Inventory of Supplemental Information

Supplementary Item	Notes
Supplementary Table S1	Contains all human and mouse bioinformatically predicted near-perfect miRNA target sites that were used to select candidates for validation in Figure 1
Supplementary Table S2	Lists the sequenced reads and their abundances with 10nt overlaps to predicted miRNA target sites with 2 or fewer non-GU mismatches. These data were used to generate Figure 3.
Supplementary Figure S1	Abundances of sequenced reads with overlaps to predicted miRNA target sites with up to 5 non-GU mismatches. Shown in contrast to Figure 3.
Supplementary Figure S2	Validation of human Plekhm1 cleavage by mir-106b by 5` RACE in human 293S cells, in addition to mouse ES cells in Figure 4.
Supplementary Figure S3	A sequence alignment showing the location of the Dgcr8 cleavage site shown in Figure 5 relative to the sites identified in Han et al, 2009.
Supplementary Table S3	All identified Drosha-dependent cleavage sites (examples of which are shown in Figure 5)
Supplementary Table S4	All identified mRNA cleavage sites (examples of which are shown in Figure 6)
Supplementary Figure S4	Validation of human TRA2A cleavage (which is shown in Figure 6)

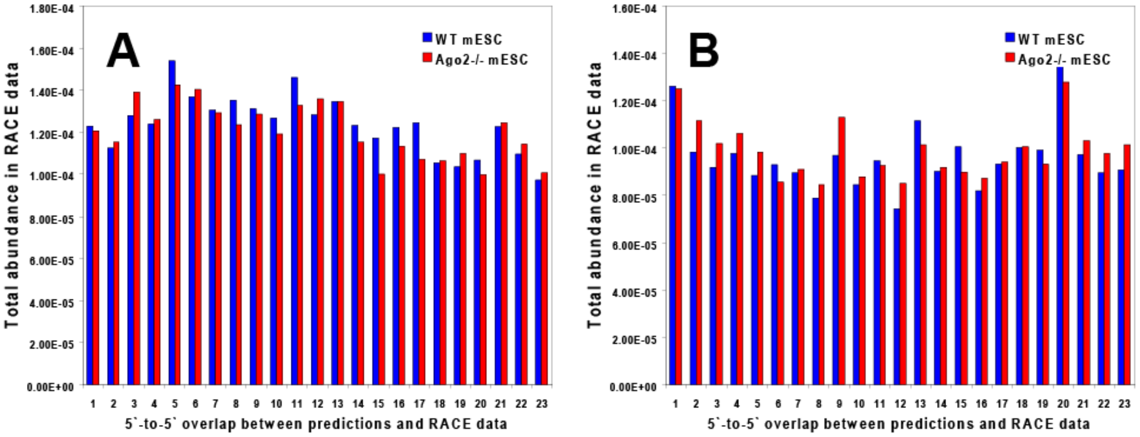
Supplementary Tables and Figures

Supplementary Table S1. All human and mouse predicted miRNA cleavage sites.
See file:
Supplementary Table S1 - Final near-perfect miRNA target predictions.xls

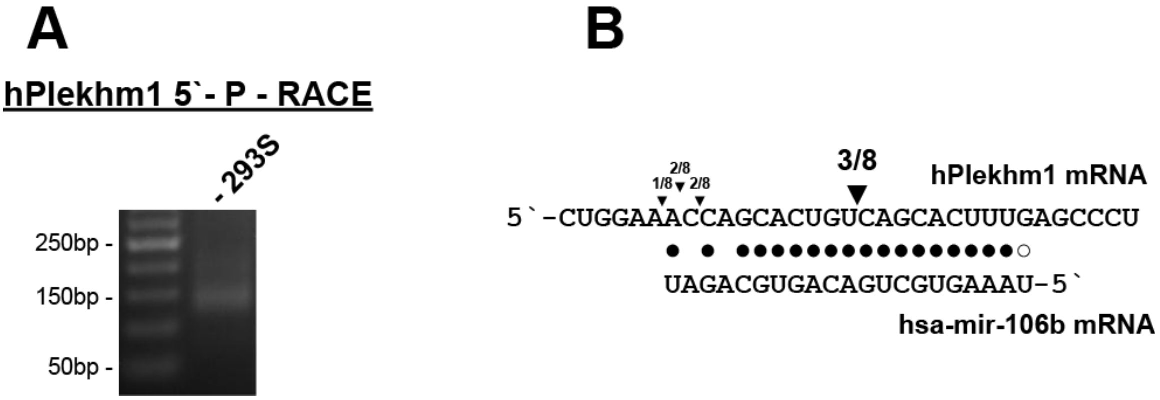
Supplementary Table S2. Sequenced reads and their abundances with 10nt overlaps to predicted miRNA binding sites with 2 or fewer non-GU mismatches.
See file:
Supplementary Table S2 - 10nt overlaps with 2nonGUmm or less predictions.xls

Supplementary Table S3. Identified Drosha-dependent cleavage sites with a 5% false discovery rate.
See file:
Supplementary Table S3 - Drosha-dependent cleavage sites q0.05.xls

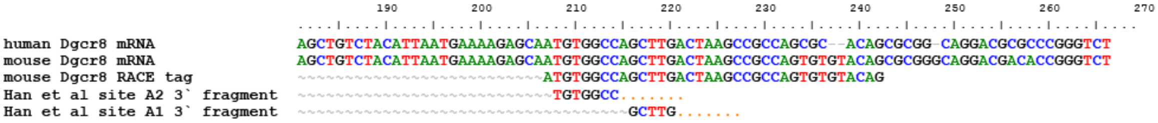
Supplementary Table S4. All identified mRNA cleavage sites.
See file:
Supplementary Table S4 - Overall cleavage sites.xls



Supplementary Figure S1. Overlap between the 5` end of miRNAs at predicted target sites and the 5` end of RACE tags. (A) Abundance of RACE tags with indicated overlap for real miRNA target predictions with up to 5 non-GU mismatches. (B) Same as in (A), but for randomized miRNA predictions.



