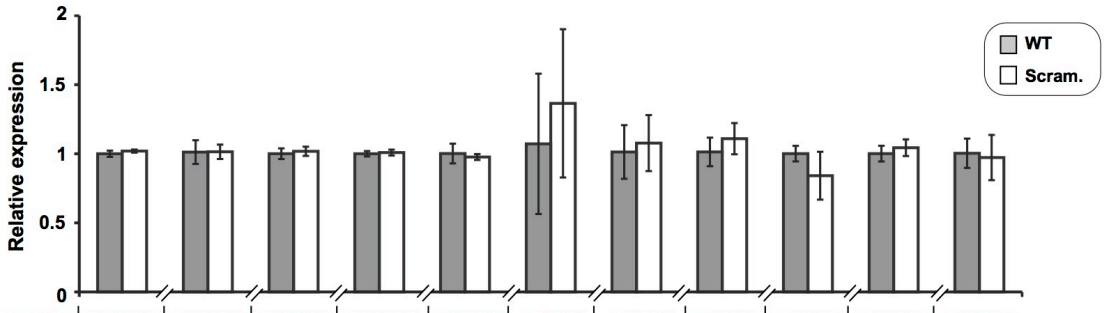
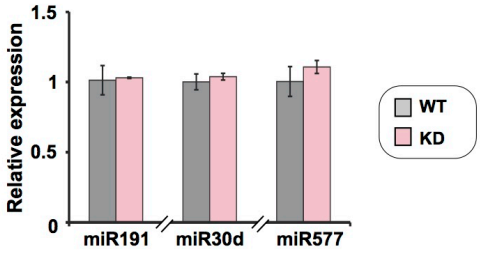
A

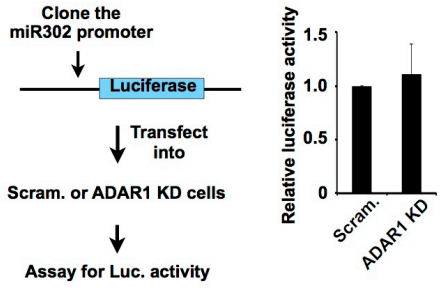


miRNA species	miR302a	miR302b	miR302c	miR302d	miR367	miR96	miR191	miR30a	miR30d	miR30e	miR577
Expression in WT at d0 (RPM)	32631	42214	22394	37919	2469	50	28249	7172	5536	12232	433

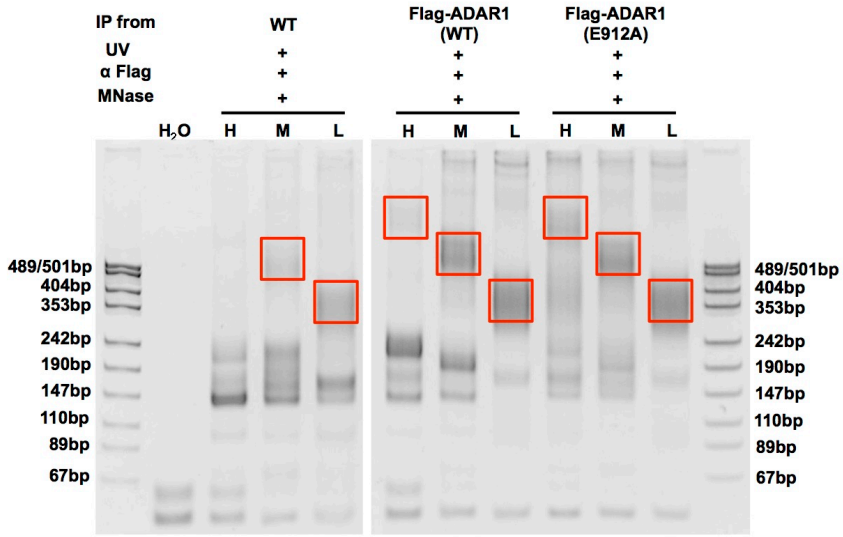
B



C



D



E

	Flag-ADAR1	Flag-E912A	hnRNP (König et al., 2010)
Raw reads	70,924,387	53,360,651	6,278,981
Mapped reads	27,142,295 (38.27%)	21,538,484 (40.36%)	4,162,812 (66.30%)
Unique reads (removing PCR duplicates)	875,955 (1.24%)	975,025 (1.83%)	641,350 (10.21%)
Clusters (FDR < 0.05)	62,093 (0.09%)	106,649 (0.20%)	33,991 (0.54%)

Supplemental Figure S5.Characterization of ADAR1 on miRNA processing.

(A) Scramble shRNA treatment in H9 cells did not alter expression of miRNAs. The expression of up-regulated or unchanged miRNAs by ADAR1 KD was not affected when treated with a scramble shRNA.

(B) Validation of unchanged miRNAs by ADAR1 KD by RT-qPCR.

(C) ADAR1 is unlikely involved in the transcriptional regulation of miR-302. Left, a schematic view of the reporter construct for miR-302 promoter. Right, the luciferase expression of miR-302 reporter construct in Scram. or ADAR1 KD HeLa cells.

(D) Visualization of Flag-ADAR1 or Flag-E912A immunoprecipitated RNAs for iCLIP assay. RNAs were isolated from protein-RNA complexes after anti-Flag IP, reversely transcribed, and then separated on urea-gels. Three banks (high, medium and low) were individually cut for sequencing after library preparation.

(E) Statistic analysis of iCLIP analysis.