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이학박사학위논문

인트론 마이크로RNA 프로세싱 과정에 있어 DROSHA의 비정형 proline-rich domain의 역할

Role of the proline-rich disordered domain of DROSHA in intronic microRNA processing

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Abstract

Role of the proline-rich disordered domain of DROSHA in intronic microRNA processing

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The biogenesis of microRNAs (miRNAs) is initiated by DROSHA, a nuclear RNase III component of the Microprocessor, which binds and cleaves primary transcripts (pri-miRNAs). DROSHA serves as a gatekeeper of the miRNA pathway, recognizing unique features of pri-miRNAs that differentiate them from thousands of other hairpins encoded in the human genome. As evidenced by numerous studies, the molecular basis of pri-miRNA processing mainly relies on the middle and C-terminal parts of DROSHA. While the functions of structured domains of DROSHA have been extensively studied, the contribution of N-terminal disordered proline-rich domain (PRD) remains elusive.

In this study, I show that the PRD promotes the processing of miRNA hairpins located within introns.[1] I identified and characterized a DROSHA isoform (p140) lacking the PRD, which is produced by proteolytic cleavage of full-length DROSHA. By performing small RNA sequencing, I revealed that p140 is significantly impaired in the maturation of intronic miRNAs. Consistently, the minigene constructs

[1] Parts of this thesis have been published in Son et al., 2023

demonstrated that PRD enhances the processing of intronic hairpins, but not those in exons. Splice site mutations did not affect PRD's enhancing effect on intronic constructs, suggesting that the PRD acts independently of splicing reaction by interacting with sequences residing within introns. The N-terminal regions from zebrafish and *Xenopus* DROSHA can replace human counterpart, indicating functional conservation despite poor sequence alignment. Moreover, I found that rapidly evolving intronic miRNAs are generally more dependent on PRD than conserved ones, suggesting a role of PRD in miRNA evolution.

This thesis reveals a new layer of miRNA regulation mediated by a low-complexity disordered domain that senses the genomic contexts of miRNA loci.

Keywords: DROSHA; disordered domain; intron; microRNA; proline-rich domain

Student ID: 2017-27756

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Nomenclature

ABC	ammonium bicarbonate
AGO	Argonaute protein
CRAPome	Contaminant Repository for Affinity Purification
DEP	Differential Enrichment analysis of Proteomics data
DROSHA-p140	DROSHA isoform of 140 kDa lacking the PRD
dsRNA	double-stranded RNA
FBS	fetal bovine serum
GSK3β	glycogen synthase kinase 3 beta
IDRs	intrinsically disordered regions
IF	immunofluorescence
IP	immunoprecipitation
KO	knockout
LC-MS/MS	liquid chromatography with tandem mass spectrometry
LFQ	label free quantification
mGHG	mismatched GHG

miRNA	microRNA
P-rich	proline-rich
p140	DROSHA-p140
p25	DROSHA-p25
PBS	phosphate buffered saline
Pol II	RNA polymerase II
PRD	P-rich disordered domain
pre-miRNA	precursor miRNA
pri-miRNA	primary transcript
RBPs	RNA-binding proteins
RdRps	RNA-dependent RNA polymerases
RS-rich	arginine/serine-rich
RT	reverse transcription
ssRNA	single-stranded RNA
UGUG	UGU/GUG

1. Introduction

MicroRNAs (miRNA) is a ~22-nt RNA that guides post-transcriptional gene silencing (Bartel, 2018). The miRNA sequence is embedded in an RNA hairpin and transcribed by RNA polymerase II (Pol II) as part of a long primary transcript (pri-miRNA) (Figure 1.1; Lee et al., 2002; Cai et al., 2004; Lee et al., 2004). Pri-miRNAs are recognized and cleaved by Microprocessor, a heterotrimeric complex composed of one molecule of DROSHA and two copies of DGCR8 (Lee et al., 2003; Denli et al., 2004; Gregory et al., 2004; Han et al., 2004; Landthaler et al., 2004; Nguyen et al., 2015; Herbert et al., 2016). DROSHA, an RNase III-type endoribonuclease, crops the hairpin by introducing a staggered cut in the lower part of the stem, releasing ~60–80 nt precursor miRNA (pre-miRNA). The pre-miRNA is subsequently cut by cytoplasmic RNase III DICER, yielding a mature miRNA duplex of ~22 nt (Bernstein et al., 2001; Grishok et al., 2001; Hutvágner et al., 2001; Ketting et al., 2001). The duplex is loaded into Argonaute protein (AGO), in which one strand remains as a mature miRNA (Mourelatos et al., 2002; Kobayashi & Tomari, 2016).

Pri-miRNAs have unique features which distinguish pri-miRNAs from numerous other hairpins encoded in the genome (Figure 1.2). A canonical and optimal pri-miRNA contains a hairpin with a stem of approximately 35 bp, an unstructured apical loop, and single-stranded RNA (ssRNA) segments flanking the hairpin (Zeng & Cullen, 2005; Zeng et al., 2005; Han et al., 2006; Ma et al., 2013). In addition to these structural features, pri-miRNAs often carry position-specific

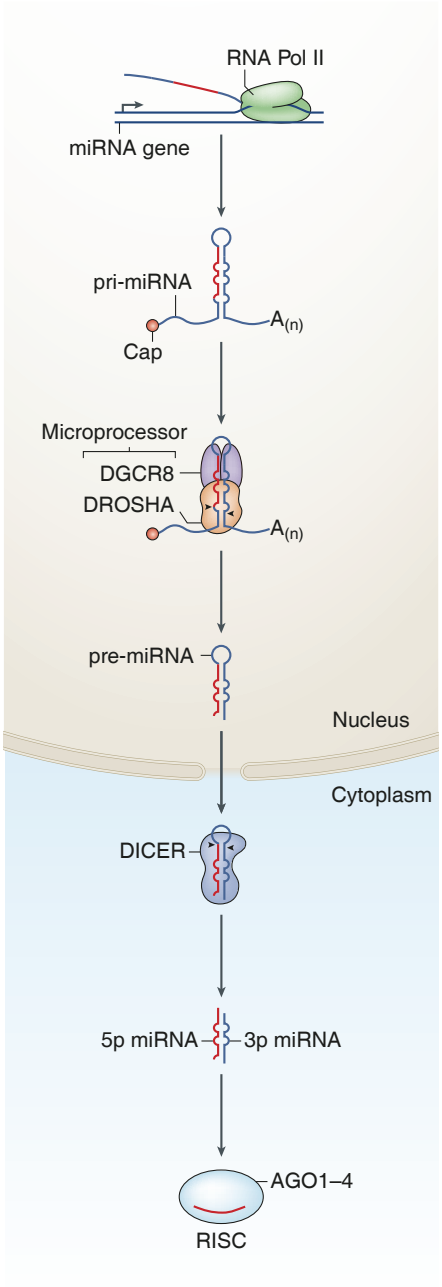

Figure 1.1 Canonical miRNA biogenesis pathway. This figure is modified from Ha & Kim, 2014.

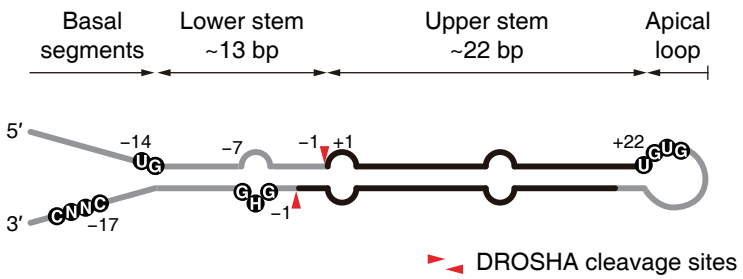

Figure 1.2 Schematic diagram of local features of a pri-miRNA hairpin.

sequence motifs: the UGU/GUG (UGUG) motif at the apical junction, the UG motif at the basal junction, the mismatched GHG (mGHG) motif in the lower stem, and the CNNC motif in the 3′ flanking segment (Auyeung et al., 2013; Fang & Bartel, 2015; Nguyen et al., 2018; Kwon et al., 2019).

While these local features of miRNA hairpins have been rigorously investigated, the surrounding genomic contexts of miRNA hairpins are less well understood (Olena & Patton, 2010). Some miRNA hairpins are clustered in the genome, and they are transcribed in a single "polycistronic" nascent transcript (Lagos-Quintana et al., 2001; Lau et al., 2001; Lee et al., 2002; Mourelatos et al., 2002). Processing of suboptimal hairpins can be assisted by their optimal neighbors, in a process known as "cluster assistance", suggesting that genomic organization relative to the other miRNA hairpins has an impact on DROSHA processing (Truscott et al., 2016; Lataniotis et al., 2017; Shang et al., 2020; Fang & Bartel, 2020; Hutter et al., 2020).

Another genomic context that may potentially impact miRNA biogenesis is their positions relative to introns. More than half of human miRNA hairpins are found in intronic loci of coding or noncoding transcripts, and introns are

thought to be hotspots for de novo miRNA evolution (Guerra-Assunção & Enright, 2012; Meunier et al., 2013). Multiple lines of evidence support that processing of intronic miRNAs occurs cotranscriptionally and is temporally coordinated with splicing (Kim & Kim, 2007; Morlando et al., 2008; Pawlicki & Steitz, 2008; Ballarino et al., 2009; Kataoka et al., 2009; Nojima et al., 2015; Yin et al., 2015; Liu et al., 2016). Both DROSHA and DGCR8 were reported to associate with pol II, supporting the cotranscriptional processing model (Gromak et al., 2013; Church et al., 2017). Efficiently processed pri-miRNAs tend to be enriched in the insoluble fraction of the nuclear extract, presumably associated with transcription machinery (Morlando et al., 2008; Pawlicki & Steitz, 2008). Both in vitro and in vivo experiments indicated that DROSHA crops the intronic hairpin prior to splicing reaction, but cleaved introns remain tethered via spliceosome and get *trans*-spliced. Splicing reaction is not prerequisite for intronic miRNA processing, judging from the observations that a purified Microprocessor complex can process minimal pri-miRNAs without intronic context and that intronic miRNAs are processed in the absence of ATP which is essential for splicing (Lee et al., 2003; Kataoka et al., 2009). However, splice site mutations appear to reduce pri-miRNA processing both in cells and in vitro, albeit modestly (Kim & Kim, 2007; Kataoka et al., 2009). Moreover, in the case of intronic pri-mir-211 located within melastatin intron 6, the mutation of $5'$ splice site and the depletion of U1 snRNP components resulted in a decrease of pri-mir-211 processing, suggesting a positive influence of splicing machinery on at least some intronic pri-miRNAs (Janas et al., 2011). Exonic pri-miRNAs show variable nucleocytoplasmic distribution, and they are cropped from either unspliced or spliced transcripts and thought to be processed less efficiently than intronic miRNAs (Pawlicki & Steitz, 2008; Slezak-Prochazka

et al., 2013; Dai et al., 2016). Overall, the associations of Microprocessor with transcription and splicing machinery are intriguing. However, it remains unknown how these machineries are mechanistically coordinated and, specifically, what role DROSHA plays in this process.

Structural and biochemical studies have elucidated how DROSHA and DGCR8 contribute to the recognition of a pri-miRNA. DROSHA recognizes the basal ssRNA and double-stranded RNA (dsRNA) junction, UG motif, and mGHG motif (Nguyen et al., 2015; Kwon et al., 2016; Jin et al., 2020; Partin et al., 2020), while DGCR8 interacts with the apical regions, including the terminal loop and the UGUG motif (Nguyen et al., 2015; Partin et al., 2017; Nguyen et al., 2018; Partin et al., 2020). Previous studies clarified that the central and C-terminal regions of DROSHA and DGCR8 (390–1365 of DROSHA and 223–751 of DGCR8) are sufficient to cover most parts of the hairpin (Kwon et al., 2016; Jin et al., 2020; Partin et al., 2020), supporting earlier biochemical data that the N termini of DROSHA and DGCR8 are dispensable for pri-miRNA processing in vitro (Han et al., 2004; Nguyen et al., 2015). More recently, it was found that the N-terminal part of DGCR8 contains a partially conserved segment that binds to ERH, which is required for cluster assistance (Kwon et al., 2020).

The N-terminal region of DROSHA possesses a proline-rich (P-rich) domain (amino acids 1–212) and an arginine/serine-rich (RS-rich) domain (amino acids 219–316) (Figure 1.3). The RS-rich domain is believed to function as a regulatory platform associated with subcellular localization and stability control of DROSHA. Phosphorylation of serines in the RS-rich domain (S300 and S302) by glycogen synthase kinase 3 beta (GSK3β) is required for the nuclear localization of DROSHA (Tang et al., 2010, 2011). Consistent with this, a smaller isoform of DROSHA

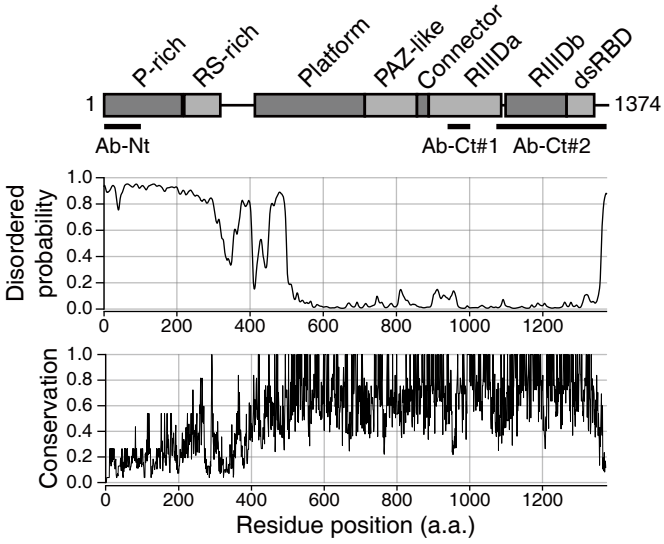

Figure 1.3 Domain structure of human DROSHA. The *lower* horizontal lines indicate the epitopes of three antibodies against DROSHA used in this study. SPOT-Disorder-Single (Hanson et al., 2018) and Valdar01 methods are used for disorderliness prediction and amino acid conservation scoring, respectively. (P-rich) Proline-rich, (RS-rich) arginine/serine-rich, (RIIID) RNase III domain, (dsRBD) double-stranded RNA-binding domain.

(~130 kDa) lacking the nuclear localization signal in the RS-rich domain (due to alternative splicing) was found in the cytoplasm of quiescent human cells (Martinez et al., 2017). The RS-rich domain is also subject to phosphorylation by p38 MAPK in stress conditions, which induces DROSHA protein degradation (Yang et al., 2015), while lysine acetylation in the RS-rich domain stabilizes DROSHA by preventing ubiquitination (Tang et al., 2013).

In contrast, the P-rich disordered domain (PRD) of DROSHA, located at the very N terminus, is the least conserved and most disordered region in DROSHA. Although several groups have observed DROSHA isoforms that may lack an intact PRD (Han et al., 2004; Gregory et al., 2004; Yang et al., 2015; Dai et al., 2016), the function of the short isoforms and the functional relevance of PRD remain unknown.

Here, I identified a major DROSHA isoform of ~140 kDa lacking the PRD (DROSHA-p140) and found that DROSHA-p140 is produced by proteolytic cleavage even in unperturbed cells. By comparing this smaller isoform and full-length protein, I discovered that the PRD of DROSHA is required for efficient processing of pri-miRNAs in intronic regions.

2. Materials & Methods

2.1 Cell lines and cultures

All cells were cultured under standard conditions: HCT116 in McCoy's 5A (WELGENE), HEK293T and HEK293E in DMEM (WELGENE), and A549 and MCF7 in RPMI (WELGENE), all of which were supplemented with 9.1% fetal bovine serum (FBS) (WELGENE). HCT116 *DROSHA* KO cells were from a previous study (Kim et al., 2016), and HEK293E *DROSHA* KO cells were generated by CRISPR/Cas9 technology. All cell lines were authenticated using short tandem repeat (STR) profiling by ATCC.

2.2 RNA interference

To knock down *DROSHA*, cells seeded 1 d before were transfected with final 30 nM siRNAs using the Lipofectamine 3000 reagent (Thermo Fisher Scientific) and harvested after 2 d. For HEK293T cells, single siRNAs (siDro-1 or siDro-2) were treated individually, whereas for MCF7 cells, a mixed siRNA pool (siDro-1, siDro-2, siDro-3, and siDro-4) was used. The control siRNA used was "AccuTarget negative control siRNA". All siRNAs were purchased from Bioneer. The sequences of synthetic siRNAs are listed in Table 2.1.

Table 2.1 Target site sequences of siRNA.

Name	Sequence (5′ to 3′)
siDro-1	GGA CCA AGT ATT CAG CAA G
siDro-2	GAC CAG ACT TTG TAC CCT T
siDro-3	CGA GTA GGC TTC GTG ACT T
siDro-4	GGT TGG AAC GAG TAG GCT T

2.3 Immunofluorescence

Cells were plated on Nunc Lab-Tek Chamber Slides (Thermo Fisher Scientific, 8-well format, 154534PK) or gelatin-coated coverslips overnight. After rinsing with phosphate buffered saline (PBS), cells were fixed in PBS-diluted 4% formaldehyde (Thermo Fisher Scientific, 28906) for 10 min at room temperature. After fixation, cells were washed three times with PBS and permeabilized in PBS with 0.1% Triton X-100 for 10 min at room temperature. The cells were washed three times with PBS. The permeabilized cells were blocked for an hour in PBS-T containing 5% BSA (Bovogen) and probed with a mixture of primary antibodies for two hours and washed three times with PBS-T. Cells were then probed with the Alexa Fluor-conjugated secondary antibodies (Thermo Fisher Scientific, 1:1000) and DAPI (Sigma-Aldrich, D9542) for an hour in the dark, and washed with PBS-T three times. The slide or coverslip was mounted and sealed. The probed proteins were detected with a fluorescence microscope (Zeiss, LSM 700), and images were analyzed by ImageJ (Schneider et al., 2012). The primary antibodies used in this study are listed in Table 2.2.

Table 2.2 Antibodies used in this study.

Name	Manufacturer, catalog #	Dilution used
DROSHA Ab-Ct#1	Cell Signaling Technology, 3364S	1:1000 (WB), 1:50 (IF)
DROSHA Ab-Ct#2	Santa Cruz Biotechnology, sc-393591	1:1000 (WB)
DROSHA Ab-Nt	Abcam, ab12286	1:1000 (WB), 1:100 (IF)
DGCR8	Abcam, ab191875	1:1000 (WB)
ERH	Abcam, ab166620	1:1000 (WB)
GAPDH	Santa Cruz Biotechnology, sc-32233	1:1000 (WB)
alpha Tubulin	Abcam, ab52866	1:1000 (WB)
GM130	BD Biosciences, 610822	1:1000 (WB), 1:100 (IF)
Lamin B1	Abcam, ab16048	1:1000 (WB)
Histone H3	Cell Signaling Technology, 4499S	1:1000 (WB)
Histone H3	Cell Signaling Technology, 3638S	1:1000 (WB)
KDEL	Enzo Life Sciences, ADI-SPA-827-F	1:1000 (WB), 1:100 (IF)
TGN46	Abcam, ab2809	1:50 (IF)
EEA1	Abcam, ab70521	1:100 (IF)
FLAG	Cell Signaling Technology, 8146S	1:1000 (WB)
HA	Thermo Fisher Scientific, 71-5500	1:1000 (WB)

2.4 Subcellular fractionation

The fractionation procedure for cytoplasm was performed following the previously described method (Holden & Horton, 2009). Briefly, the cultured cells were harvested in ice-cold PBS and placed in a 1.5-mL microtube. After centrifugation at 100g for 10 min, the PBS was removed, and the cell pellet volume was measured. The pellet was resuspended in its 10-fold volume of digitonin buffer (150 mM NaCl, 50 mM HEPES at pH 7.5, 150~200 µg/mL digitonin) supplemented with protease inhibitor cocktail (Calbiochem) by gentle pipetting. Different concentrations of digitonin (Sigma-Aldrich) were used in digitonin buffer, depending on the cell lines: 150 µg/mL for HEK293T, MCF7, and HEK293E, and 200 µg/mL for HCT116 cells. After end-over-end incubation for 10 min at 4°C, the lysate was centrifuged at 2000g for 10 min at 4°C. The supernatant was collected as the cytoplasmic fraction. The remaining pellet was washed once with 1 mL of PBS, collected by centrifugation, and used to prepare the membrane and nucleus fractions with the subcellular protein fractionation kit for cultured cells (Thermo Fisher Scientific). I followed the manufacturer's instructions with an additional PBS wash step after extracting the membrane fraction.

2.5 Western blot

Whole-cell extracts were prepared with the RIPA buffer (150 mM NaCl, 50 mM HEPES pH 7.4, 0.5% sodium deoxycholate, and 0.1% sodium dodecyl sulfate) supplemented with protease inhibitor cocktail (Calbiochem). The cell pellet was lysed in about a 20-fold volume of the RIPA buffer, incubated for 10 min on ice, and sonicated with the Bioruptor sonication system (Diagenode) or Q800R3

sonicator (Qsonica). Protein concentrations were determined using the Pierce BCA Protein Assay Kit (Thermo Fisher Scientific), and protein samples were denatured in 4× Laemmli Sample Buffer (Bio-Rad).

For Western blotting, protein samples were boiled at 95°C for 5 min before separating on Novex WedgeWell Tris-Glycine Mini Gels (Thermo Fisher Scientific). Separated proteins were transferred onto Immobilon-P PVDF membranes (Merck Millipore). Membranes were incubated with 5% skimmed milk in PBS-T (PBS (Amresco) + 0.1% Tween 20 (Anatrace)), then probed with primary antibodies overnight, and washed three times with PBS-T for 10 min each time. The membranes were incubated with HRP-conjugated secondary antibodies (Jackson) for 45 min and washed three times with PBS-T for 10 min each time. The protein bands were detected by SuperSignal West Pico PLUS Chemiluminescent Substrate (Thermo Fisher Scientific) or SuperSignal West Femto Maximum Sensitivity Substrate (Thermo Fisher Scientific) and scanned by the ChemiDoc XRS+ System (Bio-rad). The primary antibodies used in this study are listed in Table 2.2.

2.6 Small RNA sequencing

Sequencing libraries were generated as previously described (Kim et al., 2019). In brief, I mixed 20 µg of total RNAs with 10 nmol of 30 equimolar spike-in RNAs described in the previous study (Kim et al., 2019). Small RNAs were enriched by size fractionation by 15% urea–polyacrylamide gel electrophoresis and ligated to the randomized adaptor at the $5'$ and $3'$ ends. The ligated RNAs were reverse-transcribed using SuperScript IV reverse transcriptase (Thermo Fisher Scientific), amplified using Phusion high-fidelity DNA polymerase (Thermo Fisher

Scientific), and subjected to high-throughput sequencing on the MiSeq platform (Illumina).

2.7 Plasmid construction

To make the HA-DROSHA-FLAG expression plasmid, the *DROSHA* coding sequence was cloned into the pCK-FLAG vector with an additional HA tag (Lee et al., 2000). DROSHA deletion or substitution mutants were constructed by overlapping PCR, and all of the primers used are presented in Table 6.1.

To generate exonic expression vectors, exonic sequences were amplified from HCT116 genomic DNA and then assembled into the pmirGLO vector (Promega) by Gibson assembly. If necessary, the endogenous pri-miRNAs were replaced with pri-mir-627 or pri-mir-203b. For intronic expression vectors with the *BCL2L2* backbone, the previously constructed pcDNA3-BCL-let-7a vector was used as a template (Kim & Kim, 2007). The let-7a-1 was replaced with PCR-amplified pri-miRNAs, and then the whole insert, including *BCL2L2* sequences and a pri-miRNA, was moved to the pmirGLO vector. Other intronic backbones were also amplified from HCT116 genomic DNA. The primers used for cloning are provided in Table 6.1.

The deletion and insertion mutants were constructed by overlapping PCR or Gibson assembly. The primers are also listed in Table 6.1.

For hybrid DROSHA proteins, the N-terminal parts of other species were synthesized with gBlocks Gene Fragments (IDT). The N-terminal parts were assembled into the vector containing the C-terminal part of human DROSHA by Gibson assembly. The primers used in the cloning are listed in Table 6.1.

For the P>A DROSHA mutant, the N-terminal part (1–200) in which all prolines are changed to alanines was synthesized with gBlocks Gene Fragments (IDT). This fragment was then introduced into the DROSHA vector. The primers are also provided in Table 6.1.

2.8 Plasmid transfection

To ectopically express HA or FLAG-tagged DROSHA, transfection was carried out using the calcium-phosphate method for HEK293T cells. 15 hours before transfection, HEK293T cells were seeded in 100 mm culture dishes. The DNA/calcium phosphate precipitates were prepared by mixing one volume of DNA plasmid (10 µg) in 250 mM $CaCl_2$ with an equal volume of 2× HBS (50 mM HEPES, 12 mM Dextrose, 280 mM NaCl, 10 mM KCl, 1.5 mM Na_2HPO_4, pH 7.05) in a dropwise manner, and the mixture was added to the cultured cells. The cells were harvested two days after transfection for subcellular fractionation.

To rescue DROSHA expression for sequencing analysis, transfection was conducted using FuGENE HD Transfection Reagent (Promega) in HCT116 or HEK293E *DROSHA* knockout cells. One day before transfection, 100–200 × 10^4 cells were seeded in 100 mm culture dishes. For HCT116 *DROSHA* knockout cells, 1–5 µg DROSHA plasmids were diluted in 500 µL of OPTI-MEM (Thermo Fisher Scientific) and mixed with 3–15 µL of FuGENE HD Transfection Reagent (Promega, FuGENE HD Transfection Reagent:DNA = 3:1) in 500 µL of OPTI-MEM (Thermo Fisher Scientific). For HEK293E *DROSHA* knockout cells, 0.3–1.8 µg plasmids and 0.9–5.4 µL of FuGENE HD Transfection Reagent were utilized.

The mixture was added to the cells after 10 min incubation at room temperature. After two days, the cells were prepared for RNA extraction and Western blotting.

Cotransfection of DROSHA plasmids and miRNA expression vectors was performed with FuGENE HD Transfection Reagent (Promega). The overall procedures were the same as above. To express comparable amounts of the DROSHA-p140 mimic or full-length mimic, 3 µg of △N200 plasmid or 4 µg of △195–204 (or 197–198 NN →AA) plasmids were used, respectively, and 3 µg was used for exonic or intronic miRNA expression vectors.

For the experiments with the P>A mutant, 1 µg of DROSHA-p140 or full-length DROSHA mimic was used, while 5 µg of the P>A plasmid was transfected to achieve similar amounts of expressed proteins.

2.9 Immunoprecipitation

Transfected cells grown on 100 mm dishes were lysed in 600 µL of lysis buffer (20 mM Tris pH 7.5, 150 mM NaCl, 0.1 ng/µL RNase A, and protease inhibitor cocktails (Calbiochem)) and sonicated. Clear lysates were collected by centrifugation at 20,000 g at 4°C for 10 min. For FLAG-tagged protein immunoprecipitation, anti-FLAG M2 affinity gel (Sigma-Aldrich) was pre-washed three times with 1 mL of the wash buffer (20 mM Tris pH 7.5, 150 mM NaCl). Lysates and beads were incubated at 4°C for two hours with gentle rotation. Incubated beads were washed three times with the wash buffer. The remaining supernatants were removed using a 30-gauge needle. For Western blot analysis, beads were resuspended in 4× Laemmli Sample Buffer (Bio-Rad) and boiled at 95°C for 5 min.

Table 2.3 Catalog numbers for TaqMan microRNA assay.

Name	Catalog number (Thermo Fisher Scientific)
miR-19a-3p	#000395
miR-15a-5p	#000389
miR-25-3p	#000403
miR-221-3p	#000524
miR-92a-3p	#000431
miR-561-5p	#471396_mat
miR-627-5p	#001560
miR-193a-3p	#002250
miR-187-3p	#001193
miR-146b-5p	#474220_mat
miR-203b-3p	#464535_mat
U6 snRNA	#001973

2.10 TaqMan miRNA qPCR

Total RNAs were isolated using TRIzol (Thermo Fisher Scientific) and treated with DNase I (Takara Bio), and 10 ng of total RNAs was used for one reaction. Complementary DNAs (cDNAs) were then synthesized using the TaqMan microRNA reverse transcription kit (Thermo Fisher Scientific) and subjected to quantitative real-time PCR with the TaqMan microRNA assay on a StepOnePlus real-time PCR system (Thermo Fisher Scientific) or QuantStudio 3 real-time PCR system (Thermo Fisher Scientific). The catalog numbers are listed in Table 2.3.

2.11 RT-qPCR

To measure pri-miRNAs and *Renilla* luciferase levels, TRIzol (Thermo Fisher Scientific)-isolated RNAs were treated with DNase I (Takara Bio). cDNAs were synthesized from 2.5–5 µg of total RNA using random hexamer primers (Thermo Fisher Scientific) and RevertAid Reverse Transcriptase (Thermo Fisher Scientific).

Table 2.4 Primers for RT-qPCR.

Name	Sequence (5′ to 3′)
pri-miR-19a-F2	CCA ATA ATT CAA GCC AAG CAA GTA
pri-miR-19a-R2	CAT TTG AAG GAA ATA GCA GGC CA
pri-miR-15a-F1	TTT AGG CGC GAA TGT GTG TT
pri-miR-15a-R3	TAT ATT TTC TTC AGA AGA TCA GAT C
pri-miR-25-F1	TCA CAG GAC AGC TGA ACT CC
pri-miR-25-R1	AGC ATC CGC AGT GTT GG
pri-miR-221-F2	TTG CAA GCT GAA CAT CCA GGT C
pri-miR-221-R2	CCA CTG GTT TAT ACC TCC TGG AA
pri-miR-92a-1-F1	AGG GAA ACT CAA ACC CCT TTC
pri-miR-92a-1-R1	TGG TCA CAA TCC CCA CCA AA
hRluc-neo qPCR F	CGA CCA CCA AGC GAA ACA TC
hRluc-neo qPCR R	TGA TAT TCG GCA AGC AGG CA
GAPDH-F	CTC TCT GCT CCT CCT GTT CGA C
GAPDH-R	TGA GCG ATG TGG CTC GGC T

$\frac{1}{10}$–$\frac{1}{5}$ diluted cDNAs were subjected to quantitative real-time PCR with the Power SYBR Green Master Mix (Thermo Fisher Scientific) on StepOnePlus Real-Time PCR System (Thermo Fisher Scientific) or QuantStudio 3 Real-Time PCR System (Thermo Fisher Scientific). GAPDH was used as an internal control. The sequences of qPCR primers are listed in Table 2.4.

2.12 In vitro DROSHA processing

To purify the Microprocessor complex, △N200 or △195–204 DROSHA that are N-terminally HA-tagged and C-terminally FLAG tagged, and DGCR8, whose N terminus is fused to V5 tag, where cloned into the pCK expression vector (Lee et al., 2000). Both constructs were cotransfected into HEK293E *DROSHA* knockout cells with calcium phosphate. 400×10^4 cells were plated on 100 mm culture dishes 15 hours before transfection. For each 100 mm dish, 10 µg of

DROSHA and 4 µg of DGCR8 plasmids were included in DNA/calcium phosphate precipitates. The cells were scraped from the dish and harvested into pellets two days after the transfection. The pellets were resuspended in 900 µL of lysis buffer containing 500 mM NaCl, 50 mM Tris pH 7.5, and protease inhibitor cocktail (Calbiochem). The lysate was sonicated by VC 130 (Sonics & Materials) with the following settings: 35% amplitude, 2 sec pulse, and a total of 2 min. After sonication, the lysate was centrifuges at 20,000 g at 4°C for 15 min, and the supernatant was transferred into a 1.7 mL tube. Using the lysate, purification of the recombinant Microprocessor complex was performed by FLAG-IP and 3×FLAG-peptide elution as previously described (Kim & Kim, 2022).

RNA substrates were prepared through in vitro transcription with the MEGAscript T7 Transcription Kit (Thermo Fisher Scientific) from DNA templates starting with a T7 promoter. Reactions were assembled according to the manufacturer's instructions in a total volume of 20 µL with the following modifications: 2 µL of 0.75 mM UTP and 6 µL of 12.5 mM [α-32P]UTP were used instead of 2 µL of 75 mM UTP. After incubation for 5 hours at 37°C, 1 µL of TURBO DNase (2 U/µL, Thermo Fisher Scientific) was added, and the reactions were incubated for another 15 min at 37°C. The radiolabeled RNA was gel purified with 6% urea-polyacrylamide gel. The template and primer sequences for in vitro transcription are listed in Table 2.5.

4 fmol of pri-miRNA substrates were incubated with 8–120 fmol of the Microprocessor complex at 37°C for 2 hours in the 30 µL buffer containing 100 mM NaCl, 60 mM Tris-HCl pH 7.5, 1.2 mM DTT, 2 mM $MgCl_2$, and 1 µL of SUPERase · In RNase Inhibitor (20 U/µL, Thermo Fisher Scientific). The reactions were terminated by mixing with 27 µL of TBE-Urea Sample Buffer

Table 2.5 Template and primer sequences for in vitro transcription.

	Name	Sequence (5′ to 3′)
Templates	pri-mir-186	ggg CCA AAC ATT TTT TCA TTG CTT GTA ACT TTC CAA AGA ATT CTC CTT TTG GGC TTT CTG GTT TTA TTT TAA GCC CAA AGG TGA ATT TTT TGG GAA GTT TGA GCT AAA TTC CTT CAA C
	pri-mir-125a	ggg CAC ACC ATG TTG CCA GTC TCT AGG TCC CTG AGA CCC TTT AAC CTG TGA GGA CAT CCA GGG TCA CAG GTG AGG TTC TTG GGA GCC TGG CGT CTG GCC CAA CCA CAC A
Primers	186_T7_F	GAC CTA ATA CGA CTC ACT ATA GGG CCA AAC ATT TTT TCA TTG CTT
	186_R	GTT GAA GGA ATT TAG CTC AAA CT
	125a_T7_F	GAC CTA ATA CGA CTC ACT ATA GGG CAC ACC ATG TTG CCA GTC TCT
	125a_R	TGT GTG GTT GGG CCA GAC

(Bio-Rad) and 3 µL of 20 mg/mL Proteinase K (Sigma-Aldrich) at 37°C for 30 min and then 50°C for 30 min. The samples were boiled at 95°C for 5 min before the 10% urea-polyacrylamide gel electrophoresis. Radioactive signals were detected by Typhoon FLA 7000 (GE Healthcare) and analyzed using the Multi Gauge software (FujiFilm).

2.13 Serum starvation

250×10^4 HCT116 wild-type cells were plated in 100 mm culture dishes containing McCoy's 5A (WELGENE) supplemented with 9.1% FBS (WELGENE). After 15 hours, the cells were rinsed with PBS (WELGENE) and the medium was changed to McCoy's 5A (WELGENE) containing 0.1% FBS (WELGENE).

Table 2.6 Primers for RT-PCR.

Name	Sequence (5′ to 3′)
BCL2L2-splicing-F	GTT GGT AAA GCC ACC ATG GCG ACC CCA GCC
BCL2L2-splicing-R	GTT TAA ACA ACT AGA ATC ACT TGC TAG CAA AAA AGG
#8#9-region-splicing-F	CGG TAC TGT TGG TAA AGC CAC
#8#9-region-splicing-R	GCG AGC TCG TTT AAA CAA CTA G

2.14 RT-PCR

Reverse transcription (RT) was carried out using RevertAid Reverse Transcriptase (Thermo Fisher Scientific) as described above. After RT, the PCR reaction was performed with nTaq polymerase (Enzynomics). The primers used are listed in Table 2.6.

2.15 Sample preparation for LC-MS/MS

To generate cell lines stably expressing FLm or p140m, I inserted coding sequences of FLm and p140m with HA and FLAG tags into the pLVX-EF1alpha-IRES-Puro plasmid. Lentivirus was produced by forward transfecting 293T Lenti-X cells (Clontech) with 1 µg of total plasmid (5:3:2 ratio of pLVX vector:psPAX2 (Addgene #12260):pMD2.G (Addgene #12259)), 3 µL of FuGENE HD (Promega), and 250 µL of OPTI-MEM in each well of a 6-well plate seeded with 60×10^4. The medium was exchanged the following day. The media with virus particles were collected 48 hours after transfection and filtered through a 0.45 µm MF-Millipore™ Membrane Filter (Merck Millipore). Collected media were supplemented with 8 µg/mL polybrene (Merck Millipore) and immediately used for transduction.

Recipient cells were HCT116 *DROSHA* KO. One day prior to transduction, 25×10^4 cells were seeded in a well of 6-well plate. An overnight transduction was performed by $\frac{1}{10}$–$\frac{1}{2}$ diluting the virus-containing media, and the medium was changed the following day. The transduced cells were selected by maintaining the cells with 1 µg/mL puromycin (AG Scientific) for more than two weeks. The expression of DROSHA was confirmed by Western blot analysis using FLAG antibody.

For a single immunoprecipitation (IP), two or three 150 mm culture dishes were used. Cells were rinsed twice with 18 mL of PBS solution and then fixed with 18 mL of PBS-diluted 0.1% formaldehyde solution (Thermo Fisher Scientific, 28906) at room temperature for 10 min. To quench the reaction, 2 mL of 1.5 M glycine solution was added directly to the plate at room temperature for 10 min. The fixed cells were then harvested and transferred into a 1.7 mL tube after resuspending in 1 mL of PBS for each 150 mm culture dish. The PBS was removed by centrifugation and the cell pellet was resuspended in 500–650 µL of IP buffer (20 mM HEPES, 0.5% NP-40, 150 mM NaCl, 1 mM EDTA, 5% glycerol, 0.5 mM TCEP) supplemented with protease inhibitor cocktail (Calbiochem) and Phosphatase inhibitor cocktail II (AG Scientific). The lysate was sonicated by VC 130 (Sonics & Materials) with the following settings: 50% amplitude, 2 sec pulse, and a total of 10 min. After sonication, the lysate was centrifuged at 20,000 g at 4°C for 15 min. The supernatant was transferred into a new tube and the protein concentration was measured using the Pierce BCA Protein Assay Kit (Thermo Fisher Scientific). A single IP was performed using 1–1.3 mg lysate.

To perform FLAG IP, 40 µL anti-FLAG M2 affinity gel (Sigma-Aldrich) was pre-washed three times with 1 mL of the IP buffer. The lysates and beads were

mixed and incubated with 0.1% RNase A (Thermo Fisher Scientific) at 4°C for 2 hours. After incubation, the beads were washed four times with the IP buffer and twice with the IP buffer without NP-40. The remaining buffer was removed using a 30-gauge needle. For elution, 100 µL of 5 µg/µL 3×FLAG Peptide (Sigma-Aldrich) was added immediately and incubated at 37°C for 30 min on the thermomixer. The eluates were collected and subjected to the mass spectrometry analysis.

2.16 LC-MS/MS

The immunoprecipitated protein samples containing SDS were subjected to FASP digestion (Wiśniewski et al., 2009). Briefly, protein samples were first reduced and alkylated in denaturation condition (8 M urea in 50 mM ammonium bicarbonate (ABC) buffer). The alkylated samples were placed on the preconditioned 30 kDa MWCO Amicon filter (0.5 mL, Merck Millipore) and centrifuged for 30 min at 14,000 g. Washing with 200 µL of 8 M urea or 50 mM ABC and centrifuging at 14,000 g for 15 min were carried out to remove SDS in the filter unit. Then protein samples were digested with 2% (w/w) trypsin at 37°C overnight. The resulting peptide samples were subjected to C18 clean-up and loaded to the in-house packed trap column (3 cm x 150 µm i.d.) and capillary analytical column (100 cm x 75 µm i.d.) with 3 µm Jupiter C18 particles (Phenomenex) for peptide separation. A flow rate of 300 nL/min and a linear gradient ranging from 95% solvent A (water with 0.1% formic acid) to 40% of solvent B (acetonitrile with 0.1% formic acid) for 100 min were applied on nanoACQUITY UPLC (Waters) coupled with Orbitrap Eclipse mass spectrometer (Thermo Scientific), which was operated using the following parameters: m/z 300–1800 of precursor scan range, 1.4 Th of precursor isolation window, 30%

of normalized collision energy (NCE) for higher-energy collisional dissociation (HCD), 30 s of dynamic exclusion duration, 60k or 15k resolution at m/z 200 for full MS or MS/MS scan, respectively.

