SUPPLEMENTARY INFORMATION

Short Intron-Derived ncRNAs

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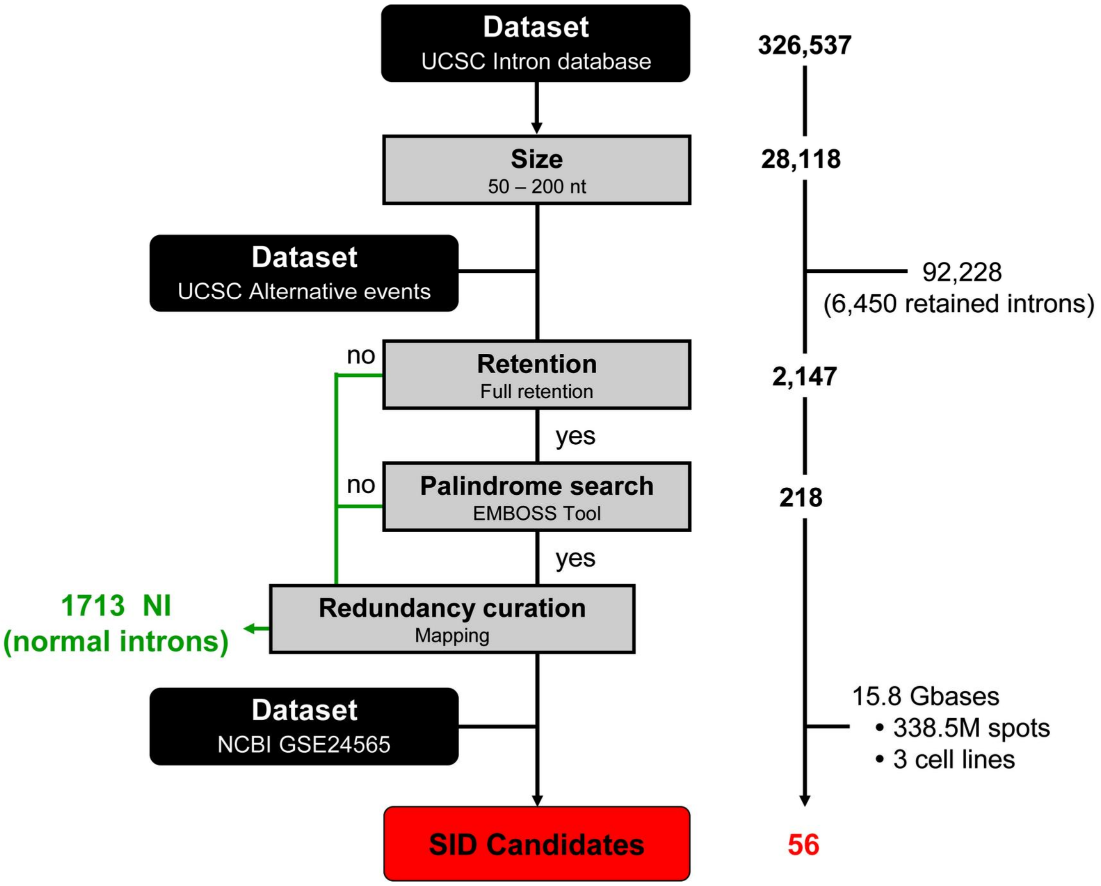
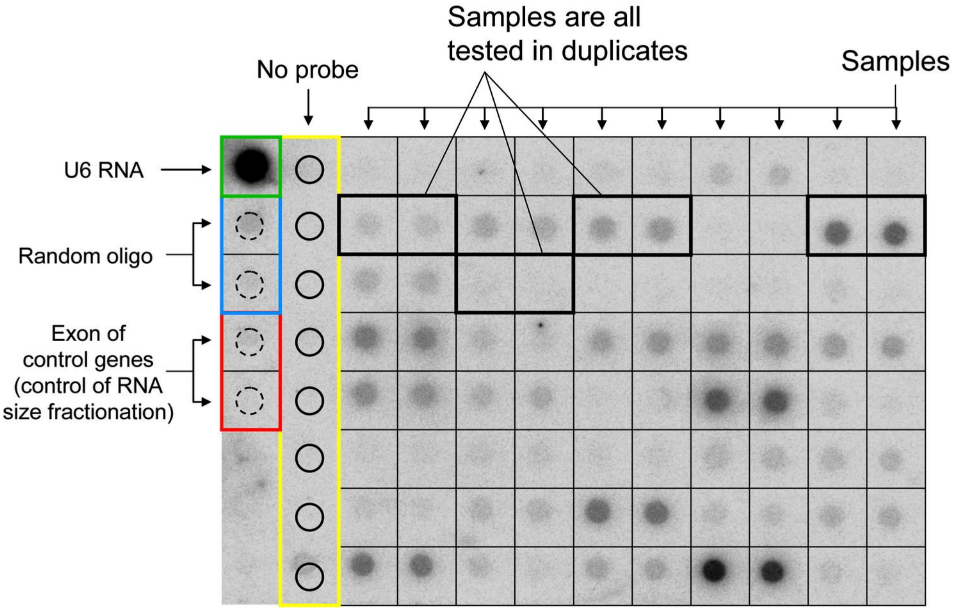
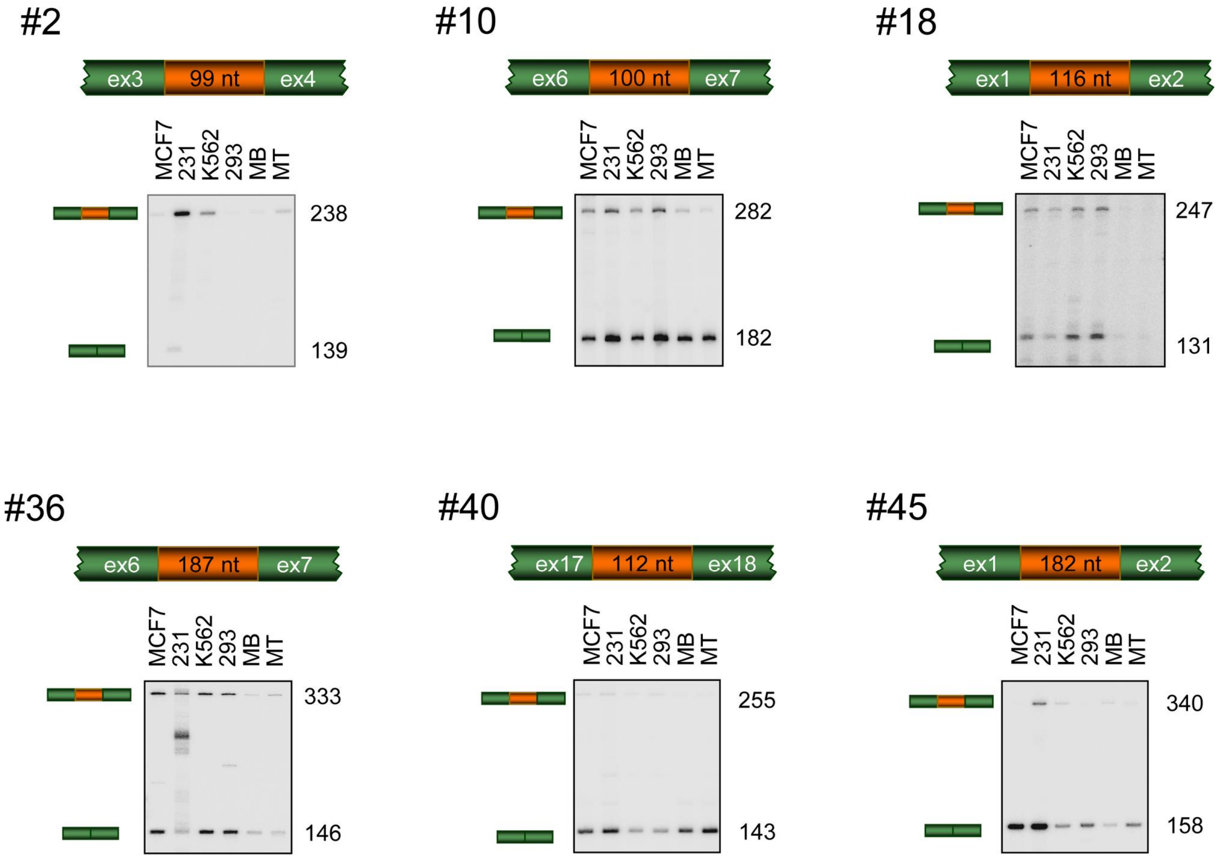


