Supplementary Table 1: List of miRNA harbouring lncRNA host genes showing termination defect following Drosha or DGCR8 depletion in HeLa cell line.

lncRNA host gene	**miRNAs**	**strand**	**Normalized Read counts (RPKM)**			**Fold increase**		**Readthrough**	
			Control siRNA	Drosha siRNA	DGCR8 siRNA	Drosha siRNA	DGCR8 siRNA	Drosha siRNA	DGCR8 siRNA
MIR17HG	hsa-miR-(17~18a~19a~19b-1~20a~92a-1)	(+)	57424.66	193251.73	339808.14	3.37	5.92	YES	YES
MIR181A2HG	hsa-miR-(181a-2~181b-2)	(+)	450.27	2687.66	4790.68	5.97	10.64	YES	YES
RP11-2B6.3	hsa-let-(7a-1~7f-1~7d)	(+)	60.04	433.49	9390.42	7.22	156.41	YES	YES
RP11-631N16.2	hsa-let-7i	(+)	6211.77	13798.26	70840.17	2.22	11.40	YES	YES
LINC00478	hsa-miR- (99a~let-7c~125b-2)	(+)	1891.14	4306.04	6127.20	2.28	3.24	YES	YES
MIR181A1HG	hsa-miR-(181a-1~181b-1)	(-)	630.38	82826.30	112737.08	131.39	178.84	YES	YES
LOC646329	hsa-miR-(29a~29b-1)	(-)	6393.86	148211.68	223252.40	23.18	34.92	YES	YES
MIR31HG	hsa-miR-31	(-)	2401.45	25821.81	26817.37	10.75	11.17	YES	YES
LINC00472	hsa-miR-(30a~30c-2)	(-)	14648.84	74459.86	114837.34	5.08	7.84	YES	YES
MIR100HG	hsa-miR-(100~125b-1~let-7a-2)	(-)	4007.42	22772.90	31538.61	5.68	7.87	YES	YES
DLEU2	hsa-miR-(15a~16-1)	(-)	26145.78	93620.31	62868.93	3.58	2.40	YES	YES
MIRLET7BHG	hsa-let-(7a-3~7b)	(+)	410.31	609.19	494.30	1.48	1.20	NO	NO
LOC284454	hsa-miR-23a~24-2~27a	(-)	2716.64	4739.54	5884.20	1.74	2.17	NO	NO
MIR22HG	hsa-miR-22	(-)	120.07	187.85	69.43	1.56	0.58	NO	NO
MIR600HG	hsa-miR-600	(-)	1921.16	2239.72	1701.04	1.17	0.89	NO	NO

RPKM fold increase ≥ 2 is considered as genes showing readthrough.

Shaded region in the table highlights lncRNA host genes that do not show termination defect following Drosha or DGCR8 depletion

Supplementary Table 2: List of miRNA harbouring lncRNA host genes showing termination defect following DGCR8 depletion in Huh7 cell line.

lncRNA host gene	**miRNAs**	**strand**	**Normalized read counts (RPKM)**		**Fold increase**	**Readthrough**
			Control siRNA	DGCR8 siRNA	DGCR8 siRNA	DGCR8 siRNA
MIR17HG	hsa-miR-(17~18a~19a~19b-1~20a~92a-1)	(+)	16404.90	72189.92	4.40	YES
MIR181A2HG	hsa-miR-(181a-2~181b-2)	(+)	810.49	8748.19	10.79	YES
RP11-2B6.3	hsa-let-(7a-1~7f-1~7d)	(+)	435.26	5901.56	13.56	YES
MIR146A	hsa-miR-(146a~3142)	(+)	1335.81	19336.27557	14.48	YES
RP11-65J21.3	hsa-miR-(193b~365a)	(+)	1651.00	7862.96	4.76	YES
RP11-631N16.2	hsa-let-7i	(+)	3347.02	12445.34	3.72	YES
AP000662.4	hsa-miR-130a	(+)	4012.84	9425.13	2.35	YES
*lnc-pri-miR-122**	hsa-miR-122	(+)	18556.81	41382.39	2.23	YES
MIR940	hsa-miR-(940~3677)	(+)	60.04	121.50	2.02	YES
MIR181A1HG	hsa-miR-(181a-1~181b-1)	(-)	120.07	20915.81	174.19	YES
LOC646329	hsa-miR-(29a~29b-1)	(-)	2671.61	63840.95	23.90	YES
AB429224	hsa-miR-194-2	(-)	285.17	2395.34	8.40	YES
MIR137HG	hsa-miR-(137~2682)	(-)	450.27	2655.70	5.90	YES
AC034220.3	hsa-miR-3936	(-)	120.07	624.87	5.20	YES
MIR210HG	hsa-miR-210	(-)	300.18	1128.24	3.76	YES
DLEU2	hsa-miR-(15a~16-1)	(-)	24629.87	83472.31	3.39	YES
LINC00472	hsa-miR-(30a~30c-2)	(-)	645.39	1614.25	2.50	YES
MIRLET7BHG	hsa-let-(7a-3~7b)	(+)	14.65	22.43	1.53	NO
LINC00478	hsa-miR-(99a~let-7c~125b-2)	(+)	420.25	833.16	1.98	NO
MIR22HG	hsa-miR-22	(-)	255.15	433.94	1.70	NO
LOC284454	hsa-miR-23a~24-2~27a	(-)	615.37	1041.45	1.69	NO
MIR600HG	hsa-miR-600	(-)	2341.41	2655.70	1.13	NO
MIR100HG	hsa-miR-(100~125b-1~let-7a-2)	(-)	2401.45	2082.90	0.87	NO

