Supplementary Table 1:

Read numbers of perfectly mapped reads in all 3 biological replicates.

	genotype	total reads E+06	miRNA reads E+06	% miRNA of total
replicate 1	wildtype	24	15	65
	Adarb1$^{-/-}$	21	11	51
	Adar$^{-/-}$, *Adarb1*$^{-/-}$	23	10	46
replicate 2	wildtype	20	7	36
	Adarb1$^{-/-}$	16	4	25
	Adar$^{-/-}$, *Adarb1*$^{-/-}$	15	3	20
replicate 3	wildtype	29	11	40
	Adarb1$^{-/-}$	30	13	43
	Adar$^{-/-}$, *Adarb1*$^{-/-}$	28	13	46

Supplementary Table 2:

Consistently deregulated miRNAs in mice deficient in ADARs

miRNAs consistently deregulated (more than 1.3 fold) in *Adarb1*$^{-/-}$ and *Adar*$^{-/-}$, *Adarb1*$^{-/-}$ mice (sorted by fold change in *Adarb1*$^{-/-}$). The underlined miRNAs are known edited ones or have been identified as edited in this study. In bold are the fold changes that are consistent over all biological replicates (Students t-test: P<0.1).

consistently deregulated miRNAs	**fold change in *Adarb1*$^{-/-}$**	P-value	**fold change in *Adar*$^{-/-}$, *Adarb1*$^{-/-}$**	P-value	possible editing context near DROSHA cleavage site	possible editing context near DICER1 cleavage site
let-7b	**-2.50**	0.000	-1.10	0.446	-	UAA
let-7c	**-2.02**	0.000	-1.59	0.106	-	UAG, UAA
miR-184	**-1.89**	0.010	**-1.51**	0.002	UAG	-
let-7d	**-1.80**	0.003	**-1.61**	0.056	UAG	UAG
let-7i	**-1.79**	0.018	**-1.74**	0.090	UAG	UAA
miR-124	**-1.72**	0.000	**-1.59**	0.007	-	UAA
miR-204	**-1.70**	0.015	**-1.44**	0.000	-	-
miR-551b	**-1.69**	0.003	-1.25	0.210	-	-
miR-720	**-1.60**	0.001	-1.16	0.104	-	-
let-7f	**-1.51**	0.028	**-1.51**	0.038	-	UAA
let-7g[1]	**-1.50**	0.010	-1.39	0.105	-	UAA
miR-140*	**-1.47**	0.025	-1.31	0.180	-	UAG, UAC
let-7e	**-1.44**	0.001	-1.27	0.127		
let-7a	**-1.43**	0.011	**-1.34**	0.089		
miR-338-3p	**-1.36**	0.005	1.14	0.388		
miR-135a-2*	**-1.30**	0.008	**-1.41**	0.000		
miR-344	-1.26	0.130	**-1.35**	0.067		
miR-3099[6]	-1.15	0.190	**-1.31**	0.030		
miR-376c[1]	-1.14	0.362	**-1.35**	0.070		
miR-30b	**-1.12**	0.042	**1.91**	0.054		
miR-598	-1.09	0.371	**-1.32**	0.028		
miR-1839-5p	-1.08	0.311	**-1.36**	0.012		
miR-350*	-1.06	0.373	**1.37**	0.087		
miR-340-3p	-1.01	0.486	**1.34**	0.008		
miR-137	1.06	0.393	**-1.53**	0.011		
miR-503*[1]	1.13	0.309	**1.30**	0.028		
miR-540-5p	1.13	0.304	**1.49**	0.074		
miR-296-3p	1.15	0.325	**1.40**	0.045		
miR-325	1.16	0.364	**1.37**	0.096		
miR-362-5p	1.16	0.327	**1.40**	0.016		
miR-673-5p	1.17	0.442	**-2.44**	0.093		
miR-708*	1.17	0.141	**1.52**	0.064		
miR-126-5p	1.19	0.317	**1.51**	0.089		
miR-30e	1.19	0.269	**1.44**	0.044		
miR-29b	1.20	0.106	**1.47**	0.020		
miR-370	1.21	0.158	**1.38**	0.042		
miR-3062	1.21	0.106	**1.42**	0.004		
miR-30c	1.25	0.229	**1.78**	0.047		
miR-101a	1.26	0.153	**1.39**	0.029		
miR-329*	1.27	0.163	**1.49**	0.007		
miR-34c	**1.27**	0.031	**1.38**	0.021		