2.17 Protein identification and MS analysis

MS raw data files were processed with MaxQuant (version 2.0.3.0) searched using the built-in Andromeda search engine in MaxQuant against the human Uniprot database (version 10/12/2022) at default settings (20 ppm or 6 ppm of precursor ion mass tolerances for initial or main search, respectively, and 0.5 Da for fragment ion masses). The label free quantification (LFQ) and Match Between Runs were used with the following search parameters: enzyme specificity was set to trypsin/P and a maximum of two missed cleavages were allowed. Cysteine carbamidomethylation and methionine oxidation were selected as fixed and variable modifications, respectively. A 1% FDR was required at both the protein- and the peptide-level.

For further statistical analysis, the LFQ values of the identified proteins were used, while contaminants from the MaxQuant contaminants database and the Contaminant Repository for Affinity Purification (CRAPome) (Mellacheruvu et al., 2013) were excluded from downstream analysis. The Differential Enrichment analysis of Proteomics data (DEP) (Zhang et al., 2018) was used to carry out differentially enrichment analysis using the imputed LFQ values.[1]

[1] DEP analysis was done by Baekgyu Kim

2.18 Conservation analysis

DROSHA protein sequences of *H. sapiens*, *M. musculus*, *X. tropicalis*, *D. rerio*, *D. melanogaster*, and *C. elegans* were used in conservation analysis (Figure 1.3). After multiple sequence alignment using Clustal Omega in Jalview (Waterhouse et al., 2009), conservation scores were calculated by using Scorecons server with the option of "valdar01" (Valdar, 2002). The conservation of a miRNA was quantified as the average of phyloP100 conservation scores (Pollard et al., 2010) of its corresponding pre-miRNA region annotated in miRBase release 21 (Kozomara & Griffiths-Jones, 2014).

2.19 Disorderliness prediction

For disorderliness prediction, the SPOT-Disorder-Single program was used (Hanson et al., 2018). Amino acid sequences of full-length proteins were used as input for the program.

2.20 Analysis of small RNA sequencing

Low-quality reads (phred quality <20 in 90% of nucleotides) were discarded with FASTX-Toolkit (http://hannonlab.cshl.edu/fastx_toolkit/). Next, the TruSeq 3′ adapter sequence was removed, and then 4 nt-long degenerate sequences at the 3′ and 5′ ends were trimmed using cutadapt (Martin, 2011). Reads shorter than 18 nt or longer than 26 nt were filtered out. Preprocessed reads were aligned to the spike-in sequences by STAR (Dobin et al., 2013). Reads mapped to spike-in sequences with at most a single mismatch were considered reliable spike-in reads. The remaining reads were mapped to the hg38 genome using STAR (STAR

--outFilterMultimapNmax 20 --outFilterMismatchNmax 0 --alignIntronMax 1). Reads were classified into annotations from miRBase release 21 by BEDTools and used for further analysis (Kozomara & Griffiths-Jones, 2014; Quinlan & Hall, 2010). After normalization with randomly selected 15 spike-ins, DESeq2 was used for differential gene expression analysis (Love et al., 2014). Outputs from DESeq2 analysis are provided in Table 6.2, 6.3, and 6.4. The DROSHA dependency was determined based on the sequencing data from HCT116 *DROSHA* WT and KO cells.

2.21 Pri-miRNA feature analysis

Based on the baseMean values from DESeq2, lowly expressed miRNAs were filtered out before pri-miRNA feature analysis. Positionally conserved primary sequence motifs were scanned based on the mature miRNA termini annotated in miRBase release 21 (the 5′ end of 5p miRNA and the 3′ end of 3p miRNA). When only one strand of the hairpin was available, the end of the available strand was used to predict the end of the opposite strand. The UG motif was scanned from −16 nt to −13 nt regions relative to the 5′ end of 5p miRNA. The UGUG motif, which was defined as UGU or GUG (Auyeung et al., 2013), was scanned from +21 nt to +23 nt positions relative to the 5′ end of 5p miRNA. Similarly, the CNNC motif was searched from −19 nt to −16 nt regions relative to the 3′ end of 3p miRNA. For the mGHG motif, I used previously defined and calculated mGHG scores (Kwon et al., 2019). The miRNAs were divided into equal-sized bins based on their mGHG scores (low, middle, and high), and the groups with low or high mGHG scores were used for the analysis.

The miRNAs were also classified according to their genomic arrangements. I assigned a pri-miRNA as 'clustered' if it is located with another pri-miRNA within 2000 bp in the genome (Shang et al., 2020). A miRNA was designated as 'intronic' if there was an intron overlapped with the miRNA; otherwise, it was classified as 'exonic'.

2.22 Data availability

All high-throughput sequencing data generated in this study (small RNA sequencing) have been deposited in GEO (accession no. GSE230544). Custom codes are publicly available online (https://github.com/wwc420/drosha_nterm).

3. Results

3.1 Proteolytic cleavage yields a DROSHA isoform (p140) lacking the proline-rich domain

To understand the functional significance of the PRD of DROSHA, I first interrogated natural isoforms of DROSHA that may lack the N terminus. I performed Western blotting using three antibodies targeting different part of DROSHA (Figure 1.3). Apart from the full-length DROSHA protein (~170 kDa), I detected a prominent band of ~140 kDa with two antibodies against the C-terminal region (Ab-Ct#1 and Ab-Ct#2) (Figure 3.1). This ~140-kDa band was not observed when *DROSHA* was knocked down or knocked out or when the N terminus targeting antibody (Ab-Nt) was used (Figure 3.1 and 3.2). Thus, this band represents a smaller isoform of DROSHA lacking the N-terminal region. This 140-kDa isoform was observed in all human cell lines that I examined, including MCF7 (human breast cancer cell line) and HCT116 (human colon cancer cell line) (Figure 3.2). I refer to this isoform as "DROSHA-p140" (Figure 3.3). Intriguingly, DROSHA-p140 (p140) was found mainly in the membrane fraction as well as in the nucleus (Figure 3.1 and 3.2). I also performed immunofluorescence (IF) staining using Ab-Ct#1 that can recognize both the full length and p140 (Figure 3.4 right, 3.5, and 3.6). The DROSHA signal was detected in the nucleus, as expected from the well-established nuclear function of DROSHA (Lee et al., 2002; Kuehbacher et al., 2007; Tang et al., 2010; Bellemer et al., 2012). However, intriguingly, I also

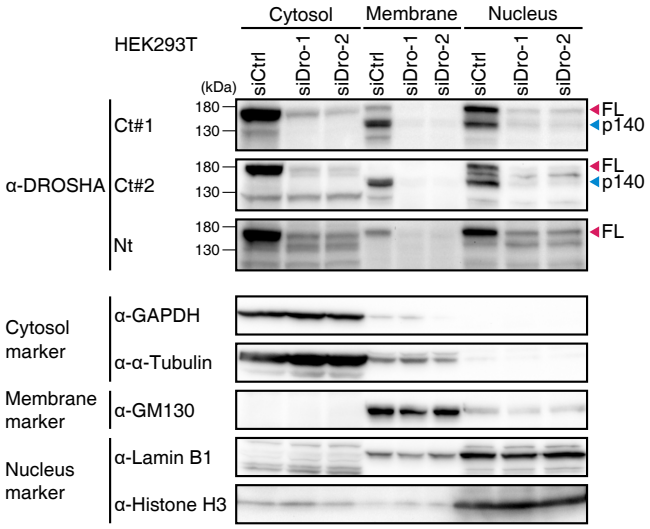

Figure 3.1 Identification of an N-terminal-truncated form of DROSHA (p140). HEK293T cells were transfected with control (siCtrl) or *DROSHA* (siDro) siRNAs for 2 d and then subjected to subcellular fractionation followed by Western blotting.

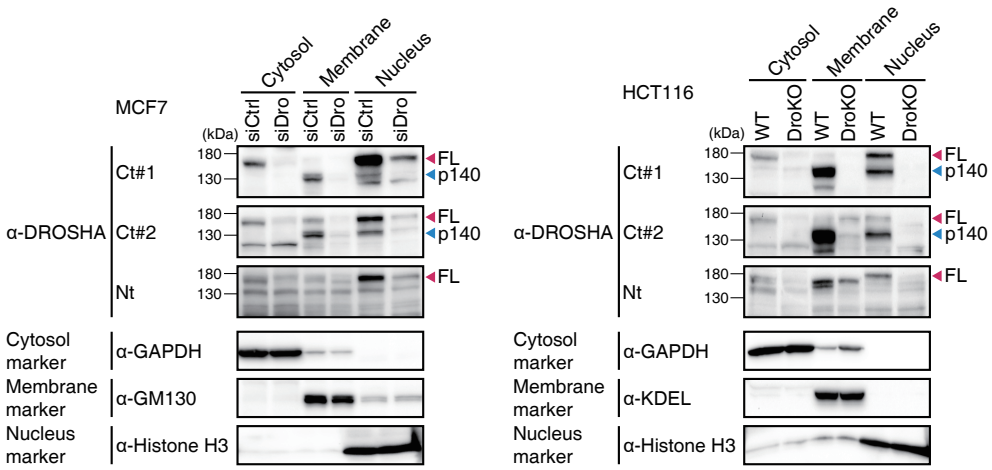

Figure 3.2 Expression of full-length DROSHA and DROSHA-p140 in MCF7 (*left*) and HCT116 (*right*) cells. MCF7 cells were transfected with control (siCtrl) or *DROSHA* (siDro) siRNAs for 2 d, and HCT116 *DROSHA* KO cells (DroKO) were from the previous study (Kim et al., 2016).

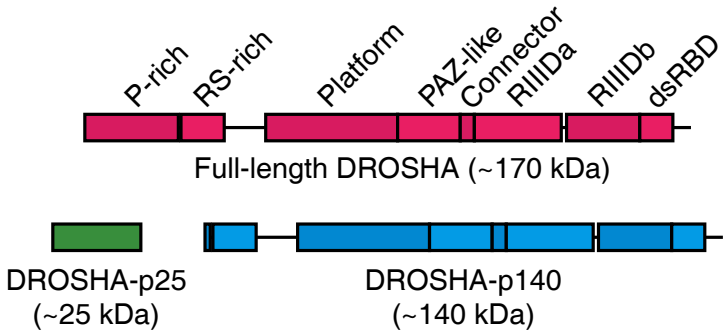

Figure 3.3 Schematics of the observed DROSHA fragments.

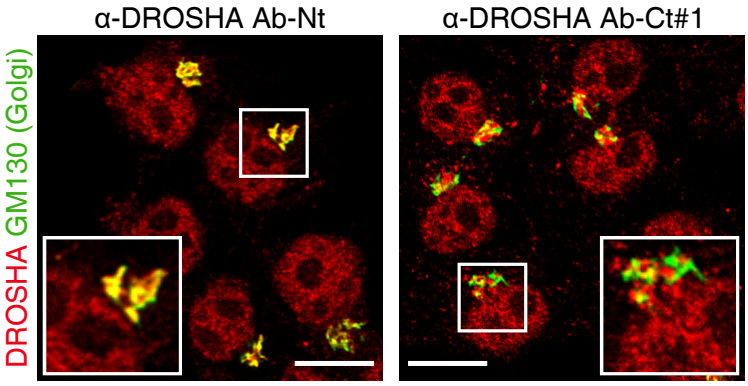

Figure 3.4 Localization of DROSHA (red) visualized using antibodies against the N terminus (*left*) or C terminus (*right*) in HEK293T cells. Costaining was done with an antibody against GM130 (green), a Golgi apparatus marker. The *insets* are enlarged views from the white rectangels. Scale bars, 10 µm.

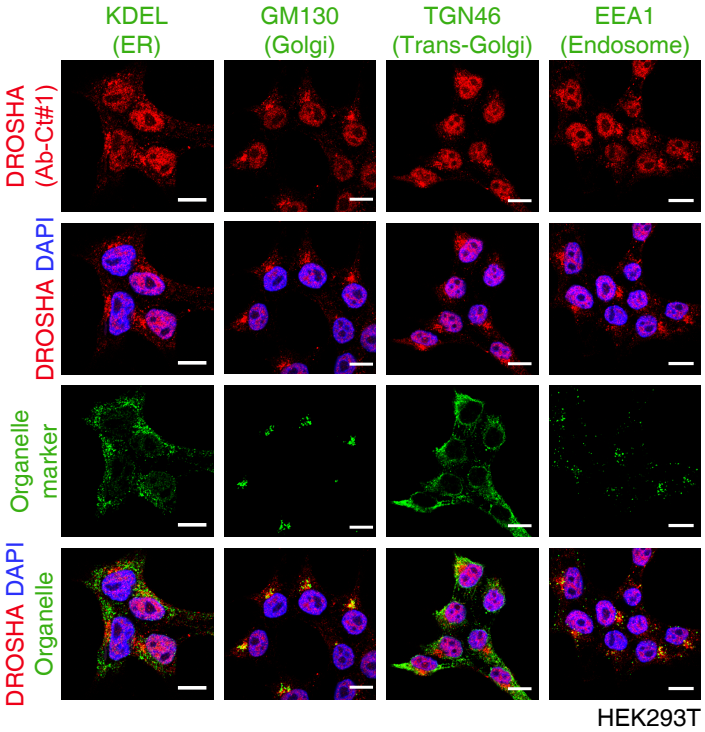

Figure 3.5 IF staining for DROSHA using Ab-Ct#1 along with various organelle markers in HEK293T cells. The signals from DROSHA were from nuclei and the perinuclear regions stained by GM130. Scale bars, 10 µm.

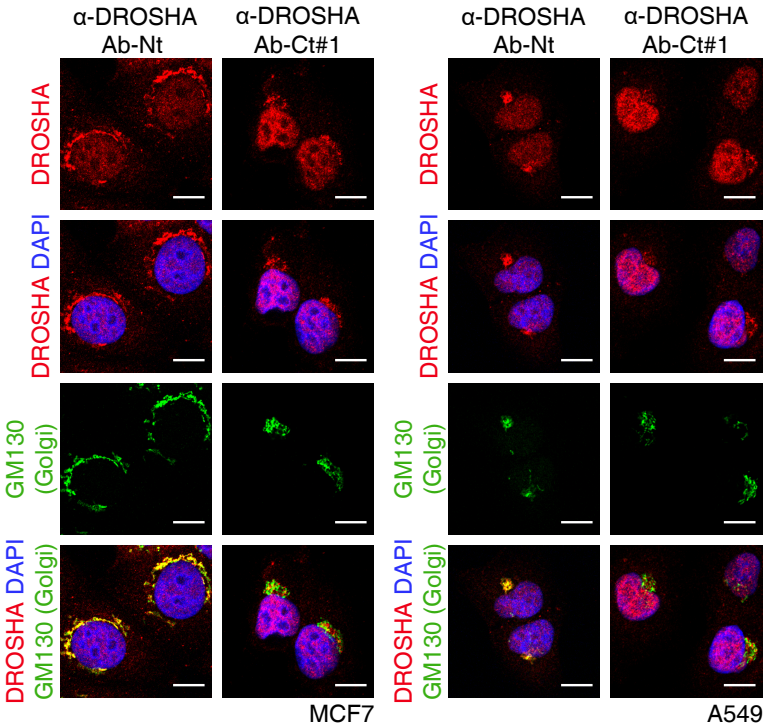

Figure 3.6 IF staining for DROSHA with N-terminal or C-terminal antibodies in MCF7 (*left*) and A549 (*right*) cells. Scale bars, 10 µm.

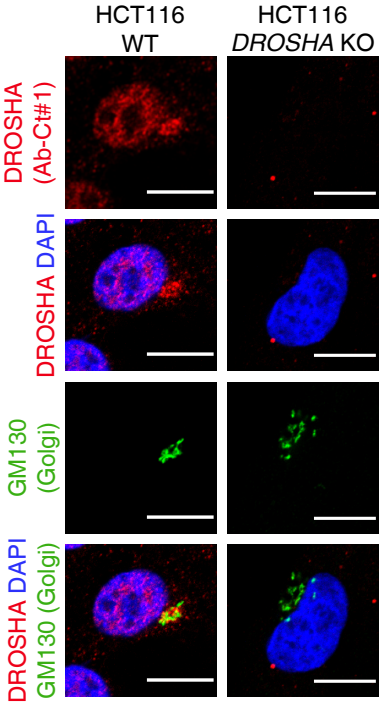

Figure 3.7 IF staining for DROSHA using Ab-Ct#1 in HCT116 *DROSHA* KO cell, showing absence of both nucleoplasmic and perinuclear signals. Scale bars, 10 µm.

detected clear DROSHA signals in specific perinuclear areas in close proximity to GM130, a marker for the Golgi apparatus (Figure 3.4 right, 3.5, and 3.6). This peri-Golgi signal as well as the nucleoplasmic signal were lost in *DROSHA* knockout (KO) cells (Figure 3.7), indicating that DROSHA indeed localizes both to the nucleus and near the Golgi. Given that p140 is the major isoform in the membrane according to the subcellular fractionation experiment (Figure 3.1 and 3.2), this peri-Golgi signal may originate from p140 rather that full-length DROSHA. Notably, the antibody Ab-Nt, targeting the N terminus of DROSHA, also gave clear signals in the Golgi (Figure 3.4 left, 3.6, and 3.8). I further found

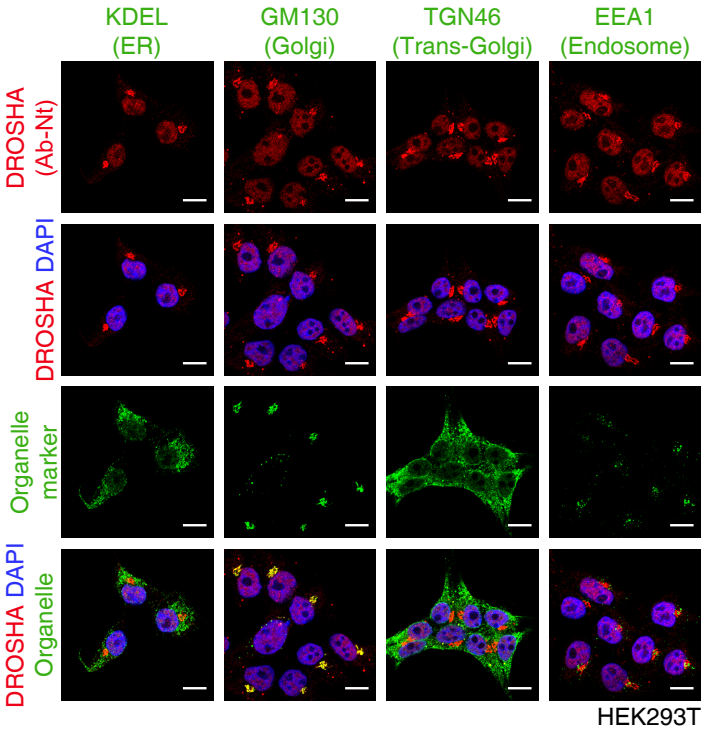

Figure 3.8 IF staining for DROSHA with Ab-Nt in HEK293T cells, showing the overlapped signals between GM130 and DROSHA. Scale bars, 10 µm.

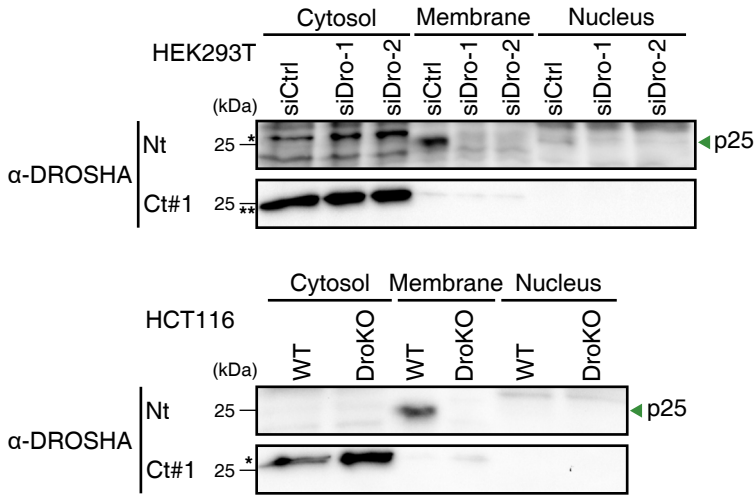

Figure 3.9 Detection of the N-terminal fragment of ~25 kDa (p25) in the membrane fraction. These blots are from the lower parts of the same blots in 3.1 and 3.2. The asterisks indicate cross-reacting bands.

that although this antibody cannot capture p140, it detects an ~25-kDa protein that is mainly in the membrane fraction (Figure 3.9). This band was not detected by the C-terminal antibody or when *DROSHA* was ablated, indicating that this ~25-kDa protein ("DROSHA-p25") detected by Ab-Nt was derived from the N terminus of DROSHA (Figure 3.9).

The presence of the separate DROSHA-p25 (p25) protein implied that p140 may be produced by proteolytic cleavage rather than alternative splicing. To test this possibility, I ectopically expressed full-length DROSHA tagged with HA and FLAG at the N and C termini, respectively (Figure 3.10). p25 was detected specifically with anti-HA antibody, while p140 was observed exclusively with anti-FLAG antibody, which indicates that p25 and p140 arise from proteolytic cleavage of the full-length protein, rather than from alternative splicing (Figure 3.3).

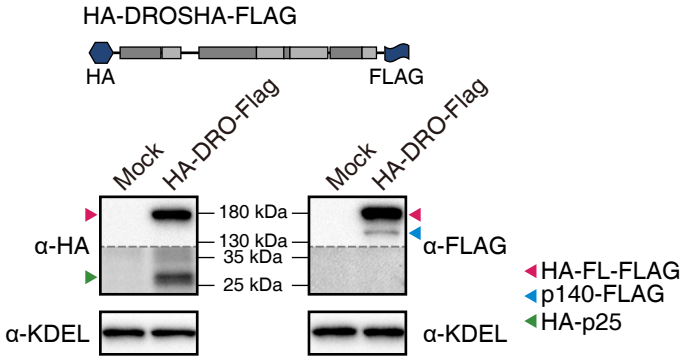

Figure 3.10 Fragments generated from ectopically expressed DROSHA. A plasmid with DROSHA coding sequence linked to the HA and FLAG tags was transfected to HEK293T cells. After 48 h, subcellular fractionation was performed, and the membrane fractions were used for Western blotting.

3.2 Identification of residues critical for proteolytic cleavage

Given the size of p25, it is likely that the cleavage occurs at the boundary between the PRD and the RS-rich domain (amino acids 180–280). To identify the residues necessary for protein cleavage, I generated deletion mutants and analyzed their products by Western blotting. Since both domains are predicted to be unstructured (Figure 1.3), and attempts to solve the structure experimentally have been unsuccessful, I had no structural guidance. Therefore, I made a series of 20 amino acid deletions within this region (Figure 3.11). The mutant lacking amino acids 180–199 failed to produce p140 and p25 (Figure 3.12 A, △180–199). To further narrow down the region, I created another set of mutants with 10 amino acid deletions (Figure 3.11) and identified two mutants that were significantly affected (Figure 3.12 B, △190–199 and △195–204). A substitution mutant (Asn197–Asn198 replaced with alanines) also showed a defect, unlike similar substitutions in

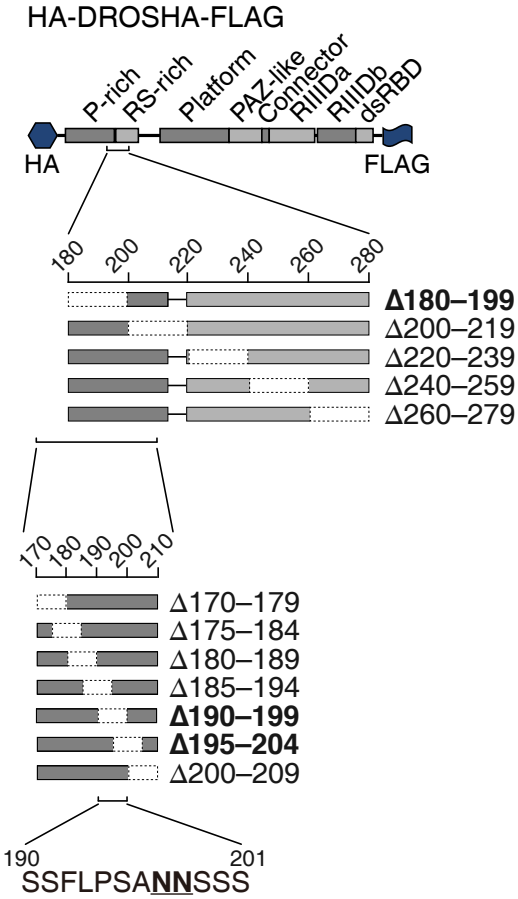

Figure 3.11 Schematics of the DROSHA constructs harboring deleted or substituted regions.

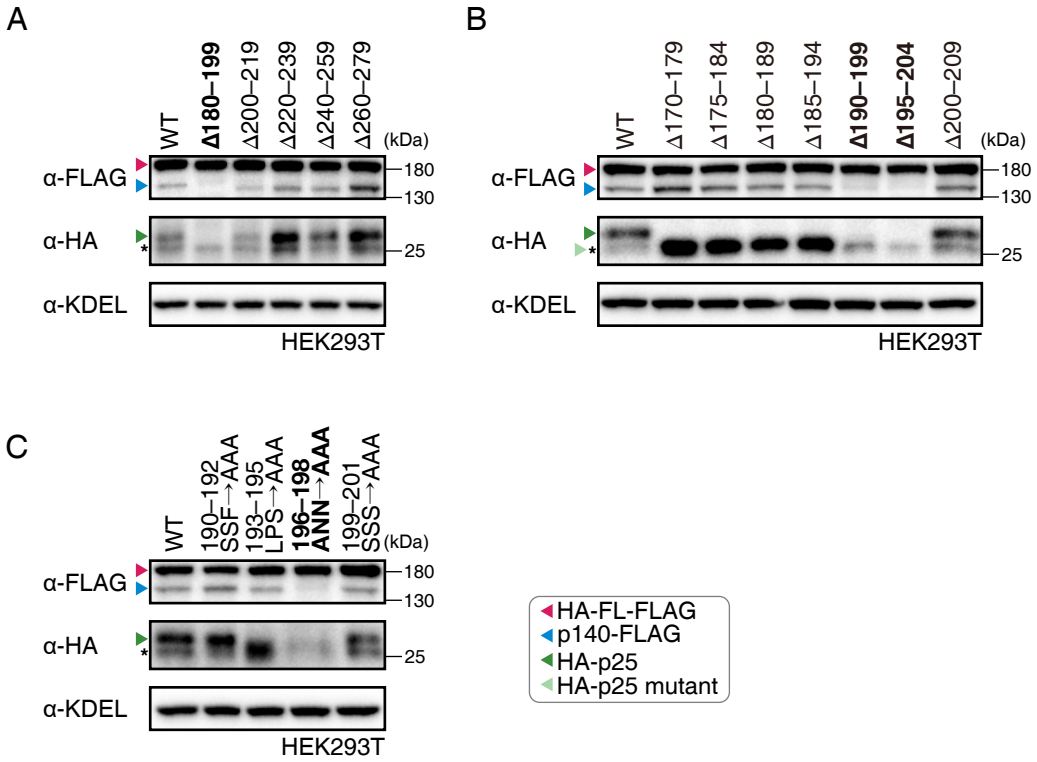

Figure 3.12 Western blot analyses of DROSHA mutants with 20 amino acid deletions (*A*), 10 amino acid deletions (*B*), or three amino acid substitutions (*C*) collectively indicate that the region around the 200th residue is crucial for the proteolytic cleavage. Subcellular fractionation was performed 48 h post-transfection, and the membrane fractions were used for Western blotting. The asterisk indicates a nonspecific band.

neighboring positions, highlighting the importance of two asparagines located at the end of PRD (Figure 3.12 C, 197–198 NN→AA). Although I attempted to map the exact cleavage site using mass spectrometry-based methods, my efforts were unsuccessful, likely because the N-terminal sequences are unsuitable for tryptic digestion necessary for mass spectrometry analysis (data not shown).

Together, my results demonstrate that proteolytic cleavage removes ~200 amino acids from the N terminus, including the PRD. The membrane association of DROSHA fragments and their localization with the Golgi marker GM130 (Figure 3.1 and 3.4) imply that a fraction of DROSHA molecules associates with the Golgi and is cleaved by a Golgi-associated protease, although the responsible protease has not been identified yet. My discovery of p140 lacking the PRD provided an opportunity to investigate the role of the PRD.

3.3 The PRD is required for efficient processing of a subset of pri-miRNAs in cells

To examine the significance of the PRD, I assessed the activity of p140 in comparison with the full-length protein. I expressed the DROSHA mutants in the *DROSHA* KO cells using a rescue strategy (Figure 3.13). The △195–204 mutant that is most strongly defective in protein cleavage was used as a full-length mimic (referred to here as "FLm") (Figure 3.12). I selected the △N200 mutant lacking the first 200 amino acids as a p140 mimic (referred to here as "p140m"). I carefully assessed the transfection conditions to match protein expression levels from two plasmids (Figure 3.14). Both FLm and p140m proteins were localized

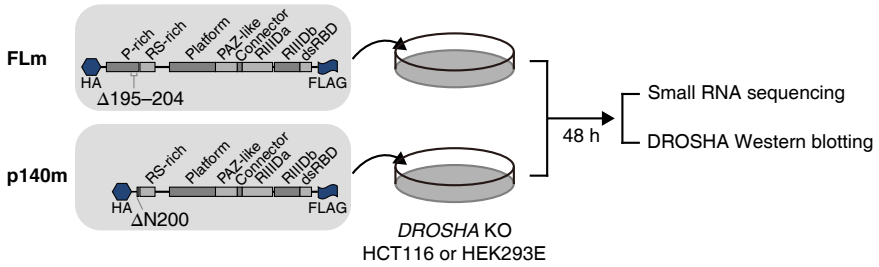

Figure 3.13 Experimental design to compare miRNA expression levels in cells expressing full-length DROSHA or p140. The △195–204 or △N200 DROSHA construct was transiently transfected to HCT116 or HEK293E *DROSHA* KO cells. Total RNAs and cell lysates were extracted for small RNA sequencing and Western blotting, respectively.

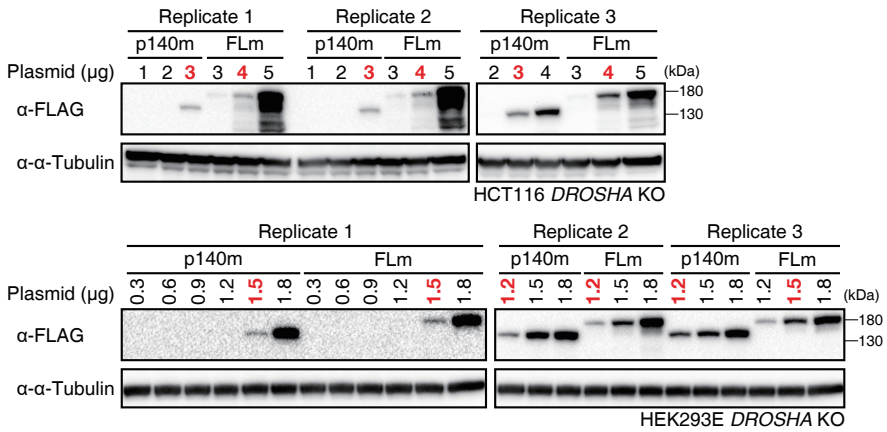

Figure 3.14 Western blotting of ectopically expressed full-length DROSHA or p140 mimic. The pairs with similar expression levels (colored in red) were chosen for small RNA sequencing. Indicated amounts of plasmids were transfected, and whole-cell extracts were prepared 2 d after transfection.

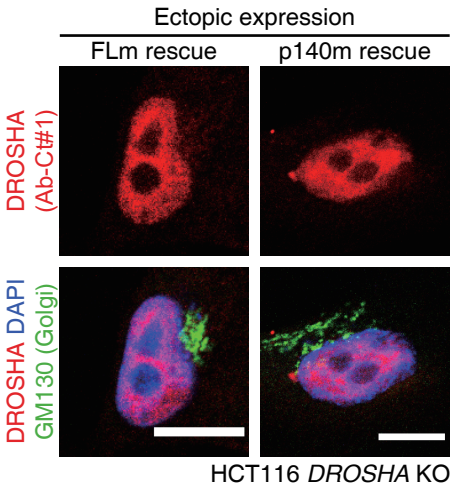

Figure 3.15 IF staining for ectopically expressed full-length DROSHA or p140 mimic. IF was carried out 2 d after transfection. Both DROSHA proteins (red) were mainly localized in the nucleus stained with DAPI (blue). Scale bars, 10 µm.

to the nucleus, as determined by immunofluorescence (Figure 3.15). Subcellular fractionation and Western blotting also showed that the nuclear localization of p140m is comparable with that of FLm (Figure 3.16). These results confirm the previous observations that the N-terminal 1–270 amino acids (including the PRD) are dispensable for nuclear localization (Tang et al., 2010; Bellemer et al., 2012). Furthermore, FLm and p140m interact with DGCR8 to similar degrees (Figure 3.17), consistent with the earlier finding that DGCR8 binds to the RIIIDs of DROSHA rather than the N terminus (Kwon et al., 2016).

To functionally assess FLm and p140m, I used two different KO cell lines generated from HCT116 and HEK293E cells (Figure 3.18 and 3.2) (Kim et al., 2016). After transient transfection of FLm or p104m, small RNA sequencing was carried out using the AQ-seq protocol, which allows accurate miRNA quantification (Kim

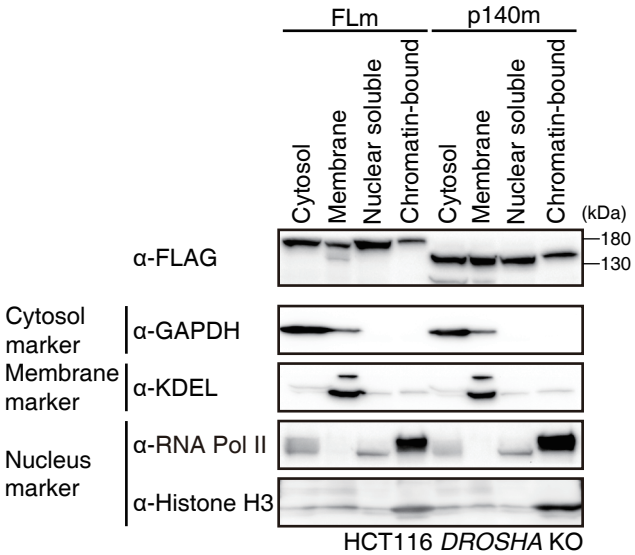

Figure 3.16 Subcellular fractionation and Western blotting analysis of cells expressing FLm or p140m.

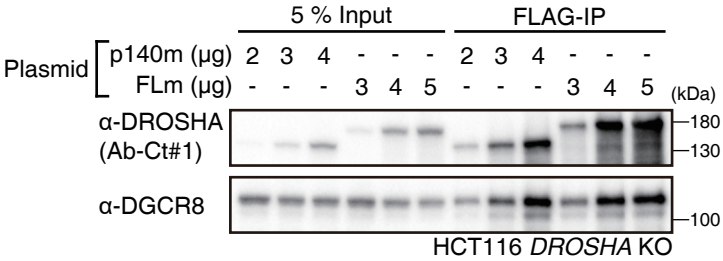

Figure 3.17 Coimmunoprecipitation of DGCR8 using p140m or FLm-expressing cells.

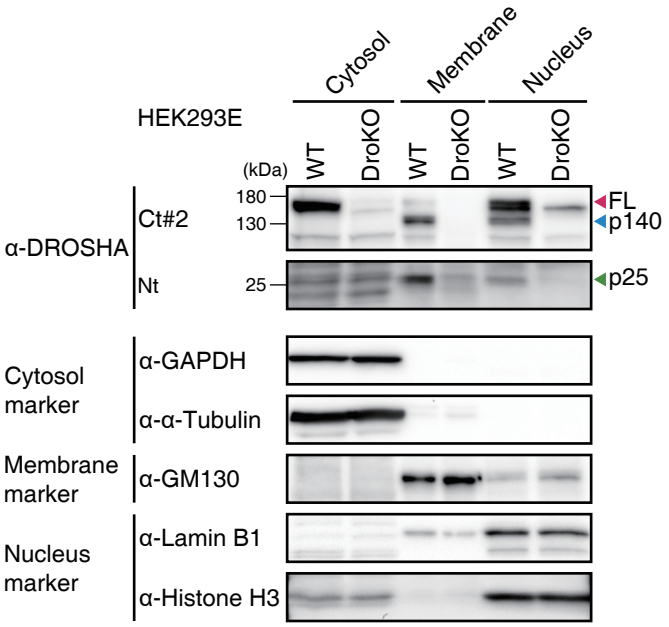

Figure 3.18 Confirmation of HEK293E *DROSHA* KO cells (DroKO) generated by CRISPR/Cas9 technology. Full-length DROSHA, p140, and p25 disappeared in the KO samples.

et al., 2019). Three independent sequencing libraries showed high reproducibility between biological replicates (Figure 3.19).

Interestingly, when rescued with p140m, some miRNAs were produced at significantly lower levels compared with the FLm-expressing condition (Figure 3.20 and 3.21). Noncanonical DROSHA-independent miRNAs were not affected or even modestly increased in p140m-expressing cells, as expected. Similar results were obtained in HCT116 and HEK293E cells, especially for canonical DROSHA-dependent miRNAs (Figure 3.22). For validation, I quantified several mature miRNAs (miR-19a, miR-15a, miR-25, miR-221, and miR-92a) and their pri-miRNAs by RT-qPCR (Figure 3.23). While mature miRNA levels were lower with p140m than with FLm, pri-miRNA levels showed the opposite patterns, indicating that the differences are attributable to the pri-miRNA-processing step. These results demonstrate that the PRD of DROSHA is required for the processing of a subset of miRNAs in cells.

The above observation appears to contradict our previous finding that the DROSHA △N390, which lacks the PRD as well as the RS-rich domain, is as active as the full-length protein in vitro, at least for pri-let-7a-1, pri-mir-16-1, and pri-mir-30a used in the studies (Han et al., 2004; Nguyen et al., 2015). To investigate further, I examined whether the PRD dependency can be demonstrated in vitro using pri-mir-186 and pri-mir-125a, which are PRD-dependent and PRD-independent, respectively, based on the rescue and sequencing data (Figure 3.24). I prepared these two representative pri-miRNAs as a minimal form of 125 nt, covering only the hairpin and its immediate surrounding sequences, by in vitro transcription and incubated them with varying concentrations of the Microprocessor complex composed of either FLm or p140m (Figure 3.24 and

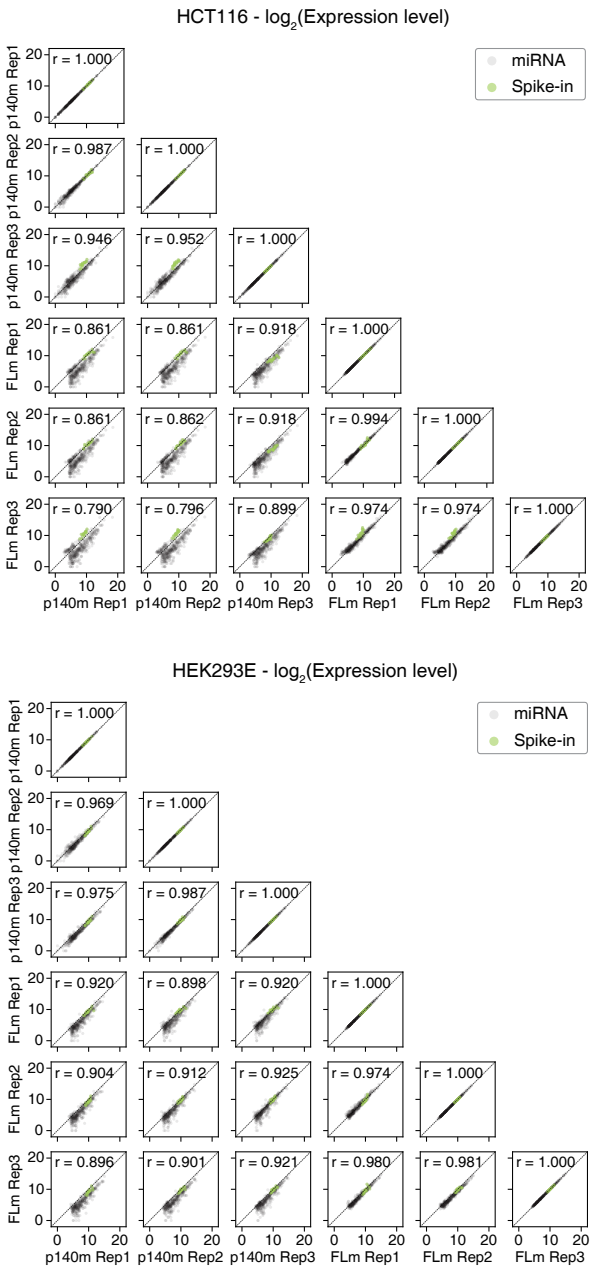

Figure 3.19 Reproducibility among three biological replicates. (r) Pearson correlation coefficient.