RPKM fold increase ≥ 2 is considered as genes showing readthrough.

Shaded region in the table highlights lncRNA host genes that do not show termination defect following DGCR8 depletion.

Genes expressed in both HeLa and Huh7 cell lines are highlighted in bold.

*Based on our data: Readthrough calculated over chromosomal region (chr18:56120306-56130306) due to lack of available gene annotation.

Supplementary Table 3: Polyadenylation status of miRNA harbouring lncRNA host genes in control vs DGCR8 depleted HeLa cells.

	Control siRNA				DGCR8 siRNA			
LncRNA host gene	**BPKM pA–**	**BPKM pA+**	**Fold change**	**polyA status**	**BPKM pA–**	**BPKM pA+**	**Fold change**	**polyA status**
MIR17HG	21.37	1.89	11.31	pA–	43.69	5.80	7.53	pA–
MIR181A2HG	3.24	0.49	6.59	pA–	4.25	1.03	4.12	pA–
RP11-2B6.3	3.37	0.37	9.03	pA–	7.3	0.95	7.70	pA–
RP11-631N16.2	6.12	1.03	5.91	pA–	13.35	2.66	5.02	pA–
LINC00478	1.46	0.17	8.45	pA–	2.17	0.32	6.78	pA–
MIR181A1HG	1.07	0.07	10.31	pA–	3.2	0.45	7.04	pA–
LOC646329	2.02	0.5	4.00	pA–	10.6	2.96	3.58	pA–
MIR31HG	4.18	0.51	8.12	pA–	6.95	1.22	5.68	pA–
LINC00472	7.65	1.02	7.62	pA–	22.9	3.81	6.01	pA–
MIR100HG	1.59	0.27	5.93	pA–	7.58	1.26	6.04	pA–
DLEU2	2.27	0.58	3.93	pA–	3.2	0.97	3.28	pA–
MIRLET7BHG	9.36	3.67	2.55	pA–	20.07	57.29	0.35	pA+
LOC284454	15.49	46.46	0.33	pA+	19.96	69.89	0.29	pA+
MIR22HG	6.05	1.58	3.82	pA–	9.82	7.27	1.35	bimorphic
MIR600HG	1.41	1.12	1.26	bimorphic	1.73	1.38	1.26	bimorphic

Shaded region in the table highlights lncRNA host genes that do not show termination defect following Drosha or DGCR8 depletion.