miR-1195	1.27	0.148	**1.35**	0.075			
miR-30a	1.28	0.179	**1.35**	0.021			
miR-486*	**1.32**	0.055	1.13	0.337			
miR-17*[4]	**1.32**	0.064	1.29	0.193			
miR-186*	1.32	0.287	**1.48**	0.001			
miR-410	**1.33**	0.012	-1.00	0.495			
miR-200a	**1.34**	0.010	**1.47**	0.008			
miR-133a*[1]	**1.34**	0.087	**1.52**	0.062			
miR-132	**1.34**	0.000	1.04	0.350			
miR-124*	**1.35**	0.091	1.18	0.140			
miR-466d-3p	**1.35**	0.008	1.24	0.301			
miR-139-5p	**1.35**	0.044	1.15	0.108			
miR-221	**1.36**	0.011	**1.39**	0.024			
miR-669l	**1.36**	0.075	1.32	0.207			
miR-384-5p	**1.36**	0.030	**1.08**	0.032			
miR-300*	**1.37**	0.024	1.10	0.199			
miR-411*[1]	**1.38**	0.004	1.12	0.305			
miR-34a	**1.38**	0.055	-1.07	0.125			
miR-196a	**1.40**	0.080	**1.32**	0.049			
miR-28	**1.41**	0.061	1.22	0.215			
miR-25	**1.41**	0.084	-1.03	0.455			
miR-32	1.42	0.265	**1.67**	0.054			
miR-210	1.42	0.199	**-1.26**	0.005			
miR-375	**1.42**	0.006	1.27	0.139			
miR-23a	**1.42**	0.039	**1.16**	0.047			
miR-200b*	**1.43**	0.046	1.18	0.279			
miR-381[6]	**1.44**	0.073	**1.24**	0.052			
miR-299	**1.45**	0.093	1.16	0.270			
miR-7a-1*	**1.46**	0.021	1.16	0.104			
miR-668	1.46	0.154	**2.18**	0.068			
miR-134	1.46	0.140	**1.36**	0.021			
miR-466i-3p	**1.47**	0.090	2.81	0.154			
miR-142-5p[3]	**1.48**	0.044	1.11	0.290			
miR-667*	**1.48**	0.016	**1.31**	0.040			
miR-669f-3p	**1.48**	0.025	1.51	0.232			
miR-380-3p	**1.49**	0.039	1.02	0.469			
miR-106b*	**1.49**	0.009	**1.51**	0.060			
miR-219-5p	**1.50**	0.066	1.29	0.240			
miR-19a	1.51	0.202	**1.81**	0.001			
miR-669a-5p	**1.51**	0.016	1.36	0.154			
miR-30c-1*	**1.52**	0.013	**1.50**	0.046			
miR-361	**1.52**	0.062	1.24	0.129			
miR-146b	**1.52**	0.054	**1.25**	0.079			
miR-200c	**1.53**	0.033	**1.46**	0.081			
miR-466p-3p	**1.53**	0.055	1.44	0.242			
miR-466e-3p	**1.53**	0.055	1.44	0.242			
miR-3095-3p	**1.53**	0.096	1.09	0.350			
miR-466b-3p	**1.54**	0.055	1.45	0.240			
miR-669o-5p	**1.54**	0.006	1.18	0.271			
miR-379*[6]	**1.55**	0.052	1.27	0.186			
miR-144*[5]	**1.55**	0.001	**1.47**	0.076			
miR-532-5p[1]	**1.55**	0.052	1.06	0.378			
miR-30c-2*	**1.56**	0.015	1.27	0.185			
miR-669c	**1.56**	0.024	**1.50**	0.019			
miR-19b[4]	1.58	0.167	**1.81**	0.000			
miR-466a-3p	**1.61**	0.038	1.43	0.250			