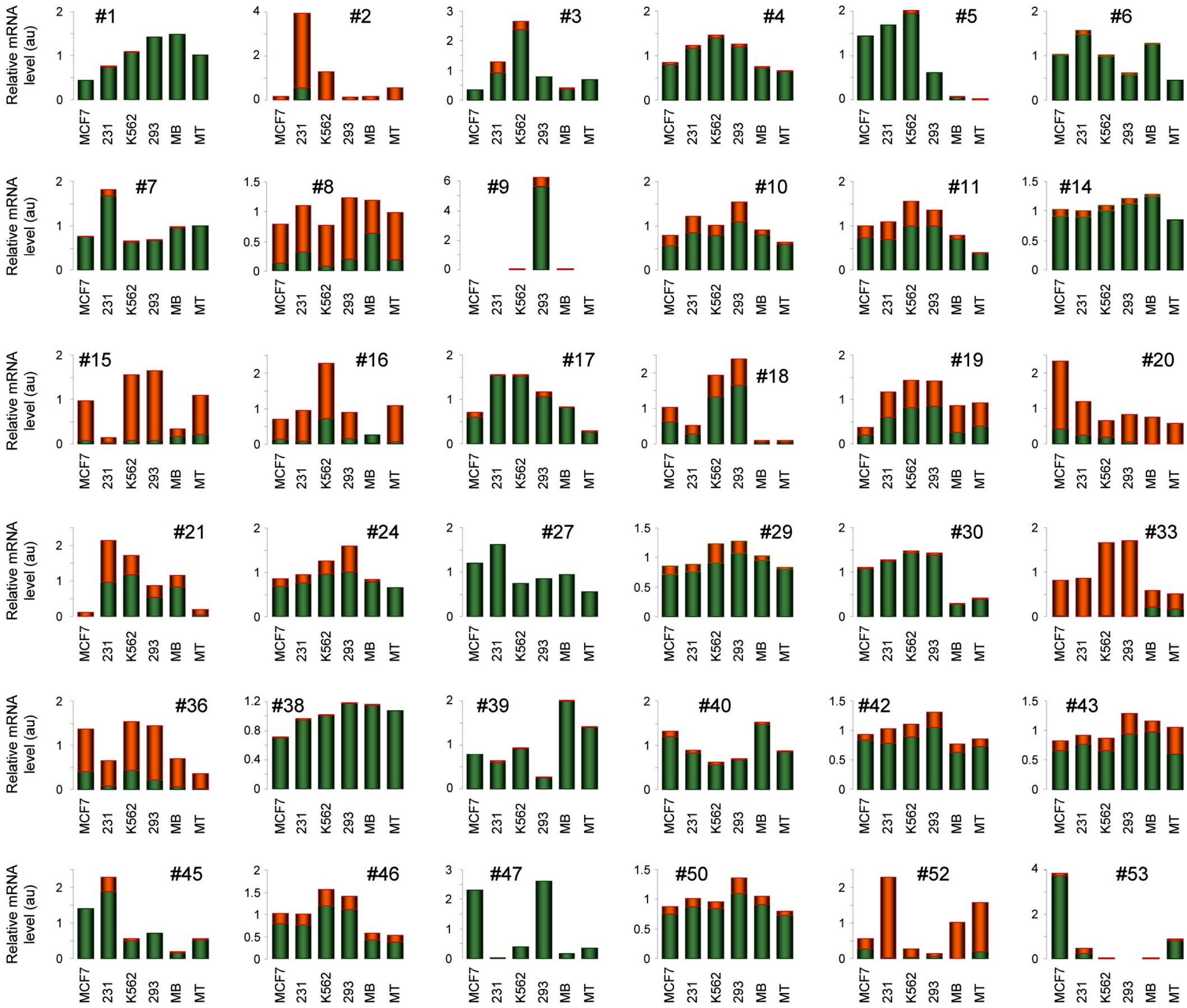
Supplementary Figure S1 Workflow for the identification of new SID. All datasets used in this study were obtained from the UCSC table browser (http://genome.ucsc.edu) using corresponding table tracks as described in the Materials and Methods section. Treatment of data was performed using Galaxy (http://main.g2.bx.psu.edu) and freely available tools. The number of sequences used to obtain the two datasets used herein, *i.e.* the SID datasets, containing 56 new candidates expressed in cells (red text), and the normal introns (NI) datasets (green text), are indicated on the right.



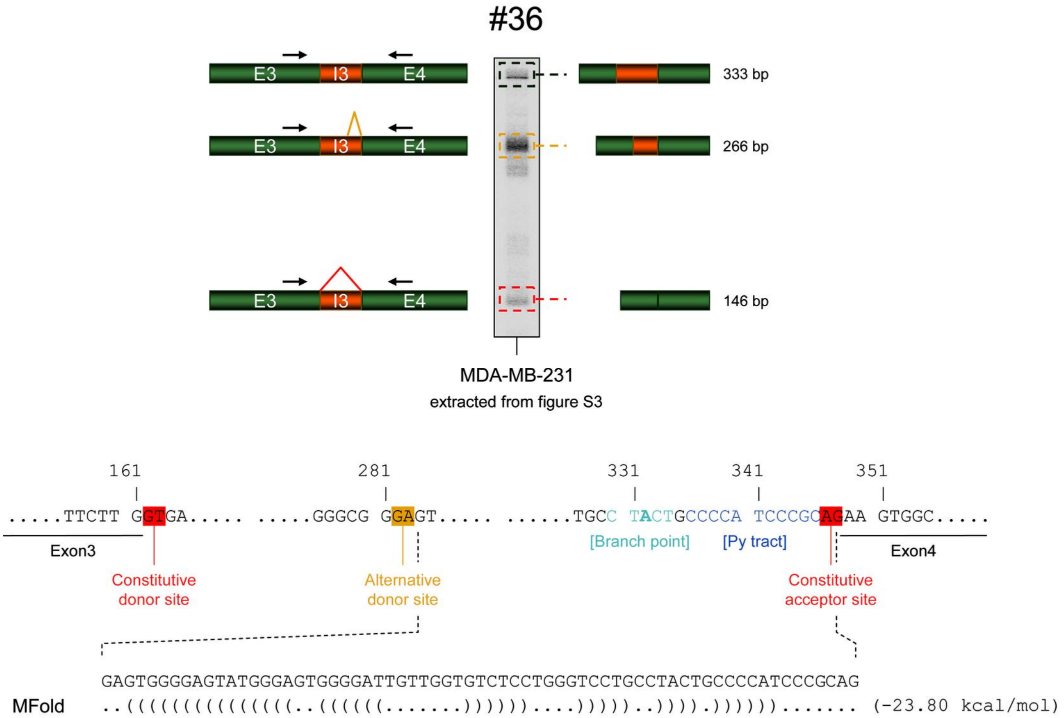
Supplementary Figure S2 Representative oligonucleotide macro-array. U6 oligonucleotide served as loading control, two random-generated oligonucleotides were used to set the baseline signal and two oligonucleotides matching constitutive exon 4 of GAPDH and exon 4 of SRA mRNA were used as size fractionation controls. All oligonucleotides were spotted as duplicates. This particular slot blot corresponds to the hybridization with small RNAs extracted from wild type HEK-293, and oligonucleotide probes were, from left to right and top to bottom, candidates #1 to #40.



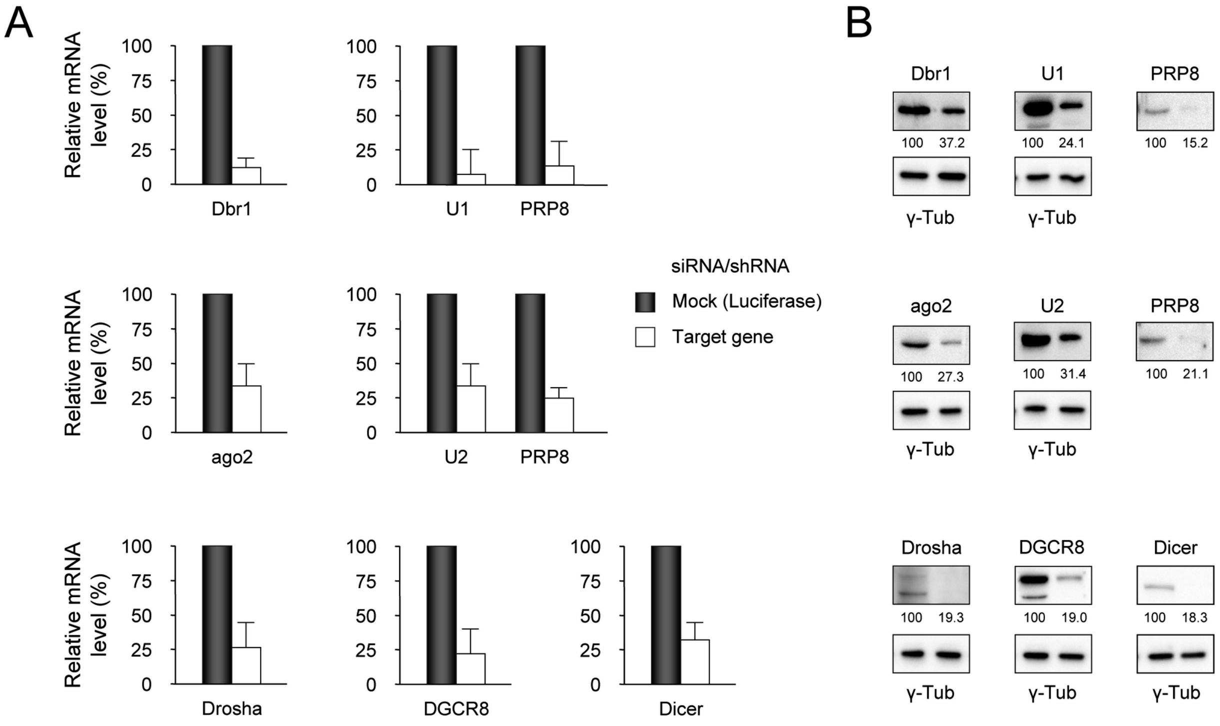
Supplementary Figure S3 Typical examples of intron retention/excision in SID host-genes in the 6 cell lines tested. Radioactive PCR data was performed as described in Material and Methods using oligonucleotides in flanking exons. The introns of interest (the number of each SID is identified on the top of each panel) is shown in red (its size is indicated), flanking exons are shown in green (the number of each exons is indicated), and size of PCR products are shown on the right of the gel. MCF7, MCF7 cells; 231, MDA-MB-231 cells; K562, K562 cells; 293, HEK-293; MB, primary human satellite (myoblast); MT, *in vitro* differentiated myotubes.



