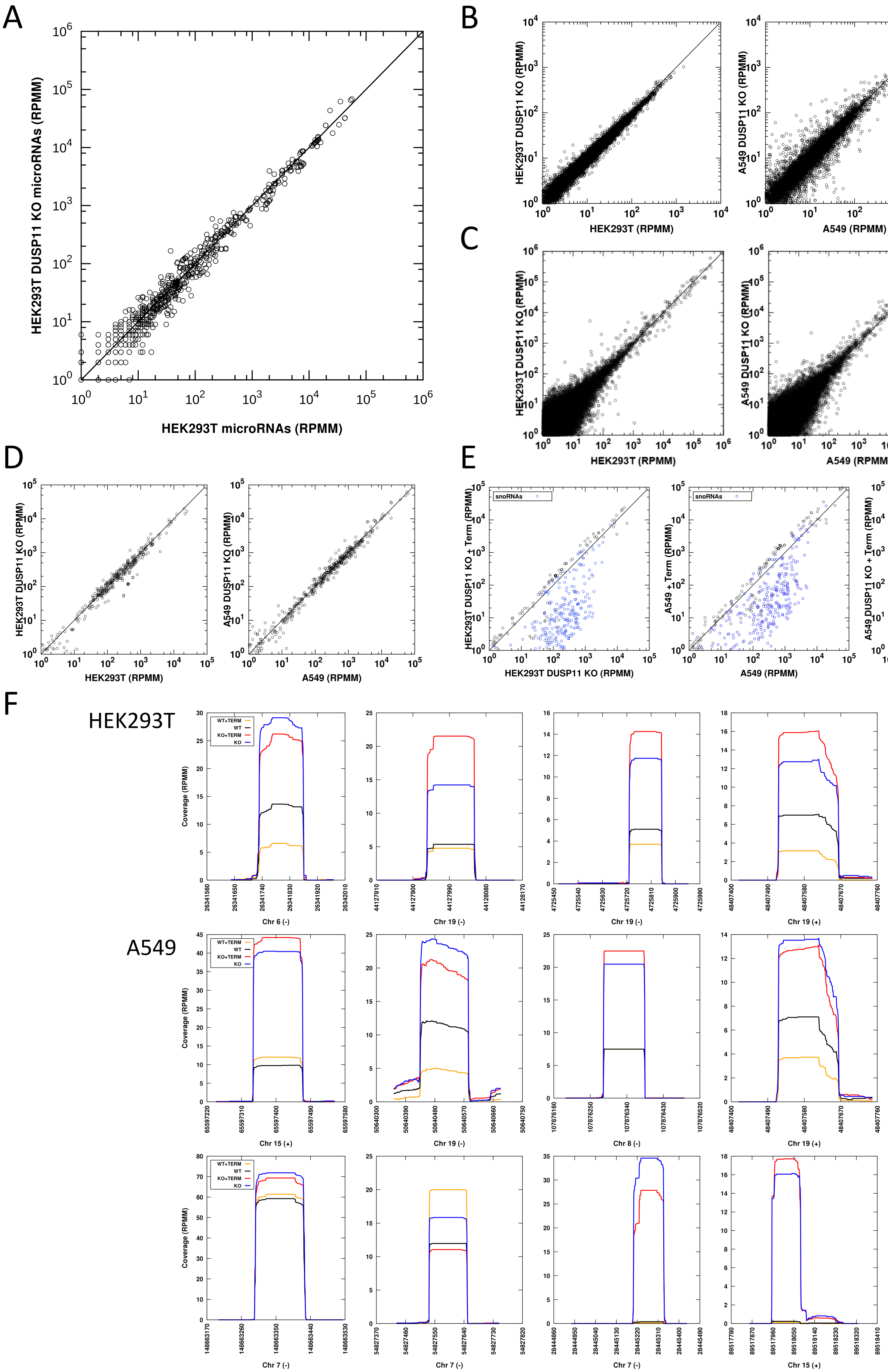

Supplemental Figure 6. TGIRT-seq analysis of DUSP11 KO cell lines.

Supplemental Figure 6 cont. TGIRT-seq analysis of DUSP11 KO cell lines.

(A) Host microRNA expression in HEK293T and HEK293T DUSP11 knockout cell lines. Read counts from HEK293T library mapping to mirBase annotated host microRNAs in reads per million mapped (RPMM) is plotted on the x axis. Read counts from HEK293T DUSP11 knockout library mapping to mirBase annotated host microRNAs in reads per million mapped (RPMM) is plotted on the y axis. Values are the average of two independent replicates. (B) Host gene expression (RefSeq genes > 500 nt with annotated coding sequence) in HEK293T, HEK293T DUSP11 knockout, A549, and A549 DUSP11 knockout cell lines assayed by fragmented TGIRT-seq. Read counts from the indicated parental cell line library mapping to annotated host genes with an annotated coding sequence in reads per million mapped (RPMM) is plotted on the x axis. Read counts from the indicated DUSP11 knockout cell line library mapping to annotated host genes with an annotated coding sequence in reads per million mapped (RPMM) is plotted on the y axis. (C) Host gene isoform expression in HEK293T, HEK293T DUSP11 knockout, A549, and A549 DUSP11 knockout cell lines assayed by fragmented TGIRT-seq. Read counts from the indicated parental cell line library mapping to Cufflinks defined isoforms in reads per million mapped (RPMM) is plotted on the x axis. Read counts from the indicated DUSP11 knockout cell library mapping to Cufflinks defined isoforms in reads per million mapped (RPMM) is plotted on the y axis. (D) Host gene expression (RefSeq genes ≤ 500 nt with no annotated coding sequence) in HEK293T, HEK293T DUSP11 knockout, A549, and A549 DUSP11 knockout cell lines assayed by unfragmented TGIRT-seq. Read counts from the indicated parental cell line library mapping to annotated host genes in reads per million mapped (RPMM) is plotted on the x axis. Read counts from the indicated DUSP11 knockout cell line library mapping to annotated host genes in reads per million mapped (RPMM) is plotted on the y axis. (E) Host gene expression (RefSeq genes ≤ 500 nt with no annotated coding sequence) in HEK293T DUSP11 knockout, A549, and A549 cells with or without terminator treatment assayed by unfragmented TGIRT-seq. Read counts from the indicated cell line library mapping to annotated host genes in reads per million mapped (RPMM) are plotted on each axis. SnoRNAs are indicated with blue circles. (F) Coverage plots of most abundant quantifiable Alu loci (≥ 10 RPMM +/- 3 nt 5' start site). Genomic position and direction of mapped reads is indicated on the x-axis. Coverage in reads per million mapped is plotted on the y-axis.