miR-18b	**1.61**	0.093	1.70	0.100		
miR-297b-3p	**1.63**	0.004	1.55	0.193		
miR-92a	**1.64**	0.000	1.24	0.255		
miR-369-3p	**1.64**	0.038	1.37	0.174		
miR-20a	**1.66**	0.076	1.32	0.121		
miR-20b*	**1.66**	0.014	**1.81**	0.059		
miR-1	**1.67**	0.011	1.17	0.287		
miR-3470a	**1.68**	0.018	**1.48**	0.074		
miR-1186b	**1.70**	0.014	**1.22**	0.068		
miR-363-3p	**1.71**	0.034	1.36	0.236		
miR-155	**1.71**	0.047	**1.68**	0.010		
miR-301a	1.72	0.137	**1.72**	0.015		
miR-467a	**1.72**	0.047	**1.74**	0.056		
miR-34b-5p	**1.73**	0.059	**1.73**	0.020		
miR-3473	**1.75**	0.020	1.72	0.121		
miR-297a	**1.76**	0.097	**1.32**	0.035		
miR-376b[1]	**1.79**	0.010	1.29	0.198		
miR-466n-3p	**1.80**	0.002	1.33	0.145		
miR-450b-3p[4]	**1.81**	0.031	1.25	0.111	-	UAC
miR-302c	**1.82**	0.071	1.94	0.174	-	-
miR-301b	**1.84**	0.054	**1.52**	0.098	-	UAC
miR-542-3p	**1.85**	0.072	**1.55**	0.001	-	UAC
miR-190	1.85	0.156	**2.20**	0.041	UAC	-
miR-106a[1]	**1.86**	0.062	1.55	0.223	UAG	-
miR-367	**1.88**	0.019	2.29	0.123	-	-
miR-335-3p	**1.90**	0.081	**1.90**	0.095	-	-
miR-19b-1*	**1.96**	0.055	**1.52**	0.055	UAG	UAC, UAG
miR-3106	**1.98**	0.078	2.36	0.140	-	UAC
miR-466c-5p	**2.02**	0.043	**1.62**	0.017	UAA	UAC
miR-493*	**2.06**	0.015	**1.50**	0.057	-	-
miR-450b-5p[4]	**2.08**	0.025	**1.51**	0.000	-	UAC
miR-574-5p	**2.09**	0.023	**1.84**	0.064	-	-
miR-20b	**2.17**	0.048	1.81	0.168	UAG	UAC
miR-219-3p*[6]	**2.41**	0.099	**1.53**	0.067	-	-
miR-712*	2.72	0.135	**3.42**	0.091	-	-
miR-690	3.35	0.123	**1.69**	0.063	-	UAA
miR-466i-5p	5.37	0.101	**2.58**	0.034	UAC	UAC

[1] (Kawahara Y et al. 2008)
[2] (Luciano DJ et al. 2004)
[3] (Yang W et al. 2006)
[4] (Landgraf P et al. 2007)
[5] (Blow MJ et al. 2006)
[6] (Chiang HR et al. 2010)

Supplementary Table 3:

Example for output of significance testing of A to G transitions in mature miRNAs.

The output for the significance of editing test for mmu-miR-378 transitions as mean of all replicates is shown per position of the reference sequence. The editing position (position 16 of mature miRNA) is marked in bold; underlined are the number of reads that have a G instead of an A at position 16.