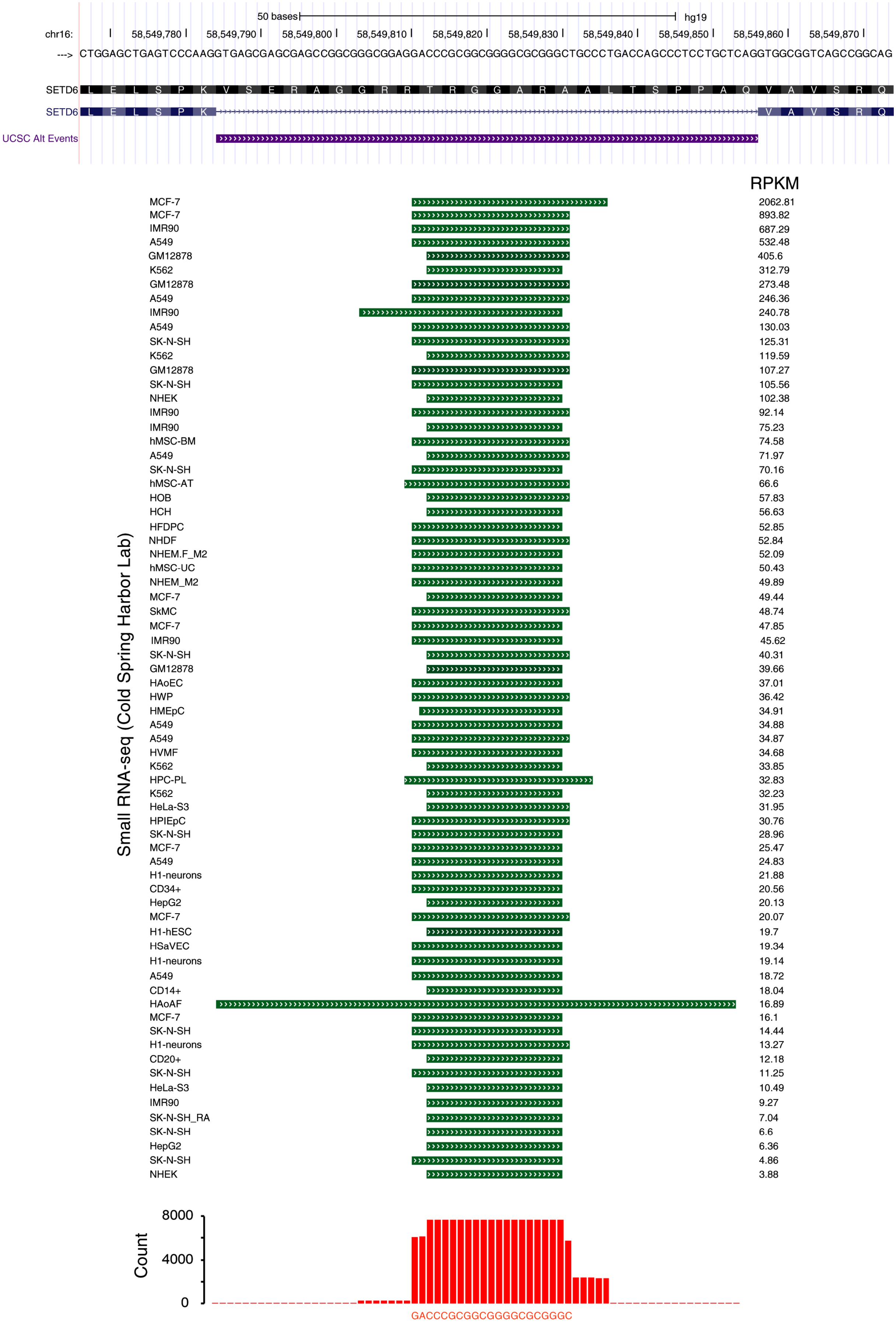
Supplementary Figure S4 Quantification of intron retention/excision in all 36 host-genes that have shown a signal above baseline levels in the oligonucleotide arrays in at least one of the 6 cell lines tested. Radioactive PCR was performed as described in Material and Methods using oligonucleotides designed in flanking exons. Results are expressed as relative mRNA levels expressed in arbitrary units (au) and corrected relative to the U6 signal for each of the 6 cell lines. The green and red colors correspond to intron excision and retention, respectively. MCF7, MCF7 cells; 231, MDA-MB-231 cells; K562, K562 cells; 293, HEK-293; MB, primary human satellite (myoblast); MT, *in vitro* differentiated myotubes.



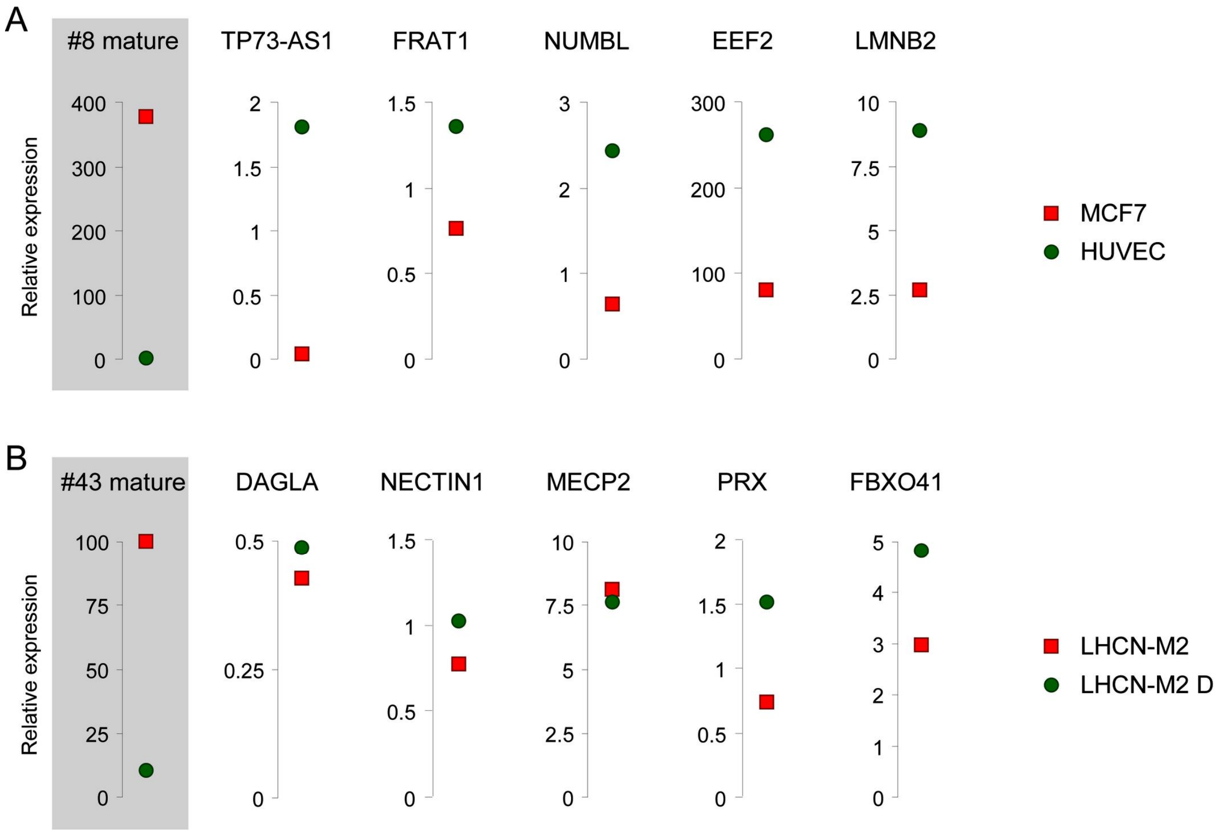
Supplementary Figure S5 Identification of an alternative donor-splicing site within intron 3 of candidate #36. The gel represents radioactive PCR data extracted from figure S3. The upper and bottom bands correspond to full intron retention and excision, respectively. The intermediate band was extracted and sequenced (Eurofins Genomics, Germany), allowing the identification of a non canonical (GT→GA) alternative splicing donor site (1). Bottom panel shows a representation of constitutive donor and acceptor sites (red), alternative donor site (orange) in addition to the branch point and pyrimidine tract (light and dark blue). Numbering is given starting at the beginning of exon 3. The sequence of the partial intron and the corresponding MFold structure are indicated at the bottom.



