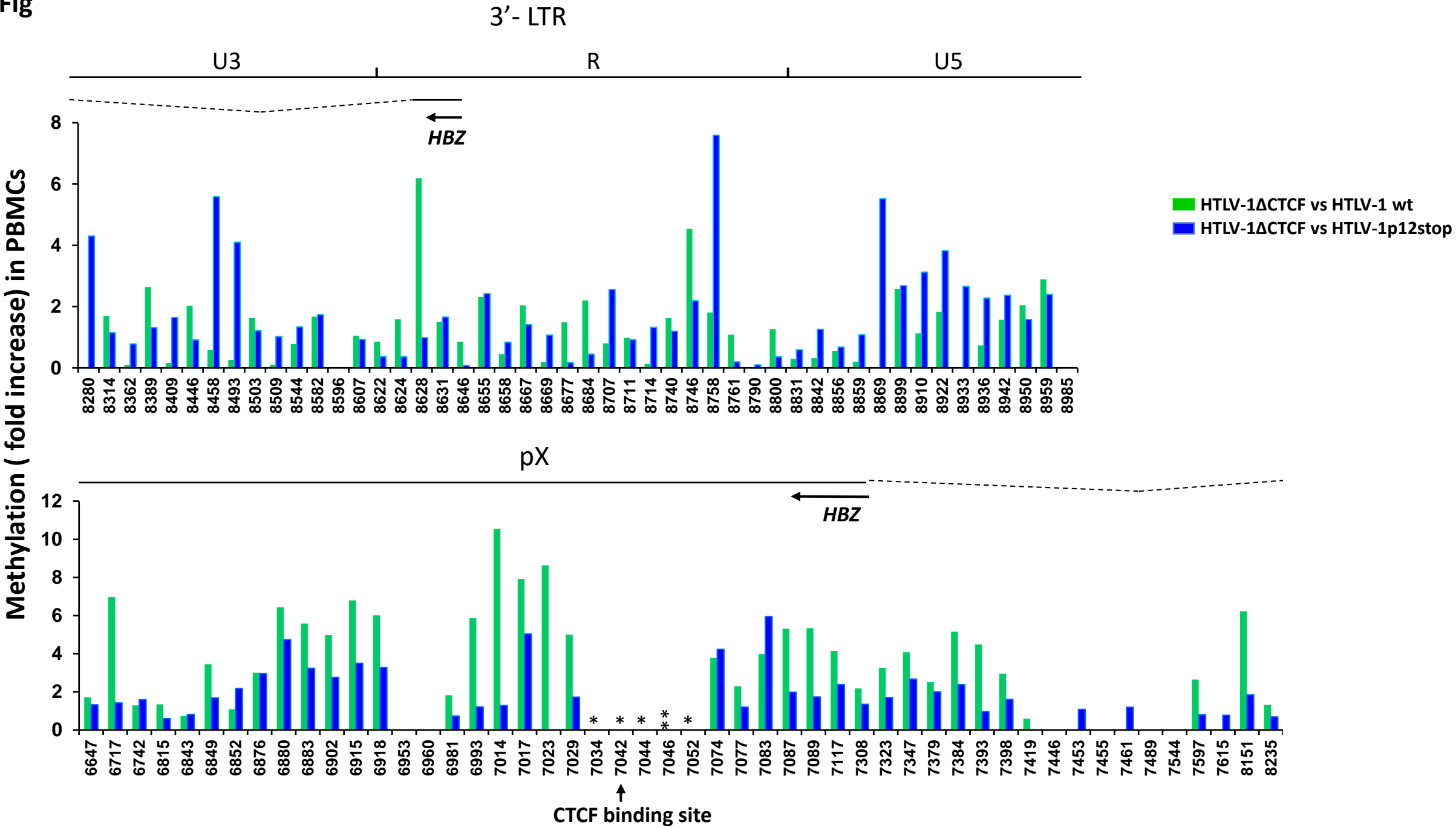
C)