	wildtype					***Adarb1*$^{-/-}$**					***Adar*$^{-/-}$, *Adarb1*$^{-/-}$**			
Ref	A	C	G	T	Ref	A	C	G	T	Ref	A	C	G	T
	5356					5510					5496			
A	8	0	0	0	A	1	0	0	0	A	1	0	0	0
C	58	57089	22	39	C	20	59094	15	38	C	16	58457	8	29
									5914					
T	22	47	11	57252	T	24	56	24	2	T	6	32	3	58530
								5917					5852	
G	24	31	57268	26	G	30	33	1	22	G	16	18	7	15
								5919					5853	
G	14	20	57313	23	G	16	25	3	27	G	7	16	9	20
	5726					5919					5850			
A	4	49	59	12	A	8	36	21	12	A	0	37	44	6
C	31	57315	24	32	C	10	59215	8	43	C	7	58572	5	24
									5925					
T	19	32	8	57384	T	2	25	3	2	T	5	18	3	58600
									5928					
T	0	0	0	57455	T	0	0	0	5	T	0	0	0	58634
								5928					5863	
G	0	0	57455	0	G	0	0	5	0	G	0	0	4	0
								5928					5863	
G	0	0	57455	0	G	0	0	5	0	G	0	0	4	0
	5745					5928					5863			
A	5	0	0	0	A	5	0	0	0	A	4	0	0	0
								5920					5855	
G	17	19	57377	41	G	13	20	0	52	G	21	22	3	37
									5900					
T	32	108	68	57203	T	35	111	88	7	T	42	134	112	58291
C	12	57359	10	30	C	10	59176	11	38	C	5	58544	2	24
	5723					**5912**					**5850**			
A	**6**	**37**	**125**	**8**	**A**	**1**	**32**	**49**	**21**	**A**	**2**	**19**	**39**	**8**
								5909					5841	
G	52	26	57300	21	G	66	24	6	29	G	57	23	1	62
	5732					5909					5848			
A	5	42	16	3	A	0	52	43	15	A	9	32	14	5
	5727					5910					5844			
A	7	64	12	5	A	4	53	18	13	A	9	21	10	12
								5906					5839	
G	25	23	57253	22	G	43	28	1	31	G	18	19	3	20
								5843					5756	
G	0	0	56574	0	G	0	0	5	0	G	0	0	1	0

Supplementary Table 4:

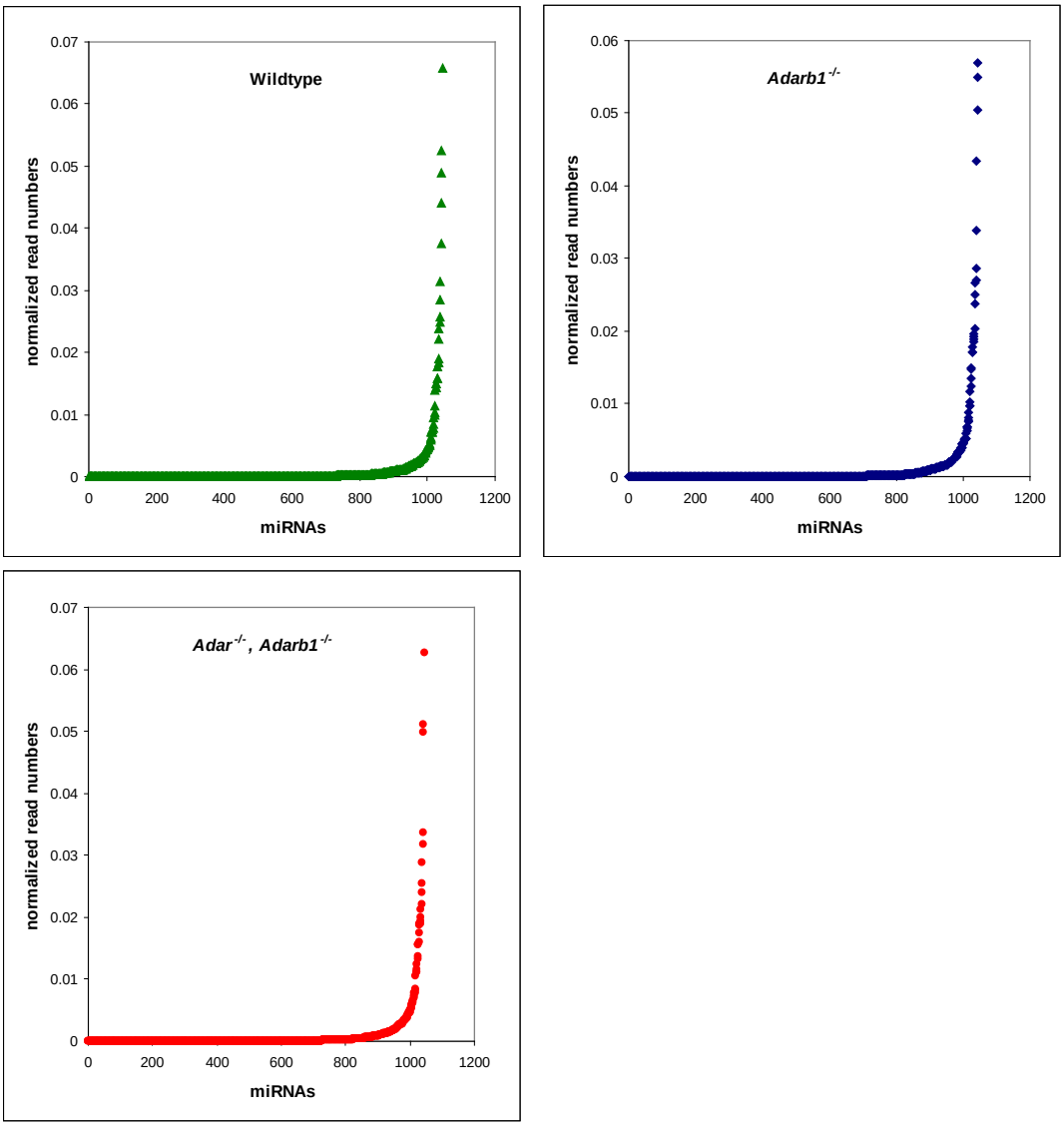
Significant editing events detected in at least 2 out of 3 replicates.