Supplementary Figure S6 Control of the efficiency of knockdown experiments. RNA interference for each factor was performed as described in Material and Methods section. Knockdown efficiency was assessed by *(A)* RT-qPCR and *(B)* Western blot. A quantification of the remaining protein levels after RNA interference and adjusted to the mock control is given below each corresponding panel. U1, snRNP70; U2, U2AF65; γ-Tub, gamma-Tubulin.


50 bases
hg19
chr16:
58,549,780
58,549,790
58,549,800
58,549,810
58,549,820
58,549,830
58,549,840
58,549,850
58,549,860
58,549,870
---> CTGGAGCTGAGTCCCAAGGTGAGCGAGCGAGCCGGCGGGCGGAGGACCCGCGGCGGGGCGCGGGCTGCCCTGACCAGCCCTCCTGCTCAGGTGGCGGTCAGCCGGCAG
SETD6 L E L S P K V S E R A G G R R T R G G A R A A L T S P P A Q V A V S R Q
SETD6 L E L S P K V A V S R Q
UCSC Alt Events
RPKM
MCF-7 2062.81
MCF-7 893.82
IMR90 687.29
A549 532.48
GM12878 405.6
K562 312.79
GM12878 273.48
A549 246.36
IMR90 240.78
A549 130.03
SK-N-SH 125.31
K562 119.59
GM12878 107.27
SK-N-SH 105.56
NHEK 102.38
IMR90 92.14
IMR90 75.23
hMSC-BM 74.58
A549 71.97
SK-N-SH 70.16
hMSC-AT 66.6
HOB 57.83
HCH 56.63
HFDPC 52.85
NHDF 52.84
NHEM.F_M2 52.09
hMSC-UC 50.43
NHEM_M2 49.89
MCF-7 49.44
SkMC 48.74
MCF-7 47.85
IMR90 45.62
SK-N-SH 40.31
GM12878 39.66
HAoEC 37.01
HWP 36.42
HMEpC 34.91
A549 34.88
A549 34.87
HVMF 34.68
K562 33.85
HPC-PL 32.83
K562 32.23
HeLa-S3 31.95
HPIEpC 30.76
SK-N-SH 28.96
MCF-7 25.47
A549 24.83
H1-neurons 21.88
CD34+ 20.56
HepG2 20.13
MCF-7 20.07
H1-hESC 19.7
HSaVEC 19.34
H1-neurons 19.14
A549 18.72
CD14+ 18.04
HAoAF 16.89
MCF-7 16.1
SK-N-SH 14.44
H1-neurons 13.27
CD20+ 12.18
SK-N-SH 11.25
HeLa-S3 10.49
IMR90 9.27
SK-N-SH_RA 7.04
SK-N-SH 6.6
HepG2 6.36
SK-N-SH 4.86
NHEK 3.88
Small RNA-seq (Cold Spring Harbor Lab)
Count
8000
4000
0
GACCCGCGGCGGGGCGCGGGC

Supplementary Figure S7 Schematic representation of the human SID #8 located within the 2nd intron of SETD6 gene. The reads extracted from Small RNA-seq of Cold Spring Harbor Lab (2) are shown in green. Cell lines are indicated on the left and associated RPKM on the right. Read counts at each position are indicated at the bottom in red, with the predicted mature miRNA sequence used in Figure S8. RPKM, Reads Per Kilobase per Million mapped reads.



Supplementary Figure S8 Anti-correlation analysis between expression levels of mature miRNA and its predicted target genes. (A) Expression levels of SID #8-derived mature miRNA and predicted target genes are indicated as mean RPKM extracted from Cold Spring Harbor Lab small and long RNA-seq databases, respectively (2). MCF7 and HUVEC cell lines represent cells with the highest and lowest expression of SID #8-derived miRNA, respectively. (B) The mature sequence of candidate #43 was cloned and sequenced in this study (Figure 7A) and was used to predict target genes. Expression levels of SID #43-derived mature miRNA were measured by Stem-loop RT-qPCR (Figure 7B), and expression levels for its predicted target genes were extracted from Caltech RNA-seq datasets (3). LHCN-M2 and LHCN-M2-D refer to myoblasts and their differentiated myotubes counterparts described in the Methods section, respectively. Target genes were predicted using TargetRank from the Burge Lab [(4); http://hollywood.mit.edu/targetrank]. The 5 genes presenting the best score were kept for further analyses. TP73-AS1, TP73 antisense RNA 1; FRAT1, frequently rearranged in advanced T-cell lymphomas 1; NUMBL, NUMB like, endocytic adaptor protein; EEF2, eukaryotic translation elongation factor 2; LMNB2, lamin B2; DAGLA, diacylglycerol lipase alpha; NECTIN1, nectin cell adhesion molecule 1; MECP2, methyl-CpG binding protein 2; PRX, periaxin; FBXO41, F-box protein 41.

Supplementary Table S1 Descriptive list of the 56 candidate SID, including quantification data of the low-density oligonucleotide arrays for the 6 cell lines tested.