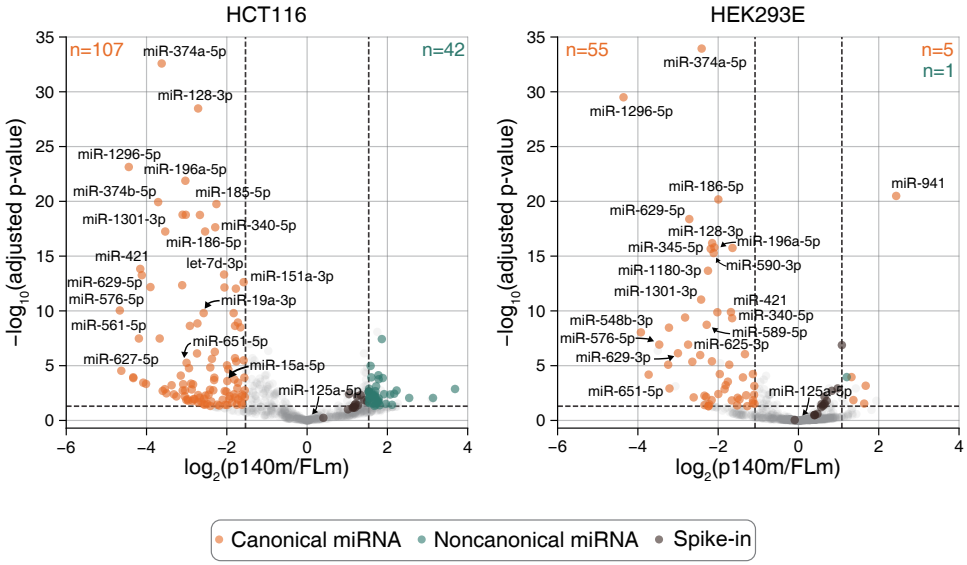

Figure 3.20 Differentially expressed miRNAs from HCT116 (*left*) or HEK293E (*right*). Vertical dotted lines were set based on the maximum fold changes of spike-in RNAs and indicate 2.9-fold and 2.1-fold enrichment in HCT116 and HEK293E, respectively. Horizontal dotted lines denote an adjusted P-value of 0.05 ($n = 3$). Only miRNAs that passed the cutoffs are colored. Numbers at the *top* corners indicate the numbers of significantly down-regulated or up-regulated miRNAs in each group. Fold changes and P-values for each miRNA are listed in Table 6.2 and 6.3.

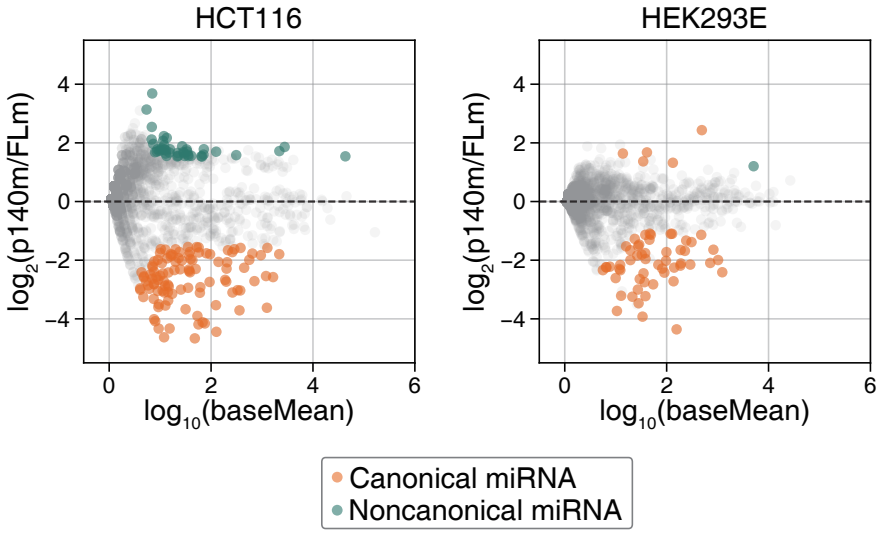

Figure 3.21 MA plots calculated from small RNA sequencing data. Colored miRNAs are differentially expressed miRNAs in Figure 3.20.

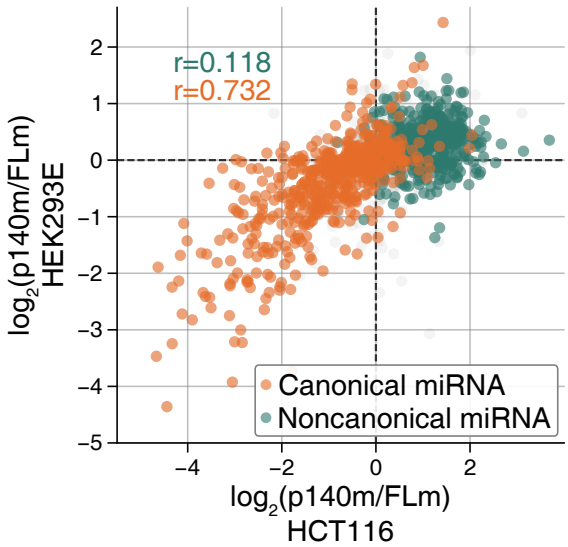

Figure 3.22 Comparison between $\log_2$ fold changes measured in two cell lines. In the case of canonical miRNAs, two values are highly correlated. (r) Pearson correlation coefficient.

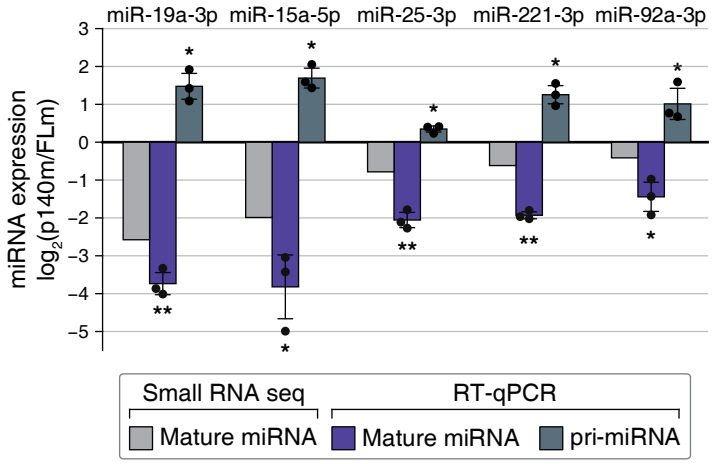

Figure 3.23 Relative expression levels of mature and pri-miRNAs for selected miRNAs. Validating the sequencing results (gray bars), mature miRNAs decreased when measured by qRT-PCR (purple bars). Pri-miRNA levels determine by RT-qPCR increased (dark blue), suggesting a defect in pri-miRNA processing. U6 snRNA and GAPDH were used as internal controls for mature miRNAs and pri-miRNAs, respectively. The abundance of pri-mir-92a-1 was measured because of the low expression of pri-mir-92a-2. The error bars indicate mean ± standard deviations ($n = 3$). Two tailed unpaired Student's t-test: (*) $P < 0.05$, (**) $P < 0.005$.

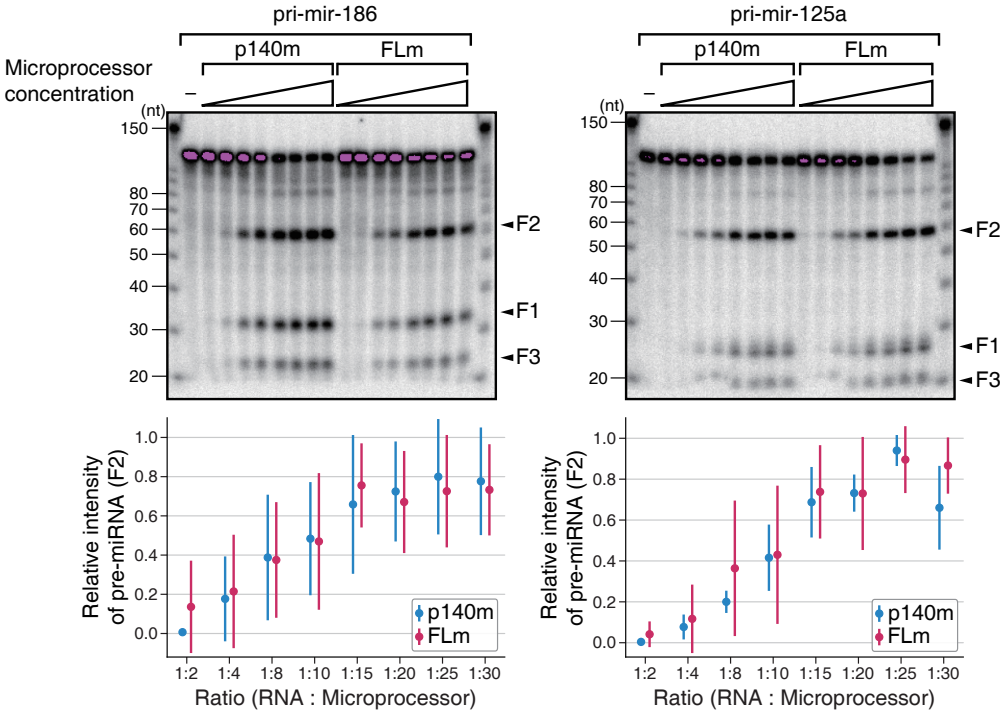

Figure 3.24 The PRD dependency cannot be recapitulated in vitro with the purified Microprocessor. (*Top*) Representative gel images from in vitro processing assays with Microprocessor composed of either recombinant p140 or full-length DROSHA mimic proteins (8–120 fmol). The $\log_2$(p140m/FLm) value of miR-186 is −2.541, and that of miR-125a is 0.165 according to the rescue and sequencing data. F2 corresponds to pre-miRNA, while F1 and F3 are the flanking fragments. (*Bottom*) Quantification of pre-miRNA (F2) band intensities from three independent replicates. The bars indicate mean ± standard deviations ($n = 3$) after minimum-maximum normalization.

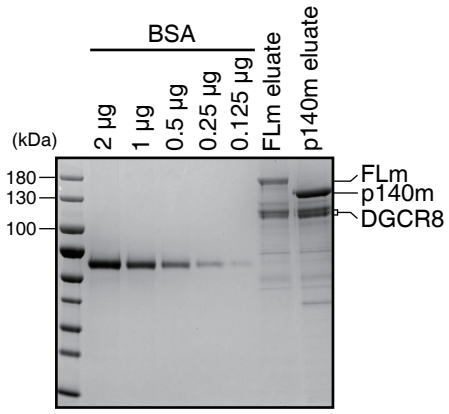

Figure 3.25 SDS-PAGE of purified Microprocessors made of either p140 or full-length DROSHA mimic. The gel was Coomassie stained.

3.25; Kim & Kim, 2022). In this assay, p140m processed both pri-miRNAs as efficiently as FLm (Figure 3.24). Thus, the purified Microprocessor and the 125-nt pri-miRNA transcripts cannot recapitulate the PRD dependency. This suggests that the PRD may required additional *trans*-acting factor(s) and/or *cis*-acting element(s) to exert its effect.

3.4 Investigating the factors contributing to PRD dependency

To identify the elements that determine the PRD dependency of certain pri-miRNAs, I analyzed various features of pri-miRNAs and their association with the PRD dependency. Initially, I examined four sequence motifs (basal UG, apical UGUG, flanking CNNC, and mGHG) known to facilitate pri-miRNA processing but could not find any significant association between these motifs and PRD

dependency (Figure 1.2 and 3.26; Auyeung et al., 2013; Fang & Bartel, 2015; Kwon et al., 2019). I also analyzed the secondary structures of pri-miRNAs but could not find substantial differences between the PRD-dependent and PRD-independent miRNAs (Figure 3.27; Reuter & Mathews, 2010). Moreover, there was no significant difference in processing efficiency between the two groups, as measured by high-throughput in vitro assays with mini-pri-miRNAs of 125 nt, which contain all the essential local elements (Figure 3.28; Kim et al., 2021). These observations suggest that the intrinsic properties of pri-miRNA hairpins that reside locally within 125 nt are unlikely to be the major determinants of the specificity of the PRD.

I then investigated the genomic arrangements of pri-miRNAs and found no difference in PRD dependency between "clustered" and "stand-alone" miRNAs (Figure 3.29). Moreover, the PRD dependency did not correlate with the depletion effects of ERH or SAFB2, which are known to facilitate the processing of clustered suboptimal miRNAs (Figure 3.30; Fang & Bartel, 2020; Hutter et al., 2020; Kwon et al., 2020). These results are consistent with the previous report that the N-terminal region of DROSHA is dispensable for cluster assistance (Fang & Bartel, 2020).

Interestingly, when I classified miRNAs based on their positions relative to the intron/exon structure, intronic miRNAs tended to be more strongly influenced by the PRD compared with exonic miRNAs (Figure 3.31). This trend was observed in both HCT116 and HEK293E cells (Figure 3.32), suggesting that the PRD may contribute to the maturation of intronic miRNAs.

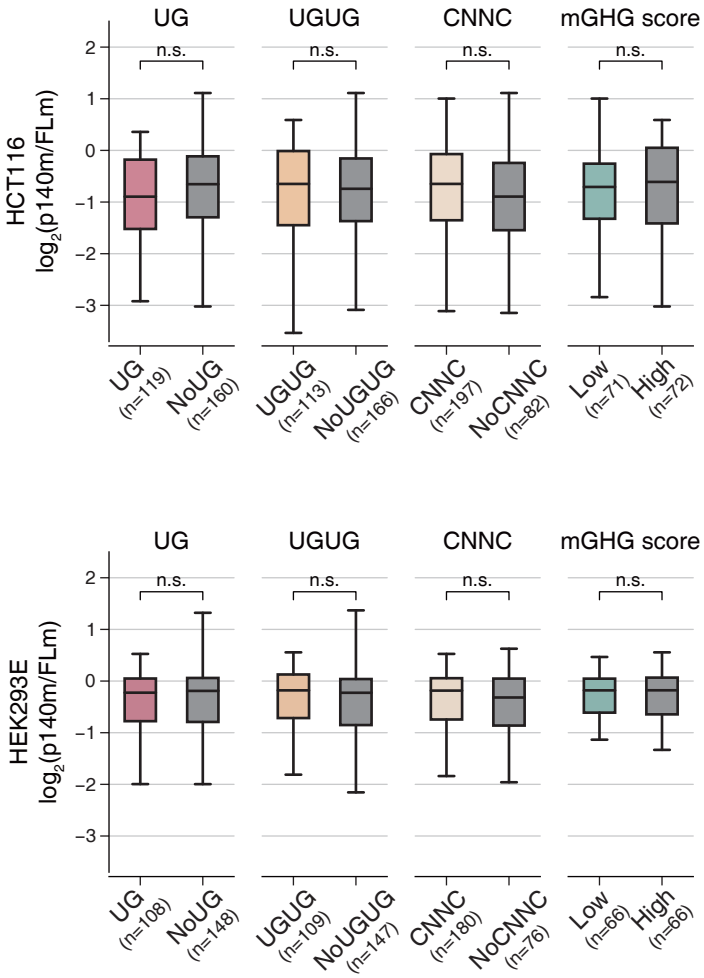

Figure 3.26 PRD dependency measured in HCT116 (*top*) and HEK293E (*bottom*) as quantified by $\log_2$ miRNA expression fold changes (p140m/FLm). miRNAs were grouped based on each sequence motif.

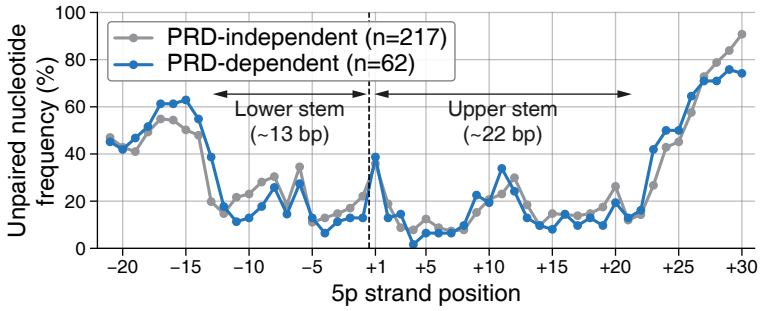

Figure 3.27 Average structures of the PRD-dependent and independent pri-miRNAs. The Y-axis shows the unpaired nucleotide frequency based on the 5p strand start site. Two groups were divided based on the sequencing result from HCT116. The secondary structure of each pri-miRNA was predicted using RNAstructure.

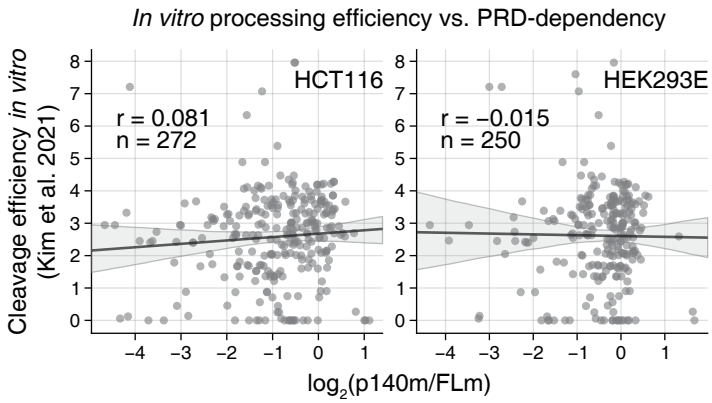

Figure 3.28 Comparisons of the PRD dependency and in vitro cleavage efficiency (Kim et al., 2021). (r) Pearson correlation coefficient.

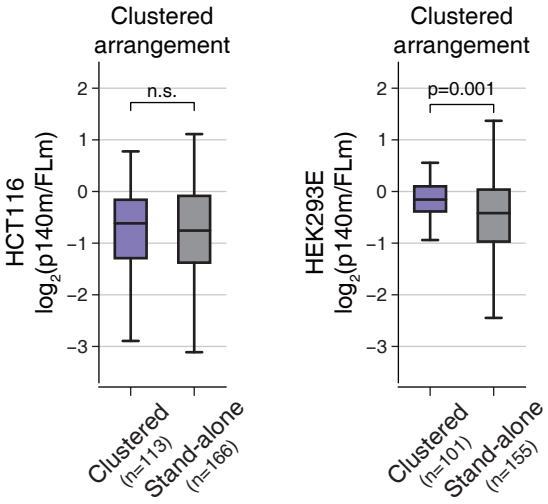

Figure 3.29 Clustered genomic arrangement and PRD dependency. PRD dependency measured in HCT116 (*left*) and HEK293E (*right*) as quantified by $\log_2$ miRNA expression fold changes (p140m/FLm). miRNAs were grouped based on clustered genomic arrangement.

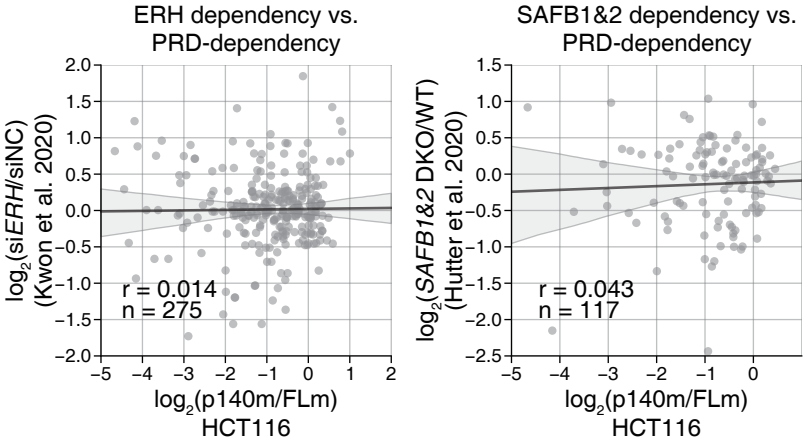

Figure 3.30 Comparisons of the PRD dependency and ERH (Kwon et al., 2020) or SAFB1/2 (Hutter et al., 2020) dependency. (r) Pearson correlation coefficient.

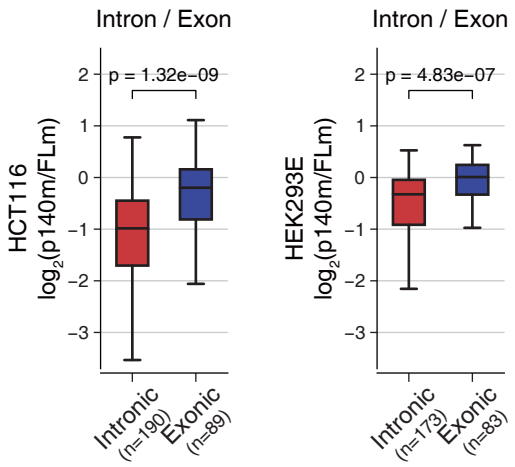

Figure 3.31 Intronic/exonic locations and PRD dependency. PRD dependency measured in HCT116 (*left*) and HEK293E (*right*) as quantified by $\log_2$ miRNA expression fold changes (p140m/FLm). miRNAs were grouped based on intronic/exonic locations.

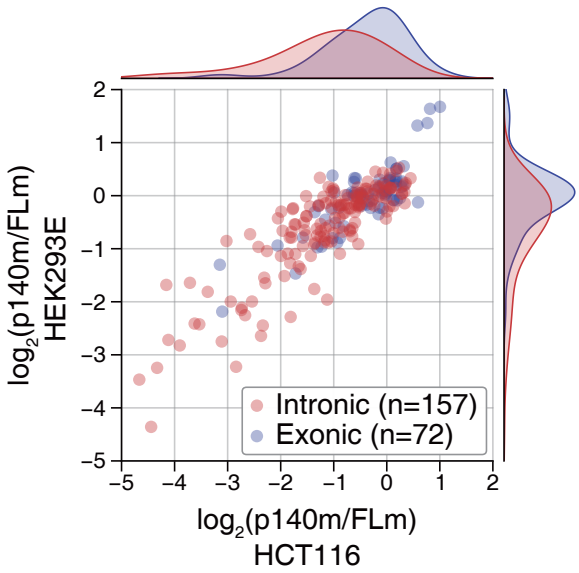

Figure 3.32 The PRD dependency of intronic and exonic miRNAs in HCT116 and HEK293E cells.

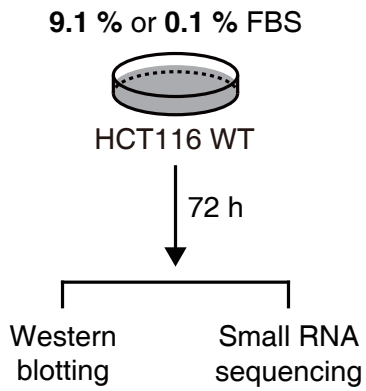

Figure 3.33 Analysis of DROSHA and miRNA expressions on HCT116 wild-type (WT) cells exposed to serum-starved conditions for 72 h.

To investigate the impact of changes in DROSHA isoform levels on miRNA biogenesis, I cultured HCT116 under serum-starved conditions, which are known to induce the production of a smaller isoform of DROSHA of ~130 kDa (Figure 3.33; Martinez et al., 2017). My results showed an increase in both the p140 and p25 isoforms, indicating that serum starvation triggers proteolytic cleavage of DROSHA (Figure 3.34). The full-length protein level was largely unaffected, possibly due to enhanced expression of DROSHA and/or differential stability of the isoforms under these conditions, resulting in a modest net increase in total DROSHA abundance. Small RNA sequencing data showed that exonic miRNAs and "PRD-independent miRNAs" were up-regulated when p140 level increased, unlike intronic miRNAs and "PRD-dependent miRNAs", which were largely insensitive to the up-regulation of p140 (Figure 3.35 and 3.36). This is consistent with the other data that PRD-dependent miRNAs cannot be processed efficiently by p140.

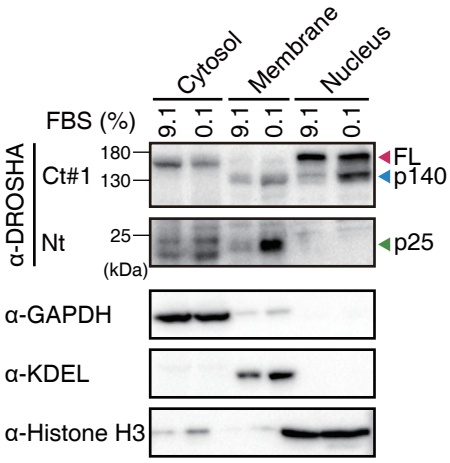

Figure 3.34 Serum deprivation induces accumulation of p140 and p25.

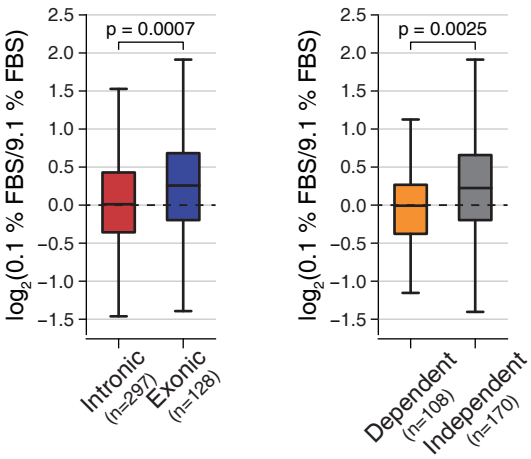

Figure 3.35 Log_2 fold changes of miRNA expression levels under normal or serum-starved conditions. miRNAs were grouped based on the intronic/exonic locations (left) or PRD dependency (*right*). Two-tailed Mann–Whitney U-test (n = 3).

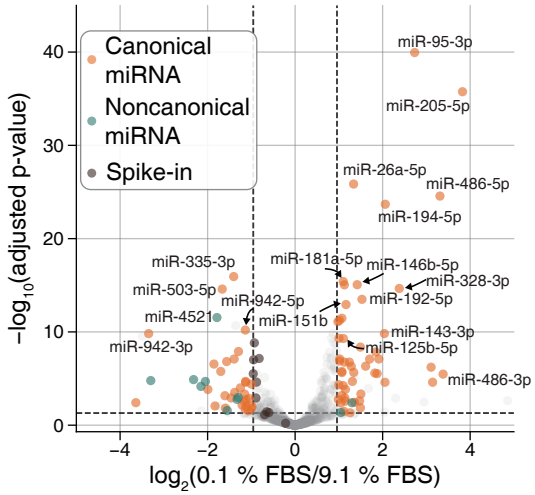

Figure 3.36 Differentially expressed miRNAs under normal and serum-starved conditions. The vertical dotted lines indicate a 2-fold enrichment, while the horizontal dotted line denotes a 0.05 adjusted *P*-value. Fold changes and *P*-values for each miRNA are listed in Table 6.4.

3.5 Intronic pri-miRNAs depend on the P-rich domain for processing

Because the endogenous miRNA abundance can be influenced by multiple factors and secondary effects, I constructed minigene plasmids that contain miRNA hairpins (of 125 nt) in either an intronic or exonic context (Figure 3.37). The plasmids were cotransfected with either FLm or p140m expression plasmids into HCT116 *DROSHA* KO cells (Figure 3.37 and 3.38). I selected miRNAs with low endogenous levels in HCT116 to reliably quantify miRNAs produced from the plasmids. When pri-mir-561 and pri-mir-627, which are originally intronic, were ectopically expressed from intronic constructs (Figure 3.39, red bars), their mature miRNA levels were substantially higher with FLm than with p140m. However, in exonic contexts, FLm only modestly induced miR-561 and miR-627 expression

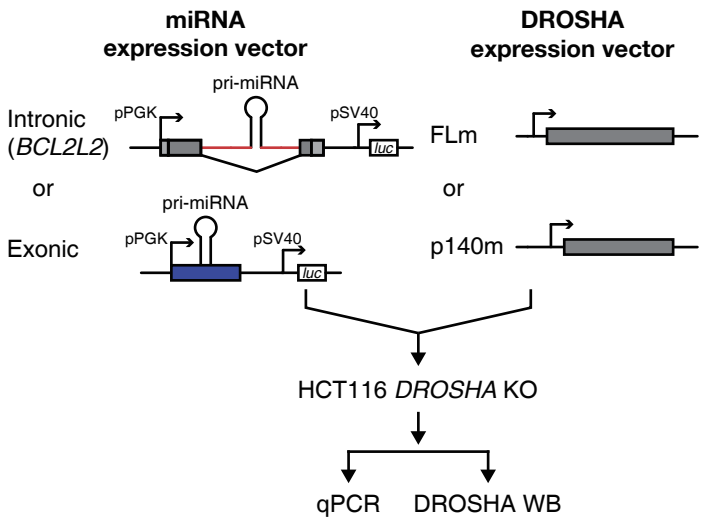

Figure 3.37 Schematics of intronic and exonic constructs. The intronic constructs include exon 3, intron 3, and exon 4 of the *BCL2L2* gene. A 125-nt pri-miRNA was inserted into the middle of the intron. In the exonic constructs, pri-miRNAs were inserted into multiple cloning sites downstream from the PGK promoter. Each construct was designed to express the *Renilla* luciferase (*luc*) from an independent promoter downstream from the miRNA cassette to normalize transfection efficiency.

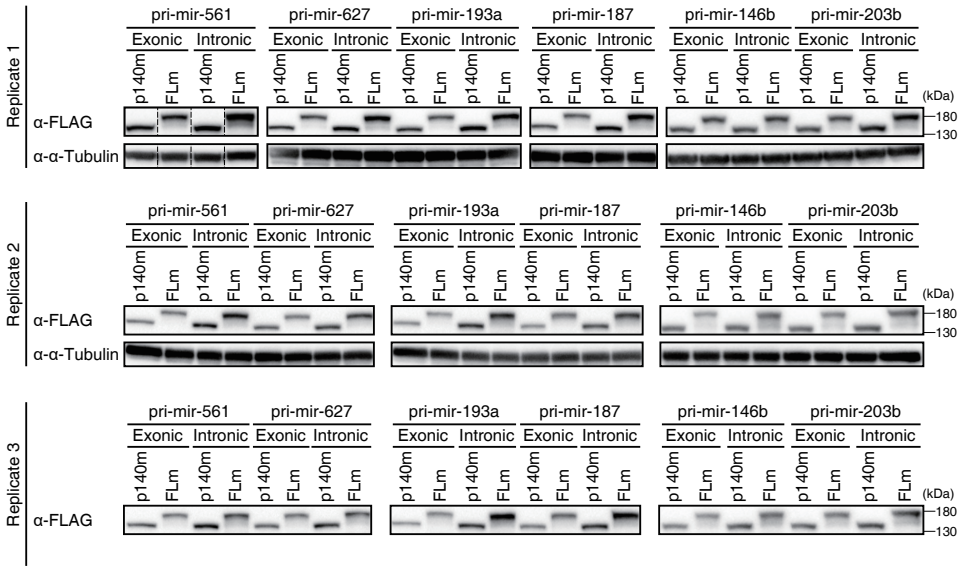

Figure 3.38 Western blotting to check the expression levels of p140m or FLm in the samples used in Figure 3.39 and 3.40.

compared with p140m (Figure 3.39, blue bars). These findings suggest that the PRD promotes intronic pri-miRNA processing preferentially.

To further validate this notion, I generated minigene constructs with different miRNAs (miR-187-3p, miR-203b-3p, miR-146b-5p, miR-193a-3p) that are originally exonic and independent of PRD (Figure 3.40 and 3.38). Remarkably when engineered into an intron, these miRNAs were produced more by FLm than by p140m (Figure 3.40, red bars). In contrast, in exonic contexts, the same hairpins were not influenced significantly by the PRD (Figure 3.40, blue bars). Thus, the PRD dependency was mainly determined by the surrounding context of the hairpin rather than by the hairpin sequences.

This phenomenon was also observed with additional constructs containing sequences from different genes (*WWP2*, *IGF2*, *CTDSP2*, and *FOCAD*) (Figure 3.41).

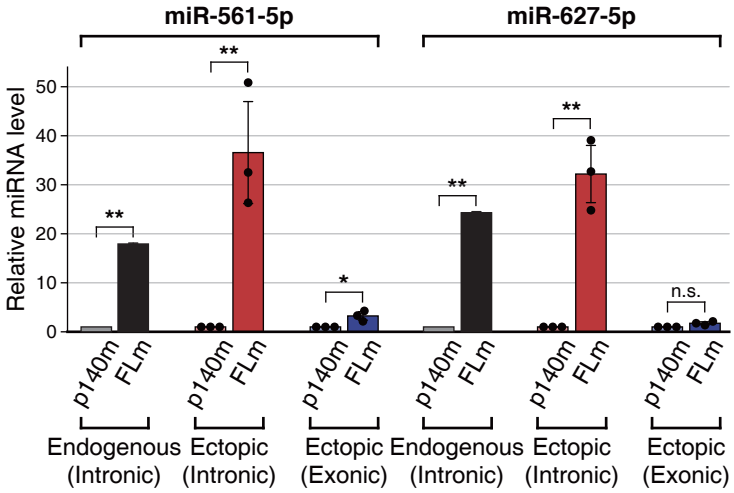

Figure 3.39 Relative expression levels of miRNAs transcribed from endogenous genomic loci (as determined by small RNA sequencing), intronic constructs, or exonic constructs (as determined by miRNA Taqman qPCR). Endogenous genomic locations of miRNA genes are intronic. All miRNAs become more dependent on the PRD in the intronic environment, regardless of the original genomic location. miRNA levels from the constructs were normalized to U6 snRNA and *Renilla* luciferase transcript. The miRNA levels in the p140m-expressing condition were set to 1. The error bars indicate mean ± standard deviations ($n = 3$). Two tailed unpaired Student's t-test: (*) $P < 0.05$, (**) $P < 0.005$, (n.s.) not significant.

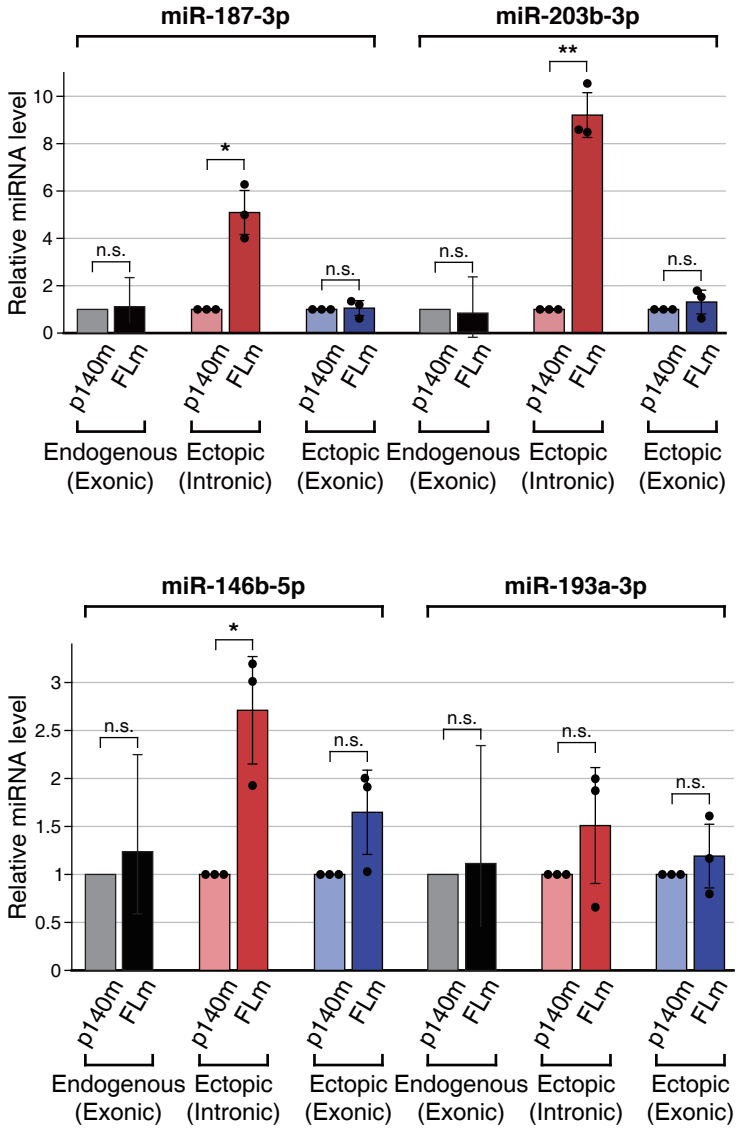

Figure 3.40 Relative expression levels of miRNAs transcribed from endogenous genomic loci (as determined by small RNA sequencing), intronic constructs, or exonic constructs (as determined by miRNA Taqman qPCR). Endogenous genomic locations of miRNA genes are exonic. All miRNAs become more dependent on the PRD in the intronic environment, regardless of the original genomic location. miRNA levels from the constructs were normalized to U6 snRNA and *Renilla* luciferase transcript. The miRNA levels in the p140m-expressing condition were set to 1. The error bars indicate mean ± standard deviations ($n = 3$). Two tailed unpaired Student's t-test: (*) $P < 0.05$, (**) $P < 0.005$, (n.s.) not significant.

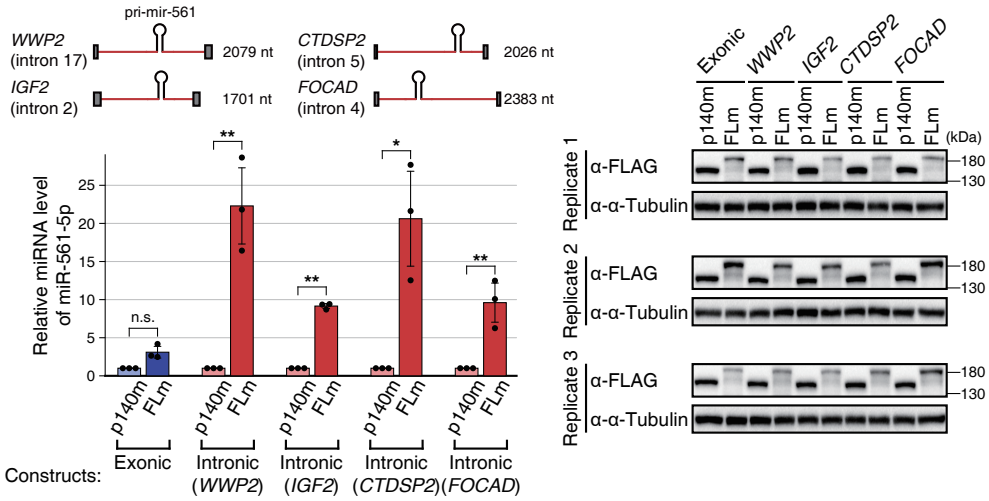

Figure 3.41 Intronic constructs with different backbones. The relative expression levels of miR-561-5p from different intronic constructs (*left*). The increased PRD dependency is not a backbone-specific phenomenon. The error bars indicate mean ± standard deviations ($n = 3$). Two tailed unpaired Student's t-test: (*) $P < 0.05$, (**) $P < 0.005$, (n.s.) not significant. The expression levels of p140 or full-length DROSHA mimics in the samples (*right*).

All of these heterologous intronic constructs exhibited PRD dependency. Additionally, to rule out the possibility that the length of the hosting transcript influences the PRD dependency, I made longer exonic constructs (*CHPF2*, *MIR3142HG*, and *MIR203bHG*) and a different intronic construct (*FOCAD*) of comparable lengths (Figure 3.42). This time, in addition to FLm, I also used WT DROSHA and the cleavage-deficient substitution mutant (197–198 NN→AA; Figure 3.12). None of the long exonic constructs showed PRD dependency, while the intronic construct exhibited strong PRD dependency (Figure 3.42). I made similar observations using another set of exon/intron constructs that contain pri-mir-203b (Figure 3.43), confirming that the length of the hosting transcript is not a significant factor and that exonic regions do not contain a determinant for PRD dependency.