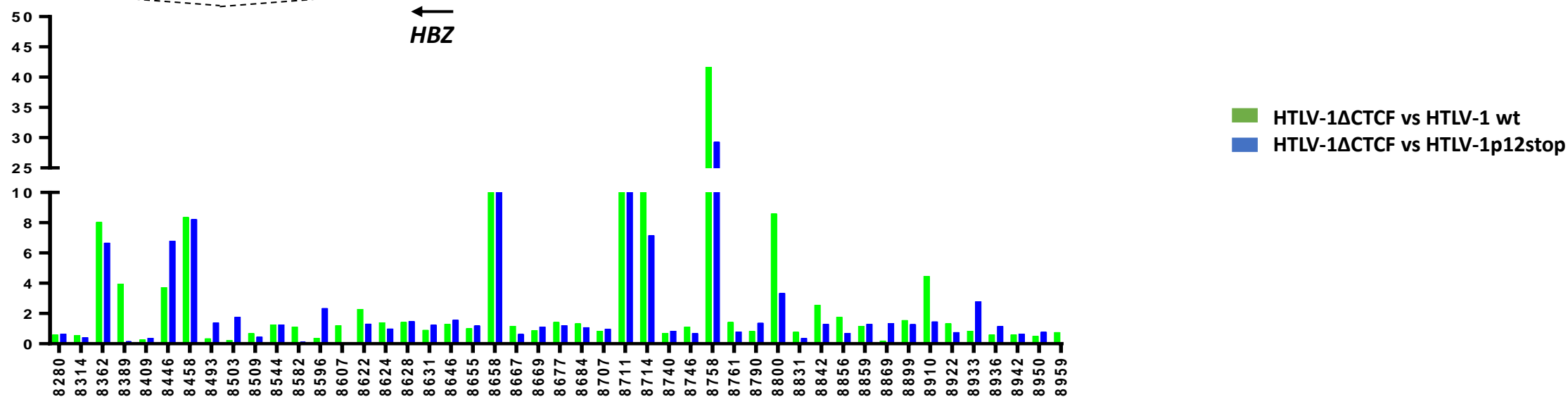
HTLV-1ΔCTCF vs HTLV-1p12stop

S5D Fig. Methylation in 3'-LTR region (antisense strand)

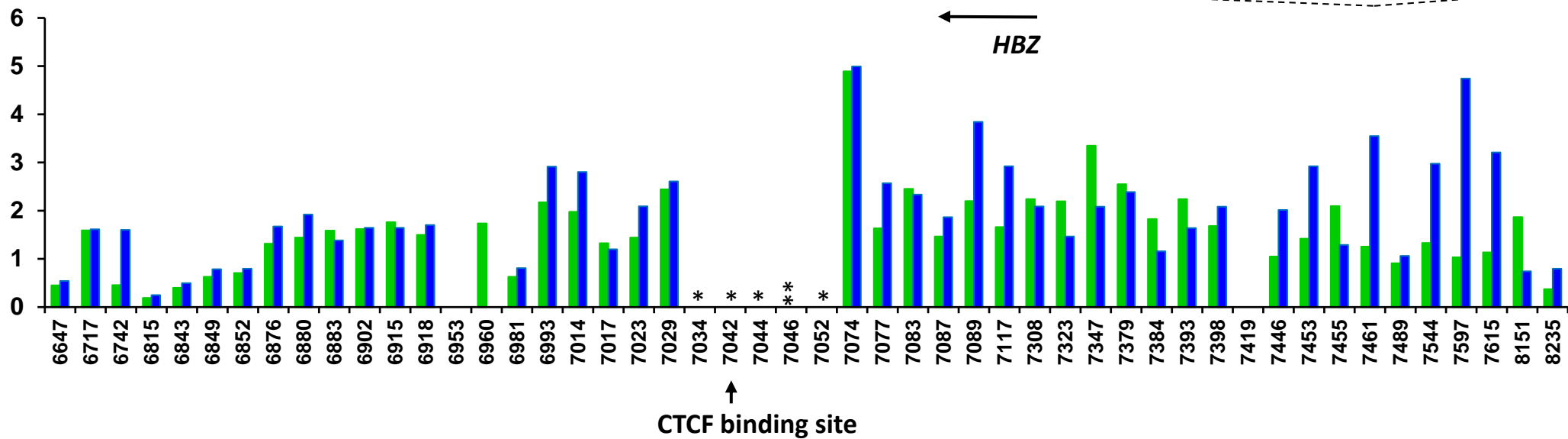




Methylation (fold increase) in JET cells



pX



S5 Fig. DNA methylation change in 5'LTR and 3'LTR of the HTLV-1 Δ CTCF compared to wild type HTLV-1 and HTLV-1p12stop provirus

A, D). DNA methylation is presented as the percentage of methylated CpG (Y- axis) in 5'LTR (A), 3'LTR and *HBZ* on anti-sense strand (D) of HTLV-1 Δ CTCF compared to wild type HTLV-1 or HTLV-1p12stop provirus at the indicated locations of the viral DNA (X- axis). Upper panel: HTLV-1 immortalized PBMCs; lower panel: HTLV-1 infected JET cells.

B, C). DNA methylation is shown as a fold increase of methylated CpG (Y- axis) in 5'LTR of HTLV-1 Δ CTCF HTLV-1 compared to wild type HTLV-1 or HTLV-1p12stop provirus in PBMCs (B) and JET cells (C).

E, F). DNA methylation is shown as a fold increase of methylated CpG in 3'LTR and *HBZ* on anti-sense strand of HTLV-1 Δ CTCF compared to wild type HTLV-1 or HTLV-1p12stop provirus in PBMCs (E) and JET cells (F). Upper panel: 3'LTR; lower panel: *HBZ*. CTCF binding site: 7041-7052 as indicated by an arrow. * Lost CpG sites, ** New CpG site due to the introduced mutations in vCTCF-BS.