Supplementary Figure S2. Validation of human Plekhm1 cleavage by mir-106b by 5` RACE in 293S cells. (A) Nested PCR of the 5` RACE produces an amplicon of the expected size for hPlekhm1. (B) Cloning and sequencing of the PCR amplicon indicates products corresponding to the expected miRNA cleavage site.



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                                      190       200       210       220       230       240       250       260       270
                               ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....
human Dgcr8 mRNA               AGCTGTCTACATTAATGAAAAGAGCAATGTGGCCAGCTTGACTAAGCCGCCAGCGC--ACAGCGCGG-CAGGACGCGCCCGGGTCT
mouse Dgcr8 mRNA               AGCTGTCTACATTAATGAAAAGAGCAATGTGGCCAGCTTGACTAAGCCGCCAGTGTGTACAGCGCGGGCAGGACGACACCGGGTCT
mouse Dgcr8 RACE tag           ~~~~~~~~~~~~~~~~~~~~~~~~~~ATGTGGCCAGCTTGACTAAGCCGCCAGTGTGTACAG
Han et al site A2 3` fragment  ~~~~~~~~~~~~~~~~~~~~~~~~~~~TGTGGCC.......
Han et al site A1 3` fragment  ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~GCTTG.......
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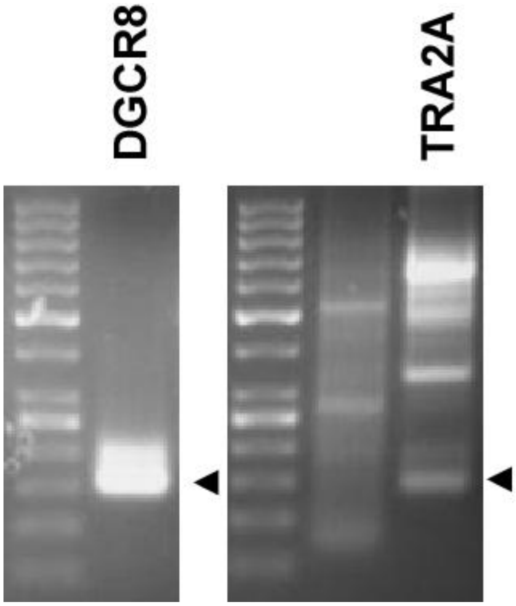
Supplementary Figure S3. Alignment of human and mouse Dgcr8 mRNA with the abundant experimental RACE tag and cleavage sites determined by Han et al, 2009.



Supplementary Figure S4. Validation of human DGCR8 and TRA2A cleavage sites by 5` RACE in 293S cells. The expected amplicon is indicated by a triangle. For DGCR8, 22/23 clones match the global RACE site; for TRA2A, 11/21 clones match and 10/21 clones begin 1 nucleotide to the 5` end.

Supplementary Materials and Methods

Primers and oligonucleotide linkers

LYPD3-151-5`Race	CAAAGTAATTAAATCTTTATTGAGGCATTTATGTGCCAGA
LYPD3-151-5`RaceNest	GAGGCATTTATGTGCCAGAAACTGATCACA
ATPAF1-151-5`Race	CAACAAAAAACTGAGTATCTTCTATGGTCCAGGCCA
ATPAF1-151-5`RaceNest	CTTCTATGGTCCAGGCCATGTCCTT
mPfkfb1-let7c-5`RACE	CTAGTCCACACCTTCAGGGAGCTGATG
mPfkfb1-let7c-5`RACEnest	TGAGACCGAATGAAGTTGGCCAG
mPfkfb1-let7c-5`RACE2	CCAGAGTCACCTCCAATGCGGC
mPfkfb1-let7c-5`RACEnest2	GCCTCTAAGGTTGAGTTCACTCTCACC
mPlekhm1-mir106b-5`RACE	GTGAGACTAAGGGTGGTGAAGCTCTGC
mPlekhm1-mir106b-5`RACEnest	GCAGCTTTGGGGCAAATTCTCCTC
hPlekhm1-mir106b-5`RACE	CAAGGTGGGCCTGGAGCATCTG
hPlekhm1-mir106b-5`RACEnest	CAGCGCCCCTGTCTGTAGAG

SBS3 (RNA)	ACACUCUUUCCCUACACGACGCUCUUCCGAUC
SBS8-N6	CGGTCTCGGCATTCCTGCTGAACCGCTCTTCCGATCTNNNNNN
PE-P5-SBS3	AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATC
PE-P7-SBS8	CAAGCAGAAGACGGCATACGAGATCGGTCTCGGCATTCCTGCTGAACCGCTCTTCCGATCT