Next, to investigate whether splicing is required for PRD's action, I introduced mutations to the 5′ splice site (changing GU to CA), 3′ splice site (changing AG to CU), branch point, and polypyrimidine tract (deletion) (Figure 3.44). RT-PCR analysis confirmed that these mutations indeed abrogated splicing (Figure 3.45). However, these splicing-defective mutants still showed PRD dependency, which is comparable with the wild-type construct (Figure 3.46), indicating that splicing events are not required for this regulation.

To identify the sequence determinant for PRD-mediated regulation, I generated a series of mutants with 120-nt deletions within the *BCL2L2* backbone (Figure 3.44). Some of the mutants exhibited impaired PRD responsiveness (Figure 3.47), indicating that the deleted regions may contribute to PRD-mediated regulation. In particular, the segment in the 3′ part of the intron spanning the △8 and △9 regions showed the strongest effect. To investigate whether this intronic segment could confer PRD dependency independently of splicing, I then

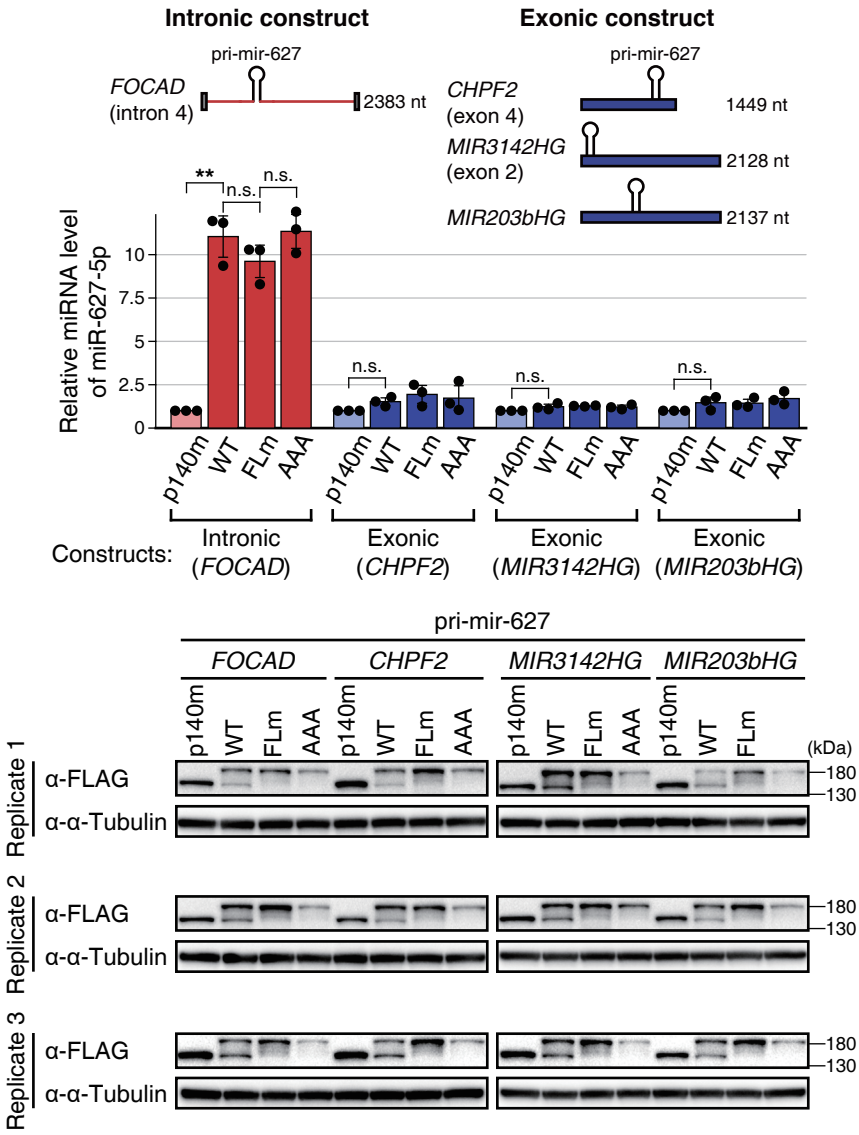

Figure 3.42 The relative expression levels of miR-627 transcribed from different intronic or exonic backbones (*top*). The number at the *right* of the schematic indicates the length of the corresponding intron or exon. The dependency is not affected by the length of the transcript. Normalization and statistical tests were performed in the same was as in Figure 3.39. Western blotting to verify DROSHA rescue levels (*bottom*).

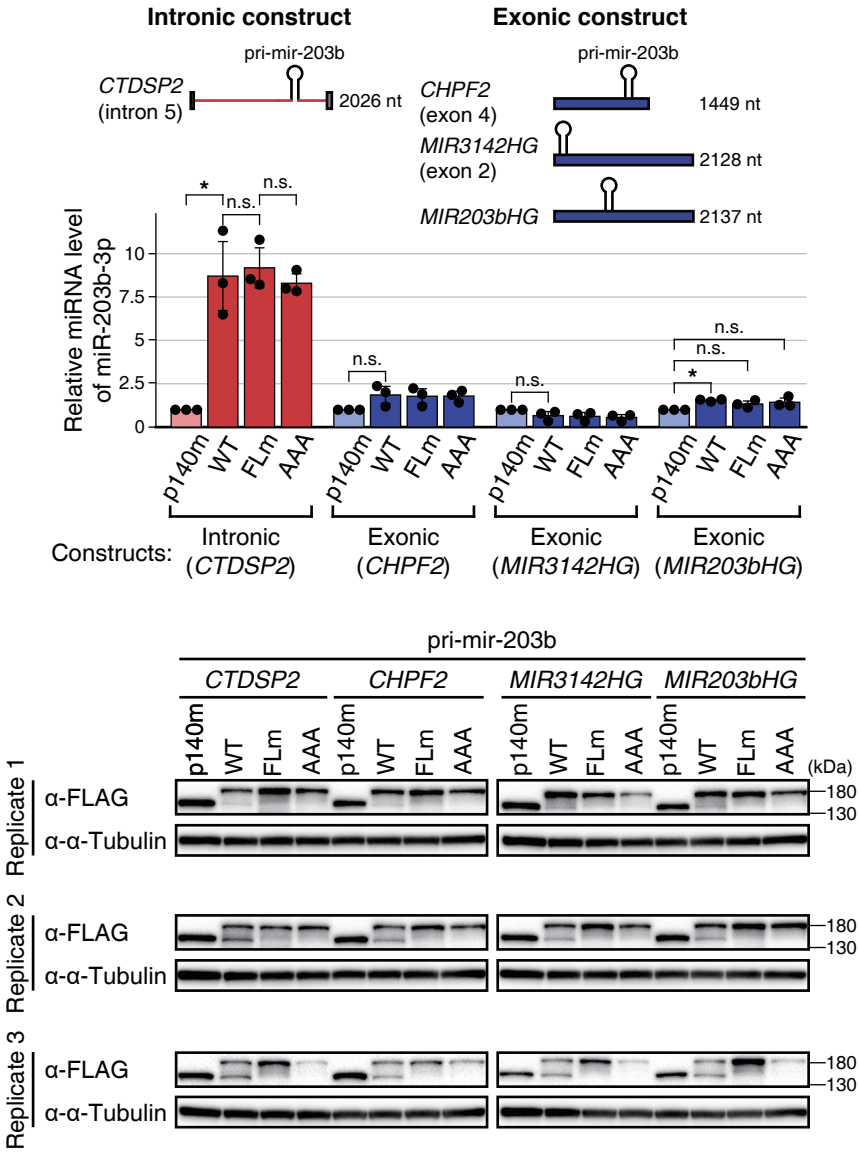

Figure 3.43 The relative expression levels of miR-203b transcribed from different intronic or exonic backbones (*top*). The number at the *right* of the schematic indicates the length of the corresponding intron or exon. The dependency is not affected by the length of the transcript. Normalization and statistical tests were performed in the same was as in Figure 3.39. Western blotting to verify DROSHA rescue levels (*bottom*).

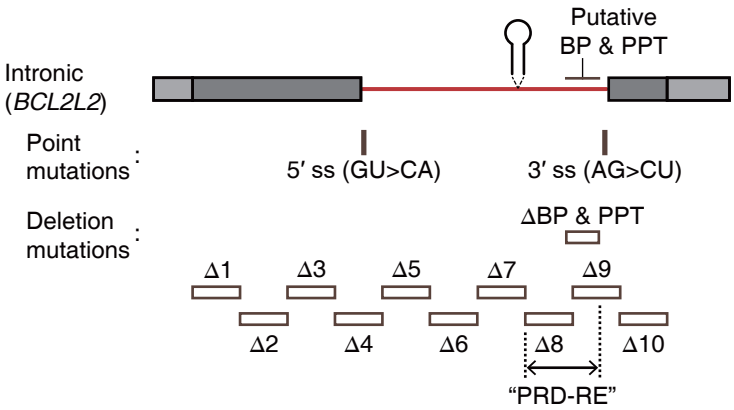

Figure 3.44 Point and deletion mutants of the *BCL2L2* intronic construct. Mutations were introduced into the 5′ /3′ splice site (ss), polypyrimidine tract (PPT), or branch point (BP). △1–△10 have a 120-nt length deletion. △4 includes the 5′ splice site, while △9 includes the 3′ splice site.

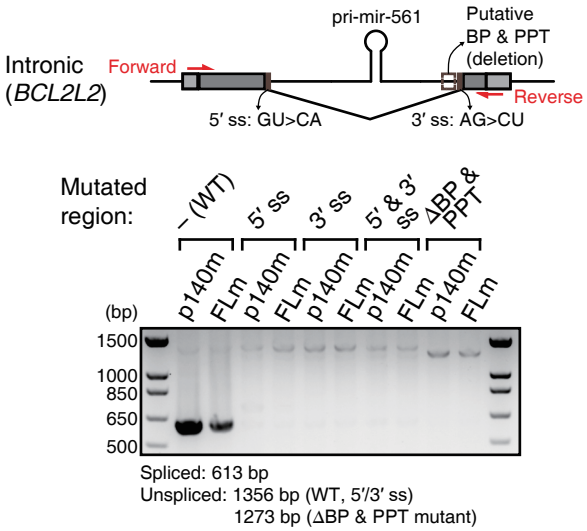

Figure 3.45 RT-PCR of splicing mutants used in Figure 3.46. The sequences of primers are listed in Table 2.6.

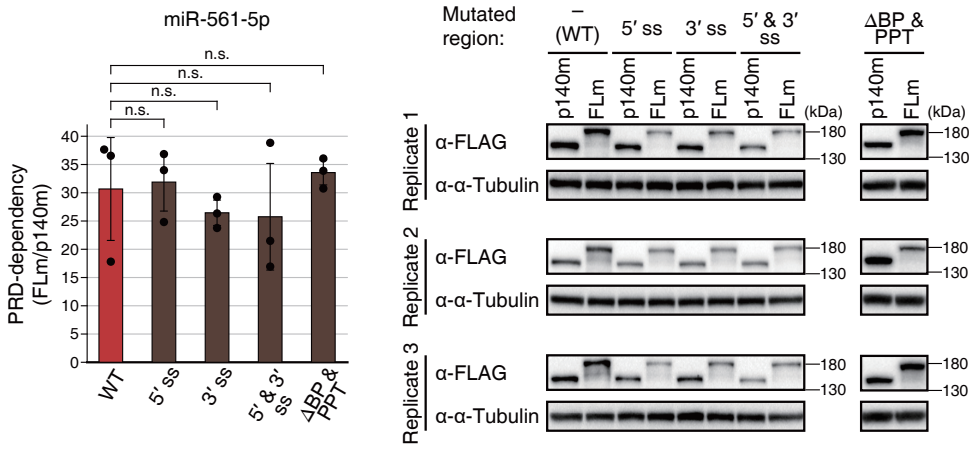

Figure 3.46 PRD dependency of intronic constructs with mutations in the core splicing elements (*left*). miRNA levels from exonic or intronic constructs were normalized to U6 snRNA and *Renilla* luciferase transcript. The error bars indicate mean ± standard deviations ($n = 3$). Two-tailed unpaired Student's t-test: (n.s.) not significant ($P = 0.05$). Western blotting to check the expression of p140m or FLm (*right*).

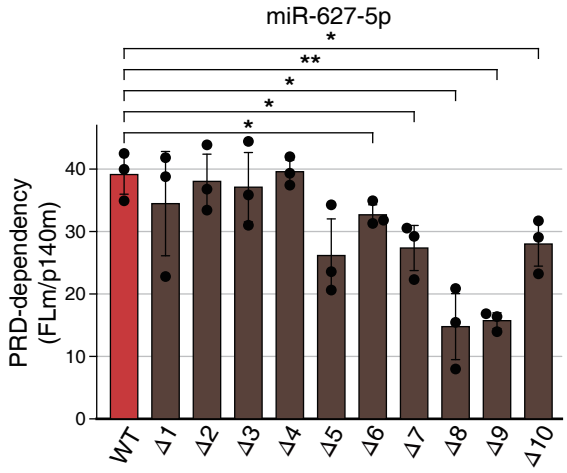

Figure 3.47 PRD dependency of deletion mutants △1–△10. Normalization and statistical tests were applied in the same way as in Figure 3.46. Two-tailed unpaired Student's t-test: ($*$) $P < 0.05$, ($**$) $P < 0.005$. The bars without an asterisk do not show statistically significant differences.

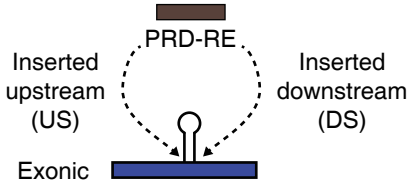

Figure 3.48 "PRD-RE" (spanning $\triangle 8$ and a part of $\triangle 9$ regions) was inserted upstream (US) of or downstream (DS) from the exonic construct.

transplanted the intronic segment (spanning the $\triangle 8$ and $\triangle 9$ regions except the splice site and downstream exon, referred to here as "PRD-RE") to an exonic construct upstream of or downstream from the miR-627 hairpin (Figure 3.48). Interestingly, the exonic constructs with PRD-RE insertion became dependent on the PRD, indicating that this intronic segment is at least partly responsible for the PRD dependency of the *BCL2L2* constructs (Figure 3.49). PRD-RE does not contain the $3'$ splice site, and, accordingly, transcripts containing PRD-RE were not spliced (Figure 3.50). These results imply that the PRD may interact with intron-enriched sequences independently of splicing.

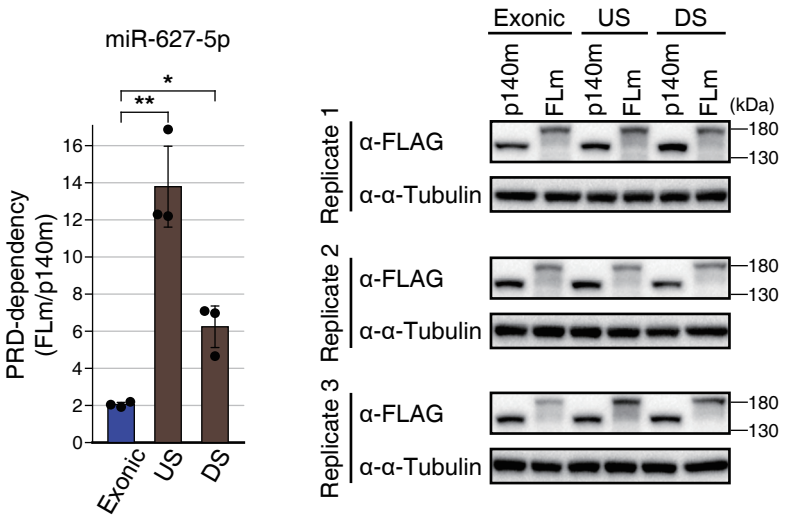

Figure 3.49 Measured PRD dependency of insertion mutants (*left*). Normalization and statistical tests were done in the same way as in Figure 3.47. Western blotting to check the expression of p140m or FLm (*right*).

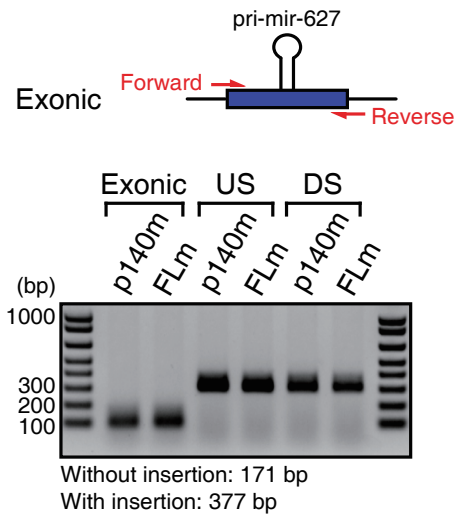

Figure 3.50 RT-PCR to detect splicing events for samples in Figure 3.49. Primer sequences are listed in Table 2.6.

3.6 Evolutionary conservation of the DROSHA PRD

The N-terminal sequences of human DROSHA (1–390 amino acids) are poorly conserved and do not align well with its homologs (Figure 1.3 and 3.51; Sievers et al., 2011; Waterhouse et al., 2009; Valdar, 2002). Nevertheless, the Drosha homologs (at least those in chordates) seem to preserve some common features in their N termini; they are intrinsically disordered with an unusually high proportion of proline residues (Figure 3.52 and 3.53). Human DROSHA contains 63 proline residues out of the first 200 amino acids (32%).

To examine the functionality of the N termini of DROSHA homologs, I generated hybrid DROSHA constructs by replacing the N terminus of human DROSHA with its counterpart from fish (*D. rerio*) or frogs (*X. tropicalis*) (Figure 3.54). After ectopic expression of these hybrid proteins in *DROSHA* KO HCT116 cells, I measured the level of miR-627-5p from minigene constructs (Figure 3.54). Despite the sequence divergence, the PRD from fish and frog homologs (dreN and xtrN) can replace the human counterpart (Figure 3.54). Thus, the proline-rich N terminus of DROSHA retains its function, at least in vertebrates, even without strict conservation in their primary sequences (Figure 3.51).

As proline richness is one of the most noticeable common features of this domain (Figure 3.52), I generated a mutant human DROSHA by substituting all prolines with alanines in the PRD (Figure 3.55). This mutant is strongly defective in processing the intronic construct (Figure 3.55), indicating that the proline residues in this disordered domain are indeed important for DROSHA's function, particularly in intronic pri-miRNA processing.

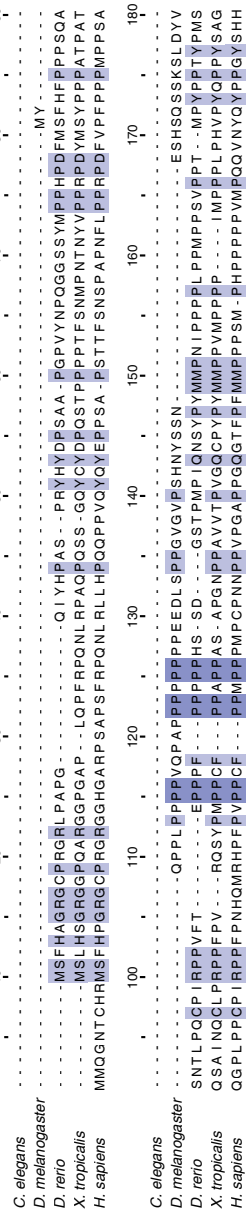

Figure 3.51 A multiple sequence alignment of the N-terminal parts of *C. elegans*, *D. melanogaster*, *D. rerio*, *X. tropicalis*, and *H. sapiens* (corresponding to 1–211 residues of human DROSHA) (Waterhouse et al., 2009). The blue color indicates the percent identity of each amino acid position.

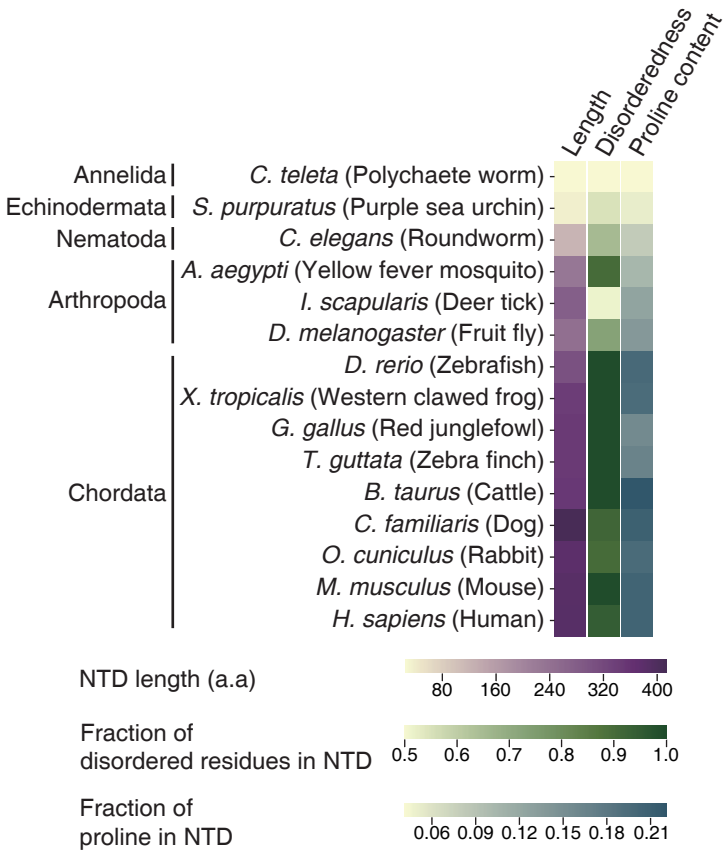

Figure 3.52 Comparison of the N-terminal part of Drosha homologs across species. The N-terminal part was defined by taking the upstream 391st amino acid of human DROSHA and the corresponding N-terminal parts from the homologs in other species. The disorderliness was predicted by SPOT-disorder-single (Hanson et al., 2018). UniProt protein IDs are listed in Table 6.5. (NTD) N-terminal domain.

Figure 3.53 The proportions of each amino acid in the N-terminal parts.

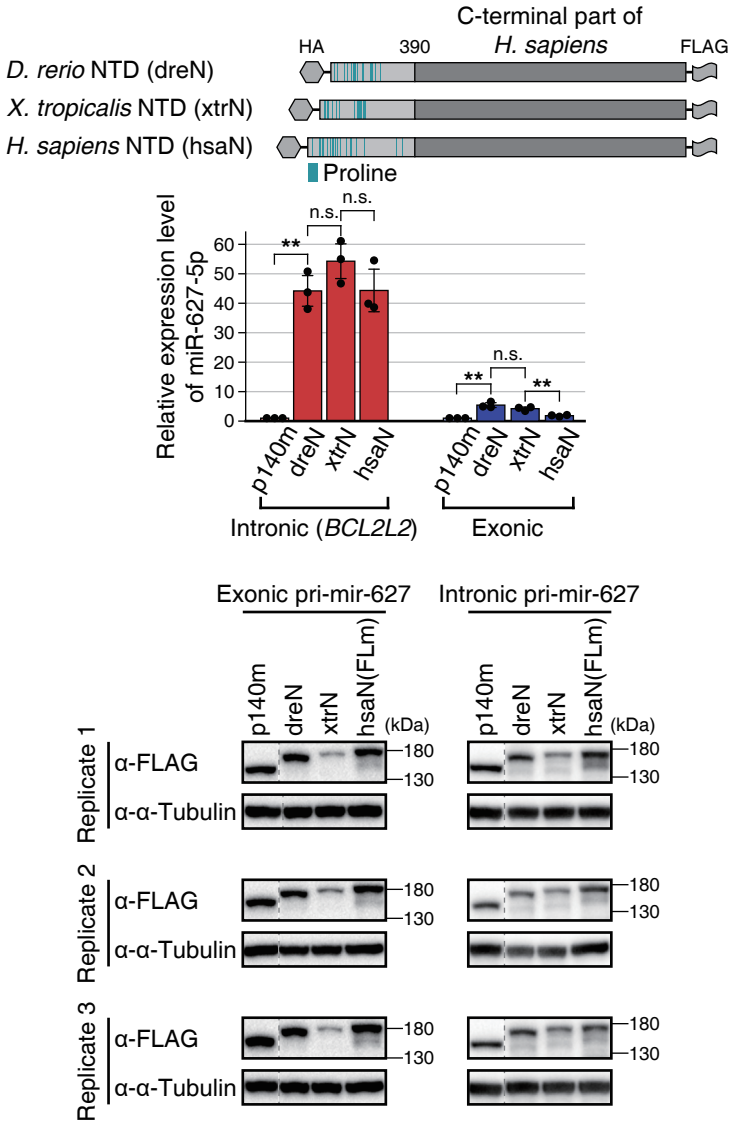

Figure 3.54 Hybrid DROSHA proteins with the N-terminal part from other species and the C-terminal part from human DROSHA. The exonic or intronic construct containing pri-mir-627 was transfected into HCT116 *DROSHA* KO cells together with one of the hybrid proteins (*top*). FLm was used for the *H. sapiens* NTD. miRNA levels were normalized to U6 snRNA and the *Renilla* luciferase transcript. The miRNA levels in the p140m-expressing condition were set to 1. The error bars indicate mean ± standard deviations ($n = 3$). Two-tailed unpaired Student's t-test: (**) $P < 0.005$, (n.s.) not significant ($P = 0.05$). The expressions of hybrid DROSHA proteins were detected by the FLAG antibody (*bottom*). The p140m samples were also analyzed on the same gels, but the lanes in between were omitted.

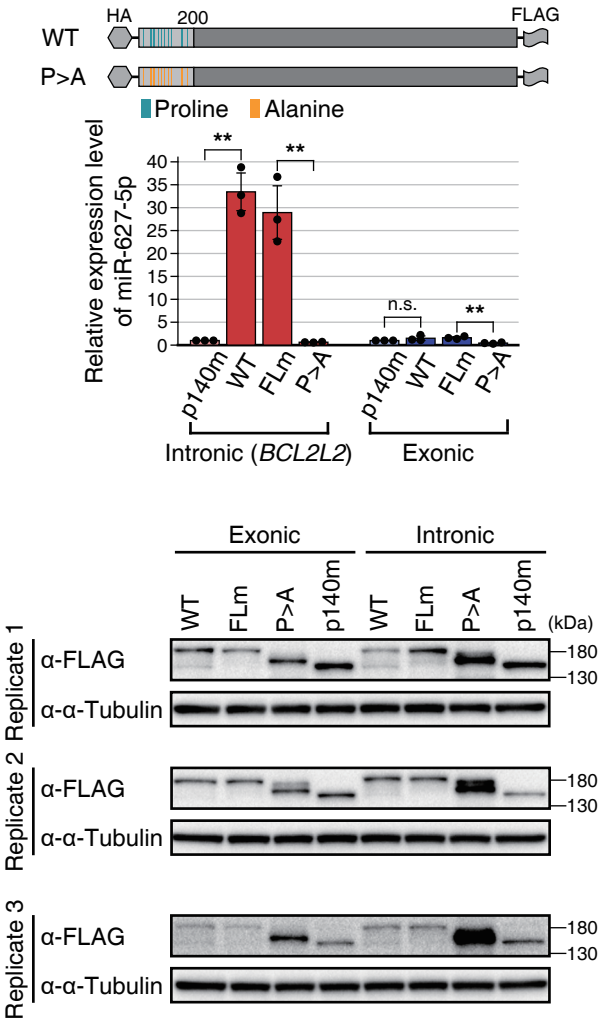

Figure 3.55 The P > A mutant in which all prolines within the first 1–200 amino acids were replaced with alanines was cloned. miRNA expression tests were done as Figure 3.54 (*top*). Western blotting to check the expression of DROSHA proteins (*bottom*).

4. Discussion

In this study, I have discovered the critical and conserved roles of the DROSHA PRD in the maturation of intronic miRNAs. The PRD has been overlooked because it is dispensable for cleavage activity in vitro and nuclear localization in cells (Figure 3.24; Han et al., 2004; Tang et al., 2010; Bellemer et al., 2012; Nguyen et al., 2015; Kwon et al., 2016). My current findings suggest that the PRD enables the Microprocessor to readily access the intron of nascent pri-miRNAs, facilitating the processing of intronic hairpins (Figure 4.1). This finding is in line with earlier observations that intronic pri-miRNA processing can occur cotranscriptionally and prior to splicing (Kim & Kim, 2007; Morlando et al., 2008; Ballarino et al., 2009; Kataoka et al., 2009). Our mutagenesis experiments on the *BCL2L2* minigene constructs suggest that the main *cis*-acting determinant(s) reside in the 3′ part of the intron, although I do not exclude a possibility that sequences outside this region also contribute to PRD dependency. DROSHA immunoprecipitation followed by liquid chromatography with tandem mass spectrometry (LC-MS/MS) provided a list of potential interactors of full-length DROSHA or p140 (Figure 4.2 and Table 6.6). However, I do not yet understand how the intronic motif(s) are recognized by the PRD and/or its protein interactors. Future studies could reveal which specific sequence(s) interact with the PRD, whether other PRD-responsive pri-miRNAs contain similar motif(s), and whether this interaction is direct or indirect through an RNA-binding protein(s).

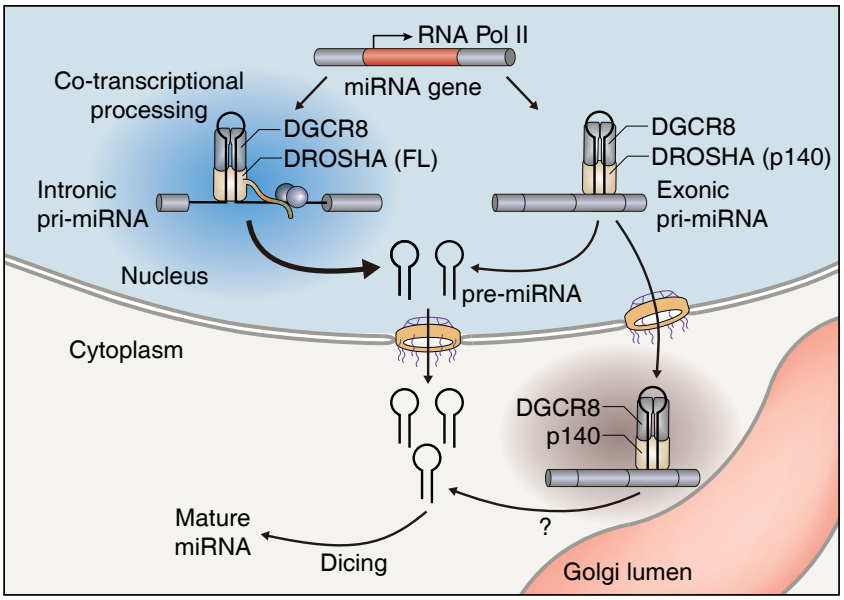

Figure 4.1 A model for the function of the DROSHA PRD in pri-miRNA processing. The PRD may interact with the intronic sequences directly or indirectly via an intron-binding protein(s), thereby assisting the Microprocessor to access the intronic miRNA hairpins.

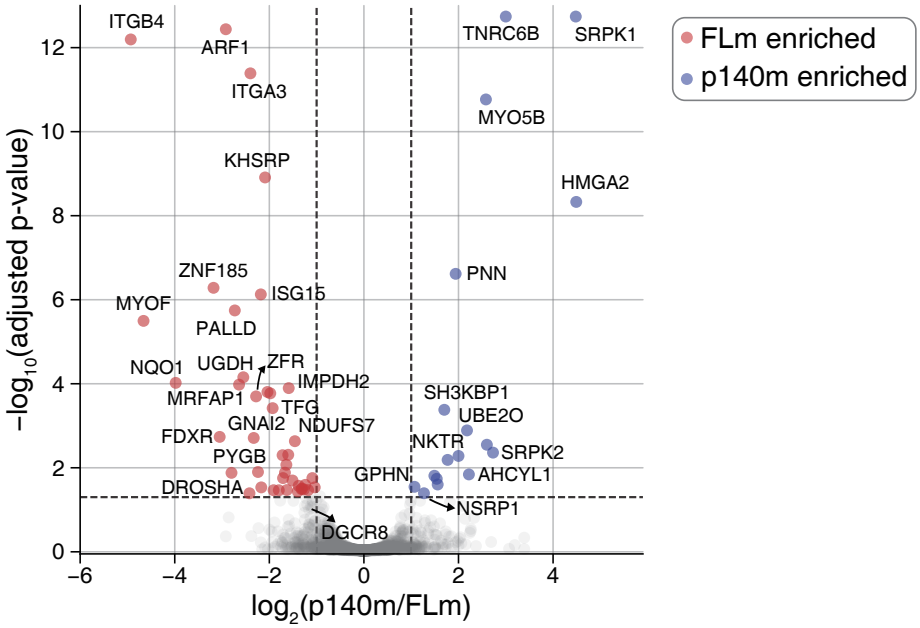

Figure 4.2 Mass spectrometry analysis to find possible interacting proteins of FLm and p140m. HCT116 *DROSHA* KO cell lines stably expressing either p140m or FLm were used for immunoprecipitation with FLAG antibody, followed by elution with FLAG peptide. Proteins were considered differentially enriched if the adjusted P-value was less than 0.05 and the absolute value of $\log_2$ fold change was greater than 1 ($n = 3$). The results are provided in Table 6.6.

This thesis has identified p140 as a major natural isoform of DROSHA, produced from proteolytic cleavage. It remains to be determined whether p140 is equivalent to the small isoforms of DROSHA described earlier (Gregory et al., 2004; Han et al., 2004; Grund et al., 2012; Yang et al., 2015; Dai et al., 2016, 2020; Link et al., 2016; Martinez et al., 2017). I found that p140 is impaired in intronic miRNA processing but can cleave exonic pri-miRNAs at a level comparable with that of the full-length protein (Figure 3.39 and 3.40). p140 may act post-transcriptionally on exonic pri-miRNAs in the nucleoplasm or in the cytoplasm, possibly near the Golgi apparatus (Figure 4.1). The production of p140 may control miRNA biogenesis, favoring PRD-independent miRNAs (Figure 3.33, 3.34, and 3.35). It is possible that p140 may provide a layer of miRNA regulation by escaping degradation via the E3 ubiquitin ligase NEDD4, which interacts with the PPxY motif of DROSHA (Jiang et al., 2021). This selective degradation of the full-length protein would alter the protein isoform ratio, resulting in changes to the miRNA profile. Additionally, p140 may have yet unknown function(s), possibly near the Golgi apparatus. It was previously proposed that DROSHA has an antiviral activity by impeding the RNA-dependent RNA polymerases (RdRps) of some positive stranded RNA viruses in the cytoplasmic membrane fraction (Aguado et al., 2017). Given that p140 is abundant in the membrane fraction and retains the region conferring steric hindrance on RdRps (Figure 3.1 and 3.3; Aguado et al., 2017), p140 may act effectively on viral RdRps. Alternatively but not mutually exclusively, p140 may bind and act on unknown cellular target RNAs localized near the membrane compartments. Further investigations will be needed to explore these intriguing hypotheses.

Our finding that the PRD is functionally conserved has evolutionary implications. Chordate Drosha homologs share several characteristics, such as length, disorderliness, and proline proportion (Figure 3.52). It was recently proposed that intrinsically disordered regions (IDRs) with shared molecular characteristics such as length, complexity, amino acid composition, and net charge can perform similar functions even if they do not exhibit detectable similarity in amino acid sequence alignments (Zarin et al., 2017, 2019). Such molecular features can be under evolutionary constraint (Zarin et al., 2017, 2019). It is noteworthy that the number of miRNA genes has increased during animal evolution (Fromm et al., 2015), and the recently emerged ones are overrepresented in intronic regions (Meunier et al., 2013). In our rescue sequencing experiments, I observed that rapidly evolving miRNAs tend to be processed more efficiently by the full-length protein than p140, while conserved miRNAs do not show such differences, which suggests that "young" miRNA genes are more dependent on PRD than the "established" ones (Figure 4.3; Pollard et al., 2010). The two groups—PRD-dependent and PRD-independent intronic miRNAs—do not significantly differ in their processing efficiency as measured in vitro with the 125-nt fragments (Figure 4.4; Kim et al., 2021), excluding the possibility that their PRD dependency is determined simply by their suboptimal local features. The mechanism underlying the differential PRD dependency should be investigated in detail in the future. However, it is tempting to speculate that the acquisition of the DROSHA PRD during evolution may have assisted the processing of emerging hairpins within introns so that the young miRNAs can establish a biological function and coevolve with their genomic contexts.

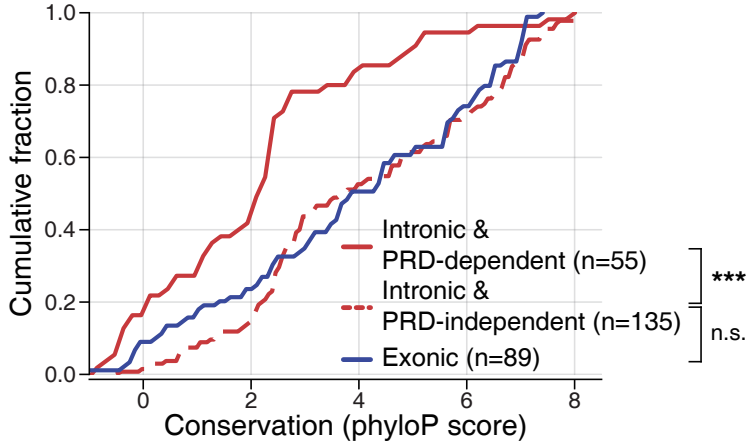

Figure 4.3 Conservation analysis of DROSHA-dependent canonical miRNAs. Conservation was quantified as the average of phyloP scores using the pre-miRNA sequence. Different miRNA groups were compared using the two-tailed Mann–Whitney U test: (∗∗∗) $P < 0.0005$, (n.s.) not significant.

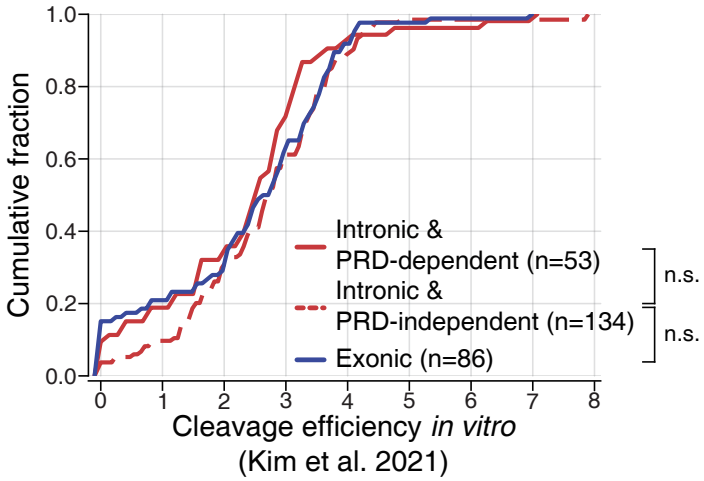

Figure 4.4 Differences in the cleavage efficiency measured in vitro DROSHA processing assay (Kim et al., 2021) between PRD-dependent or independent intronic/exonic miRNAs. The values from the two groups were compared using the two-tailed Mann–Whitney U test: (n.s.) not significant at $P = 0.05$.

5. Conclusion

miRNAs are small non-coding RNAs that play a pivotal role as guides in the process of RNA silencing. The biogenesis of miRNAs is tightly regulated, ensuring precise temporal and spatial control, and any dysregulation in this process has been associated with a wide range of cancers and diseases. Given that DROSHA initiates the biogenesis pathway and defines the terminus of an miRNA, it is crucial that Microprocessor efficiently and precisely recognizes and cleaves a pri-miRNA. Through previous structural and biochemical studies, the accurate processing of a pri-miRNA by the Microprocessor has been elucidated, along with the understanding of how RNA-binding proteins (RBPs) influence the biogenesis pathway. However, there has been a lack of extensive research conducted on the disordered domains of the Microprocessor. The work in this thesis has focused on clarifying the role of the disordered domain of DROSHA.