													Fold-above baseline						
#	Chr	Start	End	Strand	Length	intron N°/total intron	%GC	? G	-MFE	CpG island	RefSeq	Gene Symbol	MCF7	MDA-MB-231	K562	293	MB	MT	Comments
1	chr1	1274819	1274961	-	142	10/14	71,13	-68,3	0,480985915		NM_004421	DVL1	0,0	0,0	0,0	0,0	0,0	1,6	
2	chr11	65360681	65360780	-	99	3/3	67,67	-44,31	0,447575758		NM_033348	KCNK7	0,0	0,0	0,0	0,0	0,1	2,5	
3	chr16	28997890	28997977	+	87	6/11	67,82	-39,3	0,451724138		NM_001014987	LAT	0,0	0,0	0,3	0,1	0,0	2,5	
4	chr19	9929293	9929403	-	110	1/2	76,36	-50,4	0,458181818	Y	NM_017703	FBXL12	0,4	0,4	0,0	0,9	0,4	3,3	
5	chr19	55593548	55593642	+	94	7/11	78,72	-34,8	0,370212766	Y	NM_133180	EPS8L1	0,0	0,1	0,0	0,0	0,0	1,3	
6	chr1	109823538	109823729	-	191	5/7	61,78	-79,9	0,418324607		NM_001005290	PSRC1	0,2	0,4	0,2	0,5	0,3	1,3	
7	chr11	65479750	65479849	+	99	1/13	76,77	-48,7	0,491919192	Y	NM_006388	KAT5	0,2	0,3	0,2	3,7	0,9	2,5	
8	chr16	58549784	58549856	+	72	2/3	80,56	-36,8	0,511111111	Y	NM_024860	SETD6	0,9	1,4	2,9	3,7	1,6	6,3	
9	chr19	11689473	11689658	-	185	1/6	65,95	-71,7	0,387567568	Y	NM_001111035	ACP5	0,0	0,2	0,0	0,0	0,0	1,5	
10	chr2	74900703	74900803	+	100	6/8	61	-40,4	0,404		NM_004263	SEMA4F	3,1	12,3	6,5	3,9	5,7	5,0	
11	chr1	113238873	113239058	+	185	13/21	56,76	-62,6	0,338378378		NM_001130079	MOV10	0,5	0,9	0,5	2,6	0,7	1,9	
12	chr11	67815271	67815348	+	77	12/19	81,82	-32,4	0,420779221		NM_006053	TCIRG1	0,0	0,0	0,0	0,0	0,0	0,0	
13	chr16	75589871	75589968	-	97	1/6	74,23	-46,1	0,475257732	Y	NM_001077418	TMEM231	0,0	0,0	0,0	0,0	0,0	0,4	
14	chr19	14070485	14070578	+	93	8/12	74,19	-51,4	0,552688172		NM_138353	DCAF15	0,3	0,2	0,0	0,0	0,0	1,0	
15	chr2	128180747	128180849	+	102	5/8	81,37	-62,5	0,612745098	Y	NM_000312	PROC	0,2	0,2	0,0	1,2	0,0	1,1	
16	chr1	156347931	156348042	+	111	3/10	71,17	-59,5	0,536036036		NM_020407	RHBG	2,0	3,3	3,5	10,5	4,0	3,0	
17	chr12	7076942	7077054	-	112	5/8	62,5	-38,4	0,342857143		NM_001144831	PHB2	0,5	0,6	0,0	0,6	0,5	4,8	
18	chr17	27229719	27229835	-	116	1/4	80,17	-60,5	0,521551724	Y	NM_144683	DHRS13	1,2	1,5	5,7	3,0	1,5	2,7	
19	chr19	18547687	18547782	-	95	4/10	76,84	-34,2	0,36	Y	NM_016368	ISYNA1	1,8	2,9	3,5	1,2	2,5	1,2	
20	chr20	3641511	3641590	-	79	2/5	84,81	-47,9	0,606329114	Y	NM_022139	GFRA4	1,2	1,2	3,5	2,1	1,3	2,3	
21	chr1	156877843	156877919	+	76	8/22	75	-27,3	0,359210526	Y	NM_001080471	PEAR1	1,0	1,7	1,2	2,8	2,6	5,3	
22	chr13	113832290	113832487	-	197	14/14	48,22	-53,6	0,272081218		NM_018386	PCID2	0,3	0,3	0,1	0,4	0,7	0,4	
23	chr17	76116913	76117093	-	180	11/18	60	-65,6	0,364444444		NM_001127198	TMC6	0,0	0,0	0,1	0,3	0,0	0,2	
24	chr19	30312725	30312902	+	177	8/11	82,73	-56,4	0,318644068	Y	NM_001238	CCNE1	6,1	10,6	12,5	9,8	8,2	7,7	
25	chr20	32247356	32247458	-	102	8/12	70,59	-64,6	0,633333333		NM_031231	NECAB3	0,2	0,2	0,0	0,5	0,1	0,9	
26	chr11	209318	209406	+	88	2/9	69,32	-45,3	0,514772727		NM_021932	RIC8A	0,1	0,1	0,0	0,1	0,0	0,5	= hsa-miR-6743
27	chr14	35099160	35099316	-	156	1/13	74,36	-71,6	0,458974359	Y	NM_152233	SNX6	0,1	0,1	0,0	0,2	0,1	1,6	
28	chr19	436431	436629	-	198	5/12	71,72	-95,6	0,482828283	Y	NM_012435	SHC2	0,0	0,0	0,0	0,4	0,0	0,6	
29	chr19	49422379	49422450	+	71	9/11	70,42	-43,4	0,611267606		NM_006184	NUCB1	0,5	0,5	0,2	1,3	0,4	0,4	
30	chr22	50699725	50699813	-	88	1/11	87,5	-50	0,568181818	Y	NM_002969	MAPK12	0,5	0,7	0,0	0,7	0,5	1,5	
31	chr11	721991	722090	+	99	11/20	74,75	-43,3	0,437373737		NM_022772	EPS8L2	0,0	0,1	0,0	0,1	0,2	0,0	
32	chr16	111279	111382	-	103	10/17	83,5	-49,8	0,483495146	Y	NM_022450	RHBDF1	0,3	0,5	0,1	0,8	0,4	0,5	
33	chr19	1083065	1083141	+	76	20/22	75	-33,1	0,435526316	Y	NM_012292	ARHGAP45	1,2	2,8	8,8	3,6	4,9	2,1	
34	chr19	50306262	50306363	+	101	17/23	71,29	-42,9	0,424752475		NM_014203	AP2A1	0,3	0,1	0,0	0,4	0,3	0,0	
35	chr3	9882300	9882381	-	81	4/7	62,96	-35,3	0,435802469		NM_001142547	RPUSD3	0,4	0,5	0,2	0,7	0,6	0,6	
36	chr11	64064751	64064938	+	187	4/6	65,78	-73,9	0,395187166		NM_033310	KCNK4	0,8	2,3	3,9	0,8	4,9	3,8	
37	chr16	28620180	28620379	-	199	1/7	60,3	-79,07	0,397336683		NM_177530	SULT1A1	0,0	0,1	0,0	0,1	0,3	0,8	
38	chr19	1877424	1877506	-	82	5/5	84,15	-37,9	0,462195122	Y	NM_031213	ABHD17A	1,1	2,1	2,9	1,8	1,0	2,6	
39	chr19	52207439	52207522	+	83	6/7	80,72	-43,2	0,520481928	Y	NR_024330	SPACA6	6,3	15,1	11,8	9,9	20,1	6,7	
40	chr3	50311077	50311189	+	112	10/18	75,89	-64,3	0,574107143	Y	NM_004636	SEMA3B	0,1	0,4	0,0	0,2	0,2	5,1	
41	chr4	995949	996056	+	107	7/13	79,44	-43,5	0,406542056	Y	NM_000203	IDUA	0,1	0,0	0,0	0,3	0,1	0,0	
42	chr8	144917900	144917989	-	89	6/6	82,02	-46,2	0,519101124	Y	NM_178564	NRBP2	26,2	4,7	20,2	9,1	0,6	0,8	
43	chr5	139936857	139937012	-	155	1/4	70,21	-33,04	0,21316129	Y	NM_001035235	SRA1	2,2	1,1	18,8	9,6	32,0	2,6	
44	chr8	145625475	145625559	-	84	9/37	77,38	-39	0,464285714		NM_013291	CPSF1	0,6	0,0	0,0	0,0	0,0	0,0	= hsa-miR-1234
45	chr5	177558055	177558237	+	182	1/10	72,53	-88,3	0,485164835	Y	NM_022762	RMND5B	0,3	0,1	1,0	0,0	0,0	0,1	
46	chr8	145634556	145634672	-	116	1/37	83,62	-69,1	0,595689655	Y	NM_013291	CPSF1	35,5	28,7	31,1	10,7	0,6	1,6	
47	chr5	179222684	179222786	+	102	2/4	82,35	-62,4	0,611764706	Y	NM_145867	LTC4S	0,0	0,0	5,5	0,0	0,0	0,0	
48	chr8	145649305	145649423	-	118	9/9	73,73	-59,1	0,500847458		NM_016208	VPS28	0,1	0,3	0,3	0,0	0,0	0,0	
49	chr6	31938924	31939096	-	172	2/6	49,42	-50,9	0,295930233		NM_005510	DOM3Z	0,6	0,0	0,4	0,0	0,1	0,0	
50	chr9	139836918	139836998	-	80	1/4	83,75	-47,9	0,59875	Y	NM_018998	FBXW5	1,1	0,4	2,5	0,3	0,1	0,0	
51	chr6	33381334	33381512	+	178	6/14	51,69	-38,8	0,217977528		NM_024165	PHF1	0,3	0,2	0,6	0,2	0,5	0,0	
52	chr9	140128393	140128560	+	167	9/12	76,05	-47,07	0,281856287		NM_080877	SLC34A3	1,0	0,5	11,7	0,9	1,0	0,0	
53	chr7	76140054	76140219	+	165	1/6	71,52	-82,1	0,497575758		NM_182684	UPK3B	0,0	0,0	0,0	0,0	0,1	7,4	
54	chrX	135579598	135579782	+	184	1/9	79,35	-106,7	0,579891304	Y	NM_001163280	HTATSF1	0,0	0,0	0,0	0,0	0,0	0,0	
55	chr7	100174400	100174524	-	124	11/15	64,52	-40,89	0,329758065		NM_002319	LRCH4	0,0	0,0	0,0	0,0	0,1	0,0	
56	chrX	153285049	153285127	-	78	1/13	87,18	-49,2	0,630769231	Y	NM_001569	IRAK1	0,0	0,1	0,0	0,0	0,0	0,0	