miRNAs in green have already been identified as edited mature miRNAs. The red A in the "context" column marks the edited adenosine, the nucleotide after the slash is the editing site opposing base. Plausible contexts according to editing site preferences are marked in bold, rather unusual target sites are in gray. The "position" column lists the nucleotide position of the edited adenosine in the mature miRNA. Positions in blue are located within the seed sequence of the miRNA.

miRNA	average read number	abundance in *Adarb1*$^{-/-}$ in % of wildtype	abundance in *Adar*$^{-/-}$, *Adarb1*$^{-/-}$ in % of wildtype	editing in # biological replicates	position	context
miR-378	58589	101	88	2	16	CAG / U
miR-376b	13612	178	113	2	**6**	**UAG / U**
miR-1957	2704	127	181	2	15	**UAU / U**
miR-381	2206	145	118	3	**4**	**UAC / U**
miR-467d*	1145	146	201	2	9	**UAC / C**
miR-3099	684	87	77	2	**7**	**UAG / C**
miR-706	228	218	253	2	20	AAA / U
miR-1186	199	181	147	2	16	**AAG / C**
miR-3102-5p.2	196	106	95	2	18	GAG / U
miR-703	156	223	132	2	**4**	AAA / U
miR-669b*	89	192	130	2	**4**	**UAU / C**
miR-1966	80	140	124	2	20	GAG / U
miR-669h-3p	65	152	187	3	**2**	**UAU / U**
miR-669p*	56	275	373	2	23	**UAU / U**
miR-669p*	56	275	373	2	**5**	AAC / U
miR-669i	54	180	132	2	20	**UAC / U**
miR-1934*	52	305	262	2	**7**	GAC / U
miR-466h-3p	47	122	149	2	12	CAC / U
miR-293*	44	293	190	2	**7**	AAC / U
miR-344d	37	99	114	2	**6**	**UAA / U**
miR-1941-5p	36	182	217	2	15	**UAC / U**
miR-3092	33	164	159	2	**2**	GAA / C
miR-466f-5p	32	215	231	2	20	CAU / U
miR-504*	32	151	154	2	**7**	GAG / A
miR-3474	24	127	141	2	13	GAC / U
miR-1971	17	137	101	2	16	GAG / U
miR-1971	17	137	101	2	**3**	AAA / -
miR-1970	16	175	132	3	16	**UAG / -**
miR-146a*	15	301	142	2	**8**	AAA / U
miR-1298*	11	119	91	2	15	GAU / U

Supplementary Figure 1:

A small set of miRNAs contains the most abundant miRNAs in all genotypes and all biological replicates. Normalized read numbers of all detected miRNAs are plotted, showing that only few miRNAs are highly abundant.



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