Criteria for polyA status:

pA–: Fold change values ≥2

pA+: Fold change values ≤0.5

Bimorphic: Fold change values between 0.5 and 2

Supplementary Table 4: Gene length and distance of pre-miRNA from TSS in lnc-pri-miRNAs showing Microprocessor mediated transcription termination in (**a**) HeLa and (**b**) Huh7 cells. **c.** Genomic distribution of pre-miRNAs in lncRNA host genes showing Microprocessor mediated transcription termination in HeLa and Huh7 cells.

a

lncRNA host gene	Gene length	Distance from TSS ł
MIR17HG	6759	2785
MIR181A2HG	40164	33975
LINC00478	556874	468567
RP11-2B6.3	34338	9668
RP11-631N16.2	11323	934
LINC00472	76425	32616
LOC646329	39660	4255
MIR181A1HG	129936	51380
DLEU2	98587	21840
MIR31HG	104027	56473
MIR100HG	113959	10654

b

lncRNA host gene	Gene length	Distance from TSS ł
MIR210HG	2797	2429
AB429224	4987	2893
MIR940	5263	2558
MIR17HG	6759	2785
RP11-631N16.2	11323	934
AP000662.4	14766	3174
MIR146A	19158	6134
RP11-65J21.3	24065	1679
RP11-2B6.3	34338	9668
LOC646329	39660	4255
MIR181A2HG	40164	33975
AC034220.3	58630	54204
MIR137HG	61863	57242
LINC00472	76425	32616
DLEU2	98587	21840
MIR181A1HG	129936	51380

ł For miRNAs in a cluster, distance is calculated from the TSS to the first miRNA. All distances are calculated in nucleotides.

c

Cell line	**Genomic location of pre-miRNAs**	
	Introns	**Exons (Last exon)**
HeLa	**81%**	**19% (19%)**
Huh7	**74.3%**	**25.7% (18%)**

SupplementaryTable 5: RNA-seq mapping statistics.

Sample ID	RNA-seq	Cell	Read size (nt)	Number of PE reads	Mapped PE reads	% of mapped PE reads
Control siRNA	Chromatin	HeLa	51	38343118	33313212	86.88%
DGCR8 siRNA	Chromatin	HeLa	51	33569636	28805961	85.81%
Drosha siRNA	Chromatin	HeLa	51	38989688	34602536	88.75%
Dicer siRNA	Chromatin	HeLa	51	17923502	12819860	71.53%
Control siRNA	Chromatin	Huh7	100	20678124	18305816	88.53%
DGCR8 siRNA	Chromatin	Huh7	100	25042908	21524505	85.95%
Control siRNA polyA+	Nuclear	HeLa	100	22919390	15798545	68.93%
Control siRNA polyA–	Nuclear	HeLa	100	21002155	14045951	66.88%
DGCR8 siRNA polyA+	Nuclear	HeLa	100	24108556	16607260	68.89%
DGCR8 siRNA polyA–	Nuclear	HeLa	100	25086373	17768424	70.83%