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10	.((((((.((((....((((((((...(.((((((((..........(((((....)))))))))))).)))).)))))))))....)).))....)))))).
11	...(((((.((((......((((((((..................))))))))(((((((((.(....(((((......))))).....(((((.(((((((((.((..((((((((((........))))).)))))..)).)))))))....)).)))))).))))))))))))))))))..
12	..(((((..((((....))))(((((((((((......)).))).))))).......).))))..(((((....)))))
13	.............(((.((.......)).))).....((((.((((((((((...(.(((((((....)))).))).)..)))))))))).))))....
14	((((((.((((((.(((((((((((......((((((.......)))))).....)))).)))))).)))).))))))))).........
15	(((.(((((((.(((........((((((((.((((.(((((.(.((........)).).)))).)).)).)).)))))))))))))))))...)))..
16	........((((((((((((...))).((((((((((((((((...(((.(((((((.((.....)).)))))))...)))...).))))))))))))))).)))))))))
17	.....(((((((.(((...(((((((....((((((((..((....)))))))).))))))))))))))))))).((.(((.((((..........)))).))).)).....
18	.((((((..(((((.(((.((.((((((.((.(.(((((((((((((..((....))))))))))))).........))).).)).)))))))).))).))))).)))))).....
19	(((((((.(((.....((.(((...))).)).....))).)))))))................(((.......)))...((((...))))..
20	.((((((.((((..(((((((.((((..(.((((............)))).)..))))..))))))).)))))))))).
21	.((((((((.((((((..(.(....(.........)....).)..)))).))).)).))))))((.....))....
22	((((((((.((....))...))))).)))(((((...............(((.(.....((((((.((((((((..........)))))))).)))))).....).))).((((.((((((........)))))))))).((.((.((((...)))))))))))))........((((..((......))..))))
23	((((((((((.((((((.(((.((..((((.(((((...((((.((.....))..))))...)))))).))..)).))).).))).)).)))).).)).)))...))))((.(((........((((((..((.....))...)))))).((((...((((.....))))))))..))).))..
24	.(((...(((.((...((((((((((......((((.((.((((((((....((((((.....))).)))....))).((((.....)))).)))).)).))))))))).)))))...((((....((((..........))))....)))))........)).)))...)))....
25	..((((((((.(...(((.((((((((((((((.((.((((...))))))).)))))..(((.(((((....)))))).)))))))))).)))))))))))))))))
26	.((((....)))))..........((((((((.(((((((((((((........))))..))).))))))))...)))))))))....
27	..((((((((.((((((.(((.(..((((((....((......(((((.....((..(((.........(((...(((.((((((((...)))))))).))).))).)))..))))))))))....))))))..)))))).)))).))...).)))))
28	.(((((.((((((((((...(.(((((((((((.((((((.((((..(((((...(((((((.(((....(.((.......)).)....)))..)))))))(((((.(((...))).))))))))))).(.(((((...))))))..)))).)))))))..)))....))))))))))))).))))))).))))).
29	......((((((((((.(((((.((((((((((.....)).))))).))).))))).)))))).))))).
30	..((((((((.((((...(((((..(((((.((.....)).).))))...)))))...).)))))))))))..(((....)))...
31	(((((..(((.(((....)))))).))))).((..((((((.(((..((((((.....))))))..)))))))))..))..................
32	.((.((((..(((.(.((.(.((((((....((((((((..(((((.....)))))....)))))))).....).))))))))))))..))))))......
33	.......(((.....))).((((.(((((.((((..(((((.((.......)).))))))))))))))...))))..
34	.((((....(((.((((.(((((((((..(((((...(((..((...))..))).(((((......))))))))))..)))).).))))))))))))))).
35	.(((((..((.((..(.((((((..((((((((.....((((.....)))))))))))).)..)))))).)).))))))).
36	...(((((......((((.(((........).)).)))).)..)))))......(((((.(..((((......(((.((.................)))))......))))..).)))))(((((((.((((((((.((((..((((((.......))))))....))))...)))).))))))))))))..
37	........(((((((.((..((...........((((((........((((((((........))))))))....(((((((((((..(((((....))))).)))))))).)))...........((((...))))((((((.((.(((.....))).)).)))))).....))))))..))..)))))))))..
38	..(((((.(((((.(((.(((((((.(.....).)).)))))))))))))...))))).((((........)))))........
39	((((((..(.(((((.((((........))))(((((((...((......))...)))))))..))))).)..))))))..
40	....(((.(((((.((((....((((((((((((.((((((((.............)))(((((....))))))))))).).)))).))))))))..)))).))))))))..
41	(((((..(((.....)))..(((((.((.(((..(.(((...(((((...))))).))).)..))).)).)))))......((((.((.....)))))).)))))..
42	.((((...((.((..(((.(((.((.((((((((((((((......))))))...))))))))))...))).)))...)).))...)))).
43	.(((((........(((.(.......).))).......)))))((((..(((.(((((.((......))))))).)))....))))........
44	.(((((((((.(((...(((((....(((.(((....))))))..)))))..............))).))))))))).....
45	(((.(((((((.((..(((((.(((.((....)).))).((((((((((...(.(((((((.(((((....(((...)))....))))).))))))).)....))))..))))))))))..)))))))).).)))((.(((((((................))))))).))..........
46	..((((.((((((((.((((..(((((.(((((((((((((.....)).))..))))))))..))).)))))))))))))).)))).........((((((......)))))).....
47	(((.((((.((.((((((((((.(((.((((.((.((((.....)))).))((((....)))).)))).)))..))))))).)))).))))))))).....
48	...(.(((((..((((.....))))((((((...))))))....))))).)(((..(((.(((((((((((((((((((.......))))))))).))))))))))..)))..)))..
49	.(((((((.(((((((((((((...))))))....((((....((((((..(...(((.((((((.........))))))..)))...)..))))))....)))))))))))).(((....)))..((((((((...(((....)))....))))))))..)))).)))).
50	((((((((((((.(...((((...((((.(((.........)))))))....)))))))))))))))))...........
51	........((((.((((((.((((((.((((....(((.((.(.....(((((.........................((((.......))))..)))))....).)).)))....))))...))))))......(.((((((((((((...)))))))))))).)))))))))).
52	((((((...(((.........))).))).)))............((((.(((.........))).))))....(((..((...(((((..(((..(((..(((.((((.((.....)).)))))))......)))....)))...)))))...))..)))......
53	....((((((((((((((((....))))))))((((((((.((((((...))))))..))).))..)))))..((((((.((..(((...((((.....)))).))).)))))))))))))))))..........(((((.(((............))))))))..
54	((((((..((((...)))).)))))).((.(((.((((....)))).)))))((((((((((((((((.(((.((((((((...(((((.((..((((((....((((......)))))))))..)))))))...))))))...(((.......)))...)))))))))))))))))))))..
55	.((((((((((...((((((((((....(((((..(.(.......).)..)))))))))))))))...))).....................)))))))..........................
56	..((((((((((((((..(((((((((.((.....))))).))))))..))))))))).))..)))))..........

Supplementary Table S2 List of all oligonucleotides used in this study.

Oligonucleotide name	**Oligonucleotide sequence (5’ → 3’)**	**Use in ***
mir1224 RTSL	GTTGGCTCTGGTGCAGGGTCCGAGGTATTCGCACCAGAGCCAACCCACCT	RTSL
mir1224 RTSL for	GTTGTTTGTGAGGACTCGGG	qPCR
pre-mir1224 for	GTGAGGACTCGGGAGGTGG	qPCR
pre-mir1224 rev	CTGAGGAGAGAGGAGGTGGGG	qPCR
miR199a2 RTSL	GTTGGCTCTGGTGCAGGGTCCGAGGTATTCGCACCAGAGCCAACTAACCA	RTSL
miR199a2 RTSL for	TGGTGACAGTAGTCTGCACAT	qPCR
pre-mir199a2 for	GGAGGCTTTTCCTGAGGAC	qPCR
pre-mir199a2 rev	CCCTAGTGTGCAAAACCTGT	qPCR
miR10a RTSL	GTTGGCTCTGGTGCAGGGTCCGAGGTATTCGCACCAGAGCCAACCACAAA	RTSL
mir10a RTSL for	TGTTTTTTTTTACCCTGTAGATCCGAA	qPCR
SRA-miRNA RTSL	GTTGGCTCTGGTGCAGGGTCCGAGGTATTCGCACCAGAGCCAACAGCGCC	RTSL
SRA-miRNA RTSL for	GTTTTTTTGCTGGGGGCG	qPCR
pre-SRA-miRNA for	GGCGGGCTAGGGCACTAGG	qPCR
pre-SRA-miRNA rev	CGGAGGCGAGGGATGTGTGAAGC	qPCR
Universal rev	GTGCAGGGTCCGAGGT	qPCR
SRA Ex4 rev	CGCCTGGCACTGCTGCAGGAAC	PCR
SRA In1 for	GCTAGGGCACTAGGTTGTCGC	PCR
SRA In4 for	ATTGACTGGGAGGGGAGGCATGGAAG	PCR
SRA In4 rev	GAAGAGAGACGGGGGTTGAGCAAGC	PCR
U6 for	CTCGCTTCGGCAGCACA	PCR, qPCR
U6 rev	AACGCTTCACGAATTTGCGT	PCR, qPCR
GAPDH for	CTTCACCACCATGGAGAAGGC	PCR
GAPDH rev	GGCATGGACTGTGGTCATGAG	PCR

U6	TGGAACGCTTCACGAATTTGCGTGTCATCCTTGCGCAGGGGCCATG	Array
Int4 SRA	GTACAAGAGCTTCCATGCCTCCCCTCCCAGTCAATCAAAA	Array
ex4 SRA	TTGACAACTTTCCTCCAGCCCACTGTTCCTGCAGCAGTGCCAGGCG	Array
Random 1	CGAGCACAAGGAACATCCGCCCACCACGCCCTGGTAACAT	Array
Random 2	CTTGTAGTAGGGGGAGAATAAGCACCATCGAAGTCGTTAGGTCTTT	Array
ex4 GAPDH	ACAGCCTTGGCAGCGCCAGTAGAGGCAGGGATGATGTTCT	Array
mir-21	CATGAGATTCAACAGTCAACATCAGTCTGATAAGCTACCCGACA	Array
Dicer for	TGGGTCCTTTCTTTGGACTG	qPCR
Dicer rev	CTGGTTTGCAGAGTTGACCA	qPCR
DGCR8 for	CAAGCAGGAGACATCGGACAAG	qPCR
DGCR8 rev	CACAATGGACATCTTGGGCTTC	qPCR
DBR1 for	GGAAACCATGAAGCCTCAAA	qPCR
DBR1 rev	CCGATCCTTACACCTCGGTA	qPCR
Drosha for	TAGGCTGTGGGAAAGGACCAAG	qPCR
Drosha rev	GTTCGATGAACCGCTTCTGATG	qPCR
U2AF65 for	CCCAGGCTTTGAGCACATCA	qPCR
U2AF65 rev	GCATGGCCTTGTACTGCATTG	qPCR
PRP8 for	CCCCGCTACCGGACTACAT	qPCR
PRP8 rev	GCCATTTTCGAGCTTTCTCCTG	qPCR
snRNP70 for	TCGTGGCGAGAGTGAATTATGA	qPCR
snRNP70 rev	TGATAGGTCCGTACACCTCAAA	qPCR
Ago2 for	TCCACCTAGACCCGACTTTGG	qPCR
Ago2 rev	GTGTTCCACGATTTCCCTGTT	qPCR
Bait SRA Intron 1	AAGGCTGGGGGCGGTTGCGGCGCTTAGTATGGACCCTCTGTCTCCCCCAGCTATAGTGA	Pulldown
Bait Luciferase	AAGGCTTACGCTGAGTACTTCGACTTGCTTCTCGAAGTACTCAGCGTAAGTATAGTGA	Pulldown
sh DBR1-1	AAGGATCGGTGGAATCTCTGGCTTGCTTCCCAGAGATTCCACCGATCCTATAGTGA	interference