In this thesis, I report a unique DROSHA isoform called p140, which lacks a significant portion of the N-terminal disordered PRD. Through a comparative analysis of this isoform and the full-length DROSHA, I discovered that the PRD is necessary for the efficient processing of miRNAs embedded within introns. This finding was validated by the experiments with the minigene constructs. Along with the recent study suggesting the function of the disordered domain of DGCR8 (Kwon et al., 2020), my research sheds light on the unexpected contribution of disordered regions of the Microprocessor to miRNA biogenesis.

Despite the absence of the PRD, the p140 isoform retains most of its protein domains, including the catalytic center. Furthermore, it exhibits localizations not only in the nucleus but also in close proximity to membrane compartments. These unique features suggest that p140 may have the potential to interact with substrates other than pri-miRNAs, which are primarily processed in the nucleus. Exploring the noncanonical function of p140 in the cytoplasm will also be an interesting topic.

6. Long tables

Table 6.1 The sequence of cloning primers used in this study.

Name of primers	Sequence (5' to 3')	Note
[180,200)-F	GTAGTCCTCATTTCAGACATCTCCCTCCATACCCACTCCCAAAGG	
[180,200)-R	TGAAATGAGGACTACTAGGTGGGAAGTTGTGGTGAGAATAGCC	
[200,220)-F	GCTAATAACAGCAGGTCCCCAGAAAGGCTGAAACACTATGA	
[200,220)-R	CCTGCTGTTATTAGCACTGGGCAGGAAAGAACTAGGGTTGTTCTG	
[220,240)-F	AGAGGCATCGGTCCCTGGATCGGCGGGAGCGAGGCCGCAGTCCCG	
[220,240)-R	GGGACCGATGCCTCTCACCTCGTCTCTCACTGGGAGCCTTTGGGA	
[240,260)-F	GACAGCCGGTACAGATCTGATTATGACCGAGGGAGAACACCA	
[240,260)-R	TCTGTACCGGCTGTCTTGTCTCCCATGACTGTGATCTCGGTGCCT	
[260,280)-F	AGCAGAGAGCGAGAACGGGAGAGACACAGGCATCGAGACAAC	
[260,280)-R	TTCTCGCTCTCTGCTCCGTTCGTAGCTTCTCCTGTCGGGACT	
[170,180)-F	CCTCCCAGTTTTAATAGTTTCCAGAACAACCCTAGTTCTTTCCTG	
[170,180)-R	ATTAAAACTGGGAGGGTACTGATAATTAACCTGCTGCGGCAT	
[175,185)-F	GGCTATTCTCACTTCCAGAACAACCCTAGTTCTTTCCTGC	
[175,185)-R	GAAGTGAGAATAGCCCGGAGGGTACTGATAATTAACCTGCTG	
[180,190)-F	CCACCTAGTTCTTTCCTGCCCAGTGCTAATAACAGCAGTAGTCC	
[180,190)-R	GAAAGAACTAGGTGGGAAGTTGTGGTGAGAATAGCCCGGAGGGTA	
[185,195)-F	AATAGTAGTGCTAATAACAGCAGTAGTCCTCATTTCAGACAT	
[185,195)-R	ATTAGCACTACTATTAAAACTGGGAGGTGGGAAGTTGTGGTGAGA	
[190,200)-F	AACAACCCTAGTAGTCCTCATTTCAGACATCTCCCTCCATAC	
[190,200)-R	ACTACTAGGGTTGTTCTGGAAACTATTAAAACTGGGAGGTGGGAA	
[195,205)-F	CCCAGACATCTCCCTCCATACCCACTCCCAAAGGCTCCCAGT	
[195,205)-R	AGGGAGATGTCTGGGCAGGAAAGAACTAGGGTTGTTCTGGAA	
[200,210)-F	AGCTACCCACTCCCAAAGGCTCCCAGTGAGAGAAGGTCCCCA	
[200,210)-R	TGGGAGTGGGTAGCTGTTATTAGCACTGGGCAGGAAAGAACT	
[190-192]-AAA-F	AACCCTGCTGCCGCTCTGCCCAGTGCTAATAACAGCAGTAGTCCT	
[190-192]-AAA-R	AGCGGCAGCAGGGTTGTTCTGGAAACTATTAAAACTGGGAGGTGG	
[193-195]-AAA-F	TCTTTCGCTGCCGCTGCTAATAACAGCAGTAGTCCTCATTTC	
[193-195]-AAA-R	AGCGGCAGCGAAAGAACTAGGGTTGTTCTGGAAACTATTAAAACT	
[196-198]-AAA-F	GCTGCCGCTAGCAGTAGTCCTCATTTCAGACATCTCCCTCCATAC	
[196-198]-AAA-R	ACTGCTAGCGGCAGCACTGGGCAGGAAAGAACTAGGGTTGTTCTG	
new-[199-201]-AAA-F	CCAGTGCTAATAACGCTGCCGCTCCTCATTTCAGACATCTCCCT	
new-[199-201]-AAA-R	GTTATTAGCACTGGGCAGGAAAGAACTAGG	
pmirGLO-F2	TTCTAGTTGTTTAAACGAGCTCGCTAGCCTCGAGTCTAGA	
pmirGLO-R2	GGTGGCTTTACCAACAGTACCGGATTGCCAAGCTTGGGCT	
miR-561-F	GTACTGTTGGTAAAGCCACCTTGAAACTTCATCCACCAGTC	
miR-561-R	GCTCGTTTAAACAACTAGAAATAGAAATAAGGATAGCCATCCATG	
miR-627-F	GTACTGTTGGTAAAGCCACCTTACTTATTACTGAATTACTTATTACTGGTAGTG	
miR-627-R	GCTCGTTTAAACAACTAGAAGCTTATGCCCATTAGTAGTATTTCTT	
miR-193a-F	GTACTGTTGGTAAAGCCACCCACCCCGAACTCCGAGGATG	
miR-193a-R	GCTCGTTTAAACAACTAGAAAGGACCGGGGAGAAGACGCT	
miR-187-F	GTACTGTTGGTAAAGCCACCTCGGGCTCACCATGACACAG	
miR-187-R	GCTCGTTTAAACAACTAGAAAAGCGGAGCAGGCTCTGCTG	
miR-146b-F	GTACTGTTGGTAAAGCCACCCAGGCTGAAAGAACTTTGGC	
miR-146b-R	GCTCGTTTAAACAACTAGAACACGGCCTTGGCATTGATGT	
miR-203b-F	GTACTGTTGGTAAAGCCACCCTCCGTCGCTGTCGCCGCGC	
miR-203b-R	GCTCGTTTAAACAACTAGAACGAACCGACGGTGTTGGGGA	
BCL2L2-WT-backbone-F2(new)	GAATTCACTGGAGGCAGAGTGGGCAGATGAACCAGTCTCT	
BCL2L2-WT-backbone-R2(new)	TCCATCCTTTCCTTGGCGAAAAATTCTGCTCAGAACTAGC	
BCL2L2-miR-561-F3(new)	TTCGCCAAGGAAAGGATGGATTGAAACTTCATCCACCAGT	
BCL2L2-miR-561-R3(new)	ACTCTGCCTCCAGTGAATTCATAGAAATAAGGATAGCCATCCAT	
BCL2L2-5M-F	GGCTGGCAAAGAAGCTTCTCAATTGCCG	
BCL2L2-5M-R	GAAGCTTCTTTGCCAGCCCCCACTGCTGTGGA	
BCL2L2-3M-F	CCCACCTGCGGAGTTCACAGCTCTATACG	
BCL2L2-3M-R	GTGAACTCCGCAGGTGGGAGAGAAGGGAAGCAG	
561-Mut9.2-F	ACAGGCGGAGTTCACAGCTCTATACG	BP&PPT mut
561-Mut9.3-R	GAGCTGTGAACTCCGCCTGTCCAGTTCCATCCACTGCGAGCAC	BP&PPT mut
pmirGLO-F	TTCTAGTTGTTTAAACGAGCTCG	

Table 6.1 (continued from the previous page)

pmirGLO-R	GGTGGCTTTACCAACAGTACCG	
BCL2L2_exon3_F	GTACTGTTGGTAAAGCCACCATGGCGACCCCAGCCTCGGC	
BCL2L2_exon4-R	GCTCGTTTAAACAACTAGAATCACTTGCTAGCAAAAAAGGCCC	
BCL2L2-miR-627-F3	TTCGCCAAGGAAAGGATGGATTACTTATTACTGAATTACTTATTACTGGTAGTGAG	
BCL2L2-miR-627-R3	ACTCTGCCTCCAGTGAATTCGCTTATGCCCATTAGTAGTATTTCTTATT	
BCL2L2-miR-193a-F2	TTCGCCAAGGAAAGGATGGACACCCCGAACTCCGAGGATG	
BCL2L2-miR-193a-R2	ACTCTGCCTCCAGTGAATTCAGGACCGGGGAGAAGACGCT	
BCL2L2-miR-187-F2	TTCGCCAAGGAAAGGATGGATCGGGCTCACCATGACACAG	
BCL2L2-miR-187-R2	ACTCTGCCTCCAGTGAATTCAAGCGGAGCAGGCTCTGCTG	
BCL2L2-146b-F	TTCGCCAAGGAAAGGATGGACAGGCTGAAAGAACTTTGGC	
BCL2L2-146b-R	ACTCTGCCTCCAGTGAATTCCACGGCCTTGGCATTGATGT	
WT-203b-long-F	TGCGCTACAGAACTGTTGAACTGTTAAGAACCACTGGACCCAGCGCGCGAGTCCCCAACACCGTCGGT TCGGAATTCACTGGAGGCAGAGT	
WT-203b-long-R	AACAGTTCTGTAGCGCAATTGTGAAATGTTTAGGACCACTAGACCCGGCGGGCGCGGCGACAGCGACG GAGTCCATCCTTTCCTTGGCGAA	
WWP2-exon17-F	GTACTGTTGGTAAAGCCACCATCATGAACATGAAACCCTATGACC	
WWP2-intron17-R	TGGAGAGGAGGTCACCACGGAAAAAAGGAACATC	
WWP2-561-F	CCGTGGTGACCTCCTCTCCATTGAAACTTCATCCACCAGTCC	
WWP2-561-R	CCAGTCCCCAGCTGCTGGGCATAGAAATAAGGATAGCCATCCATGG	
WWP2-intron17-F	GCCCAGCAGCTGGGGACTGGCC	
WWP2-exon18-R	GCTCGTTTAAACAACTAGAACATGGCGATGAATCTGCCTATAA	
IGF2-exon2-F	GTACTGTTGGTAAAGCCACCACACCAATGGGAATCCCAATGGGG	
IGF2-intron3-R	GGGGCTCCACCTTGGGGTGCCAAAG	
IGF2-561-F	GCACCCCAAGGTGGAGCCCCTTGAAACTTCATCCACCAGTCC	
IGF2-561-R	TAGGAGGCTGGAGGGGCCCAATAGAAATAAGGATAGCCATCCATGG	
IGF2-intron3-F	TGGGCCCCTCCAGCCTCCTAGGTG	
IGF2-exon3-R	GCTCGTTTAAACAACTAGAACGGAAGCACGGTCGGAGGGGTC	
CTDSP2-exon5-F	GTACTGTTGGTAAAGCCACCCCAATCAACAATGCTGACTTCATAGT	
CTDSP2-intron5-R	TGTCCAGGTCATGATTAGGTAATGAATTG	
CTDSP2-561-F	ACCTAATCATGACCTGGACATTGAAACTTCATCCACCAGTCC	
CTDSP2-561-R	CAGGAAGAAGCGCACACACCATAGAAATAAGGATAGCCATCCATGG	
CTDSP2-intron5-F	GGTGTGTGCGCTTCTTCCTGAGCCAG	
CTDSP2-exon6-R	GCTCGTTTAAACAACTAGAACTTGGCCAGGCTGGCAGTGAAGAGAAC	
FOCAD-exon4-F	GTACTGTTGGTAAAGCCACCAAGCTGCACACATACATGTAAGAGAAG	
FOCAD-intron4-R	TCCAAGGTGCTGTATGTTGTTAAGTC	
FOCAD-561-F	ACAACATACAGCACCTTGGATTGAAACTTCATCCACCAGTCC	
FOCAD-561-R	GAATAGTATCCTCCAAGCCTATAGAAATAAGGATAGCCATCCATGG	
FOCAD-intron4-F	AGGCTTGGAGGATACTATTCACAGTT	
FOCAD-exon5-R	GCTCGTTTAAACAACTAGAACTGATTTGTAGATTGGTGAATCTTTTCTG	
FOCAD-627-long-F	GGAGGTGGTTGTTTTCCTCCTCTTTTCTTTGAGACTCACTACCAATAATAAGAAATACTACTAATGGG CATAAGCAGGCTTGGAGGATACTATTCACAG	
FOCAD-627-long-R	AGGAGGAAAACAACCACCTCCTCTTTTCTTAGAGACTCACTACCAGTAATAAGTAATTCAGTAATAAG TAATCCAAGGTGCTGTATGTTGTTAA	
CTDSP2-203b-long-F	AATTGCGCTACAGAACTGTTGAACTGTTAAGAACCACTGGACCCAGCGCGCGAGTCCCCAACACCGTC GGTTCGGGTGTGTGCGCTTCTTCCTGAGCCAG	
CTDSP2-203b-long-R	AACAGTTCTGTAGCGCAATTGTGAAATGTTTAGGACCACTAGACCCGGCGGGCGCGGCGACAGCGACG GAGTGTCCAGGTCATGATTAGGTAATG	
CHPF2-exon4-F	GTACTGTTGGTAAAGCCACCGCTCAGATCCGGAACCTGAC	
CHPF2-exon4-R	GCTCGTTTAAACAACTAGAATTTGGCAGAAGACATGTTTAATAAC	
MIR3142-exon2-F	GTACTGTTGGTAAAGCCACCGGCTGGGACAGGCCTGGACTGCAA	
MIR3142-exon2-R	GCTCGTTTAAACAACTAGAATTGTCTTCAATAACTTTATTGTTGTAACCAAAC	
near203b-region-F	GTACTGTTGGTAAAGCCACCATTCGACCCTTTGCTGAGTCC	
near203b-region-R	GCTCGTTTAAACAACTAGAACCTTGGCTCCTGAGCACTTG	
CHPF2-F	AGAACTCTACCACCGCTGCCGC	
CHPF2-R	CAGCCCTCCGCAGAAGCCTG	
CHPF2-627-F	GGCTTCTGCGGAGGGCTGTTACTTATTACTGAATTACTTATTACTGGTAGTGAGTCTC	
CHPF2-627-R	CAGCGGTGGTAGAGTTCTGCTTATGCCCATTAGTAGTATTTCTTATTATTG	
CHPF2-203b-F	GGCTTCTGCGGAGGGCTGCTCCGTCGCTGTCGCCGCGC	
CHPF2-203b-R	CAGCGGTGGTAGAGTTCTCGAACCGACGGTGTTGGGGA	
MIR3142-F	TTCAGTCTGCTGAAGAGCTTGGAAG	
MIR3142-R	GCCTGTCCCAGCCGGTGGCT	
MIR3142-627-F	CCACCGGCTGGGACAGGCTTACTTATTACTGAATTACTTATTACTGGTAGTGAGTCTC	
MIR3142-627-R	GCTCTTCAGCAGACTGAAGCTTATGCCCATTAGTAGTATTTCTTATTATTG	
MIR3142-203b-F	CCACCGGCTGGGACAGGCCTCCGTCGCTGTCGCCGCGC	
MIR3142-203b-R	GCTCTTCAGCAGACTGAACGAACCGACGGTGTTGGGGA	

Table 6.1 (continued from the previous page)

203bnear-F	CCGAGCTGCGGAGAGAGGAGCCC	
203bnear-R	CGTCCCACGCGCGGCCTGGAGTCAGAGTCACA	
203bnear-627-F	CAGGCCGCGCGTGGGACGTTACTTATTACTGAATTACTTATTACTGGTAGTGAGTCTC	
203bnear-627-R	CCTCTCTCCGCAGCTCGGGCTTATGCCCATTAGTAGTATTTCTTATTATTG	
1_del1-120-F	GTACTGTTGGTAAAGCCACCCCGCTGCACCAAGCCATG	Mut #1
2_del121-240-F	GGGAGGGCCCAGCAGCTGACCAGGTCTCCGATGAACTTTTTC	Mut #2
2_del121-240-R	GTCAGCTGCTGGGCCCTCCCCG	Mut #2
3_del241-360-F	CAGCCCAACAACGCTTCACCCAAGTGCAGGAGTGGATGGT	Mut #3
3_del241-360-R	GGTGAAGCGTTGTTGGGCTGAG	Mut #3
4_del361-480-F	AGATGGAACCACTGGTGGGATCTCCAGGGGGAAGATGGGG	Mut #4
4_del361-480-R	TCCCACCAGTGGTTCCATCTCC	Mut #4
5_del481-600-F	ACATCCTTCTGCAAAGCTGGTCCAGGGCTGCCATGCAGTC	Mut #5
5_del481-600-R	CCAGCTTTGCAGAAGGATGTGC	Mut #5
6_del601-720-F	GAGATGCCTGGACTCTGCACGCGTGGGAGGTGGGGAGGAC	Mut #6
6_del601-720-R	GTGCAGAGTCCAGGCATCTCTC	Mut #6
7_del721-840-Insert-F	CTTTTTACATCTGAGTCATGTTACTTATTACTGAATTACTTATTACTGGTAGTGAGTCT	Mut #7
7_del721-840-Backbone-R	CATGACTCAGATGTAAAAAGTCCCT	Mut #7
7_del721-840-Backbone-F	GGCAGATGAACCAGTCTCTCAG	Mut #7
7_del721-840-Insert-R	GAGAGACTGGTTCATCTGCCGCTTATGCCCATTAGTAGTATTTCTTATTATTG	Mut #7
8_del841-960-F	AATTCACTGGAGGCAGAGTGTGGAACTCTTCCTCTCCTCTTCTCTC	Mut #8
8_del841-960-R	CACTCTGCCTCCAGTGAATTCG	Mut #8
9_del961-1080-F	GTGCTCGCAGTGGATGGAACGCCCTGGAGGAGGCGCGGCG	Mut #9
9_del961-1080-R	GTTCCATCCACTGCGAGCACTA	Mut #9
10_del1081-1200-F	CAGCTCTATACGGGGACGGGTTCTAGTTGTTTAAACGAGCTCGCTAGC	Mut #10
10_del1081-1200-R	CCCGTCCCCGTATAGAGCTGTG	Mut #10
#8#9-region-F	GGCAGATGAACCAGTCTCTCAGG	US/DS
#8#9-region-R	GGGAGAGAAGGGAAGCAGGAGA	US/DS
front-#8#9-F	TCCTGCTTCCCTTCTCTCCCTTACTTATTACTGAATTACTTATTACTGGTAGTGAGTCTCTAA	US
front-#8#9-R	GAGAGACTGGTTCATCTGCCGGTGGCTTTACCAACAGTACCGGA	US
back-#8#9-F	TCCTGCTTCCCTTCTCTCCCTTCTAGTTGTTTAAACGAGCTCGCTAGC	DS
back-#8#9-R	GAGAGACTGGTTCATCTGCCGCTTATGCCCATTAGTAGTATTTCTTATTATTG	DS
DroN-common-F	AAAGAGCCCGAGGAGACCATG	
DroN-common-R	CGAAGCTTGAGCTCGAGATCT	
DroN-dre-F	GATCTCGAGCTCAAGCTTCGATGTCTTTCCATGCTGGCCGT	
DroN-dre-R	ATGGTCTCCTCGGGCTCTTTGCTCCTGCTGGAGTTCACAG	
DroN-xtr-F	GATCTCGAGCTCAAGCTTCGATGTCTCTGCATTCAGGAAGAGG	
DroN-xtr-R	ATGGTCTCCTCGGGCTCTTTCTTCTCTTTAAAAGAAATGCTGGAC	
DRO(PtoA)-F	AGTCCTCATTTCAGACATCTCCC	
DRO(PtoA)-gBlock-F	GATCTCGAGCTCAAGCTTCGATGATGCAGGGAAACACATG	
DRO(PtoA)-gBlock-R	AGATGTCTGAAATGAGGACTACTGCTGTTATTAGCACTAGCCAG	

Table 6.2 DESeq2 output from small RNA sequencing of HCT116 *DROSHA* KO rescued with FLm or p140m.

mature	baseMean	log2FC	padj
hsa-let-7a-2-3p	52.4	-0.901	0.067
hsa-let-7a-3p	410.8	-0.089	0.740
hsa-let-7a-5p	15216.7	0.009	0.982
hsa-let-7b-3p	113.5	-0.584	0.076
hsa-let-7b-5p	3288.2	-0.136	0.692
hsa-let-7c-3p	0.7	-0.248	
hsa-let-7c-5p	86.7	-0.235	0.582
hsa-let-7d-3p	205.7	-2.069	0.000
hsa-let-7d-5p	2176.3	-1.795	0.000
hsa-let-7e-3p	19.7	-1.400	0.013
hsa-let-7e-5p	1016.3	-0.500	0.077
hsa-let-7f-1-3p	35.9	-2.316	0.000
hsa-let-7f-2-3p	47.6	-0.160	0.742
hsa-let-7f-5p	6602.4	-0.859	0.000
hsa-let-7g-3p	47.3	-0.355	0.479
hsa-let-7g-5p	4175.6	0.184	0.570
hsa-let-7i-3p	190.7	-1.379	0.000
hsa-let-7i-5p	7062.5	-0.967	0.000
hsa-miR-1-3p	0.7	-0.313	
hsa-miR-100-3p	73.5	-0.214	0.701
hsa-miR-100-5p	6033.7	-0.516	0.029
hsa-miR-101-3p	1746.6	-0.336	0.265
hsa-miR-101-5p	3.8	-0.071	0.959
hsa-miR-103a-2-5p	7.9	-0.548	0.563
hsa-miR-103a-3p	7589.8	-0.199	0.350
hsa-miR-105-5p	0.1	0.075	
hsa-miR-106a-5p	183.4	-0.373	0.354
hsa-miR-106b-3p	360.9	-0.598	0.035
hsa-miR-106b-5p	2614.4	-0.254	0.345
hsa-miR-107	769.0	-0.375	0.110
hsa-miR-10a-3p	135.8	-0.151	0.772
hsa-miR-10a-5p	4827.3	-0.455	0.194
hsa-miR-10b-3p	8.8	0.499	0.516
hsa-miR-10b-5p	470.3	0.035	0.912
hsa-miR-1178-3p	0.5	1.080	
hsa-miR-1179	1.0	0.172	
hsa-miR-1180-3p	187.8	-2.670	0.000
hsa-miR-1180-5p	6.0	-2.185	0.044
hsa-miR-1181	0.4	0.365	
hsa-miR-1185-1-3p	2.9	0.987	0.397
hsa-miR-1185-2-3p	1.4	0.860	
hsa-miR-1185-5p	0.3	0.517	
hsa-miR-1193	0.3	0.517	
hsa-miR-1197	0.3	0.517	
hsa-miR-1204	0.3	0.517	
hsa-miR-122-5p	4.0	0.763	0.453
hsa-miR-1224-3p	15.3	1.227	0.063
hsa-miR-1273a	0.1	0.075	
hsa-miR-1273c	0.9	-0.614	
hsa-miR-1273d	1.1	-1.620	
hsa-miR-1273e	2.0	0.547	
hsa-miR-1273h-5p	0.1	0.075	
hsa-miR-1275	140.0	1.730	0.002
hsa-miR-1276	2.2	-2.601	
hsa-miR-1277-3p	16.4	-0.691	0.447
hsa-miR-1277-5p	120.8	-0.652	0.328
hsa-miR-1278	0.9	-0.646	
hsa-miR-1279	0.1	0.075	
hsa-miR-128-1-5p	8.2	-2.675	0.008
hsa-miR-128-3p	708.7	-2.715	0.000
hsa-miR-1281	0.1	0.075	
hsa-miR-1283	3.5	0.470	0.673
hsa-miR-1284	0.6	-0.861	
hsa-miR-1285-3p	6.6	-2.387	0.019
hsa-miR-1285-5p	0.1	0.075	
hsa-miR-1286	3.2	-1.707	0.155
hsa-miR-1287-3p	3.6	-1.057	0.335
hsa-miR-1287-5p	34.1	-1.348	0.003
hsa-miR-1288-3p	0.1	0.075	
hsa-miR-1289	1.3	1.334	
hsa-miR-129-1-3p	0.1	0.075	

mature	baseMean	log2FC	padj
hsa-miR-1224-5p	71.0	1.784	0.000
hsa-miR-1225-3p	1.1	0.700	
hsa-miR-1225-5p	1.0	1.048	
hsa-miR-1226-3p	253.5	1.497	0.000
hsa-miR-1226-5p	65.6	1.535	0.002
hsa-miR-1227-3p	18.9	1.290	0.038
hsa-miR-1227-5p	0.1	0.075	
hsa-miR-1228-3p	102.6	1.446	0.002
hsa-miR-1228-5p	22.7	1.493	0.015
hsa-miR-1229-3p	310.7	1.582	0.000
hsa-miR-1229-5p	4.1	1.823	0.105
hsa-miR-1231	0.5	1.080	
hsa-miR-1233-3p	5.1	1.482	0.127
hsa-miR-1233-5p	1.0	1.047	
hsa-miR-1234-3p	6.2	0.726	0.384
hsa-miR-1236-3p	32.2	1.777	0.000
hsa-miR-1236-5p	5.9	1.726	0.055
hsa-miR-1237-3p	26.0	1.885	0.000
hsa-miR-1237-5p	1.7	0.493	
hsa-miR-1238-3p	1.2	0.513	
hsa-miR-1238-5p	0.3	0.517	
hsa-miR-124-3p	0.5	0.098	
hsa-miR-124-5p	0.0		
hsa-miR-1243	1.4	-1.970	
hsa-miR-1244	0.3	0.517	
hsa-miR-1246	14.7	0.900	0.169
hsa-miR-1247-3p	3.3	-0.474	0.703
hsa-miR-1247-5p	59.3	0.307	0.465
hsa-miR-1248	2.9	0.164	0.904
hsa-miR-1249-3p	14.5	-0.896	0.140
hsa-miR-1249-5p	0.2	-0.124	
hsa-miR-1250-3p	1.5	1.710	
hsa-miR-1250-5p	1.7	1.140	
hsa-miR-1252-5p	0.3	0.517	
hsa-miR-1254	99.6	1.622	0.002
hsa-miR-1255a	0.4	-0.662	
hsa-miR-1255b-2-3p	0.1	0.075	
hsa-miR-1255b-5p	0.1	0.075	
hsa-miR-1256	0.2	-0.124	
hsa-miR-1257	2.1	1.098	
hsa-miR-1258	1.0	0.014	
hsa-miR-125a-3p	33.9	0.230	0.667
hsa-miR-125a-5p	1143.2	0.165	0.582
hsa-miR-125b-1-3p	136.8	-0.548	0.116
hsa-miR-125b-2-3p	1.1	-1.310	
hsa-miR-125b-5p	2895.5	-0.447	0.071
hsa-miR-126-3p	696.9	0.448	0.212
hsa-miR-126-5p	336.4	0.286	0.441
hsa-miR-1260a	4.2	-0.024	0.986
hsa-miR-1260b	535.4	1.750	0.000
hsa-miR-1262	1.2	-1.709	
hsa-miR-1263	0.1	0.075	
hsa-miR-1266-3p	0.4	-0.487	
hsa-miR-1266-5p	1.1	-1.651	
hsa-miR-1268b	35.8	1.730	0.008
hsa-miR-127-3p	0.4	0.378	
hsa-miR-1271-3p	0.1	0.075	
hsa-miR-1272	5.2	1.128	0.212
hsa-miR-141-5p	0.3	-0.319	
hsa-miR-142-3p	8.8	-0.428	0.686
hsa-miR-142-5p	3.3	-0.472	0.691
hsa-miR-143-3p	5.0	0.360	0.735
hsa-miR-143-5p	0.3	0.517	
hsa-miR-144-3p	0.5	0.097	
hsa-miR-144-5p	1.0	1.010	
hsa-miR-145-3p	15.7	0.529	0.465
hsa-miR-145-5p	108.8	0.777	0.086
hsa-miR-1468-5p	0.6	-0.769	
hsa-miR-1469	0.3	0.517	
hsa-miR-146a-5p	11.2	0.307	0.697
hsa-miR-146b-3p	1.2	-0.182	

mature	baseMean	log2FC	padj
hsa-miR-3917	3.0	1.407	0.231
hsa-miR-3919	0.1	0.075	
hsa-miR-3922-3p	1.3	0.380	
hsa-miR-3922-5p	0.3	0.517	
hsa-miR-3923	0.1	0.075	
hsa-miR-3926	0.2	-0.124	
hsa-miR-3928-3p	81.1	1.164	0.051
hsa-miR-3928-5p	1.5	0.771	
hsa-miR-3929	87.2	1.271	0.002
hsa-miR-3934-5p	3.8	-0.125	0.912
hsa-miR-3935	0.5	0.170	
hsa-miR-3936	0.4	-0.487	
hsa-miR-3939	0.7	-0.239	
hsa-miR-3940-3p	6.7	1.362	0.104
hsa-miR-3940-5p	2.5	0.522	
hsa-miR-3941	0.1	0.075	
hsa-miR-3942-3p	0.1	0.075	
hsa-miR-3942-5p	0.8	-0.442	
hsa-miR-3943	3.1	0.389	0.750
hsa-miR-3944-3p	3.0	2.041	0.063
hsa-miR-3944-5p	0.8	0.315	
hsa-miR-3960	0.3	0.517	
hsa-miR-3973	0.1	0.075	
hsa-miR-3975	0.3	0.517	
hsa-miR-3976	0.1	0.075	
hsa-miR-409-3p	1.8	-0.866	
hsa-miR-409-5p	0.5	0.098	
hsa-miR-410-3p	1.1	-0.029	
hsa-miR-410-5p	0.3	0.517	
hsa-miR-411-3p	1.7	2.267	
hsa-miR-411-5p	1.4	1.021	
hsa-miR-412-3p	0.3	0.517	
hsa-miR-412-5p	0.4	0.371	
hsa-miR-421	74.6	-4.156	0.000
hsa-miR-423-3p	2229.3	-0.358	0.195
hsa-miR-423-5p	923.7	-0.214	0.503
hsa-miR-424-3p	23.9	0.319	0.566
hsa-miR-424-5p	359.9	0.314	0.641
hsa-miR-425-3p	79.9	-1.766	0.000
hsa-miR-425-5p	645.3	-1.774	0.000
hsa-miR-4251	0.3	0.517	
hsa-miR-4252	0.3	0.517	
hsa-miR-4254	0.8	-1.194	
hsa-miR-4255	0.1	0.075	
hsa-miR-4257	0.3	0.517	
hsa-miR-4261	3.2	1.556	0.197
hsa-miR-4263	0.3	0.517	
hsa-miR-4265	0.5	0.810	
hsa-miR-4266	3.5	1.737	0.111
hsa-miR-4268	0.3	0.517	
hsa-miR-4269	0.6	-0.096	
hsa-miR-4281	0.5	0.810	
hsa-miR-4283	0.1	0.075	
hsa-miR-4284	13.5	0.769	0.208
hsa-miR-4285	0.1	0.075	
hsa-miR-4286	100.4	1.771	0.000
hsa-miR-4289	0.3	0.517	
hsa-miR-429	8.6	0.578	0.466
hsa-miR-4290	0.5	-0.817	
hsa-miR-4292	0.1	0.075	
hsa-miR-4295	0.1	0.075	
hsa-miR-4296	0.3	0.517	
hsa-miR-4297	0.2	-0.124	
hsa-miR-4298	0.4	0.371	
hsa-miR-4306	0.3	-0.310	
hsa-miR-431-5p	0.4	0.369	
hsa-miR-4314	1.6	-0.660	
hsa-miR-4315	0.3	0.517	
hsa-miR-4317	0.1	0.075	
hsa-miR-4319	0.3	0.517	
hsa-miR-4324	0.2	-0.135	

Table 6.2 (continued from the previous page)

hsa-miR-129-5p	0.7	-0.181	
hsa-miR-1290	1.0	0.009	
hsa-miR-1291	2.4	1.281	
hsa-miR-1292-3p	5.9	2.543	0.009
hsa-miR-1292-5p	112.9	1.395	0.010
hsa-miR-1293	10.0	1.301	0.080
hsa-miR-1294	0.6	-0.974	
hsa-miR-1295a	0.9	-0.653	
hsa-miR-1296-3p	1.6	-0.081	
hsa-miR-1296-5p	126.1	-4.442	0.000
hsa-miR-1297	0.6	-0.093	
hsa-miR-1301-3p	123.7	-3.534	0.000
hsa-miR-1301-5p	2.0	-2.402	
hsa-miR-1302	0.0		
hsa-miR-1304-3p	0.3	0.517	
hsa-miR-1304-5p	5.8	-1.499	0.127
hsa-miR-1306-3p	4.7	-0.257	0.797
hsa-miR-1306-5p	11.2	-0.972	0.166
hsa-miR-1307-3p	1301.3	-0.547	0.021
hsa-miR-1307-5p	961.5	-0.797	0.004
hsa-miR-130a-3p	593.2	0.060	0.925
hsa-miR-130a-5p	25.7	-0.071	0.904
hsa-miR-130b-3p	378.0	-1.582	0.000
hsa-miR-130b-5p	138.9	-2.059	0.000
hsa-miR-132-3p	103.9	-0.487	0.154
hsa-miR-132-5p	8.9	-0.329	0.688
hsa-miR-1321	0.1	0.075	
hsa-miR-133a-3p	0.2	-0.124	
hsa-miR-133a-5p	0.1	0.075	
hsa-miR-134-3p	0.3	0.517	
hsa-miR-134-5p	0.3	0.517	
hsa-miR-1343-3p	1.5	-0.552	
hsa-miR-1343-5p	2.1	-1.751	
hsa-miR-135a-5p	0.5	1.080	
hsa-miR-135b-3p	1.9	-0.395	
hsa-miR-135b-5p	34.0	-1.158	0.058
hsa-miR-136-5p	0.1	0.075	
hsa-miR-137	0.1	0.075	
hsa-miR-138-1-3p	0.1	0.075	
hsa-miR-138-2-3p	0.2	-0.148	
hsa-miR-138-5p	6.6	-0.541	0.531
hsa-miR-139-3p	16.0	-1.362	0.071
hsa-miR-139-5p	144.2	-1.356	0.001
hsa-miR-140-3p	475.1	-0.763	0.004
hsa-miR-140-5p	163.1	-0.514	0.230
hsa-miR-141-3p	35.0	-0.900	0.084
hsa-miR-200c-3p	78.6	-1.248	0.000
hsa-miR-200c-5p	0.6	-0.861	
hsa-miR-202-3p	0.1	0.075	
hsa-miR-202-5p	0.7	-0.239	
hsa-miR-203a-3p	1358.0	-0.134	0.690
hsa-miR-203a-5p	12.6	-0.346	0.686
hsa-miR-203b-3p	226.5	0.323	0.377
hsa-miR-203b-5p	5.4	0.945	0.292
hsa-miR-204-5p	0.6	-0.715	
hsa-miR-205-5p	0.1	0.075	
hsa-miR-208a-3p	0.3	0.517	
hsa-miR-208a-5p	0.3	0.517	
hsa-miR-208b-3p	0.4	0.369	
hsa-miR-208b-5p	0.4	0.369	
hsa-miR-20a-3p	75.5	-0.677	0.181
hsa-miR-20a-5p	3534.2	-0.446	0.361
hsa-miR-20b-5p	0.7	-0.862	
hsa-miR-21-3p	1943.9	-1.360	0.000
hsa-miR-21-5p	164514.0	-1.047	0.000
hsa-miR-210-3p	529.0	-1.178	0.000
hsa-miR-210-5p	1.9	-0.414	
hsa-miR-211-3p	0.4	0.375	
hsa-miR-211-5p	1.2	-0.193	
hsa-miR-2110	81.6	1.004	0.005
hsa-miR-2114-3p	1.2	-0.194	
hsa-miR-2114-5p	6.5	-0.283	0.772

hsa-miR-146b-5p	59.8	-0.306	0.453
hsa-miR-1470	0.5	1.080	
hsa-miR-147b	2.2	-1.837	
hsa-miR-148a-3p	1161.8	-0.736	0.002
hsa-miR-148a-5p	16.7	-0.610	0.336
hsa-miR-148b-3p	1164.5	-1.249	0.000
hsa-miR-148b-5p	34.3	-1.550	0.007
hsa-miR-149-3p	1.8	-0.263	
hsa-miR-149-5p	56.1	-1.564	0.000
hsa-miR-150-5p	0.3	-0.319	
hsa-miR-151a-3p	1272.2	-1.581	0.000
hsa-miR-151a-5p	1657.3	-1.313	0.000
hsa-miR-151b	93.9	-1.160	0.000
hsa-miR-152-3p	13.1	-1.372	0.074
hsa-miR-153-3p	167.5	-1.521	0.000
hsa-miR-153-5p	12.9	-0.859	0.225
hsa-miR-1537-3p	0.6	-0.821	
hsa-miR-1537-5p	0.2	-0.135	
hsa-miR-1538	17.8	1.433	0.048
hsa-miR-154-3p	3.6	0.371	0.742
hsa-miR-154-5p	0.7	0.574	
hsa-miR-15a-3p	4.0	-1.614	0.140
hsa-miR-15a-5p	561.7	-1.989	0.000
hsa-miR-15b-3p	121.0	-1.195	0.001
hsa-miR-15b-5p	1132.7	-1.521	0.000
hsa-miR-16-1-3p	24.8	-0.556	0.427
hsa-miR-16-2-3p	210.2	-0.043	0.902
hsa-miR-16-5p	7618.2	-0.185	0.573
hsa-miR-17-3p	239.0	-0.717	0.139
hsa-miR-17-5p	3581.7	-0.485	0.295
hsa-miR-181a-2-3p	23.9	-0.649	0.252
hsa-miR-181a-3p	232.1	0.344	0.213
hsa-miR-181a-5p	5508.8	0.254	0.307
hsa-miR-181b-2-3p	1.0	-0.695	
hsa-miR-181b-3p	11.6	-1.639	0.022
hsa-miR-181b-5p	1459.3	-0.937	0.001
hsa-miR-181c-3p	5.7	0.015	0.986
hsa-miR-181c-5p	83.0	-0.556	0.146
hsa-miR-181d-3p	0.5	-0.660	
hsa-miR-181d-5p	39.4	-0.858	0.058
hsa-miR-182-3p	19.1	0.116	0.855
hsa-miR-182-5p	2615.3	0.276	0.285
hsa-miR-1825	0.3	0.517	
hsa-miR-183-3p	58.4	0.589	0.201
hsa-miR-183-5p	1286.6	0.133	0.620
hsa-miR-184	1.7	0.511	
hsa-miR-185-3p	23.7	-2.310	0.000
hsa-miR-185-5p	444.7	-2.259	0.000
hsa-miR-186-3p	15.1	-1.866	0.022
hsa-miR-186-5p	1196.8	-2.541	0.000
hsa-miR-187-3p	19.9	-0.154	0.817
hsa-miR-187-5p	0.2	-0.124	
hsa-miR-188-3p	2.9	0.538	0.676
hsa-miR-188-5p	74.2	-0.201	0.676
hsa-miR-18a-3p	56.7	-1.738	0.001
hsa-miR-18a-5p	1088.1	-1.448	0.002
hsa-miR-18b-5p	17.4	-1.023	0.173
hsa-miR-1908-3p	2.6	-0.921	
hsa-miR-1908-5p	2.5	-1.326	
hsa-miR-1909-3p	8.3	1.015	0.244
hsa-miR-1909-5p	1.1	0.700	
hsa-miR-190a-3p	1.5	-2.021	
hsa-miR-190a-5p	52.1	-1.353	0.002
hsa-miR-190b	8.0	-1.990	0.038
hsa-miR-191-3p	30.3	-1.097	0.043
hsa-miR-191-5p	1544.8	-0.830	0.004
hsa-miR-1910-3p	6.6	-0.505	0.619
hsa-miR-1910-5p	12.3	-0.507	0.472
hsa-miR-1913	0.2	-0.138	
hsa-miR-1914-3p	5.6	-0.910	0.320
hsa-miR-1914-5p	1.9	-0.346	
hsa-miR-1915-3p	8.4	-3.504	0.003

hsa-miR-4325	0.5	1.080	
hsa-miR-4326	14.4	-4.330	0.000
hsa-miR-4330	0.4	0.378	
hsa-miR-4418	0.3	0.517	
hsa-miR-4422	0.3	0.517	
hsa-miR-4423-3p	1.0	0.162	
hsa-miR-4423-5p	0.7	-1.178	
hsa-miR-4660	0.4	-0.477	
hsa-miR-4661-3p	0.5	-0.640	
hsa-miR-4661-5p	3.9	-1.567	0.151
hsa-miR-4662a-3p	0.2	-0.159	
hsa-miR-4662a-5p	0.7	-1.052	
hsa-miR-4662b	0.2	-0.138	
hsa-miR-4664-3p	2.9	-2.213	0.071
hsa-miR-4664-5p	13.2	-3.088	0.000
hsa-miR-4665-5p	1.6	-0.063	
hsa-miR-4666a-3p	0.4	0.365	
hsa-miR-4666a-5p	0.5	0.138	
hsa-miR-4667-3p	4.1	1.840	0.060
hsa-miR-4667-5p	1.2	0.477	
hsa-miR-4668-3p	0.5	0.156	
hsa-miR-4668-5p	0.6	0.919	
hsa-miR-4669	4.1	0.969	0.366
hsa-miR-4670-3p	0.5	0.156	
hsa-miR-4670-5p	0.4	0.376	
hsa-miR-4671-3p	0.9	-1.115	
hsa-miR-4673	0.7	-0.240	
hsa-miR-4674	0.8	-0.401	
hsa-miR-4676-3p	0.5	-0.660	
hsa-miR-4676-5p	0.5	-0.869	
hsa-miR-4677-3p	1.6	-2.136	
hsa-miR-4677-5p	0.3	-0.357	
hsa-miR-4682	0.2	-0.148	
hsa-miR-4684-3p	0.1	0.075	
hsa-miR-4684-5p	0.1	0.075	
hsa-miR-4685-3p	4.2	-0.020	0.986
hsa-miR-4685-5p	0.9	1.470	
hsa-miR-4686	0.5	0.138	
hsa-miR-4687-3p	0.7	0.484	
hsa-miR-4687-5p	0.1	0.075	
hsa-miR-4688	3.3	2.123	0.058
hsa-miR-4689	0.2	-0.148	
hsa-miR-4690-3p	5.5	1.396	0.136
hsa-miR-4690-5p	3.9	1.576	0.172
hsa-miR-4691-3p	0.4	-0.662	
hsa-miR-4691-5p	0.1	0.075	
hsa-miR-4694-3p	0.1	0.075	
hsa-miR-4694-5p	0.1	0.075	
hsa-miR-4695-3p	2.4	1.029	
hsa-miR-4695-5p	1.0	1.032	
hsa-miR-4697-3p	3.3	2.123	0.058
hsa-miR-4697-5p	1.2	0.551	
hsa-miR-4700-3p	1.0	0.132	
hsa-miR-4700-5p	1.7	0.496	
hsa-miR-4701-3p	3.3	2.119	0.058
hsa-miR-4701-5p	1.9	0.207	
hsa-miR-4706	1.0	-0.778	
hsa-miR-4707-3p	10.9	0.545	0.415
hsa-miR-4707-5p	20.1	-0.620	0.252
hsa-miR-4709-5p	0.9	1.088	
hsa-miR-4710	1.2	0.543	
hsa-miR-4713-3p	0.1	0.075	
hsa-miR-4713-5p	4.5	-1.368	0.217
hsa-miR-4714-3p	0.3	0.517	
hsa-miR-4714-5p	0.1	0.075	
hsa-miR-4716-5p	0.4	0.369	
hsa-miR-4717-3p	0.4	0.365	
hsa-miR-4717-5p	0.1	0.075	
hsa-miR-4720-3p	0.5	0.810	
hsa-miR-4720-5p	0.7	0.573	
hsa-miR-4721	0.3	0.517	
hsa-miR-4722-3p	27.6	1.308	0.014