PE denotes paired end

Supplementary Table 6: Oligonucleotide primers and siRNAs used in study

Primer (qPCR)	**Gene**	**Sequence (5'-3')**
EX1 (spliced) forward	lnc-pri-miR-122	CAGAAGCTGTGGAAGGCGC
EX2 (spliced) reverse	lnc-pri-miR-122	GAAACAGTGAGAGGTGAACAATTCA
INT1(unspliced) forward	lnc-pri-miR-122	TGCCACTCAGCACAGCACTA
INT1 (unspliced) reverse	lnc-pri-miR-122	TGAACCCATCCTGCTCATA
GAPDH mRNA forward	GAPDH	AAGGTGAAGGTCGGAGTCAA
GAPDH mRNA reverse	GAPDH	AATGAAGGGGTCATTGATGG
U6 snRNA forward	U6 snRNA	CTCGCTTCGGCAGCACA
U6 snRNA reverse	U6 snRNA	AACGCTTCACGAATTTGCGT
EXON2 forward	lnc-pri-miR-122	ACATGCCTGTGTCCACTGCT
EXON2 reverse	lnc-pri-miR-122	CTCTAGGTGGCCCCAGTCAC
TSS forward	lnc-pri-miR-122	TTTGACCAAAGGTGGTGCTG
TSS reverse	lnc-pri-miR-122	TTAGGCCTCTCCCCTCTCC
MIR122 forward	lnc-pri-miR-122	CCCGTGATGCTTCTTTTCTC
MIR122 reverse	lnc-pri-miR-122	CCATTGTCACACTCCACAGC
MIR+2.5kb forward	lnc-pri-miR-122	GGACTGGGTCTTCCATGCTC
MIR+2.5kb reverse	lnc-pri-miR-122	AAACGAATCCAGGCAGCAAT
MIR+4.5kb forward	lnc-pri-miR-122	CATTCACTCCTGCACGCATT
MIR+4.5kb reverse	lnc-pri-miR-122	GGTTCTGGGGAGAGCATCAC
MIR+7.5kb forward	lnc-pri-miR-122	GCAACTGAAGCAGCATCGTT
MIR+7.5kb reverse	lnc-pri-miR-122	CACGGGGGAGCTTTTCTCTT
INT1 forward	GAPDH	CCCCTTCATACCCTCACGTA
INT1 reverse	GAPDH	GACAAGCTTCCCGTTCTCAG
PAS forward	GAPDH	CTGAATCTCCCCTCCTCACA
PAS reverse	GAPDH	TGCCCCAGACCCTAGAATAA
PAS+1.1kb forward	GAPDH	TCCAGCCTAGGCAACAGAGT
PAS+1.1kb reverse	GAPDH	TGTGCACTTTGGTGTCACTG
Exon1 forward	GPC5	TCGGCTAGGGAAGAAGACCA
Exon1 reverse	GPC5	GCAGTTAGCTCTTCCCGGAG
-2kb GPC5 forward	GPC5	TGACCTCCCACCTGTTTTGT
-2kb GPC5 reverse	GPC5	AACGGTGTGTCTTGCAAGGA
exon1-2 forward	GPC5	GAAACTTTTCCAGTGGCGGC
exon1-2 reverse	GPC5	CTCCTCCATCTTCCTGGTGC
exon3-4 forward	OGFRL1	TCCATTCAAGCCAGATGGTGT
exon3-4 reverse	OGFRL1	AGTGTGGTTGTGCTCCAGTT
Primer (PCR-Gel)	**Gene**	**Sequence (5'-3')**
exon2 (Total) forward	lnc-pri-miR-122	GGTGAAGAGGTGAGAGTTGGA
exon2 (Total) reverse	lnc-pri-miR-122	CAGCAAACCCCTTCTGCAAA
EX1 (spliced) forward	lnc-pri-miR-122	CAGAAGCTGTGGAAGGCGC
EX2 (spliced) reverse	lnc-pri-miR-122	GAAACAGTGAGAGGTGAACAATTCA
INT1 (unspliced) forward	lnc-pri-miR-122	ACAACTGGGCTCAAGGGATC
INT1 (unspliced) reverse	lnc-pri-miR-122	TCTGTTTAGCTTCCCTGGGC
GAPDH mRNA forward	GAPDH	AAGGTGAAGGTCGGAGTCAA
GAPDH mRNA reverse	GAPDH	AATGAAGGGGTCATTGATGG
fwd1 (3'end mapping)	lnc-pri-miR-122	CCCGTGATGCTTCTTTTCTC
Linker (3'end mapping)		GCTGTCAACGATACGCTACGTAACG
3'RACE-(dT)$_{24}$V		GCTGTCAACGATACGCTACGTAACG(T)$_{24}$V
Anti-miR-122 **(Northern blot)**		AACACCAUUGUCACACUCCAUA (RNA oligo)
siRNA	**Gene**	**siRNA Forward Strand**
Control	Luciferase	GAUUAUGUCCGGUUAUGUAUU
DGCR8	DGCR8	CAUCGGACAAGAGUGUGAU.dTdT
Drosha	Drosha	CGAGUAGGCUUCGUGACUU.dTdT
CPSF73	CPSF3	ON-TARGETPLUS SMARTPOOL CAT NO. L-006365-01
Dicer	Dicer	UGCUUGAAGCAGCUCUGG.dTdT
Primers for pri-miR-122 cloning and mutagenesis		**Sequence (5'-3')**
Open_Beta qR		AGCTTTATTGAGGCTTAAGC
B10 qF		CAGGAAACTATTACTCAAAGGG
Pri122 qF		CAGAAGCTGTGGAAGGCGC
Pri122 qR		ACTGTGTTCTCTGCTGCCTC
DELTA mir qF		GTTTCCTTAGCAGAGCTGCAATCCTTCCCTCGATAA
DELTA mir qR		TTATCGAGGGAAGGATTGCAGCTCTGCTAAGGAAAC
pA1MTqF		CAATCTTGTGTACTTACTGAAGAAAGTCTGGCTCTTTTGCACT
pA1MTqR		AGTGCAAAAGAGCCAGACTTTCTTCAGTAAGTACACAAGATTG