sh DBR1-2	AAGGCGAGGCGGATCTACGCTGCCTTGCTTCGCAGCGTAGATCCGCCTCGCCTATAGTGA	interference
sh DBR1-3	AAGGTGTGACTGGGCGCCTGTGGCTTGCTTCCCACAGGCGCCCAGTCACACCTATAGTGA	interference
sh snRNP70	AAGGTCTACAGTAAGCGGTCATTCTTGCTTCAATGACCGCTTACTGTAGACCTATAGTGA	interference
sh PRP8	AAGGCCCATCATGTGAACAACGATTCTTGCTTCAATCGTTGTTCACATGATGGGTATAGTGA	interference
sh U2AF65	AAGGCCAACTACCTGAACGATGATTCTTGCTTCAATCATCGTTCAGGTAGTTGGTATAGTGA	interference
sh Ago2-1	AAGCACGACTGTGGACACGAACTTGCTTCTTCGTGTCCACAGTCGTGCTATAGTGA	interference
sh Ago2-2	AACAAGCAGGCCTTCGCACTACTTGCTTCTAGTGCGAAGGCCTGCTTGTATAGTGA	interference
sh Luc	AAGGCTTACGCTGAGTACTTCGACTTGCTTCTCGAAGTACTCAGCGTAAGTATAGTGA	interference
Cand1	GGGCACAGAGGAGAGAGGCCTTCAGGCTAGGTAGGCGCCCC	Array
Cand2	CCCCGCCCACCTCCCAGCGCAGTGACTTGCCCTGGCAACT	Array
Cand3	GGGTAACGACACAGGGGTCAGCCTAGTCCAGGACGGACCC	Array
Cand4	ACGCGCGGTTAGAACGACCCCAGCCCCGGGCCACATCGCATCTC	Array
Cand5	GGTTGGCGTGGGTGCGGGGACGGGACAGGTTCGTCGTGCCC	Array
Cand6	TGCTGGTAGAAGGCTGTGGGGCCAGGACGGATCTGATGGGGGTGGGT	Array
Cand7	GCGCGACGCCAGGGTCGGCTACTGGGGGGCCTCGGGCTCTAC	Array
Cand8	GCCCCGCCGCGGGTCCTCCGCCCGCCGGCTCGCTCGCTCAC	Array
Cand9	CGAGCGCGGACCCGGGAGAGAGCTCTCATTCAACGCTGAGGCCACT	Array
Cand10	ACACAACCTAGGACTTCCCAGACTCCACCCCATCGGTCTCCCCA	Array
Cand11	TCCCAGGCTGGCTTCTCAGCACCCACCACCCCACTCCGGAAACCAT	Array
Cand12	TGCGGCAACGCAGGGGAGGGCGGTCAGGGCTGCGGGTGCTGC	Array
Cand13	CTGAGTTAAAGAGGGCGGTAGGGAGGCGGTTAGGGAGGCCGGCC	Array
Cand14	CTGCGGGTGAGTGGGTAGGCGCAGGGGACGGTGCCAACTG	Array
Cand15	CTGCGGGCAGGGGAGGGCGCGGGCAGCTGGTGCTGGTGCC	Array
Cand16	AGAGGCTGACCTTGACCACCCCCCACCCCCGACTCCATCCCTCC	Array
Cand17	AGGGAGACCCTGTCCTGGGTCAGGAGCCCCACCCATGGAGTCTTTC	Array
Cand18	GGCCTCCTCTCCGCGCGCCCCGCCAGCTCGCACTCACCCG	Array

Cand19	ACTCGGCCCTGCCCGGATCCTGGGCCCCTCCAGACCCCATC	Array
Cand20	GCGGTGAGCCGGAGAGAGGCCCCGTCCCCACCCTCGCCAC	Array
Cand21	CTGGGCACCTAGCTGAGTGAGCCTGGCGGCGCCCCACCTCCTCCCTCCC	Array
Cand22	CTCAGCCTCAGCATCCCTGGGAAAAGCGCCTCCAAGAGTTCCG	Array
Cand23	GGTCACACCGGCCTCATCCTAAGTAGGTTTGGATACACCCGGAGCT	Array
Cand24	GTGAGCACCCGCGGCCGCCCCTCCCCCACGCCACCCGTCC	Array
Cand25	TACCAGGAGGGTCCTCCCTTGTGGGGCCCTGGCCCCACGGC	Array
Cand26	GGCAGGGAGAAGAGCGGCTCCACCAGGCCCTTCTTCCTGGGGCCACC	Array
Cand27	AGGATGAGATGGGGGAGACACAAAGGGAGACATTAGTGACAGGCTGGCG	Array
Cand28	GCACAGGGTACGTTAGGCGGGCTCTGGGGAAGGATGAGAGGGTCTCGC	Array
Cand29	GAGCCAGATAAGGGTGAGTGACAGAGCTGGGGGCCCGTCCTCTCC	Array
Cand30	GCGGACCGCTTAGCGGGAAGGCCGGGCACCCCGCGCAGGC	Array
Cand31	GTGGGAACAAGTGAGCAGGTGCCGGGGCGGGGCGGGGCCTC	Array
Cand32	GGCGAGGGAGACGAGCGGCCGCAGTCCGGGGCCTCCTGCC	Array
Cand33	GCTCCCGGGACCCCGCGCCCTCCACTCCATATGCCGGGACTC	Array
Cand34	GGGGCGCAAGATGACGGGGGTGCCTGTCTGCACCTGGCCTGGGCTCCG	Array
Cand35	CACAGGGTGGCTTGCTGGGACCTCCCCACCACTCTAGGAACCTCCCAG	Array
Cand36	CAGGAGACACCAACAATCCCCACTCCCATACTCCCCACTCCC	Array
Cand37	CAGTGGCGGGGCTGGGGCTGAAAACCAGGTCGGGCTCTAATGCGGTGGT	Array
Cand38	GTCGTGGAGCCGGTGAGACTTCGCGCCCGGCCCGGGCCCC	Array
Cand39	AGGCACGAGCCCCACCCCTCTCCCGACCCCGCTCACTCAC	Array
Cand40	CTGCGGGGAAGGGGCCTAGCTGGGGTAGGGCGCACAGCCC	Array
Cand41	GTGGCGCGGCCACCGCTCGCCTGTCCCGTCTCGGGAGGAA	Array
Cand42	GCCTGCCCCGTGCGCCCCCTCCGCCAGGCCGCGCCGCACC	Array
Cand43	AGAGGGTCCATACTAAGCGCCGCAACCGCCCCCAGCCTAGGCCGGGGCG	Array
Cand44	CTGTGGGGTGGGTGGTCAGGCCGACTAGGCAGGCCCAAGC	Array

Cand45	CAAGCCCAAGGGCAGATTGTTCGGGGCTTAGTCGTGGGTAGCAGGGGT	Array
Cand46	CGCACCGCGCCCCTCCCCGGCCTCGCGCTGCCGCCTCGGC	Array
Cand47	GCGGGTGGGATGAGCGCGCCGGCCGGGATGGTCCTGCGAC	Array
Cand48	GCAGCACAGGGCATGTGGGGGCTGAGGGCCTCAGGGGCACTGCGGG	Array
Cand49	GGAGTTACAGGCTGAAGGTCTGACACAAGCATTAGTGAGATGCTCCCCTC	Array
Cand50	GGCCCCAGGAGGGCAGCCCCGCCCCTAGCCCCGCACGCAC	Array
Cand51	CTGAGGGGGAACACAGGACTTCTGGCCTCCAGAAACCCCCTTCCCCA	Array
Cand52	CGGGGCTGTGCTGTTCCTCTCCATGTAGGGGCCGGTGAGGGGGAG	Array
Cand53	TGTGGCCACGGGGGACAAAAGGTGAGCCACGGAGACGGGC	Array
Cand54	AGCAGTCCCCGGGAAATCGCGGCCGCTCGGCGGCTGCACC	Array
Cand55	AACCAGGGACACAGCGACAGGGGCAGGTGAGACAGGCATC	Array
Cand56	GGGGGGCGTCAGGCGTCGGCGCCAGGAGCCCGCGCGCCTC	Array
#1F	CATCAGCCTCACTGTGGCCAAG	rPCR
#1R	CTCCTGTCAGTGCCGCCGTGTG	rPCR
#2F	GAGGGACCTCACTCCAGGGCAC	rPCR
#2R	GACCTGCGGCAGCTCAGAGAAG	rPCR
#3F	GCTCCCACCGGACGCCATCTTC	rPCR
#3R	GGTAGCCTGGGTTGTGATAGTC	rPCR
#4F	CATGGCGACTTTGGTCGAACTG	rPCR
#4R	GTGTAGAGCGTCAGGTCGACATG	rPCR
#5F	CTTGCTGACGCTGCGGGCCAAG	rPCR
#5R	GTGCAACAGCTCCGGAGAGGAG	rPCR
#6F	GAGTCACCCACTTGCAATCTG	rPCR
#6R	CGAGTTGACAGAGAATCCGGAG	rPCR
#7F	CCGGAAGTGACGTCTCCCAGAG	rPCR
#7R	CCACTCATCTTCGTTGTCCTGG	rPCR