Table 6.2 (continued from the previous page)

hsa-miR-2115-3p	0.3	0.517	
hsa-miR-2115-5p	0.3	0.517	
hsa-miR-2116-3p	0.9	0.178	
hsa-miR-212-3p	0.9	0.379	
hsa-miR-212-5p	0.4	0.371	
hsa-miR-214-3p	1.0	0.171	
hsa-miR-215-3p	0.1	0.075	
hsa-miR-215-5p	0.4	-0.477	
hsa-miR-216a-3p	0.1	0.075	
hsa-miR-216a-5p	1.6	-2.168	
hsa-miR-216b-3p	0.5	0.809	
hsa-miR-216b-5p	1.2	-1.034	
hsa-miR-217	0.7	-0.862	
hsa-miR-218-1-3p	1.7	-0.780	
hsa-miR-218-2-3p	0.3	0.517	
hsa-miR-218-5p	98.4	-1.091	0.003
hsa-miR-219a-1-3p	3.8	-2.548	0.037
hsa-miR-219a-2-3p	0.4	0.365	
hsa-miR-219a-5p	25.7	-2.010	0.002
hsa-miR-219b-3p	1.0	-0.792	
hsa-miR-219b-5p	1.9	-0.966	
hsa-miR-22-3p	3483.5	0.158	0.639
hsa-miR-22-5p	204.9	0.066	0.870
hsa-miR-221-3p	21915.7	-0.617	0.007
hsa-miR-221-5p	339.3	-0.990	0.001
hsa-miR-222-3p	45538.8	0.180	0.494
hsa-miR-222-5p	1728.9	0.174	0.466
hsa-miR-224-3p	2.3	-0.159	
hsa-miR-224-5p	158.8	-0.129	0.686
hsa-miR-2276-3p	1.2	-1.081	
hsa-miR-2276-5p	0.2	-0.135	
hsa-miR-2277-3p	5.8	-1.260	0.161
hsa-miR-2277-5p	9.0	-1.750	0.037
hsa-miR-2278	2.0	-0.427	
hsa-miR-2355-3p	6.5	-2.805	0.012
hsa-miR-2355-5p	5.1	-2.976	0.012
hsa-miR-23a-3p	2992.7	-0.038	0.896
hsa-miR-23a-5p	64.3	-0.198	0.750
hsa-miR-23b-3p	761.5	0.077	0.843
hsa-miR-23b-5p	6.7	0.044	0.971
hsa-miR-23c	3.2	0.321	0.775
hsa-miR-24-1-5p	16.6	-0.238	0.728
hsa-miR-24-2-5p	86.4	-0.281	0.404
hsa-miR-24-3p	3894.7	0.056	0.817
hsa-miR-2467-3p	0.1	0.075	
hsa-miR-2467-5p	1.3	-0.376	
hsa-miR-25-3p	4249.7	-0.783	0.003
hsa-miR-25-5p	51.5	-0.958	0.041
hsa-miR-2681-3p	0.6	0.919	
hsa-miR-2681-5p	0.6	0.919	
hsa-miR-26a-1-3p	7.3	0.018	0.986
hsa-miR-26a-2-3p	10.0	-0.437	0.591
hsa-miR-26a-5p	5774.8	0.033	0.896
hsa-miR-26b-3p	15.2	-0.016	0.986
hsa-miR-26b-5p	1933.6	0.358	0.151
hsa-miR-27a-3p	4452.6	-0.029	0.919
hsa-miR-27a-5p	84.9	-0.571	0.123
hsa-miR-27b-3p	1120.1	0.063	0.870
hsa-miR-27b-5p	18.4	-0.020	0.983
hsa-miR-28-3p	259.8	-1.725	0.000
hsa-miR-28-5p	261.2	-1.528	0.000
hsa-miR-2861	0.3	0.517	
hsa-miR-296-3p	2.8	-1.035	
hsa-miR-296-5p	1.9	0.221	
hsa-miR-298	0.4	0.378	
hsa-miR-299-3p	1.5	1.676	
hsa-miR-299-5p	1.4	1.855	
hsa-miR-29a-3p	19252.0	-0.225	0.427
hsa-miR-29a-5p	375.2	0.189	0.725
hsa-miR-29b-1-5p	400.7	0.488	0.096
hsa-miR-29b-2-5p	19.7	0.017	0.985
hsa-miR-29b-3p	6156.0	0.217	0.751

hsa-miR-1915-5p	2.1	-2.525	
hsa-miR-192-3p	0.7	0.444	
hsa-miR-192-5p	19.1	-2.052	0.002
hsa-miR-193a-3p	37.8	-0.025	0.983
hsa-miR-193a-5p	36.6	-0.080	0.890
hsa-miR-193b-3p	293.7	-0.524	0.404
hsa-miR-193b-5p	29.6	-0.627	0.208
hsa-miR-194-3p	0.7	-0.314	
hsa-miR-194-5p	58.5	-0.559	0.171
hsa-miR-195-3p	1.2	-1.065	
hsa-miR-195-5p	25.2	-1.151	0.056
hsa-miR-196a-3p	1.3	-1.190	
hsa-miR-196a-5p	372.4	-3.033	0.000
hsa-miR-196b-3p	36.8	-0.883	0.045
hsa-miR-196b-5p	2210.0	-1.042	0.000
hsa-miR-197-3p	193.5	-1.308	0.001
hsa-miR-197-5p	1.8	-0.898	
hsa-miR-1973	1.5	0.883	
hsa-miR-1976	11.2	1.771	0.015
hsa-miR-198	0.1	0.075	
hsa-miR-199a-3p	22.3	0.213	0.702
hsa-miR-199a-5p	1.7	-0.181	
hsa-miR-199b-3p	19.1	0.184	0.750
hsa-miR-199b-5p	17.7	0.163	0.804
hsa-miR-19a-3p	1646.9	-2.577	0.000
hsa-miR-19a-5p	4.8	-2.283	0.055
hsa-miR-19b-1-5p	38.6	-0.879	0.142
hsa-miR-19b-2-5p	0.2	-0.159	
hsa-miR-19b-3p	3916.1	-0.808	0.005
hsa-miR-200a-3p	13.7	-0.548	0.410
hsa-miR-200a-5p	1.7	1.109	
hsa-miR-200b-3p	12.8	-0.272	0.726
hsa-miR-200b-5p	3.2	1.142	0.300
hsa-miR-30c-2-3p	0.2	-0.148	
hsa-miR-30c-5p	2911.7	0.108	0.681
hsa-miR-30d-3p	23.9	-0.474	0.403
hsa-miR-30d-5p	2095.7	-0.151	0.595
hsa-miR-30e-3p	250.3	-1.041	0.002
hsa-miR-30e-5p	2240.1	-1.014	0.000
hsa-miR-31-3p	1274.9	0.049	0.902
hsa-miR-31-5p	14789.0	0.061	0.817
hsa-miR-3115	4.1	0.043	0.979
hsa-miR-3118	0.1	0.075	
hsa-miR-3120-3p	0.9	1.306	
hsa-miR-3120-5p	0.8	1.575	
hsa-miR-3121-3p	0.2	-0.135	
hsa-miR-3121-5p	0.1	0.075	
hsa-miR-3124-3p	0.4	0.378	
hsa-miR-3124-5p	0.3	0.517	
hsa-miR-3125	0.3	0.517	
hsa-miR-3126-5p	0.4	0.365	
hsa-miR-3127-3p	1.7	-1.472	
hsa-miR-3127-5p	1.6	-1.387	
hsa-miR-3128	1.0	-0.793	
hsa-miR-3129-3p	2.4	-1.266	
hsa-miR-3129-5p	1.3	-0.314	
hsa-miR-3130-3p	0.6	-0.974	
hsa-miR-3130-5p	0.7	-1.211	
hsa-miR-3131	0.1	0.075	
hsa-miR-3132	0.2	-0.138	
hsa-miR-3133	0.6	-0.069	
hsa-miR-3134	0.2	-0.124	
hsa-miR-3135b	0.4	-0.487	
hsa-miR-3136-3p	0.3	0.517	
hsa-miR-3136-5p	1.3	-1.156	
hsa-miR-3138	1.1	0.727	
hsa-miR-3140-3p	0.8	-0.474	
hsa-miR-3140-5p	0.1	0.075	
hsa-miR-3141	1.8	0.917	
hsa-miR-3143	22.3	1.273	0.016
hsa-miR-3145-3p	1.3	-1.003	
hsa-miR-3145-5p	0.8	-0.495	

hsa-miR-4722-5p	28.4	1.252	0.014
hsa-miR-4723-3p	6.6	1.430	0.113
hsa-miR-4723-5p	1.9	1.547	
hsa-miR-4724-5p	0.1	0.075	
hsa-miR-4725-3p	0.2	-0.138	
hsa-miR-4725-5p	0.3	-0.346	
hsa-miR-4726-3p	3.2	1.607	0.139
hsa-miR-4726-5p	11.0	1.919	0.004
hsa-miR-4727-3p	2.9	1.121	0.337
hsa-miR-4727-5p	1.4	0.185	
hsa-miR-4728-3p	11.6	1.260	0.075
hsa-miR-4728-5p	1.1	1.795	
hsa-miR-4730	0.5	0.810	
hsa-miR-4731-3p	0.3	0.517	
hsa-miR-4731-5p	0.8	-1.311	
hsa-miR-4733-3p	0.3	0.517	
hsa-miR-4733-5p	0.4	0.365	
hsa-miR-4734	5.4	0.659	0.486
hsa-miR-4736	1.1	-0.133	
hsa-miR-4737	0.6	0.754	
hsa-miR-4738-3p	7.9	1.493	0.062
hsa-miR-4738-5p	0.5	0.809	
hsa-miR-4739	0.8	-1.346	
hsa-miR-4741	43.8	1.533	0.004
hsa-miR-4742-3p	14.6	1.785	0.010
hsa-miR-4742-5p	5.8	1.186	0.191
hsa-miR-4743-3p	0.5	0.810	
hsa-miR-4743-5p	0.8	1.581	
hsa-miR-4744	0.2	-0.135	
hsa-miR-4745-3p	63.4	1.544	0.001
hsa-miR-4745-5p	39.8	1.558	0.009
hsa-miR-4746-3p	0.4	0.368	
hsa-miR-4746-5p	1.5	-1.279	
hsa-miR-4747-3p	2.1	1.171	
hsa-miR-4747-5p	5.9	2.002	0.058
hsa-miR-4748	0.5	0.098	
hsa-miR-4749-3p	0.8	0.564	
hsa-miR-4749-5p	10.0	1.340	0.072
hsa-miR-4750-3p	0.3	0.517	
hsa-miR-4750-5p	2.0	1.353	
hsa-miR-4753-3p	0.1	0.075	
hsa-miR-4754	0.2	-0.138	
hsa-miR-4755-5p	0.3	-0.256	
hsa-miR-4756-3p	0.3	0.517	
hsa-miR-4756-5p	0.3	0.517	
hsa-miR-4757-3p	0.4	0.378	
hsa-miR-4758-3p	7.0	1.680	0.047
hsa-miR-4758-5p	7.6	1.446	0.067
hsa-miR-4761-3p	0.1	0.075	
hsa-miR-4761-5p	0.5	0.098	
hsa-miR-4762-3p	0.7	-0.240	
hsa-miR-4762-5p	0.9	-0.654	
hsa-miR-4763-5p	0.6	0.739	
hsa-miR-5187-5p	5.1	1.134	0.230
hsa-miR-5188	5.5	1.399	0.129
hsa-miR-518a-5p	0.1	0.075	
hsa-miR-518e-5p	2.2	0.940	
hsa-miR-5190	0.6	0.743	
hsa-miR-5193	0.1	0.075	
hsa-miR-5196-3p	0.4	-0.477	
hsa-miR-519a-3p	4.2	0.267	0.825
hsa-miR-519a-5p	2.2	0.940	
hsa-miR-519b-3p	0.2	-0.135	
hsa-miR-519b-5p	2.2	0.940	
hsa-miR-519c-5p	2.2	0.940	
hsa-miR-519d-3p	0.1	0.075	
hsa-miR-519d-5p	0.3	0.517	
hsa-miR-520a-5p	0.3	0.517	
hsa-miR-520d-5p	0.1	0.075	
hsa-miR-520f-5p	0.3	0.517	
hsa-miR-521	1.8	-0.218	
hsa-miR-522-3p	2.1	-0.014	

Table 6.2 (continued from the previous page)

hsa-miR-29c-3p	365.0	-0.656	0.160
hsa-miR-29c-5p	14.7	-0.500	0.445
hsa-miR-300	0.3	0.517	
hsa-miR-301a-3p	1260.1	-0.559	0.195
hsa-miR-301a-5p	85.4	-0.698	0.088
hsa-miR-301b-3p	157.1	-1.242	0.025
hsa-miR-301b-5p	19.1	-1.629	0.006
hsa-miR-302a-3p	0.1	0.075	
hsa-miR-302b-3p	0.3	0.517	
hsa-miR-3064-3p	8.8	1.355	0.090
hsa-miR-3064-5p	8.3	1.016	0.223
hsa-miR-3065-3p	9.0	-2.531	0.005
hsa-miR-3065-5p	30.6	-3.672	0.000
hsa-miR-3074-3p	3.0	2.006	0.073
hsa-miR-3074-5p	1.5	0.075	
hsa-miR-30a-3p	19.0	-0.474	0.425
hsa-miR-30a-5p	199.9	-0.621	0.102
hsa-miR-30b-3p	13.1	0.122	0.870
hsa-miR-30b-5p	1327.6	0.009	0.986
hsa-miR-30c-1-3p	16.4	0.229	0.742
hsa-miR-330-5p	122.7	-1.083	0.004
hsa-miR-331-3p	337.0	-0.331	0.354
hsa-miR-331-5p	19.4	-0.610	0.273
hsa-miR-335-3p	91.0	-0.243	0.704
hsa-miR-335-5p	109.3	-0.242	0.595
hsa-miR-338-3p	3.7	1.089	0.276
hsa-miR-338-5p	3.0	1.988	0.086
hsa-miR-339-3p	112.3	-0.975	0.001
hsa-miR-339-5p	644.3	-1.154	0.000
hsa-miR-33a-3p	39.4	0.338	0.617
hsa-miR-33a-5p	307.3	0.333	0.674
hsa-miR-33b-3p	39.1	-0.525	0.225
hsa-miR-33b-5p	112.6	-0.509	0.454
hsa-miR-340-3p	22.1	-1.929	0.006
hsa-miR-340-5p	200.2	-2.288	0.000
hsa-miR-342-3p	203.8	0.289	0.483
hsa-miR-342-5p	7.0	0.331	0.712
hsa-miR-345-3p	2.5	-1.927	
hsa-miR-345-5p	261.9	-3.102	0.000
hsa-miR-346	12.7	-1.937	0.011
hsa-miR-34a-3p	92.6	-0.258	0.441
hsa-miR-34a-5p	3036.1	0.292	0.345
hsa-miR-34b-3p	0.6	0.904	
hsa-miR-34b-5p	2.8	0.246	0.838
hsa-miR-34c-3p	0.7	0.587	
hsa-miR-34c-5p	5.9	-0.503	0.609
hsa-miR-3529-3p	0.2	-0.124	
hsa-miR-3529-5p	0.2	-0.124	
hsa-miR-3591-5p	0.1	0.075	
hsa-miR-3605-3p	88.3	1.494	0.010
hsa-miR-3605-5p	18.1	1.121	0.081
hsa-miR-3607-3p	3.3	0.294	0.805
hsa-miR-3607-5p	1.3	0.349	
hsa-miR-3609	3.6	1.618	0.108
hsa-miR-361-3p	66.1	-0.100	0.797
hsa-miR-361-5p	487.9	-0.284	0.279
hsa-miR-3610	0.5	1.080	
hsa-miR-3611	3.6	-1.881	0.119
hsa-miR-3613-3p	13.6	-0.013	0.986
hsa-miR-3613-5p	136.5	-0.550	0.127
hsa-miR-3614-3p	31.8	1.111	0.038
hsa-miR-3614-5p	30.1	1.023	0.053
hsa-miR-3615	1309.5	1.354	0.009
hsa-miR-3617-5p	0.7	0.572	
hsa-miR-3618	0.2	-0.124	
hsa-miR-3619-3p	1.6	-2.161	
hsa-miR-3619-5p	6.5	-3.319	0.004
hsa-miR-362-3p	65.2	-1.033	0.008
hsa-miR-362-5p	44.4	-0.602	0.200
hsa-miR-3620-3p	69.8	1.600	0.000
hsa-miR-3620-5p	25.1	1.473	0.039
hsa-miR-3621	3.2	1.597	0.146

hsa-miR-3149	0.4	-0.662	
hsa-miR-3150a-3p	0.7	-0.291	
hsa-miR-3150a-5p	1.2	-0.201	
hsa-miR-3150b-3p	0.1	0.075	
hsa-miR-3150b-5p	0.1	0.075	
hsa-miR-3152-5p	0.9	-1.349	
hsa-miR-3153	0.2	-0.124	
hsa-miR-3155b	0.1	0.075	
hsa-miR-3157-3p	0.2	-0.124	
hsa-miR-3157-5p	1.8	-0.810	
hsa-miR-3158-3p	7.5	-2.568	0.011
hsa-miR-3158-5p	1.0	-0.828	
hsa-miR-3159	1.1	-0.029	
hsa-miR-3160-3p	0.4	-0.477	
hsa-miR-3160-5p	0.2	-0.148	
hsa-miR-3163	0.1	0.075	
hsa-miR-3164	0.4	0.369	
hsa-miR-3165	0.1	0.075	
hsa-miR-3166	0.9	1.309	
hsa-miR-3168	2.6	0.858	
hsa-miR-3170	0.1	0.075	
hsa-miR-3173-3p	0.9	-0.587	
hsa-miR-3173-5p	2.6	-1.397	
hsa-miR-3174	1.0	0.132	
hsa-miR-3175	3.3	-0.443	0.726
hsa-miR-3176	13.2	-2.841	0.001
hsa-miR-3177-3p	3.9	-2.065	0.075
hsa-miR-3177-5p	1.0	-1.467	
hsa-miR-3178	0.6	-0.030	
hsa-miR-3179	1.7	0.414	
hsa-miR-3180	4.4	-1.029	0.301
hsa-miR-3180-3p	4.3	-0.985	0.333
hsa-miR-3180-5p	0.4	0.368	
hsa-miR-3181	0.9	0.346	
hsa-miR-3182	0.5	0.156	
hsa-miR-3183	0.4	-0.487	
hsa-miR-3184-5p	0.1	0.075	
hsa-miR-3185	0.3	0.517	
hsa-miR-3187-3p	37.2	-1.720	0.000
hsa-miR-3187-5p	1.4	-0.461	
hsa-miR-3188	15.5	1.837	0.002
hsa-miR-3189-3p	0.6	-1.022	
hsa-miR-3189-5p	0.6	-1.014	
hsa-miR-3190-3p	3.0	1.481	0.181
hsa-miR-3190-5p	1.9	0.219	
hsa-miR-3191-3p	0.6	-0.030	
hsa-miR-3191-5p	0.3	0.517	
hsa-miR-3193	3.4	0.931	0.384
hsa-miR-3194-3p	1.4	-1.945	
hsa-miR-3194-5p	4.8	-2.858	0.016
hsa-miR-3195	0.1	0.075	
hsa-miR-3196	0.2	-0.135	
hsa-miR-3197	0.3	-0.256	
hsa-miR-3198	0.7	-0.323	
hsa-miR-3199	4.2	2.259	0.028
hsa-miR-32-3p	31.9	-1.367	0.013
hsa-miR-32-5p	284.9	-1.625	0.004
hsa-miR-3200-3p	106.7	-0.071	0.848
hsa-miR-3200-5p	5.0	-0.122	0.907
hsa-miR-3201	5.4	1.484	0.146
hsa-miR-3202	1.5	0.630	
hsa-miR-320a	43250.8	1.541	0.002
hsa-miR-320b	2109.4	1.354	0.008
hsa-miR-320c	960.3	1.250	0.014
hsa-miR-320d	488.6	1.066	0.037
hsa-miR-320e	75.5	0.778	0.044
hsa-miR-323a-3p	1.2	-0.946	
hsa-miR-323a-5p	0.3	0.517	
hsa-miR-323b-3p	0.5	0.098	
hsa-miR-323b-5p	0.3	0.517	
hsa-miR-324-3p	283.6	0.049	0.887
hsa-miR-324-5p	555.8	0.179	0.610

hsa-miR-522-5p	2.2	0.940	
hsa-miR-523-5p	2.2	0.940	
hsa-miR-524-3p	0.1	0.075	
hsa-miR-527	0.1	0.075	
hsa-miR-532-3p	31.2	-0.890	0.109
hsa-miR-532-5p	123.6	-0.994	0.001
hsa-miR-539-3p	0.3	0.517	
hsa-miR-539-5p	0.7	-0.314	
hsa-miR-541-3p	0.3	0.517	
hsa-miR-541-5p	0.3	0.517	
hsa-miR-542-3p	42.8	-0.884	0.034
hsa-miR-542-5p	8.2	-0.443	0.647
hsa-miR-543	1.9	0.168	
hsa-miR-544a	0.3	0.517	
hsa-miR-545-3p	5.6	-1.440	0.146
hsa-miR-545-5p	10.2	-3.041	0.002
hsa-miR-548a-3p	8.9	-0.005	0.996
hsa-miR-548a-5p	2.1	-0.526	
hsa-miR-548ab	1.1	-0.920	
hsa-miR-548ac	0.3	-0.256	
hsa-miR-548ad-5p	0.1	0.075	
hsa-miR-548ae-3p	0.1	0.075	
hsa-miR-548ae-5p	0.3	-0.256	
hsa-miR-548ag	0.6	-0.094	
hsa-miR-548ai	1.6	-1.437	
hsa-miR-548al	1.5	0.579	
hsa-miR-548am-5p	0.1	0.075	
hsa-miR-548an	0.4	-0.503	
hsa-miR-548ap-3p	0.3	0.517	
hsa-miR-548ap-5p	0.5	0.122	
hsa-miR-548aq-3p	0.6	0.902	
hsa-miR-548aq-5p	5.0	-1.971	0.061
hsa-miR-548ar-3p	1.1	-1.571	
hsa-miR-548as-3p	0.3	-0.310	
hsa-miR-548at-3p	0.1	0.075	
hsa-miR-548at-5p	0.3	0.517	
hsa-miR-548au-3p	0.1	0.075	
hsa-miR-548au-5p	0.1	0.075	
hsa-miR-548av-3p	0.1	0.075	
hsa-miR-548av-5p	0.1	0.075	
hsa-miR-548aw	1.2	0.553	
hsa-miR-548ay-3p	1.3	-1.862	
hsa-miR-548ay-5p	0.1	0.075	
hsa-miR-548b-3p	8.0	-3.050	0.006
hsa-miR-548bb-5p	0.1	0.075	
hsa-miR-548d-3p	5.4	-2.490	0.031
hsa-miR-548d-5p	0.3	0.517	
hsa-miR-548e-3p	11.0	-3.099	0.002
hsa-miR-548e-5p	4.3	-2.192	0.058
hsa-miR-548h-5p	0.0		
hsa-miR-548i	0.7	-0.248	
hsa-miR-548j-3p	0.6	-0.093	
hsa-miR-548j-5p	3.2	-1.279	0.255
hsa-miR-548k	8.4	-4.331	0.000
hsa-miR-548l	1.6	-1.383	
hsa-miR-548n	1.5	-0.614	
hsa-miR-548o-3p	2.0	-1.709	
hsa-miR-548o-5p	0.4	0.369	
hsa-miR-548p	0.2	-0.135	
hsa-miR-548q	0.8	0.341	
hsa-miR-548s	0.9	-1.306	
hsa-miR-548t-5p	0.1	0.075	
hsa-miR-548u	1.6	-1.208	
hsa-miR-548v	0.6	-0.974	
hsa-miR-549a	0.1	0.075	
hsa-miR-550a-3-5p	1.0	-1.252	
hsa-miR-550a-3p	48.8	-2.299	0.000
hsa-miR-550a-5p	7.1	-1.580	0.079
hsa-miR-550b-2-5p	1.2	0.576	
hsa-miR-550b-3p	1.2	0.576	
hsa-miR-551a	60.6	-2.920	0.000
hsa-miR-551b-3p	21.4	0.003	0.996

Table 6.2 (continued from the previous page)

hsa-miR-3622a-3p	0.1	0.075	
hsa-miR-3622a-5p	0.2	-0.138	
hsa-miR-3622b-3p	0.4	-0.477	
hsa-miR-3622b-5p	0.4	-0.477	
hsa-miR-3648	17.9	1.031	0.179
hsa-miR-3651	1.4	1.005	
hsa-miR-3652	1.0	1.028	
hsa-miR-3653-3p	1.5	1.366	
hsa-miR-3653-5p	4.9	1.355	0.165
hsa-miR-3654	0.3	0.517	
hsa-miR-3656	0.4	0.368	
hsa-miR-3657	2.6	-2.554	
hsa-miR-3658	0.1	0.075	
hsa-miR-3659	0.8	-1.319	
hsa-miR-365a-3p	237.5	-1.279	0.006
hsa-miR-365a-5p	6.2	-1.341	0.152
hsa-miR-365b-3p	237.1	-1.291	0.005
hsa-miR-365b-5p	0.7	-0.314	
hsa-miR-3660	0.3	0.517	
hsa-miR-3661	0.8	-1.063	
hsa-miR-3662	4.9	1.608	0.143
hsa-miR-3663-3p	5.8	0.205	0.839
hsa-miR-3663-5p	0.7	-0.249	
hsa-miR-3664-3p	1.1	-1.633	
hsa-miR-3664-5p	0.6	-0.094	
hsa-miR-3667-3p	9.5	-0.301	0.715
hsa-miR-3667-5p	6.7	0.629	0.502
hsa-miR-3670	0.3	0.517	
hsa-miR-3672	0.4	-0.477	
hsa-miR-3674	0.1	0.075	
hsa-miR-3677-3p	0.5	-0.817	
hsa-miR-3677-5p	0.1	0.075	
hsa-miR-3678-5p	0.4	0.368	
hsa-miR-3679-3p	0.1	0.075	
hsa-miR-3679-5p	0.9	-0.586	
hsa-miR-3680-3p	0.3	0.517	
hsa-miR-3680-5p	0.8	0.319	
hsa-miR-3681-5p	0.1	0.075	
hsa-miR-3682-3p	0.3	0.517	
hsa-miR-3684	1.6	-0.622	
hsa-miR-3685	0.1	0.075	
hsa-miR-3687	15.1	1.301	0.083
hsa-miR-3688-3p	0.7	-1.041	
hsa-miR-3688-5p	0.1	0.075	
hsa-miR-3689a-3p	1.2	1.608	
hsa-miR-3689a-5p	1.5	1.584	
hsa-miR-3689b-3p	1.2	1.608	
hsa-miR-3689b-5p	1.5	1.584	
hsa-miR-3689c	1.2	1.608	
hsa-miR-3689d	1.2	1.608	
hsa-miR-3689e	1.5	1.584	
hsa-miR-3689f	1.2	1.608	
hsa-miR-369-3p	4.0	-0.197	0.871
hsa-miR-369-5p	0.4	0.371	
hsa-miR-3691-3p	0.7	-0.285	
hsa-miR-3691-5p	2.6	-2.061	
hsa-miR-3692-3p	0.5	1.077	
hsa-miR-3692-5p	0.6	0.902	
hsa-miR-371a-3p	0.6	-0.093	
hsa-miR-371a-5p	2.0	-0.942	
hsa-miR-372-3p	4.4	-0.121	0.923
hsa-miR-372-5p	0.1	0.075	
hsa-miR-373-3p	3.3	-0.114	0.924
hsa-miR-373-5p	0.4	0.371	
hsa-miR-374a-3p	52.9	-3.902	0.000
hsa-miR-374a-5p	1245.4	-3.622	0.000
hsa-miR-4424	0.3	0.517	
hsa-miR-4425	0.4	0.365	
hsa-miR-4429	6.0	1.062	0.205
hsa-miR-4431	0.1	0.075	
hsa-miR-4434	0.1	0.075	
hsa-miR-4435	26.8	1.612	0.003

hsa-miR-325	0.3	0.517	
hsa-miR-326	50.2	-0.599	0.122
hsa-miR-328-3p	36.5	0.250	0.597
hsa-miR-328-5p	1.5	0.881	
hsa-miR-329-3p	2.0	-0.990	
hsa-miR-329-5p	0.3	0.517	
hsa-miR-330-3p	232.6	-1.319	0.000
hsa-miR-374b-3p	13.4	-3.375	0.001
hsa-miR-374b-5p	360.2	-3.711	0.000
hsa-miR-374c-5p	8.2	-3.598	0.002
hsa-miR-375	5.6	-0.157	0.879
hsa-miR-376a-2-5p	0.4	0.378	
hsa-miR-376a-3p	3.0	0.481	0.719
hsa-miR-376a-5p	0.4	0.371	
hsa-miR-376b-3p	1.0	0.162	
hsa-miR-376b-5p	0.3	0.517	
hsa-miR-376c-3p	5.1	0.327	0.765
hsa-miR-376c-5p	0.3	0.517	
hsa-miR-377-3p	0.7	-0.240	
hsa-miR-377-5p	0.3	0.517	
hsa-miR-378a-3p	1262.4	-0.831	0.006
hsa-miR-378a-5p	55.5	-0.537	0.331
hsa-miR-378b	0.1	0.075	
hsa-miR-378c	69.0	-0.812	0.062
hsa-miR-378d	15.8	-1.378	0.037
hsa-miR-378e	0.1	0.075	
hsa-miR-378g	4.3	1.504	0.152
hsa-miR-379-3p	0.7	0.651	
hsa-miR-379-5p	1.9	2.501	
hsa-miR-380-3p	0.3	0.517	
hsa-miR-380-5p	0.3	0.517	
hsa-miR-381-3p	2.3	-0.140	
hsa-miR-381-5p	0.4	0.368	
hsa-miR-382-3p	1.3	1.163	
hsa-miR-382-5p	2.7	1.350	
hsa-miR-384	0.3	0.517	
hsa-miR-3907	0.3	0.517	
hsa-miR-3908	0.1	0.075	
hsa-miR-3909	4.2	-0.526	0.676
hsa-miR-3910	0.2	-0.124	
hsa-miR-3911	0.6	-0.096	
hsa-miR-3912-3p	7.9	1.085	0.181
hsa-miR-3912-5p	2.1	2.091	
hsa-miR-3913-3p	3.0	1.478	0.181
hsa-miR-3913-5p	6.8	1.310	0.105
hsa-miR-3914	0.3	0.517	
hsa-miR-3916	0.8	-0.415	
hsa-miR-659-5p	4.7	1.201	0.198
hsa-miR-660-3p	11.8	-0.795	0.257
hsa-miR-660-5p	218.7	-0.570	0.112
hsa-miR-661	0.6	0.778	
hsa-miR-662	0.6	0.940	
hsa-miR-663a	6.8	0.804	0.349
hsa-miR-663b	3.7	0.310	0.777
hsa-miR-664a-3p	75.5	1.270	0.003
hsa-miR-664a-5p	20.0	1.339	0.072
hsa-miR-664b-3p	11.8	1.637	0.030
hsa-miR-664b-5p	4.2	1.589	0.152
hsa-miR-668-3p	0.5	1.080	
hsa-miR-668-5p	0.3	0.517	
hsa-miR-671-3p	51.3	-0.350	0.432
hsa-miR-671-5p	578.2	0.073	0.828
hsa-miR-6716-3p	3.8	0.909	0.432
hsa-miR-6717-5p	0.1	0.075	
hsa-miR-6721-5p	10.3	1.539	0.048
hsa-miR-6723-5p	59.4	1.283	0.018
hsa-miR-6724-5p	58.2	1.392	0.012
hsa-miR-6726-3p	3.7	1.841	0.085
hsa-miR-6726-5p	0.1	0.075	
hsa-miR-6727-3p	0.7	0.661	
hsa-miR-6727-5p	2.4	1.974	
hsa-miR-6728-3p	6.4	0.794	0.362

hsa-miR-551b-5p	1.3	-0.302	
hsa-miR-552-3p	0.2	-0.135	
hsa-miR-552-5p	0.2	-0.124	
hsa-miR-556-3p	10.8	-2.714	0.005
hsa-miR-556-5p	6.7	-2.825	0.011
hsa-miR-5579-3p	0.1	0.075	
hsa-miR-5579-5p	0.1	0.075	
hsa-miR-5580-3p	0.7	-0.300	
hsa-miR-5580-5p	0.3	-0.343	
hsa-miR-5581-3p	1.0	-0.805	
hsa-miR-5581-5p	0.1	0.075	
hsa-miR-5582-3p	3.7	-3.256	0.006
hsa-miR-5583-3p	2.3	-2.645	
hsa-miR-5583-5p	1.1	-0.950	
hsa-miR-5584-3p	0.4	0.375	
hsa-miR-5584-5p	0.4	0.375	
hsa-miR-5586-3p	0.2	-0.148	
hsa-miR-5586-5p	0.1	0.075	
hsa-miR-5587-3p	0.9	1.330	
hsa-miR-5587-5p	1.2	0.547	
hsa-miR-5588-3p	0.6	-0.071	
hsa-miR-5588-5p	0.5	0.170	
hsa-miR-559	0.1	0.075	
hsa-miR-561-3p	11.7	-3.545	0.001
hsa-miR-561-5p	55.6	-4.190	0.000
hsa-miR-5680	0.4	0.365	
hsa-miR-5681b	0.1	0.075	
hsa-miR-6513-5p	0.9	1.325	
hsa-miR-6514-3p	2.4	1.140	
hsa-miR-6514-5p	5.2	1.348	0.190
hsa-miR-6515-3p	9.2	1.760	0.022
hsa-miR-6515-5p	1.6	0.684	
hsa-miR-6516-3p	8.1	0.963	0.230
hsa-miR-6516-5p	21.2	1.602	0.009
hsa-miR-652-3p	213.5	-1.660	0.000
hsa-miR-652-5p	13.3	-1.166	0.094
hsa-miR-653-3p	3.7	-1.474	0.184
hsa-miR-653-5p	2.7	-2.827	
hsa-miR-654-3p	3.4	-0.194	0.871
hsa-miR-654-5p	0.3	0.517	
hsa-miR-655-3p	1.8	-0.231	
hsa-miR-655-5p	0.3	0.517	
hsa-miR-656-3p	0.3	0.517	
hsa-miR-656-5p	0.3	0.517	
hsa-miR-657	2.8	1.864	
hsa-miR-658	0.1	0.075	
hsa-miR-659-3p	2.7	0.851	
hsa-miR-6847-5p	8.6	1.724	0.028
hsa-miR-6848-3p	1.3	0.386	
hsa-miR-6848-5p	2.7	1.142	
hsa-miR-6849-3p	0.8	-0.473	
hsa-miR-6849-5p	0.5	0.170	
hsa-miR-6850-3p	12.1	1.494	0.043
hsa-miR-6850-5p	34.9	1.549	0.008
hsa-miR-6851-3p	0.7	0.631	
hsa-miR-6851-5p	1.8	0.918	
hsa-miR-6852-3p	0.8	1.230	
hsa-miR-6852-5p	0.6	0.941	
hsa-miR-6853-3p	3.1	0.854	0.447
hsa-miR-6853-5p	0.5	0.810	
hsa-miR-6854-3p	0.1	0.075	
hsa-miR-6855-3p	2.2	2.666	
hsa-miR-6855-5p	0.1	0.075	
hsa-miR-6856-3p	0.6	0.919	
hsa-miR-6856-5p	0.4	0.365	
hsa-miR-6857-3p	2.1	1.126	
hsa-miR-6857-5p	0.6	0.920	
hsa-miR-6858-3p	15.7	1.263	0.047
hsa-miR-6858-5p	4.9	1.260	0.213
hsa-miR-6859-3p	3.8	0.253	0.842
hsa-miR-6859-5p	4.4	1.122	0.217
hsa-miR-6861-3p	0.4	0.368	

