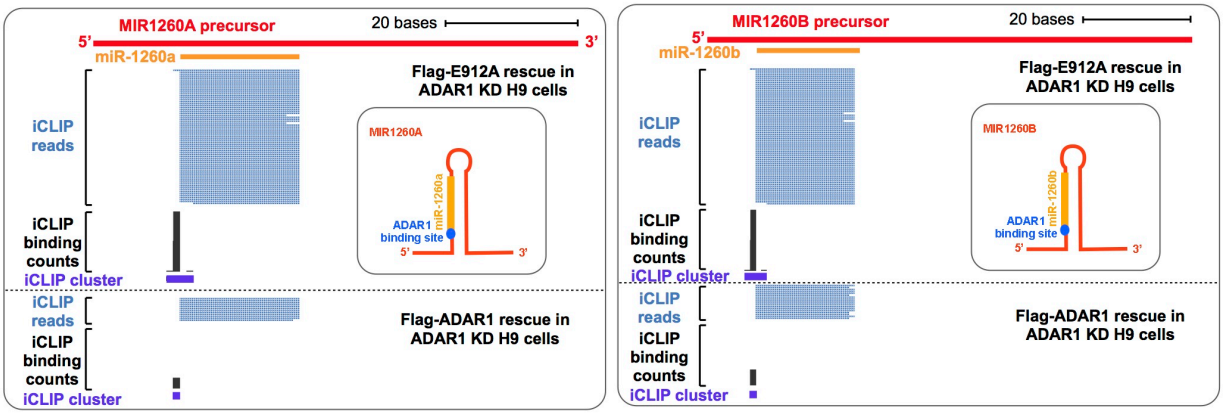
A



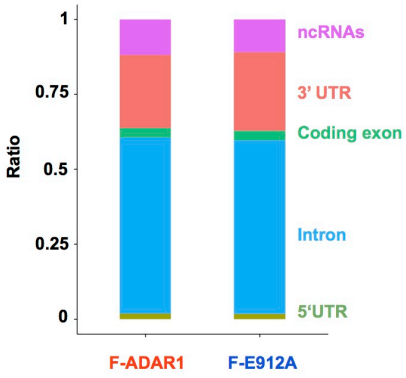
B

	Exp. in WT H9 cells	Exp. in ADAR1 KD H9 cells
miR-1260a	537	1351
miR-1260b	671	1245

C

	iCLIP peaks	miRNA regions with peaks	Clusters (FDR < 0.05)	miRNA regions with clusters
Flag-ADAR1	3478	725	1291	335
Flag-E912A	7449	848	2105	373

D



Supplemental Figure S6. Genome-wide analysis of ADAR1 binding sites from iCLIP-seq datasets in H9 cells.

(A) Flag-ADAR1 and Flag-ADAR1-E912A iCLIP-seq reads (in blue) or iCLIP binding counts (in black) aligned to pri-miR1260s, with the mature miRNA boundaries depicted below (orange bars). The iCLIP clusters are depicted as purple rectangles.

(B) The normalized expression of miR1260a/b (RPM) in WT and ADAR1 KD H9 cells. Note that no A-to-I editing site could be detected in pri-miR1260s.

(C) Genome-wide analyses of ADAR1 binding sites. About 20% of ADAR1 binding sites were located in pri-miRNA regions.

(D) Genomic distribution of ADAR1 binding sites.