#8F	GATCCTGTGGCCTGCTTCCTGA	rPCR
#8Rb	GATGGAGCAGGTGTGCTGCGAC	rPCR
#9F	GGAGTGCGATCGCCTGCGGATC	rPCR
#9R	CCTGCCTGCCTCCTCCGTGCTG	rPCR
#10F	GTCCTCTATGCTGCCACTGTGAA	rPCR
#10R	TCGTCGTCTCCATCTTCATCCC	rPCR
#11F	GAAGCTGCAGGAATACCGGGTC	rPCR
#11R	GACTCTCAGGCTCCATGCAGTG	rPCR
#14F	CGTGGTGACTGATCTTCGTGGC	rPCR
#14R	GTCGTGGCGGATGACCTCATTG	rPCR
#15F	CATCGACGGCATCGGCAGCTTC	rPCR
#15R	CCACCTCCTCTAGGCAGTAATG	rPCR
#16F	CCTGCTGGAGGTGGTGCTGTT	rPCR
#16R	CTGGCGGTGCTTGCTCTTCTC	rPCR
#17F	CATCTTGGCAGCCTCGGCCTCAC	rPCR
#17R	GCCGAGAGTACACAGCTGCTG	rPCR
#18Fb	AGCTCCAGCGCCGTCATCTTTC	rPCR
#18R	GGCGCTTACGTGCTTGTCTACT	rPCR
#19F	CGTGAGCCTGGGCCTGGAC	rPCR
#19R	CTCCATGTGCGGCCACAGTTG	rPCR
#20F	GAGACCTGAAAGGCCAGGAG	rPCR
#20Rb	GCGTCGGCGCCAGACCTTCGTG	rPCR
#21F	CCAGGAATGTCGCTGCCACAA	rPCR
#21R	TGAAGCCGTGTTCGCACAGAC	rPCR
#24F	GTTTGCGTATGTGACAGATGGAGC	rPCR
#24R	GCGGCAGTAGCACTTCATGTAAGT	rPCR

#27F	TCGCCTCGGAGCAGCCATGATG	rPCR
#27R	TCCACCTGCAGAGCAGCATCAC	rPCR
#29F	GAGATGGAGGAGGAGCGACTGC	rPCR
#29R	CCTTCCTCTGAGTGGATGCGAG	rPCR
#30F	GACCAAGACGGCCTGGGAGGTG	rPCR
#30R	GCTTGGCGAACAGCTCGGACTG	rPCR
#33Fb	CGGCTCGGAGAGCGAGGCAGTG	rPCR
#33R	TGTTGTCCTGCTCCACCTCCA	rPCR
#36F	GCATCGGTCACATTGAAGCCATC	rPCR
#36R	CCAGTCCTCCATATAGCAGAACAC	rPCR
#38F	GACCTACTGCTTCGACGCCTTC	rPCR
#38R	GTCCTCCGTGCCGTGGATGAT	rPCR
#39Fb	CGAAGGATACCTGGCGCGGATC	rPCR
#39R	GCCTGCAACTCTGTCTCCGC	rPCR
#40F	CAAGTGGACGACGTTCCTGAAG	rPCR
#40R	TGGAGAAGACGGCATAGAGCAG	rPCR
#42F	GCTCGTGCACTATGGCTTCC	rPCR
#42R	GGTCCCACGGTACTTGAGG	rPCR
#43F	ATGGCGGAGCTGTACGTGAAGCCG	rPCR
#43R	GCGACCCTCTTGGTAAGCAG	rPCR
#45Fb	GCTTCCGGTTCCGATGACAGTG	rPCR
#45Rb	GACGTTTGAGTCCGAGCAACTC	rPCR
#46F	GGACTGAGTTCGCTGCTGTC	rPCR
#46R	GGTTGCGCTCGCTGTTGTTG	rPCR
#47F	CTTCTCCCTGCAGGTGATCTCG	rPCR
#47R	ATGCCGGCGACCCAGAGCG	rPCR

#50F	CTATGACGTGTTTGGCTGTTGGC	rPCR
#50R	GTGCTGGCATTGAGGTTCTGG	rPCR
#52F	GGCCCGTGCACAGAGAAGAAC	rPCR
#52R	GACCAGGCAGCCGCAGAG	rPCR
#53F	TCACCTAGGGCTGCAGATGCTC	rPCR
#53R	TGGTGGCTGTGACCTTCCCTTC	rPCR
In8F	GTGAGCGAGCGAGCCGGCG	RIP
In8R	CCTGACCAGCCCTCCTGCTCAG	RIP
In16F	GAGAGTCTGGGGAGGGATG	RIP
In16R	GTCAAGGTCAGCCTCTGAGCCAG	RIP
In18F	GGCGGGAGCCGAGCTGAG	RIP
In18R	GGCCTCCTCTCCGCGCGCCCCGCCAGCTCGCACTCACCCG	RIP
In19F	GGGGGACCCTCACACTCG	RIP
In19R	AGACCCCATCTCCCATCC	RIP
In20F	GCGGTGAGCCGGAGAGAGGCCCCGTCCCCACCCTCGCCAC	RIP
In20R	CACGGCCCCGCCGCCG	RIP
In24F	CCAGTGAATTTTCCGGCCATT	RIP
In24R	GCATGGAACATGGCTGCATT	RIP
In39F	AGTGAGCGGGGTCGGGAGAG	RIP
In39R	CTCGTGCCTGGCTGACGTG	RIP
In45F	CTTCTCCAGAACCCCTGCTACCC	RIP
In45R	GCCCTTGGGCTTGTTCTCTTCG	RIP
In46F	TGCGCAAGGCCGGGAGA	RIP
In46R	GTGAGCGGGGTCGCCCA	RIP

* RTSL, Stem Loop RT-qPCR; qPCR, quantitative PCR ; PCR, RT-PCR; Pulldown, RNA pull down; interference, RNA interference; rPCR, radioactive PCR; RIP, native RNA Immunoprecipitation.

Supplementary Table S3 Synthesis of data shown in Figures 3, 4 and 5. ***, p<0.05; ns, not significant; nd, not determined; sh, RNA interference; RIP, native RIP.

	Drosha		DGCR8		U1+PRP8	U1	U2+PRP8	U2	DBR1		Dicer		Ago2		
	sh	RIP	sh	RIP	sh	RIP	sh	RIP	sh	RIP	sh	RIP	sh	RIP	
#8	ns	***	ns	ns	ns	***	ns	ns	***	***	***	nd	ns	ns	mirtron-like
#10	ns	nd	ns	nd	ns	nd	ns	nd	ns	nd	***	nd	ns	nd	
#16	***	***	***	***	ns	ns	ns	ns	ns	ns	***	nd	ns	***	miRNA
#18	***	***	***	***	ns	ns	ns	ns	ns	ns	***	nd	ns	***	miRNA
#19	***	***	***	***	ns	ns	ns	ns	ns	ns	***	nd	ns	ns	miRNA
#20	***	***	***	***	ns	ns	ns	ns	ns	ns	***	nd	ns	***	miRNA
#21	ns	nd	ns	nd	ns	nd	ns	nd	ns	nd	***	nd	ns	nd	
#24	***	***	***	***	ns	ns	ns	ns	***	***	***	nd	ns	ns	
#33	***	nd	ns	nd	ns	nd	ns	nd	ns	nd	***	nd	ns	nd	
#36	ns	nd	ns	nd	ns	nd	ns	nd	ns	nd	ns	nd	***	nd	
#38	ns	nd	ns	nd	ns	nd	ns	nd	ns	nd	***	nd	ns	nd	
#39	***	***	***	***	ns	ns	ns	ns	***	***	***	nd	ns	***	
#42	***	nd	***	nd	ns	nd	***	nd	***	nd	***	nd	ns	nd	
#43	***	***	***	***	***	ns	***	ns	***	***	***	nd	***	***	
#45	***	***	ns	ns	ns	***	***	ns	ns	ns	***	nd	ns	***	simtron-like
#46	***	***	***	***	***	ns	***	ns	***	***	***	nd	ns	***	
#47	***	nd	ns	nd	ns	nd	***	nd	***	nd	***	nd	ns	nd	
#50	ns	nd	ns	nd	ns	nd	ns	nd	ns	nd	***	nd	***	nd	
#52	***	nd	***	nd	ns	nd	***	nd	***	nd	***	nd	***	nd	

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