Table 6.2 (continued from the previous page)

hsa-miR-4436b-3p	0.4	0.368	
hsa-miR-4440	1.8	-0.876	
hsa-miR-4442	0.2	-0.135	
hsa-miR-4443	27.2	1.878	0.005
hsa-miR-4444	5.4	1.913	0.039
hsa-miR-4445-3p	0.1	0.075	
hsa-miR-4445-5p	0.1	0.075	
hsa-miR-4448	3.3	0.697	0.494
hsa-miR-4449	10.2	1.174	0.186
hsa-miR-4451	2.4	1.283	
hsa-miR-4453	0.1	0.075	
hsa-miR-4454	84.1	1.402	0.001
hsa-miR-4457	4.2	0.993	0.295
hsa-miR-4458	10.2	1.615	0.025
hsa-miR-4461	14.7	1.434	0.051
hsa-miR-4463	2.9	1.050	0.335
hsa-miR-4466	18.7	1.747	0.007
hsa-miR-4467	0.7	0.554	
hsa-miR-4469	1.2	0.543	
hsa-miR-4470	7.4	1.139	0.200
hsa-miR-4473	0.4	0.378	
hsa-miR-4474-3p	0.5	0.138	
hsa-miR-4478	0.1	0.075	
hsa-miR-4479	24.9	1.245	0.038
hsa-miR-4482-3p	0.6	-1.022	
hsa-miR-4483	2.1	1.129	
hsa-miR-4484	28.8	0.827	0.170
hsa-miR-4485-3p	44.9	1.000	0.016
hsa-miR-4485-5p	70.4	0.855	0.061
hsa-miR-4487	0.4	0.376	
hsa-miR-4488	1.8	0.923	
hsa-miR-4489	1.9	1.323	
hsa-miR-4492	0.6	0.774	
hsa-miR-4493	0.2	-0.138	
hsa-miR-4497	0.5	0.122	
hsa-miR-4498	3.0	3.102	0.012
hsa-miR-449a	45.4	0.123	0.861
hsa-miR-449b-3p	0.3	-0.425	
hsa-miR-449b-5p	18.3	-1.123	0.139
hsa-miR-449c-3p	0.2	-0.159	
hsa-miR-449c-5p	13.8	-2.894	0.000
hsa-miR-4500	5.3	-0.305	0.746
hsa-miR-4501	0.3	-0.256	
hsa-miR-4502	0.1	0.075	
hsa-miR-4504	0.1	0.075	
hsa-miR-4507	16.7	1.369	0.051
hsa-miR-4508	2.0	0.119	
hsa-miR-450a-1-3p	2.2	-2.500	
hsa-miR-450a-2-3p	1.2	-1.745	
hsa-miR-450a-5p	37.6	-2.412	0.000
hsa-miR-450b-3p	0.1	0.075	
hsa-miR-450b-5p	16.2	-3.147	0.000
hsa-miR-4510	0.1	0.075	
hsa-miR-4511	9.6	1.116	0.205
hsa-miR-4512	0.9	0.194	
hsa-miR-4515	0.3	-0.319	
hsa-miR-4516	0.3	0.517	
hsa-miR-4517	7.9	0.893	0.228
hsa-miR-4519	0.6	0.778	
hsa-miR-451a	2.6	-0.913	
hsa-miR-452-3p	9.9	-0.845	0.295
hsa-miR-452-5p	27.5	-0.910	0.065
hsa-miR-4520-2-3p	0.4	0.369	
hsa-miR-4520-3p	0.3	0.517	
hsa-miR-4520-5p	0.1	0.075	
hsa-miR-4521	2778.6	1.861	0.000
hsa-miR-4522	1.9	0.753	
hsa-miR-4523	7.0	-1.327	0.128
hsa-miR-4525	0.2	-0.124	
hsa-miR-4526	0.6	-0.094	
hsa-miR-4529-3p	0.3	0.517	
hsa-miR-4529-5p	0.3	0.517	

hsa-miR-6728-5p	3.2	1.068	0.374
hsa-miR-6729-3p	4.4	3.136	0.009
hsa-miR-6729-5p	3.0	1.427	0.208
hsa-miR-6730-5p	0.1	0.075	
hsa-miR-6731-3p	1.7	0.432	
hsa-miR-6731-5p	1.0	1.044	
hsa-miR-6732-3p	5.2	0.787	0.385
hsa-miR-6732-5p	0.4	0.378	
hsa-miR-6733-3p	2.1	1.083	
hsa-miR-6733-5p	2.7	0.888	
hsa-miR-6734-3p	2.8	1.331	
hsa-miR-6734-5p	3.8	1.900	0.058
hsa-miR-6735-3p	5.8	2.115	0.037
hsa-miR-6735-5p	6.1	1.545	0.071
hsa-miR-6736-5p	1.1	0.592	
hsa-miR-6737-3p	4.9	1.688	0.083
hsa-miR-6737-5p	2.3	0.830	
hsa-miR-6738-3p	1.7	2.338	
hsa-miR-6738-5p	0.8	1.573	
hsa-miR-6739-3p	2.0	1.369	
hsa-miR-6739-5p	0.9	1.289	
hsa-miR-6740-3p	4.7	1.505	0.121
hsa-miR-6740-5p	1.8	0.332	
hsa-miR-6741-3p	10.5	1.253	0.129
hsa-miR-6741-5p	0.5	0.122	
hsa-miR-6742-3p	5.2	1.388	0.128
hsa-miR-6742-5p	4.0	1.473	0.186
hsa-miR-6743-3p	4.6	1.336	0.140
hsa-miR-6743-5p	2.9	1.611	0.167
hsa-miR-6744-3p	0.1	0.075	
hsa-miR-6744-5p	0.1	0.075	
hsa-miR-6745	0.8	1.816	
hsa-miR-6746-3p	2.7	1.484	
hsa-miR-6746-5p	1.6	0.665	
hsa-miR-6747-3p	34.1	1.597	0.003
hsa-miR-6747-5p	1.1	1.949	
hsa-miR-6748-3p	0.8	0.319	
hsa-miR-6748-5p	0.6	-0.071	
hsa-miR-6749-3p	0.6	0.743	
hsa-miR-6749-5p	0.4	0.378	
hsa-miR-675-3p	1.2	-1.061	
hsa-miR-675-5p	3.3	-2.412	0.048
hsa-miR-6750-3p	3.5	0.800	0.488
hsa-miR-6750-5p	2.0	1.293	
hsa-miR-6751-3p	1.1	2.197	
hsa-miR-6751-5p	1.3	2.225	
hsa-miR-6752-3p	0.4	0.369	
hsa-miR-6753-3p	1.0	0.165	
hsa-miR-6753-5p	0.4	0.368	
hsa-miR-6754-3p	0.7	-0.249	
hsa-miR-6754-5p	1.7	0.484	
hsa-miR-6755-5p	0.6	0.920	
hsa-miR-6756-3p	0.8	1.575	
hsa-miR-6756-5p	0.4	0.368	
hsa-miR-6757-3p	0.4	0.368	
hsa-miR-6757-5p	0.1	0.075	
hsa-miR-6758-3p	8.0	1.245	0.106
hsa-miR-6758-5p	3.1	1.801	0.109
hsa-miR-6759-3p	0.6	0.941	
hsa-miR-6759-5p	2.9	1.004	0.388
hsa-miR-676-3p	4.3	-2.717	0.023
hsa-miR-676-5p	0.3	-0.425	
hsa-miR-6760-3p	0.3	0.517	
hsa-miR-6760-5p	0.3	0.517	
hsa-miR-6761-3p	0.4	0.371	
hsa-miR-6761-5p	0.6	0.902	
hsa-miR-6762-3p	1.4	1.080	
hsa-miR-6762-5p	0.5	1.080	
hsa-miR-6763-3p	0.7	0.661	
hsa-miR-6763-5p	7.7	0.724	0.441
hsa-miR-6764-3p	2.8	0.709	
hsa-miR-6764-5p	3.4	0.903	0.432

hsa-miR-6861-5p	0.6	0.919	
hsa-miR-6862-3p	2.7	0.870	
hsa-miR-6862-5p	5.7	0.758	0.399
hsa-miR-6863	0.1	0.075	
hsa-miR-6864-3p	0.4	0.365	
hsa-miR-6864-5p	1.0	0.919	
hsa-miR-6865-3p	0.8	0.317	
hsa-miR-6865-5p	1.0	1.002	
hsa-miR-6866-3p	1.1	1.583	
hsa-miR-6866-5p	2.8	1.312	
hsa-miR-6867-5p	0.1	0.075	
hsa-miR-6868-3p	4.5	0.725	0.469
hsa-miR-6868-5p	0.6	0.754	
hsa-miR-6869-3p	0.8	-0.392	
hsa-miR-6869-5p	2.5	1.715	
hsa-miR-6870-3p	2.1	1.787	
hsa-miR-6870-5p	0.3	0.517	
hsa-miR-6871-3p	1.4	1.018	
hsa-miR-6871-5p	2.8	0.734	
hsa-miR-6873-3p	4.0	1.573	0.110
hsa-miR-6873-5p	0.5	1.080	
hsa-miR-6874-3p	3.6	1.053	0.350
hsa-miR-6875-3p	0.8	0.386	
hsa-miR-6875-5p	1.9	1.557	
hsa-miR-6876-3p	0.9	1.330	
hsa-miR-6876-5p	1.0	1.011	
hsa-miR-6877-3p	2.3	2.288	
hsa-miR-6877-5p	12.5	2.170	0.004
hsa-miR-6878-3p	0.3	0.517	
hsa-miR-6878-5p	1.1	1.583	
hsa-miR-6879-3p	0.6	-0.096	
hsa-miR-6880-3p	0.5	0.170	
hsa-miR-6880-5p	0.8	1.581	
hsa-miR-6881-3p	4.0	1.093	0.272
hsa-miR-6881-5p	0.7	0.646	
hsa-miR-6882-3p	1.7	1.057	
hsa-miR-6882-5p	3.5	1.154	0.309
hsa-miR-6883-3p	2.1	1.152	
hsa-miR-6883-5p	0.6	0.902	
hsa-miR-6884-3p	2.2	0.449	
hsa-miR-6884-5p	1.6	0.675	
hsa-miR-6885-3p	5.8	1.214	0.181
hsa-miR-6885-5p	1.7	0.498	
hsa-miR-6886-3p	9.7	1.508	0.041
hsa-miR-6886-5p	124.7	1.699	0.002
hsa-miR-6889-3p	1.2	0.582	
hsa-miR-6889-5p	4.1	1.418	0.168
hsa-miR-6890-5p	0.6	0.902	
hsa-miR-6891-3p	3.7	0.954	0.395
hsa-miR-6891-5p	20.9	1.495	0.011
hsa-miR-6892-3p	9.2	1.024	0.160
hsa-miR-6892-5p	8.4	1.416	0.062
hsa-miR-6893-3p	3.2	1.192	0.253
hsa-miR-6893-5p	1.9	1.376	
hsa-miR-6894-3p	0.8	0.404	
hsa-miR-6894-5p	2.2	0.959	
hsa-miR-6895-3p	12.4	1.554	0.026
hsa-miR-8089	0.6	0.904	
hsa-miR-873-3p	0.3	0.517	
hsa-miR-873-5p	0.3	0.517	
hsa-miR-874-3p	1.2	-1.753	
hsa-miR-875-5p	0.1	0.075	
hsa-miR-876-3p	0.3	0.517	
hsa-miR-876-5p	0.3	0.517	
hsa-miR-877-3p	298.5	1.468	0.000
hsa-miR-877-5p	2187.9	1.719	0.001
hsa-miR-889-3p	0.9	0.379	
hsa-miR-889-5p	0.3	0.517	
hsa-miR-6780a-5p	1.9	1.560	
hsa-miR-6780b-3p	3.0	1.832	0.140
hsa-miR-6780b-5p	1.5	1.697	
hsa-miR-6781-3p	1.7	0.484	

Table 6.2 (continued from the previous page)

hsa-miR-4530	0.3	0.517	
hsa-miR-4532	0.5	0.122	
hsa-miR-4533	0.8	-0.474	
hsa-miR-454-3p	329.7	-3.022	0.000
hsa-miR-454-5p	13.5	-2.419	0.002
hsa-miR-455-3p	182.0	-0.370	0.284
hsa-miR-455-5p	57.6	-0.013	0.986
hsa-miR-4632-3p	0.4	0.378	
hsa-miR-4632-5p	0.4	0.378	
hsa-miR-4635	0.4	0.369	
hsa-miR-4637	0.1	0.075	
hsa-miR-4638-3p	3.9	0.173	0.890
hsa-miR-4638-5p	1.4	0.955	
hsa-miR-4639-3p	0.5	0.170	
hsa-miR-4639-5p	0.4	0.375	
hsa-miR-4640-3p	2.2	0.951	
hsa-miR-4640-5p	3.3	2.128	0.062
hsa-miR-4641	1.6	1.378	
hsa-miR-4642	0.1	0.075	
hsa-miR-4644	0.2	-0.148	
hsa-miR-4645-3p	1.3	0.315	
hsa-miR-4645-5p	0.6	0.774	
hsa-miR-4646-3p	1.5	0.849	
hsa-miR-4646-5p	0.3	0.517	
hsa-miR-4647	1.7	2.284	
hsa-miR-4648	0.6	0.754	
hsa-miR-4651	2.0	2.109	
hsa-miR-4652-3p	0.6	-0.097	
hsa-miR-4652-5p	0.5	0.156	
hsa-miR-4653-3p	0.3	-0.343	
hsa-miR-4653-5p	0.3	-0.346	
hsa-miR-4654	0.6	-1.014	
hsa-miR-4655-3p	0.1	0.075	
hsa-miR-4655-5p	0.1	0.075	
hsa-miR-4656	0.9	1.448	
hsa-miR-4657	0.9	1.334	
hsa-miR-4658	0.7	-0.239	
hsa-miR-4659a-3p	1.3	-1.875	
hsa-miR-4659a-5p	0.1	0.075	
hsa-miR-466	0.1	0.075	
hsa-miR-4764-3p	0.3	0.517	
hsa-miR-4764-5p	0.3	0.517	
hsa-miR-4766-3p	2.6	-0.871	
hsa-miR-4766-5p	0.4	0.369	
hsa-miR-4767	1.7	-0.201	
hsa-miR-4768-5p	0.1	0.075	
hsa-miR-4769-3p	0.1	0.075	
hsa-miR-4771	0.4	0.364	
hsa-miR-4774-3p	0.2	-0.124	
hsa-miR-4775	1.2	0.489	
hsa-miR-4776-3p	0.1	0.075	
hsa-miR-4776-5p	0.1	0.075	
hsa-miR-4777-3p	0.2	-0.138	
hsa-miR-4781-3p	0.8	1.581	
hsa-miR-4781-5p	0.1	0.075	
hsa-miR-4783-3p	9.1	-1.574	0.052
hsa-miR-4783-5p	0.2	-0.148	
hsa-miR-4784	0.3	0.517	
hsa-miR-4785	22.8	1.237	0.031
hsa-miR-4786-3p	1.1	0.786	
hsa-miR-4787-3p	34.5	0.766	0.127
hsa-miR-4787-5p	1.4	0.917	
hsa-miR-4788	0.3	0.517	
hsa-miR-4791	2.5	1.167	
hsa-miR-4793-3p	0.1	0.075	
hsa-miR-4795-3p	0.6	0.941	
hsa-miR-4796-3p	0.6	-0.861	
hsa-miR-4796-5p	0.2	-0.135	
hsa-miR-4797-3p	0.5	0.170	
hsa-miR-4797-5p	0.3	0.517	
hsa-miR-4799-3p	0.1	0.075	
hsa-miR-4799-5p	0.1	0.075	

hsa-miR-6765-3p	63.8	1.469	0.000
hsa-miR-6827-5p	2.2	1.646	
hsa-miR-6828-3p	0.3	0.517	
hsa-miR-6828-5p	0.3	0.517	
hsa-miR-6829-3p	0.3	0.517	
hsa-miR-6829-5p	0.2	-0.135	
hsa-miR-6830-3p	2.7	2.073	
hsa-miR-6830-5p	0.8	1.216	
hsa-miR-6831-3p	1.5	1.397	
hsa-miR-6831-5p	0.7	0.568	
hsa-miR-6832-3p	4.3	1.545	0.117
hsa-miR-6832-5p	6.0	3.685	0.001
hsa-miR-6833-3p	2.5	1.174	
hsa-miR-6833-5p	0.5	0.810	
hsa-miR-6834-3p	10.0	1.505	0.049
hsa-miR-6834-5p	1.4	-0.400	
hsa-miR-6835-5p	0.4	0.365	
hsa-miR-6836-3p	0.5	0.170	
hsa-miR-6836-5p	0.4	0.376	
hsa-miR-6837-3p	1.6	0.620	
hsa-miR-6837-5p	0.5	0.170	
hsa-miR-6838-3p	2.6	0.037	
hsa-miR-6838-5p	1.0	0.138	
hsa-miR-6839-3p	0.5	0.817	
hsa-miR-6839-5p	0.5	0.817	
hsa-miR-6840-3p	0.3	-0.357	
hsa-miR-6840-5p	0.4	-0.547	
hsa-miR-6841-3p	0.3	0.517	
hsa-miR-6841-5p	0.3	0.517	
hsa-miR-6842-3p	2.5	1.174	
hsa-miR-6843-3p	2.1	1.150	
hsa-miR-6844	93.8	1.197	0.062
hsa-miR-6845-3p	1.8	0.936	
hsa-miR-6845-5p	0.5	0.156	
hsa-miR-6846-3p	1.9	0.216	
hsa-miR-6846-5p	1.9	1.391	
hsa-miR-6847-3p	3.5	1.321	0.197
hsa-miR-5701	0.3	-0.287	
hsa-miR-5702	0.3	0.517	
hsa-miR-5703	1.0	1.101	
hsa-miR-5707	0.3	0.517	
hsa-miR-572	2.4	-0.281	
hsa-miR-573	15.8	1.344	0.049
hsa-miR-574-3p	118.8	-0.560	0.092
hsa-miR-574-5p	0.3	0.517	
hsa-miR-576-3p	7.0	-4.082	0.000
hsa-miR-576-5p	47.0	-4.665	0.000
hsa-miR-577	18.1	-2.337	0.002
hsa-miR-578	0.1	0.075	
hsa-miR-5787	0.1	0.075	
hsa-miR-579-3p	1.3	-1.784	
hsa-miR-579-5p	1.1	-1.578	
hsa-miR-580-3p	0.7	-1.193	
hsa-miR-583	0.1	0.075	
hsa-miR-584-3p	5.7	-0.436	0.641
hsa-miR-584-5p	230.7	-0.750	0.002
hsa-miR-588	0.2	-0.159	
hsa-miR-589-3p	17.2	-1.124	0.063
hsa-miR-589-5p	35.6	-1.812	0.000
hsa-miR-590-3p	197.5	-2.732	0.000
hsa-miR-590-5p	92.4	-2.742	0.000
hsa-miR-592	1.5	0.072	
hsa-miR-595	0.1	0.075	
hsa-miR-596	0.1	0.075	
hsa-miR-597-3p	1.6	-1.384	
hsa-miR-597-5p	3.1	-2.269	0.064
hsa-miR-598-3p	0.2	-0.124	
hsa-miR-600	0.8	-0.392	
hsa-miR-601	0.5	0.809	
hsa-miR-602	1.5	1.676	
hsa-miR-605-5p	0.1	0.075	
hsa-miR-606	0.4	-0.365	

hsa-miR-6781-5p	1.6	0.678	
hsa-miR-6782-3p	1.2	-0.167	
hsa-miR-6782-5p	0.2	-0.159	
hsa-miR-6783-3p	7.3	0.569	0.493
hsa-miR-6783-5p	4.7	0.840	0.393
hsa-miR-6784-3p	10.8	2.229	0.002
hsa-miR-6784-5p	0.8	0.404	
hsa-miR-6785-5p	1.7	2.303	
hsa-miR-6786-3p	11.6	1.246	0.101
hsa-miR-6786-5p	3.5	1.040	0.415
hsa-miR-6787-3p	6.3	1.963	0.031
hsa-miR-6787-5p	0.3	0.517	
hsa-miR-6789-3p	5.6	1.668	0.068
hsa-miR-6789-5p	33.0	1.703	0.007
hsa-miR-6790-3p	3.7	1.318	0.255
hsa-miR-6790-5p	1.2	1.759	
hsa-miR-6791-3p	3.6	2.202	0.056
hsa-miR-6791-5p	2.1	2.018	
hsa-miR-6792-3p	7.0	1.421	0.083
hsa-miR-6792-5p	2.3	1.465	
hsa-miR-6793-3p	1.5	0.704	
hsa-miR-6793-5p	3.1	1.737	0.138
hsa-miR-6794-3p	7.0	0.713	0.427
hsa-miR-6794-5p	1.0	1.082	
hsa-miR-6795-3p	1.5	1.649	
hsa-miR-6795-5p	0.3	0.517	
hsa-miR-6796-3p	1.3	0.380	
hsa-miR-6796-5p	0.3	-0.256	
hsa-miR-6797-3p	28.0	1.382	0.006
hsa-miR-6797-5p	3.0	0.083	0.953
hsa-miR-6798-3p	2.4	1.868	
hsa-miR-6798-5p	0.3	0.517	
hsa-miR-6799-3p	14.2	1.670	0.006
hsa-miR-6799-5p	2.5	1.730	
hsa-miR-6800-3p	20.7	1.539	0.021
hsa-miR-6800-5p	0.8	0.544	
hsa-miR-6801-3p	7.6	1.405	0.130
hsa-miR-6801-5p	3.8	1.268	0.256
hsa-miR-6802-3p	1.0	-0.813	
hsa-miR-6802-5p	0.6	-0.071	
hsa-miR-6803-3p	7.9	1.781	0.021
hsa-miR-6803-5p	0.3	0.517	
hsa-miR-6804-3p	0.7	0.599	
hsa-miR-6804-5p	6.1	1.549	0.072
hsa-miR-6805-3p	1.6	0.702	
hsa-miR-6805-5p	13.8	1.225	0.158
hsa-miR-6806-3p	2.6	0.423	
hsa-miR-6807-3p	35.1	1.342	0.004
hsa-miR-6807-5p	14.7	1.366	0.031
hsa-miR-6808-3p	1.7	1.130	
hsa-miR-6808-5p	0.6	0.941	
hsa-miR-6810-3p	1.6	1.379	
hsa-miR-6810-5p	1.4	1.809	
hsa-miR-6811-3p	1.2	0.551	
hsa-miR-6811-5p	3.9	1.193	0.247
hsa-miR-6812-3p	6.9	1.141	0.208
hsa-miR-6812-5p	0.4	0.378	
hsa-miR-6813-3p	0.6	0.941	
hsa-miR-6813-5p	1.4	0.217	
hsa-miR-6814-3p	0.3	0.517	
hsa-miR-6814-5p	0.3	0.517	
hsa-miR-6815-3p	2.9	0.983	0.445
hsa-miR-6815-5p	1.9	0.808	
hsa-miR-6816-3p	8.0	1.236	0.114
hsa-miR-6816-5p	0.5	0.810	
hsa-miR-6817-3p	4.2	0.897	0.361
hsa-miR-6817-5p	1.0	1.022	
hsa-miR-6818-3p	2.7	0.785	
hsa-miR-6818-5p	2.2	1.819	
hsa-miR-6819-3p	2.5	0.556	
hsa-miR-6819-5p	1.1	0.581	
hsa-miR-6820-3p	3.2	0.768	0.473

Table 6.2 (continued from the previous page)

hsa-miR-4800-3p	0.3	0.517	
hsa-miR-4800-5p	0.3	0.517	
hsa-miR-4802-5p	0.1	0.075	
hsa-miR-4803	0.2	-0.148	
hsa-miR-4804-3p	0.2	-0.148	
hsa-miR-4804-5p	0.7	-0.313	
hsa-miR-483-3p	97.4	-1.179	0.001
hsa-miR-483-5p	35.9	-0.649	0.150
hsa-miR-484	4112.4	1.417	0.000
hsa-miR-485-3p	1.8	0.366	
hsa-miR-485-5p	0.3	0.517	
hsa-miR-486-3p	0.4	0.364	
hsa-miR-486-5p	3.4	-1.830	0.130
hsa-miR-487a-3p	1.0	2.193	
hsa-miR-487a-5p	0.3	0.517	
hsa-miR-487b-3p	2.3	0.799	
hsa-miR-487b-5p	0.3	0.517	
hsa-miR-488-3p	0.3	0.517	
hsa-miR-488-5p	0.3	0.517	
hsa-miR-489-3p	7.5	-1.402	0.130
hsa-miR-489-5p	0.3	-0.346	
hsa-miR-491-3p	4.4	-0.398	0.711
hsa-miR-491-5p	36.0	-2.371	0.000
hsa-miR-493-5p	0.1	0.075	
hsa-miR-494-3p	0.5	0.098	
hsa-miR-494-5p	0.3	0.517	
hsa-miR-495-3p	3.6	0.032	0.986
hsa-miR-495-5p	0.3	0.517	
hsa-miR-496	0.4	0.378	
hsa-miR-497-3p	0.6	-1.006	
hsa-miR-497-5p	26.7	-1.281	0.011
hsa-miR-4999-3p	1.1	-0.023	
hsa-miR-4999-5p	1.6	-0.051	
hsa-miR-499a-3p	0.8	0.307	
hsa-miR-499a-5p	19.9	0.063	0.925
hsa-miR-499b-5p	0.1	0.075	
hsa-miR-5001-3p	22.8	0.815	0.101
hsa-miR-5001-5p	2.8	1.185	0.269
hsa-miR-5002-5p	0.1	0.075	
hsa-miR-5003-5p	0.1	0.075	
hsa-miR-5004-3p	0.2	-0.135	
hsa-miR-5004-5p	0.3	0.517	
hsa-miR-5006-3p	2.6	1.434	
hsa-miR-5006-5p	0.3	0.517	
hsa-miR-5007-5p	0.3	0.517	
hsa-miR-5008-3p	3.1	-3.009	0.014
hsa-miR-5008-5p	1.9	-2.413	
hsa-miR-5009-3p	0.1	0.075	
hsa-miR-5009-5p	0.1	0.075	
hsa-miR-500a-3p	38.7	-1.964	0.000
hsa-miR-500a-5p	31.3	-1.514	0.004
hsa-miR-500b-3p	0.1	0.075	
hsa-miR-500b-5p	31.3	-1.514	0.004
hsa-miR-501-3p	22.9	-1.720	0.012
hsa-miR-501-5p	41.6	-1.051	0.017
hsa-miR-5010-3p	35.4	1.506	0.001
hsa-miR-5010-5p	4.2	1.337	0.155
hsa-miR-5011-3p	0.1	0.075	
hsa-miR-5011-5p	0.1	0.075	
hsa-miR-502-3p	42.0	-1.995	0.000
hsa-miR-502-5p	7.2	-1.365	0.108
hsa-miR-503-3p	2.2	-0.617	
hsa-miR-503-5p	234.9	-0.298	0.427
hsa-miR-504-5p	0.4	0.376	
hsa-miR-5047	2.2	0.329	
hsa-miR-505-3p	111.5	-1.108	0.001
hsa-miR-505-5p	7.6	-0.441	0.620
hsa-miR-508-3p	0.3	0.517	
hsa-miR-5087	1.4	2.049	
hsa-miR-5088-3p	10.4	2.071	0.004
hsa-miR-5088-5p	4.7	1.982	0.055
hsa-miR-5089-3p	0.4	-0.365	

hsa-miR-607	0.9	0.362	
hsa-miR-6071	0.3	0.517	
hsa-miR-6073	0.1	0.075	
hsa-miR-6076	0.1	0.075	
hsa-miR-6077	0.5	1.080	
hsa-miR-6080	0.1	0.075	
hsa-miR-6084	0.1	0.075	
hsa-miR-6086	0.1	0.075	
hsa-miR-6087	10.6	0.647	0.371
hsa-miR-611	0.4	0.369	
hsa-miR-612	0.1	0.075	
hsa-miR-6124	0.1	0.075	
hsa-miR-6125	0.4	0.365	
hsa-miR-6127	0.3	0.517	
hsa-miR-6131	0.1	0.075	
hsa-miR-6132	0.3	0.517	
hsa-miR-6134	0.2	-0.138	
hsa-miR-615-3p	87.7	-0.812	0.018
hsa-miR-615-5p	2.9	-1.070	0.363
hsa-miR-616-3p	0.6	-1.006	
hsa-miR-616-5p	3.8	-2.583	0.032
hsa-miR-618	3.9	-2.043	0.079
hsa-miR-620	0.3	0.517	
hsa-miR-621	0.3	0.517	
hsa-miR-623	0.3	0.517	
hsa-miR-624-3p	3.0	-2.962	0.016
hsa-miR-624-5p	6.7	-2.041	0.037
hsa-miR-625-3p	59.3	-3.112	0.000
hsa-miR-625-5p	34.4	-2.942	0.000
hsa-miR-627-3p	6.6	-4.013	0.000
hsa-miR-627-5p	11.0	-4.629	0.000
hsa-miR-628-3p	9.8	-2.104	0.013
hsa-miR-628-5p	8.9	-1.533	0.056
hsa-miR-629-3p	11.4	-2.873	0.001
hsa-miR-629-5p	67.3	-4.117	0.000
hsa-miR-632	0.4	0.368	
hsa-miR-635	0.1	0.075	
hsa-miR-636	88.3	1.690	0.000
hsa-miR-637	0.3	0.517	
hsa-miR-638	0.2	-0.159	
hsa-miR-639	0.2	-0.135	
hsa-miR-641	10.4	-2.454	0.004
hsa-miR-642a-3p	10.4	-1.276	0.077
hsa-miR-642a-5p	28.0	-1.237	0.016
hsa-miR-642b-3p	0.6	-0.093	
hsa-miR-642b-5p	2.5	0.089	
hsa-miR-643	2.8	-1.522	0.214
hsa-miR-644a	0.1	0.075	
hsa-miR-646	1.0	0.001	
hsa-miR-647	0.7	0.573	
hsa-miR-6501-3p	2.5	1.723	
hsa-miR-6501-5p	7.4	0.555	0.492
hsa-miR-6503-3p	0.2	-0.148	
hsa-miR-6504-3p	0.4	0.368	
hsa-miR-6504-5p	0.4	0.368	
hsa-miR-6505-3p	0.6	0.920	
hsa-miR-6505-5p	2.4	0.237	
hsa-miR-6509-3p	0.3	-0.346	
hsa-miR-6509-5p	0.1	0.075	
hsa-miR-651-3p	0.3	-0.357	
hsa-miR-651-5p	24.6	-3.003	0.000
hsa-miR-6510-3p	0.4	0.365	
hsa-miR-6510-5p	0.1	0.075	
hsa-miR-6511a-3p	52.3	1.427	0.004
hsa-miR-6511a-5p	36.2	1.430	0.011
hsa-miR-6511b-3p	28.3	1.645	0.005
hsa-miR-6511b-5p	36.4	1.444	0.010
hsa-miR-6512-3p	0.3	0.517	
hsa-miR-6512-5p	0.3	0.517	
hsa-miR-6513-3p	1.3	1.423	
hsa-miR-6765-5p	1.5	1.571	
hsa-miR-6766-3p	1.6	0.485	

hsa-miR-6820-5p	4.9	1.002	0.310
hsa-miR-6821-3p	4.6	1.663	0.070
hsa-miR-6821-5p	2.2	1.729	
hsa-miR-6822-5p	0.5	1.080	
hsa-miR-6823-3p	0.5	0.809	
hsa-miR-6823-5p	0.8	1.816	
hsa-miR-6824-3p	2.6	0.442	
hsa-miR-6824-5p	0.6	0.778	
hsa-miR-6825-3p	0.8	0.350	
hsa-miR-6825-5p	2.5	1.158	
hsa-miR-6826-3p	0.6	0.920	
hsa-miR-6826-5p	1.4	1.084	
hsa-miR-6827-3p	2.2	0.990	
hsa-miR-6895-5p	1.8	0.871	
hsa-miR-7-1-3p	111.3	-0.915	0.028
hsa-miR-7-2-3p	0.6	0.904	
hsa-miR-7-5p	4213.0	-0.933	0.007
hsa-miR-708-3p	0.1	0.075	
hsa-miR-708-5p	0.6	0.920	
hsa-miR-7106-3p	0.5	0.122	
hsa-miR-7106-5p	1.0	1.007	
hsa-miR-7108-3p	7.2	1.274	0.132
hsa-miR-7108-5p	11.9	1.743	0.017
hsa-miR-7109-3p	2.3	1.336	
hsa-miR-7109-5p	2.8	1.223	
hsa-miR-711	0.3	0.517	
hsa-miR-7110-3p	5.8	1.179	0.225
hsa-miR-7110-5p	0.3	0.517	
hsa-miR-7111-3p	63.4	1.457	0.001
hsa-miR-7111-5p	8.0	1.161	0.181
hsa-miR-7112-3p	5.8	-0.032	0.983
hsa-miR-7112-5p	5.1	1.056	0.345
hsa-miR-7113-3p	0.4	0.369	
hsa-miR-7113-5p	1.9	0.775	
hsa-miR-7114-3p	1.7	0.528	
hsa-miR-7114-5p	4.2	1.213	0.304
hsa-miR-7150	0.5	0.809	
hsa-miR-7152-3p	0.2	-0.124	
hsa-miR-7152-5p	0.5	0.170	
hsa-miR-7154-3p	0.1	0.075	
hsa-miR-7154-5p	0.1	0.075	
hsa-miR-7155-3p	0.5	0.156	
hsa-miR-7155-5p	0.6	0.920	
hsa-miR-7159-3p	0.3	0.517	
hsa-miR-7159-5p	0.3	0.517	
hsa-miR-718	0.3	0.517	
hsa-miR-744-3p	15.2	-1.797	0.008
hsa-miR-744-5p	651.8	-1.432	0.000
hsa-miR-758-3p	0.5	1.080	
hsa-miR-758-5p	0.3	0.517	
hsa-miR-759	0.2	-0.148	
hsa-miR-760	27.7	0.577	0.292
hsa-miR-762	0.3	0.517	
hsa-miR-7641	10.2	0.879	0.351
hsa-miR-765	2.8	1.851	0.108
hsa-miR-766-3p	13.8	-1.005	0.140
hsa-miR-766-5p	1.3	-1.121	
hsa-miR-767-5p	0.2	-0.124	
hsa-miR-769-3p	105.7	-0.933	0.004
hsa-miR-769-5p	267.4	-1.024	0.001
hsa-miR-7703	5.4	1.172	0.244
hsa-miR-7704	2.6	1.501	
hsa-miR-7705	14.1	1.443	0.016
hsa-miR-7706	257.6	1.456	0.002
hsa-miR-7844-5p	0.6	0.778	
hsa-miR-7845-5p	0.3	0.517	
hsa-miR-7846-3p	0.4	0.378	
hsa-miR-7847-3p	0.1	0.075	
hsa-miR-7850-5p	0.1	0.075	
hsa-miR-7851-3p	9.3	-1.624	0.037
hsa-miR-7854-3p	3.9	-1.575	0.152
hsa-miR-7855-5p	0.3	0.517	

Table 6.2 (continued from the previous page)

hsa-miR-5089-5p	0.7	-0.239	
hsa-miR-5090	5.9	1.704	0.071
hsa-miR-5091	0.5	1.080	
hsa-miR-5092	0.2	-0.135	
hsa-miR-5093	0.9	1.289	
hsa-miR-5094	16.2	1.555	0.011
hsa-miR-5100	19.1	1.348	0.019
hsa-miR-511-3p	0.3	-0.319	
hsa-miR-511-5p	0.3	0.517	
hsa-miR-512-5p	0.1	0.075	
hsa-miR-516a-5p	2.6	-0.406	
hsa-miR-517a-3p	0.5	0.138	
hsa-miR-517b-3p	0.5	0.138	
hsa-miR-5187-3p	1.2	-0.253	
hsa-miR-5683	0.2	-0.148	
hsa-miR-5684	0.6	0.920	
hsa-miR-5690	0.7	-1.043	
hsa-miR-5692a	0.1	0.075	
hsa-miR-5692b	0.5	0.810	
hsa-miR-5693	0.6	-0.108	
hsa-miR-5695	1.0	1.007	
hsa-miR-5696	1.9	0.237	
hsa-miR-5697	0.7	0.661	
hsa-miR-5699-3p	6.1	-2.238	0.036
hsa-miR-5699-5p	3.7	-1.042	0.350
hsa-miR-570-3p	6.0	-2.634	0.021
hsa-miR-570-5p	1.6	-1.437	
hsa-miR-936	0.1	0.075	
hsa-miR-937-3p	51.6	1.304	0.013
hsa-miR-937-5p	9.7	1.810	0.041
hsa-miR-938	0.5	0.170	
hsa-miR-939-3p	11.5	0.721	0.381
hsa-miR-939-5p	27.7	1.685	0.004
hsa-miR-940	60.1	-0.895	0.102
hsa-miR-941	177.3	1.428	0.000
hsa-miR-942-3p	1.3	-1.053	
hsa-miR-942-5p	16.5	-1.821	0.004
hsa-miR-943	2.7	1.358	
hsa-miR-95-3p	78.8	-0.734	0.079
hsa-miR-95-5p	2.1	-0.037	
hsa-miR-96-3p	11.4	0.031	0.979
hsa-miR-96-5p	375.2	-0.072	0.901
hsa-miR-98-3p	51.0	-1.553	0.002
hsa-miR-98-5p	1003.9	-1.261	0.000
hsa-miR-99a-5p	7.0	-0.438	0.674
hsa-miR-99b-3p	94.6	-1.795	0.000
hsa-miR-99b-5p	947.9	-1.830	0.000
hsa-miR-6766-5p	0.9	1.334	
hsa-miR-6767-3p	20.6	1.515	0.008
hsa-miR-6767-5p	21.1	1.658	0.006
hsa-miR-6768-3p	21.4	1.558	0.006
hsa-miR-6768-5p	29.1	1.554	0.003
hsa-miR-6769a-3p	0.6	-0.071	
hsa-miR-6769a-5p	1.9	0.775	
hsa-miR-6769b-3p	2.1	1.154	
hsa-miR-6770-3p	4.6	0.873	0.413
hsa-miR-6770-5p	7.5	1.304	0.108
hsa-miR-6771-3p	0.3	0.517	
hsa-miR-6771-5p	0.9	1.059	
hsa-miR-6772-3p	2.1	1.176	
hsa-miR-6772-5p	0.5	1.080	
hsa-miR-6773-3p	1.0	1.116	
hsa-miR-6773-5p	1.7	1.130	
hsa-miR-6775-3p	5.5	0.607	0.499
hsa-miR-6775-5p	0.4	0.365	
hsa-miR-6776-3p	3.0	2.237	0.055
hsa-miR-6776-5p	1.3	0.315	
hsa-miR-6777-3p	38.7	1.434	0.007
hsa-miR-6777-5p	7.6	1.706	0.036
hsa-miR-6778-3p	0.6	0.940	
hsa-miR-6778-5p	1.0	0.923	
hsa-miR-6779-3p	1.2	0.530	
hsa-miR-6779-5p	1.8	1.892	
hsa-miR-6780a-3p	0.9	1.071	
hsa-miR-7973	0.1	0.075	
hsa-miR-7974	190.5	1.149	0.044
hsa-miR-7975	0.8	1.569	
hsa-miR-7976	3.1	-2.343	0.055
hsa-miR-7977	2.3	1.230	
hsa-miR-8052	0.1	0.075	
hsa-miR-8065	0.3	0.517	
hsa-miR-8071	0.3	0.517	
hsa-miR-8072	3.1	0.854	0.458
hsa-miR-8074	1.3	2.222	
hsa-miR-8077	0.4	0.365	
hsa-miR-891a-5p	0.5	0.138	
hsa-miR-892c-3p	1.1	0.700	
hsa-miR-9-3p	23.4	-0.415	0.524
hsa-miR-9-5p	94.9	-0.239	0.746
hsa-miR-920	0.3	0.517	
hsa-miR-922	0.3	0.517	
hsa-miR-924	0.8	-0.415	
hsa-miR-92a-1-5p	43.3	-0.401	0.337
hsa-miR-92a-3p	6872.4	-0.414	0.139
hsa-miR-92b-3p	494.9	0.051	0.908
hsa-miR-92b-5p	44.7	0.181	0.722
hsa-miR-93-3p	210.0	-0.150	0.657
hsa-miR-93-5p	5988.3	0.072	0.759
hsa-miR-933	8.3	1.945	0.019
hsa-miR-934	0.3	0.517	
hsa-miR-935	13.1	-1.230	0.117
spk_1	462.7	1.334	0.005
spk_4	1131.9	1.152	0.066
spk_7	1329.3	1.136	0.070
spk_9	750.2	1.535	0.002
spk_10	2536.2	1.018	0.097
spk_11	1130.8	1.187	0.039
spk_12	3092.4	1.166	0.058
spk_20	2018.2	1.266	0.041
spk_21	1631.8	1.207	0.031
spk_22	869.8	1.498	0.018
spk_24	2604.3	1.192	0.067
spk_25	523.2	1.044	0.004
spk_26	1567.5	1.425	0.014
spk_29	2227.5	0.406	0.579
spk_30	934.1	1.244	0.006

