

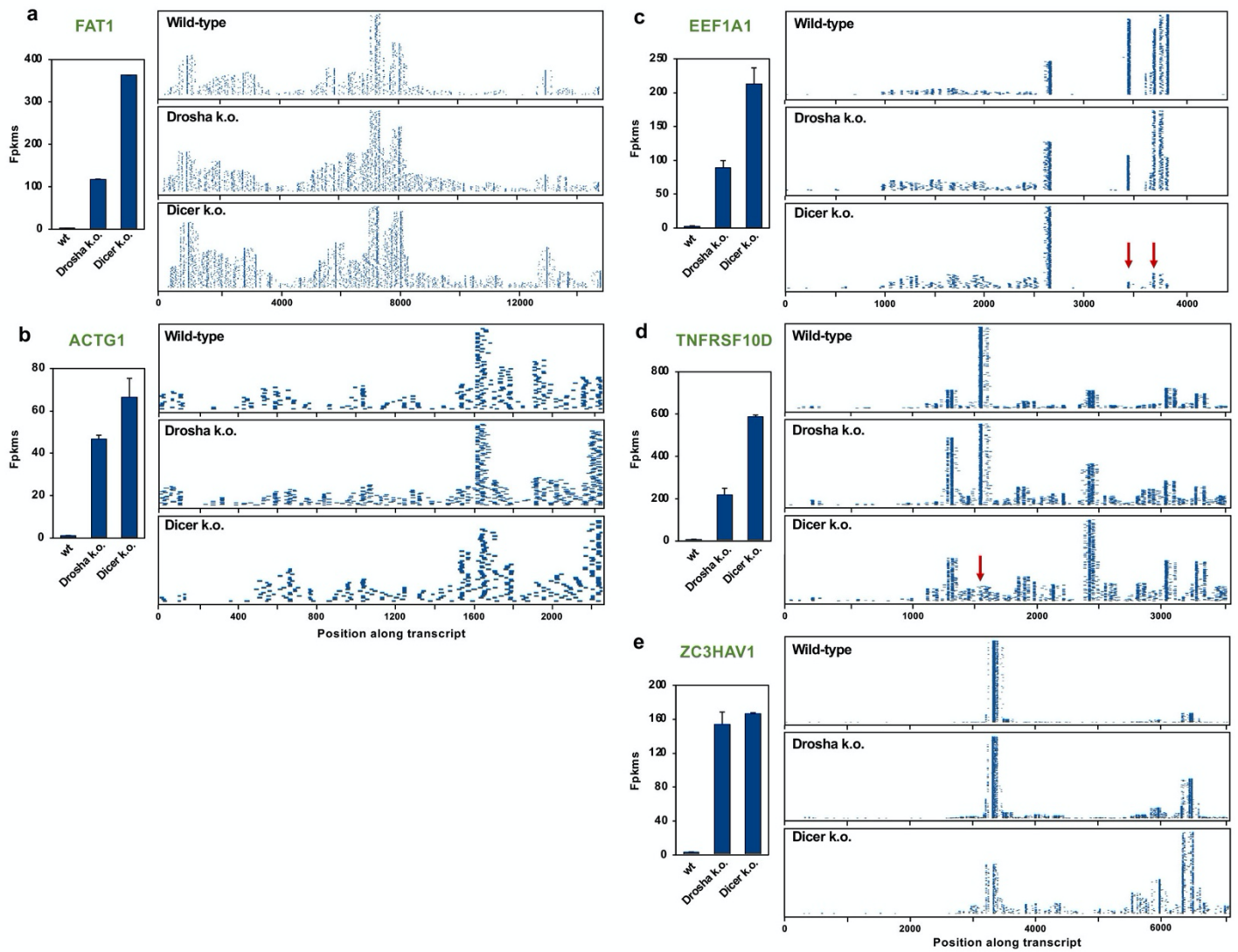


Figure S4 - Endogenous mRNAs are processed and loaded into the RISC of Dicer k.o. cells

(a-e) Mapping of R-sRNAs to the transcripts of five selected highly processed mRNAs in cells infected with pLenti-CD95L NP. One horizontal line represents one read in the RISC of HCT116 wild-type (top), Drosha k.o. (center), and Dicer k.o. cells (bottom). *Left*, Reads from both replicates are combined and error bars show SD. *Right*, normalized read counts (fpkms) by genotype. Selected processed mRNAs (a) FAT1, (b) ACTG1, (c) EEF1A1, (d) TNFRSF10D, and (e) ZC3HAV1. Red arrows indicate stacks with few reads in Dicer k.o. cells.