Table 6.3 DESeq2 output from small RNA sequencing of HEK293E *DROSHA* KO rescued with FLm or p140m.

mature	baseMean	log2FC	padj
hsa-let-7a-2-3p	0.1	-0.010	
hsa-let-7a-3p	106.6	0.194	0.797
hsa-let-7a-5p	3465.8	0.303	0.449
hsa-let-7b-3p	22.0	0.327	0.793
hsa-let-7b-5p	399.2	0.303	0.508
hsa-let-7c-3p	9.8	-0.147	0.939
hsa-let-7c-5p	717.6	-0.188	0.765
hsa-let-7d-3p	5.8	-0.310	0.886
hsa-let-7d-5p	76.2	-0.680	0.148
hsa-let-7e-3p	10.6	-0.519	0.753
hsa-let-7e-5p	625.6	0.044	0.957
hsa-let-7f-1-3p	0.3	0.124	
hsa-let-7f-2-3p	20.0	0.133	0.929
hsa-let-7f-5p	1379.3	0.329	0.326
hsa-let-7g-3p	7.4	-0.311	0.874
hsa-let-7g-5p	875.2	0.466	0.163
hsa-let-7i-3p	4.9	-0.296	0.896
hsa-let-7i-5p	173.3	-0.513	0.196
hsa-miR-1-3p	7.6	-0.393	0.838
hsa-miR-1-5p	0.3	-0.153	
hsa-miR-100-5p	46.9	-0.178	0.855
hsa-miR-101-3p	1149.1	0.131	0.855
hsa-miR-101-5p	6.7	0.137	0.956
hsa-miR-103a-2-5p	4.4	-0.332	0.886
hsa-miR-103a-3p	4064.2	0.166	0.780
hsa-miR-103b	0.4	0.127	
hsa-miR-105-3p	0.1	-0.010	
hsa-miR-105-5p	0.3	-0.179	
hsa-miR-106a-5p	185.0	-0.168	0.810
hsa-miR-106b-3p	356.6	-0.172	0.765
hsa-miR-106b-5p	3254.0	0.032	0.970
hsa-miR-107	613.5	0.127	0.848
hsa-miR-10a-3p	308.6	-0.004	0.994
hsa-miR-10a-5p	12450.2	-0.010	0.990
hsa-miR-10b-3p	20.7	0.155	0.912
hsa-miR-10b-5p	1348.8	0.277	0.455
hsa-miR-1178-3p	0.5	0.289	
hsa-miR-1178-5p	0.3	0.114	
hsa-miR-1179	2.1	-0.360	0.886
hsa-miR-1180-3p	139.4	-2.253	0.000
hsa-miR-1180-5p	4.2	-0.995	0.534
hsa-miR-1185-1-3p	0.5	0.538	
hsa-miR-1193	0.1	-0.010	
hsa-miR-1199-3p	0.4	-0.272	
hsa-miR-1199-5p	0.4	-0.272	
hsa-miR-1200	0.2	0.244	
hsa-miR-122-5p	3.2	0.884	0.625
hsa-miR-1273d	2.6	-2.048	0.063
hsa-miR-1273e	2.7	0.662	0.765
hsa-miR-1273f	0.1	-0.010	
hsa-miR-1273g-3p	0.1	-0.010	
hsa-miR-1273g-5p	0.1	-0.010	
hsa-miR-1273h-3p	1.1	-0.971	
hsa-miR-1275	198.0	0.885	0.031
hsa-miR-1276	0.7	-0.699	
hsa-miR-1277-3p	14.0	-0.670	0.616
hsa-miR-1277-5p	86.4	-0.765	0.322
hsa-miR-1278	0.6	-0.640	
hsa-miR-128-1-5p	4.8	-1.173	0.419
hsa-miR-128-3p	290.1	-2.150	0.000
hsa-miR-1281	0.3	0.114	
hsa-miR-1284	2.4	-1.451	0.294
hsa-miR-1285-3p	5.2	-1.541	0.211
hsa-miR-1286	3.1	-1.384	0.334
hsa-miR-1287-3p	0.6	-0.160	
hsa-miR-1287-5p	10.0	-1.071	0.316
hsa-miR-1288-3p	0.1	-0.010	
hsa-miR-1289	0.0		
hsa-miR-129-1-3p	3.3	-0.202	0.930
hsa-miR-129-2-3p	30.6	0.441	0.626
hsa-miR-129-5p	38.1	0.022	0.989

mature	baseMean	log2FC	padj
hsa-miR-1224-3p	5.0	-0.220	0.922
hsa-miR-1224-5p	9.1	0.458	0.781
hsa-miR-1225-3p	0.8	-0.460	
hsa-miR-1225-5p	0.5	-0.162	
hsa-miR-1226-3p	203.3	0.408	0.449
hsa-miR-1226-5p	26.4	0.813	0.248
hsa-miR-1227-3p	20.3	-0.119	0.935
hsa-miR-1227-5p	0.3	0.114	
hsa-miR-1228-3p	19.6	0.434	0.737
hsa-miR-1228-5p	6.0	1.083	0.415
hsa-miR-1229-3p	114.9	0.592	0.216
hsa-miR-1229-5p	0.8	0.450	
hsa-miR-1233-3p	5.4	0.428	0.838
hsa-miR-1233-5p	1.0	0.530	
hsa-miR-1234-3p	2.5	0.079	0.983
hsa-miR-1236-3p	5.5	0.581	0.770
hsa-miR-1236-5p	1.0	-0.294	
hsa-miR-1237-3p	21.5	0.479	0.674
hsa-miR-1237-5p	1.7	0.815	
hsa-miR-1238-3p	0.6	0.177	
hsa-miR-124-3p	18.3	-0.698	0.477
hsa-miR-124-5p	2.2	0.018	0.994
hsa-miR-1243	0.7	-0.606	
hsa-miR-1246	3.2	0.702	0.736
hsa-miR-1248	1.4	0.342	
hsa-miR-1249-3p	16.4	-0.608	0.595
hsa-miR-1249-5p	0.4	-0.272	
hsa-miR-1250-3p	1.2	-0.353	
hsa-miR-1250-5p	12.3	-3.064	0.001
hsa-miR-1252-3p	0.9	0.019	
hsa-miR-1252-5p	1.4	-0.932	
hsa-miR-1254	78.5	0.794	0.051
hsa-miR-1255a	1.3	-0.500	
hsa-miR-1256	1.4	-0.322	
hsa-miR-1257	13.0	0.667	0.595
hsa-miR-1258	0.6	-0.222	
hsa-miR-125a-3p	22.0	0.525	0.595
hsa-miR-125a-5p	867.5	0.148	0.798
hsa-miR-125b-1-3p	1.4	0.938	
hsa-miR-125b-2-3p	70.7	-0.177	0.840
hsa-miR-125b-5p	845.0	-0.092	0.873
hsa-miR-126-3p	353.0	0.329	0.389
hsa-miR-126-5p	237.0	0.035	0.961
hsa-miR-1260a	29.6	0.358	0.757
hsa-miR-1260b	2141.9	0.386	0.181
hsa-miR-1262	2.6	-2.033	0.066
hsa-miR-1265	0.3	0.244	
hsa-miR-1266-3p	0.1	-0.010	
hsa-miR-1266-5p	1.0	-1.025	
hsa-miR-1267	1.7	-0.790	
hsa-miR-1268b	47.6	0.425	0.616
hsa-miR-1269b	26.6	-0.495	0.616
hsa-miR-127-3p	0.2	0.244	
hsa-miR-1271-3p	7.2	-1.301	0.291
hsa-miR-1271-5p	1.2	-1.153	
hsa-miR-1272	1.4	-0.145	
hsa-miR-1273a	0.3	0.244	
hsa-miR-1273c	0.6	-0.504	
hsa-miR-141-3p	11.2	-0.112	0.957
hsa-miR-141-5p	0.5	0.538	
hsa-miR-142-3p	2.5	-0.446	0.848
hsa-miR-142-5p	1.4	-0.173	
hsa-miR-143-3p	1.0	0.082	
hsa-miR-143-5p	0.1	-0.010	
hsa-miR-144-3p	0.3	0.114	
hsa-miR-144-5p	0.7	-0.261	
hsa-miR-145-3p	0.1	-0.010	
hsa-miR-145-5p	0.6	0.176	
hsa-miR-146a-5p	4.1	0.152	0.956
hsa-miR-146b-3p	0.4	0.463	
hsa-miR-146b-5p	35.3	-0.231	0.840

mature	baseMean	log2FC	padj
hsa-miR-5088-5p	1.8	0.424	
hsa-miR-5089-3p	0.2	0.244	
hsa-miR-509-3-5p	0.3	0.244	
hsa-miR-5699-5p	2.0	-0.334	
hsa-miR-570-3p	3.1	-1.390	0.340
hsa-miR-570-5p	1.2	-0.574	
hsa-miR-5701	0.4	0.463	
hsa-miR-5702	0.2	0.244	
hsa-miR-5703	0.4	0.142	
hsa-miR-5704	0.3	0.124	
hsa-miR-572	1.0	0.180	
hsa-miR-573	26.8	0.500	0.595
hsa-miR-574-3p	35.9	-0.047	0.974
hsa-miR-574-5p	0.3	0.244	
hsa-miR-576-3p	3.3	-1.119	0.506
hsa-miR-576-5p	27.2	-3.468	0.000
hsa-miR-577	34.1	-2.448	0.000
hsa-miR-579-3p	9.6	-3.732	0.000
hsa-miR-579-5p	0.7	-0.157	
hsa-miR-580-3p	0.4	-0.273	
hsa-miR-581	0.1	-0.010	
hsa-miR-582-3p	14.1	-1.359	0.082
hsa-miR-582-5p	45.4	-1.950	0.000
hsa-miR-584-3p	0.2	0.244	
hsa-miR-584-5p	0.5	-0.162	
hsa-miR-585-3p	2.4	-1.524	0.287
hsa-miR-585-5p	0.2	-0.126	
hsa-miR-588	0.4	0.433	
hsa-miR-589-3p	37.5	-1.960	0.000
hsa-miR-589-5p	81.0	-2.286	0.000
hsa-miR-590-3p	189.6	-2.112	0.000
hsa-miR-590-5p	67.7	-2.155	0.000
hsa-miR-591	0.2	0.244	
hsa-miR-592	6.3	-1.011	0.472
hsa-miR-597-3p	1.2	-0.251	
hsa-miR-597-5p	4.6	-2.340	0.039
hsa-miR-598-3p	151.8	-0.254	0.709
hsa-miR-598-5p	2.3	-0.025	0.994
hsa-miR-601	0.2	-0.126	
hsa-miR-602	1.2	0.066	
hsa-miR-604	0.2	0.244	
hsa-miR-605-3p	0.1	-0.010	
hsa-miR-605-5p	2.4	-1.429	0.289
hsa-miR-6069	0.7	0.428	
hsa-miR-607	1.2	-0.463	
hsa-miR-6072	0.3	0.244	
hsa-miR-608	0.1	-0.010	
hsa-miR-6082	0.2	0.244	
hsa-miR-6084	0.2	0.244	
hsa-miR-6086	0.3	0.244	
hsa-miR-6087	4.4	-0.435	0.840
hsa-miR-6088	0.2	0.244	
hsa-miR-611	0.4	-0.028	
hsa-miR-612	0.1	-0.010	
hsa-miR-6124	0.8	0.411	
hsa-miR-6125	0.3	-0.179	
hsa-miR-6127	0.6	0.508	
hsa-miR-6133	0.4	0.127	
hsa-miR-615-3p	161.0	-0.177	0.810
hsa-miR-615-5p	2.7	-0.181	0.949
hsa-miR-616-3p	0.6	-0.222	
hsa-miR-616-5p	2.2	-1.479	0.308
hsa-miR-618	10.8	-2.299	0.007
hsa-miR-622	0.2	0.244	
hsa-miR-624-3p	0.9	-0.897	
hsa-miR-624-5p	5.5	-2.239	0.050
hsa-miR-625-3p	35.8	-2.749	0.000
hsa-miR-625-5p	18.4	-1.996	0.004
hsa-miR-626	0.6	0.508	
hsa-miR-627-3p	2.9	-1.428	0.326
hsa-miR-627-5p	3.2	-1.892	0.125

Table 6.3 (continued from the previous page)

hsa-miR-1290	0.9	0.662	
hsa-miR-1291	5.4	-0.121	0.961
hsa-miR-1292-3p	1.9	-0.045	
hsa-miR-1292-5p	82.9	0.765	0.074
hsa-miR-1293	11.0	0.160	0.928
hsa-miR-1294	1.0	0.126	
hsa-miR-1295a	5.1	-1.588	0.185
hsa-miR-1296-3p	1.5	-1.064	
hsa-miR-1296-5p	155.7	-4.358	0.000
hsa-miR-1297	1.1	0.613	
hsa-miR-1299	0.2	0.244	
hsa-miR-1301-3p	89.2	-2.425	0.000
hsa-miR-1301-5p	2.7	-1.625	0.216
hsa-miR-1302	0.2	0.244	
hsa-miR-1303	11.8	-1.474	0.077
hsa-miR-1304-3p	0.3	0.124	
hsa-miR-1304-5p	2.2	-1.075	0.549
hsa-miR-1305	25.2	-3.504	0.000
hsa-miR-1306-3p	12.6	-0.399	0.793
hsa-miR-1306-5p	51.0	-0.515	0.434
hsa-miR-1307-3p	562.6	-0.188	0.758
hsa-miR-1307-5p	581.2	-0.325	0.506
hsa-miR-130a-3p	174.4	0.333	0.850
hsa-miR-130a-5p	19.5	0.230	0.880
hsa-miR-130b-3p	201.9	-0.790	0.029
hsa-miR-130b-5p	91.3	-0.940	0.010
hsa-miR-132-3p	134.1	0.053	0.955
hsa-miR-132-5p	12.2	-0.111	0.956
hsa-miR-1322	1.3	0.536	
hsa-miR-133a-3p	4.8	-0.278	0.896
hsa-miR-133a-5p	0.5	0.010	
hsa-miR-133b	0.1	-0.010	
hsa-miR-1343-3p	1.7	-1.074	
hsa-miR-1343-5p	0.1	-0.010	
hsa-miR-135a-3p	0.1	-0.010	
hsa-miR-135a-5p	0.4	0.044	
hsa-miR-135b-3p	0.2	0.244	
hsa-miR-135b-5p	1.6	-0.040	
hsa-miR-137	7.5	0.454	0.810
hsa-miR-138-1-3p	2.6	0.274	0.907
hsa-miR-138-2-3p	0.1	-0.010	
hsa-miR-138-5p	44.5	0.479	0.548
hsa-miR-139-3p	0.2	0.244	
hsa-miR-139-5p	3.2	-0.190	0.939
hsa-miR-140-3p	255.0	-0.163	0.806
hsa-miR-140-5p	93.3	-0.182	0.838
hsa-miR-202-5p	0.4	0.142	
hsa-miR-203a-3p	13.8	-0.227	0.891
hsa-miR-203a-5p	0.1	-0.010	
hsa-miR-203b-3p	0.3	0.244	
hsa-miR-204-3p	0.5	-0.162	
hsa-miR-204-5p	33.2	-0.271	0.811
hsa-miR-208b-3p	0.2	0.244	
hsa-miR-20a-3p	105.6	-0.240	0.780
hsa-miR-20a-5p	4396.9	-0.045	0.960
hsa-miR-20b-5p	0.4	-0.309	
hsa-miR-21-3p	18.7	-0.311	0.840
hsa-miR-21-5p	1992.0	-0.258	0.449
hsa-miR-210-3p	94.5	-0.879	0.076
hsa-miR-210-5p	1.1	-0.736	
hsa-miR-211-3p	0.8	-0.020	
hsa-miR-211-5p	1.0	0.160	
hsa-miR-2110	40.0	1.675	0.001
hsa-miR-2114-3p	0.1	-0.010	
hsa-miR-2114-5p	2.6	0.845	0.663
hsa-miR-2116-3p	0.7	0.208	
hsa-miR-2116-5p	1.1	1.168	
hsa-miR-2117	0.2	0.244	
hsa-miR-212-3p	10.6	0.181	0.916
hsa-miR-212-5p	1.6	0.079	
hsa-miR-214-3p	0.5	0.400	
hsa-miR-215-3p	0.9	0.750	

hsa-miR-147b	2.4	-0.894	0.622
hsa-miR-148a-3p	2233.2	0.015	0.985
hsa-miR-148a-5p	38.0	0.051	0.974
hsa-miR-148b-3p	763.6	-0.533	0.036
hsa-miR-148b-5p	16.6	-0.652	0.609
hsa-miR-149-3p	2.1	0.215	0.929
hsa-miR-149-5p	70.2	-0.510	0.374
hsa-miR-150-3p	0.3	0.114	
hsa-miR-150-5p	0.4	-0.028	
hsa-miR-151a-3p	359.5	-0.948	0.000
hsa-miR-151a-5p	658.0	-0.749	0.004
hsa-miR-151b	21.5	-0.453	0.685
hsa-miR-152-3p	43.0	-0.916	0.080
hsa-miR-152-5p	0.4	0.127	
hsa-miR-153-3p	48.1	-1.133	0.015
hsa-miR-153-5p	2.2	-0.132	0.961
hsa-miR-1537-3p	1.0	-0.978	
hsa-miR-1537-5p	0.1	-0.010	
hsa-miR-1538	3.0	0.298	0.902
hsa-miR-1539	0.4	0.154	
hsa-miR-154-3p	0.4	0.142	
hsa-miR-155-5p	35.2	0.274	0.805
hsa-miR-15a-3p	11.0	-0.652	0.626
hsa-miR-15a-5p	1207.6	-0.301	0.731
hsa-miR-15b-3p	215.5	-0.020	0.985
hsa-miR-15b-5p	2462.2	-0.009	0.991
hsa-miR-16-1-3p	29.8	0.061	0.978
hsa-miR-16-2-3p	150.8	0.231	0.757
hsa-miR-16-5p	6533.8	-0.001	0.999
hsa-miR-17-3p	253.0	-0.239	0.798
hsa-miR-17-5p	4228.0	-0.050	0.942
hsa-miR-181a-2-3p	14.4	-0.612	0.609
hsa-miR-181a-3p	83.1	0.209	0.781
hsa-miR-181a-5p	2104.0	0.287	0.423
hsa-miR-181b-2-3p	3.0	-0.224	0.924
hsa-miR-181b-3p	10.0	0.059	0.983
hsa-miR-181b-5p	1252.0	0.123	0.819
hsa-miR-181c-3p	8.3	-0.214	0.908
hsa-miR-181c-5p	113.9	-0.025	0.985
hsa-miR-181d-3p	1.9	-0.428	
hsa-miR-181d-5p	118.1	-0.174	0.838
hsa-miR-182-3p	5.8	-0.109	0.961
hsa-miR-182-5p	837.5	0.166	0.781
hsa-miR-183-3p	17.7	-0.126	0.930
hsa-miR-183-5p	459.2	-0.084	0.906
hsa-miR-184	0.9	1.114	
hsa-miR-185-3p	12.3	-1.546	0.063
hsa-miR-185-5p	209.4	-1.044	0.001
hsa-miR-186-3p	12.1	-1.093	0.305
hsa-miR-186-5p	1021.3	-1.995	0.000
hsa-miR-187-3p	14.1	-0.351	0.810
hsa-miR-187-5p	1.0	1.076	
hsa-miR-188-3p	0.9	0.019	
hsa-miR-188-5p	57.0	0.191	0.840
hsa-miR-18a-3p	92.1	-0.540	0.248
hsa-miR-18a-5p	1616.4	-0.204	0.789
hsa-miR-18b-5p	20.6	0.379	0.793
hsa-miR-1908-3p	9.1	-1.176	0.325
hsa-miR-1908-5p	11.8	-1.596	0.068
hsa-miR-1909-3p	2.0	1.139	
hsa-miR-1909-5p	0.8	-0.019	
hsa-miR-190a-3p	0.4	0.127	
hsa-miR-190a-5p	29.1	-0.885	0.189
hsa-miR-190b	3.2	-0.603	0.780
hsa-miR-191-3p	25.8	0.165	0.896
hsa-miR-191-5p	1220.9	-0.342	0.368
hsa-miR-1910-3p	3.6	1.347	0.326
hsa-miR-1910-5p	6.9	1.245	0.273
hsa-miR-1913	0.4	0.143	
hsa-miR-1914-3p	5.4	-0.222	0.916
hsa-miR-1914-5p	1.3	-0.150	
hsa-miR-1915-3p	9.0	-2.610	0.008

hsa-miR-628-3p	15.0	-1.527	0.043
hsa-miR-628-5p	17.6	-1.168	0.119
hsa-miR-629-3p	26.2	-3.002	0.000
hsa-miR-629-5p	135.7	-2.719	0.000
hsa-miR-634	0.1	-0.010	
hsa-miR-636	86.1	0.787	0.036
hsa-miR-637	0.1	-0.010	
hsa-miR-638	0.5	-0.058	
hsa-miR-639	0.7	0.627	
hsa-miR-641	15.8	-1.036	0.248
hsa-miR-642a-3p	0.9	0.127	
hsa-miR-642a-5p	3.8	-0.405	0.855
hsa-miR-643	1.9	-0.783	
hsa-miR-646	5.4	0.508	0.793
hsa-miR-647	1.1	0.059	
hsa-miR-650	0.1	-0.010	
hsa-miR-6500-3p	1.1	0.327	
hsa-miR-6500-5p	0.3	0.114	
hsa-miR-6501-3p	0.2	-0.126	
hsa-miR-6501-5p	0.6	0.452	
hsa-miR-6504-3p	5.3	0.402	0.848
hsa-miR-6504-5p	5.3	0.402	0.848
hsa-miR-6505-3p	1.7	1.206	
hsa-miR-6505-5p	3.7	1.073	0.504
hsa-miR-6508-3p	0.4	0.331	
hsa-miR-6508-5p	0.3	0.114	
hsa-miR-6509-3p	0.1	-0.010	
hsa-miR-651-3p	0.1	-0.010	
hsa-miR-651-5p	11.8	-3.213	0.001
hsa-miR-6511a-3p	68.0	0.339	0.685
hsa-miR-6511a-5p	15.3	0.714	0.547
hsa-miR-6511b-3p	46.7	0.394	0.663
hsa-miR-6511b-5p	15.6	0.654	0.596
hsa-miR-6513-3p	0.5	-0.149	
hsa-miR-6513-5p	0.3	0.244	
hsa-miR-6514-3p	4.5	0.300	0.896
hsa-miR-6514-5p	7.7	0.753	0.595
hsa-miR-6515-3p	25.3	0.655	0.469
hsa-miR-6515-5p	4.2	0.418	0.840
hsa-miR-6516-3p	13.4	0.344	0.838
hsa-miR-6516-5p	47.3	0.234	0.822
hsa-miR-652-3p	241.0	-1.333	0.000
hsa-miR-652-5p	13.5	-0.840	0.421
hsa-miR-653-3p	2.9	-1.346	0.375
hsa-miR-653-5p	1.9	-1.214	
hsa-miR-654-3p	0.2	0.244	
hsa-miR-656-3p	0.1	-0.010	
hsa-miR-657	0.8	0.017	
hsa-miR-658	0.2	0.244	
hsa-miR-659-3p	1.5	0.514	
hsa-miR-6774-5p	0.1	-0.010	
hsa-miR-6775-3p	1.4	-0.021	
hsa-miR-6775-5p	0.2	0.244	
hsa-miR-6776-3p	2.5	0.321	0.896
hsa-miR-6776-5p	0.9	0.237	
hsa-miR-6777-3p	9.9	0.059	0.983
hsa-miR-6777-5p	0.9	0.098	
hsa-miR-6778-3p	1.2	-0.092	
hsa-miR-6778-5p	1.1	0.247	
hsa-miR-6779-3p	2.2	-0.052	0.986
hsa-miR-6779-5p	2.0	0.068	
hsa-miR-6780a-3p	1.2	0.357	
hsa-miR-6780a-5p	1.9	0.465	
hsa-miR-6780b-3p	2.0	0.316	
hsa-miR-6780b-5p	0.8	0.295	
hsa-miR-6781-3p	5.6	0.656	0.718
hsa-miR-6781-5p	1.5	0.078	
hsa-miR-6782-3p	0.2	0.244	
hsa-miR-6782-5p	0.3	0.114	
hsa-miR-6783-3p	6.5	0.866	0.552
hsa-miR-6783-5p	3.7	0.391	0.855
hsa-miR-6784-3p	5.6	0.230	0.911

Table 6.3 (continued from the previous page)

hsa-miR-215-5p	11.4	-0.237	0.896
hsa-miR-216a-3p	0.1	-0.010	
hsa-miR-216a-5p	4.0	0.828	0.625
hsa-miR-216b-3p	0.4	0.331	
hsa-miR-216b-5p	7.5	-0.891	0.525
hsa-miR-217	3.4	-0.024	0.994
hsa-miR-218-1-3p	119.3	-1.104	0.005
hsa-miR-218-2-3p	5.0	-0.316	0.855
hsa-miR-218-5p	13821.7	-0.807	0.000
hsa-miR-219a-1-3p	5.1	-1.300	0.325
hsa-miR-219a-5p	11.2	-2.163	0.014
hsa-miR-219b-3p	1.0	-0.123	
hsa-miR-219b-5p	1.8	-0.731	
hsa-miR-22-3p	385.5	0.263	0.552
hsa-miR-22-5p	28.2	0.293	0.797
hsa-miR-221-3p	10430.4	0.259	0.525
hsa-miR-221-5p	198.8	0.059	0.939
hsa-miR-222-3p	12481.7	0.323	0.326
hsa-miR-222-5p	448.6	0.278	0.524
hsa-miR-224-3p	0.3	0.114	
hsa-miR-224-5p	12.0	-0.053	0.983
hsa-miR-2276-3p	2.1	-0.695	0.765
hsa-miR-2276-5p	0.4	-0.257	
hsa-miR-2277-3p	12.5	-0.702	0.552
hsa-miR-2277-5p	16.6	-0.749	0.458
hsa-miR-2278	1.7	-0.648	
hsa-miR-2355-3p	1.1	-0.702	
hsa-miR-2355-5p	0.4	0.009	
hsa-miR-23a-3p	270.6	0.090	0.902
hsa-miR-23a-5p	3.0	-0.597	0.781
hsa-miR-23b-3p	577.3	0.148	0.781
hsa-miR-23b-5p	3.7	-0.908	0.609
hsa-miR-23c	1.4	0.922	
hsa-miR-24-1-5p	11.7	0.126	0.956
hsa-miR-24-2-5p	5.1	0.669	0.723
hsa-miR-24-3p	813.5	0.118	0.840
hsa-miR-2467-3p	0.2	-0.126	
hsa-miR-2467-5p	1.2	-0.029	
hsa-miR-25-3p	5940.2	0.010	0.990
hsa-miR-25-5p	88.3	-0.114	0.912
hsa-miR-2681-3p	0.4	-0.273	
hsa-miR-2681-5p	0.4	-0.273	
hsa-miR-2682-3p	0.8	-0.052	
hsa-miR-26a-1-3p	2.4	0.623	0.777
hsa-miR-26a-2-3p	8.4	0.085	0.974
hsa-miR-26a-5p	2615.2	0.213	0.616
hsa-miR-26b-3p	18.4	-0.433	0.745
hsa-miR-26b-5p	1628.3	0.239	0.558
hsa-miR-27a-3p	344.7	0.009	0.992
hsa-miR-27a-5p	5.7	0.252	0.903
hsa-miR-27b-3p	1029.8	0.146	0.797
hsa-miR-27b-5p	21.3	0.100	0.956
hsa-miR-28-3p	127.0	-1.100	0.001
hsa-miR-28-5p	148.9	-0.742	0.036
hsa-miR-2861	0.3	0.244	
hsa-miR-2909	0.3	0.244	
hsa-miR-296-3p	75.5	-0.250	0.770
hsa-miR-296-5p	50.1	-0.167	0.868
hsa-miR-299-3p	0.3	0.244	
hsa-miR-29a-3p	674.4	0.106	0.872
hsa-miR-29a-5p	14.9	-0.090	0.961
hsa-miR-29b-1-5p	11.4	-0.086	0.968
hsa-miR-29b-2-5p	9.1	0.167	0.928
hsa-miR-29b-3p	327.6	0.099	0.960
hsa-miR-29c-3p	299.1	0.061	0.956
hsa-miR-29c-5p	19.3	0.012	0.994
hsa-miR-301a-3p	820.4	-0.127	0.832
hsa-miR-301a-5p	65.2	-0.645	0.203
hsa-miR-301b-3p	45.0	-0.666	0.309
hsa-miR-301b-5p	9.3	-0.630	0.663
hsa-miR-3064-3p	11.5	0.785	0.525
hsa-miR-3064-5p	10.5	0.807	0.524

hsa-miR-1915-5p	2.9	-1.706	0.183
hsa-miR-192-3p	1.2	0.147	
hsa-miR-192-5p	33.7	-0.428	0.626
hsa-miR-193a-3p	30.1	0.039	0.986
hsa-miR-193a-5p	14.7	0.048	0.983
hsa-miR-193b-3p	205.7	-0.219	0.770
hsa-miR-193b-5p	10.1	-0.463	0.780
hsa-miR-194-3p	1.0	-0.078	
hsa-miR-194-5p	38.8	0.157	0.886
hsa-miR-195-3p	4.2	0.098	0.974
hsa-miR-195-5p	63.8	-0.141	0.881
hsa-miR-196a-3p	1.4	-0.230	
hsa-miR-196a-5p	715.9	-2.094	0.000
hsa-miR-196b-3p	45.6	-1.095	0.030
hsa-miR-196b-5p	2869.2	-0.864	0.000
hsa-miR-197-3p	171.3	-0.974	0.001
hsa-miR-197-5p	0.9	-0.590	
hsa-miR-1973	2.4	0.463	0.840
hsa-miR-1976	6.6	0.430	0.840
hsa-miR-199a-3p	14.8	0.609	0.614
hsa-miR-199a-5p	1.1	0.730	
hsa-miR-199b-3p	12.6	0.508	0.733
hsa-miR-199b-5p	6.6	-0.092	0.974
hsa-miR-19a-3p	2396.8	-0.726	0.005
hsa-miR-19a-5p	11.7	-0.207	0.912
hsa-miR-19b-1-5p	70.6	-0.191	0.874
hsa-miR-19b-3p	4812.0	-0.076	0.896
hsa-miR-200a-3p	7.9	-0.688	0.663
hsa-miR-200a-5p	0.1	-0.010	
hsa-miR-200b-3p	5.8	-0.305	0.886
hsa-miR-200b-5p	0.7	-0.144	
hsa-miR-200c-3p	18.2	-0.772	0.464
hsa-miR-200c-5p	1.1	0.613	
hsa-miR-3121-3p	0.2	-0.126	
hsa-miR-3121-5p	0.1	-0.010	
hsa-miR-3124-3p	0.1	-0.010	
hsa-miR-3124-5p	0.4	-0.345	
hsa-miR-3126-3p	0.2	0.244	
hsa-miR-3127-3p	3.1	-1.490	0.312
hsa-miR-3127-5p	3.7	-0.923	0.609
hsa-miR-3128	0.1	-0.010	
hsa-miR-3129-3p	0.1	-0.010	
hsa-miR-3130-3p	0.3	-0.153	
hsa-miR-3130-5p	0.5	-0.456	
hsa-miR-3131	3.3	-2.347	0.028
hsa-miR-3133	0.7	-0.536	
hsa-miR-3136-3p	0.1	-0.010	
hsa-miR-3136-5p	1.2	-0.573	
hsa-miR-3138	0.3	0.244	
hsa-miR-3139	0.1	-0.010	
hsa-miR-3140-3p	1.0	-0.571	
hsa-miR-3140-5p	0.3	0.124	
hsa-miR-3141	1.3	0.456	
hsa-miR-3143	33.6	1.150	0.032
hsa-miR-3144-3p	53.9	1.093	0.010
hsa-miR-3144-5p	4.2	-0.215	0.924
hsa-miR-3145-3p	0.4	0.009	
hsa-miR-3145-5p	0.4	-0.309	
hsa-miR-3146	0.3	0.136	
hsa-miR-3147	0.2	0.244	
hsa-miR-3148	0.2	0.244	
hsa-miR-3149	0.3	-0.153	
hsa-miR-3150a-3p	0.9	-0.194	
hsa-miR-3150a-5p	1.4	-1.380	
hsa-miR-3150b-3p	1.4	0.523	
hsa-miR-3150b-5p	1.4	0.523	
hsa-miR-3155a	0.3	-0.179	
hsa-miR-3156-3p	0.1	-0.010	
hsa-miR-3156-5p	0.0		
hsa-miR-3157-3p	0.7	-0.366	
hsa-miR-3157-5p	3.2	-0.891	0.622
hsa-miR-3158-3p	2.9	-1.124	0.506

hsa-miR-6784-5p	1.1	0.937	
hsa-miR-6785-3p	0.2	-0.126	
hsa-miR-6785-5p	1.1	0.705	
hsa-miR-6786-3p	1.8	-0.027	
hsa-miR-6786-5p	0.2	-0.126	
hsa-miR-6787-3p	0.5	0.011	
hsa-miR-6787-5p	0.4	0.142	
hsa-miR-6788-3p	0.4	-0.309	
hsa-miR-6789-3p	2.3	-0.247	0.916
hsa-miR-6789-5p	7.0	0.953	0.482
hsa-miR-6790-3p	1.9	-0.151	
hsa-miR-6791-3p	7.9	0.523	0.777
hsa-miR-6791-5p	3.1	0.448	0.840
hsa-miR-6792-3p	0.7	0.539	
hsa-miR-6792-5p	0.1	-0.010	
hsa-miR-6793-3p	5.1	0.172	0.939
hsa-miR-6793-5p	4.0	0.601	0.775
hsa-miR-6794-3p	1.3	0.862	
hsa-miR-6794-5p	0.9	1.064	
hsa-miR-6795-3p	0.6	0.350	
hsa-miR-6795-5p	0.2	0.244	
hsa-miR-6796-3p	0.2	0.244	
hsa-miR-6797-3p	29.8	0.409	0.709
hsa-miR-6797-5p	1.9	-0.046	
hsa-miR-6798-3p	5.6	0.118	0.961
hsa-miR-6798-5p	0.6	0.711	
hsa-miR-6799-3p	29.4	0.865	0.185
hsa-miR-6799-5p	3.1	0.937	0.595
hsa-miR-6800-3p	5.6	0.450	0.828
hsa-miR-6800-5p	0.3	0.365	
hsa-miR-6801-3p	1.6	-0.141	
hsa-miR-6801-5p	1.3	0.863	
hsa-miR-6802-3p	5.9	0.312	0.880
hsa-miR-6802-5p	3.8	0.755	0.686
hsa-miR-6803-3p	22.6	0.356	0.781
hsa-miR-6803-5p	0.3	0.124	
hsa-miR-6804-3p	1.4	-0.020	
hsa-miR-6804-5p	7.2	0.579	0.754
hsa-miR-6805-3p	2.8	0.273	0.908
hsa-miR-6805-5p	5.1	0.810	0.620
hsa-miR-6806-3p	0.9	-0.183	
hsa-miR-6806-5p	0.1	-0.010	
hsa-miR-6807-3p	11.8	0.791	0.508
hsa-miR-6807-5p	4.6	0.092	0.974
hsa-miR-6808-3p	1.8	0.118	
hsa-miR-6808-5p	0.4	-0.316	
hsa-miR-6810-3p	1.5	0.981	
hsa-miR-6810-5p	1.5	1.190	
hsa-miR-6811-3p	0.1	-0.010	
hsa-miR-6811-5p	0.1	-0.010	
hsa-miR-6812-3p	9.3	0.859	0.496
hsa-miR-6812-5p	1.9	0.344	
hsa-miR-6813-3p	0.1	-0.010	
hsa-miR-6813-5p	1.6	-0.596	
hsa-miR-6814-3p	1.9	0.108	
hsa-miR-6814-5p	1.2	0.531	
hsa-miR-6815-3p	1.8	0.285	
hsa-miR-6815-5p	2.2	-0.003	0.999
hsa-miR-6816-3p	14.1	0.395	0.781
hsa-miR-6816-5p	1.6	0.784	
hsa-miR-6817-3p	4.5	0.429	0.840
hsa-miR-6817-5p	1.1	-0.583	
hsa-miR-6818-3p	6.9	0.359	0.855
hsa-miR-6818-5p	4.4	0.767	0.665
hsa-miR-6819-3p	5.6	0.427	0.840
hsa-miR-6819-5p	0.5	-0.427	
hsa-miR-6820-3p	13.6	0.620	0.622
hsa-miR-6820-5p	6.7	0.735	0.665
hsa-miR-6821-3p	2.5	-0.251	0.914
hsa-miR-6821-5p	0.4	-0.309	
hsa-miR-6822-5p	0.1	-0.010	
hsa-miR-6823-3p	0.2	0.244	

Table 6.3 (continued from the previous page)

hsa-miR-3065-3p	1.2	-1.153	
hsa-miR-3065-5p	11.3	-2.342	0.005
hsa-miR-3074-3p	11.2	1.942	0.016
hsa-miR-3074-5p	10.1	1.234	0.248
hsa-miR-30a-3p	158.3	0.015	0.989
hsa-miR-30a-5p	1697.1	-0.004	0.994
hsa-miR-30b-3p	19.0	-0.083	0.961
hsa-miR-30b-5p	1678.7	0.079	0.891
hsa-miR-30c-1-3p	5.3	0.371	0.855
hsa-miR-30c-2-3p	17.1	-0.898	0.320
hsa-miR-30c-5p	2172.7	-0.024	0.974
hsa-miR-30d-3p	28.1	-0.190	0.896
hsa-miR-30d-5p	2578.2	0.154	0.765
hsa-miR-30e-3p	126.7	0.080	0.916
hsa-miR-30e-5p	1014.2	0.135	0.810
hsa-miR-31-3p	58.4	-0.200	0.832
hsa-miR-31-5p	531.9	0.410	0.326
hsa-miR-3115	2.2	-1.369	0.326
hsa-miR-3116	0.1	-0.010	
hsa-miR-3120-3p	0.4	0.127	
hsa-miR-342-5p	25.0	0.233	0.857
hsa-miR-345-3p	2.1	-0.146	0.960
hsa-miR-345-5p	185.3	-2.185	0.000
hsa-miR-346	25.4	-1.840	0.001
hsa-miR-34a-3p	24.7	-0.071	0.961
hsa-miR-34a-5p	616.9	0.267	0.731
hsa-miR-34b-3p	0.7	0.388	
hsa-miR-34b-5p	0.4	0.154	
hsa-miR-34c-3p	0.1	-0.010	
hsa-miR-34c-5p	1.6	-0.536	
hsa-miR-3605-3p	16.7	0.455	0.741
hsa-miR-3605-5p	3.8	0.797	0.663
hsa-miR-3607-3p	5.8	0.229	0.911
hsa-miR-3607-5p	1.0	0.948	
hsa-miR-3609	5.2	0.652	0.731
hsa-miR-361-3p	118.2	-0.025	0.983
hsa-miR-361-5p	1014.1	-0.100	0.855
hsa-miR-3610	0.2	0.244	
hsa-miR-3611	3.4	-1.620	0.248
hsa-miR-3612	0.4	0.463	
hsa-miR-3613-3p	26.5	0.181	0.889
hsa-miR-3613-5p	346.9	0.152	0.788
hsa-miR-3615	219.9	0.585	0.063
hsa-miR-3616-5p	0.1	-0.010	
hsa-miR-3617-5p	0.1	-0.010	
hsa-miR-3618	1.0	-0.534	
hsa-miR-3619-3p	2.3	-0.708	0.754
hsa-miR-3619-5p	11.8	-1.415	0.111
hsa-miR-362-3p	33.0	-0.232	0.840
hsa-miR-362-5p	33.8	-0.308	0.780
hsa-miR-3620-3p	53.2	0.489	0.506
hsa-miR-3620-5p	16.5	0.622	0.558
hsa-miR-3621	6.9	0.560	0.770
hsa-miR-3622a-3p	0.1	-0.010	
hsa-miR-3622b-3p	0.6	0.377	
hsa-miR-3622b-5p	0.6	0.377	
hsa-miR-3648	11.1	1.323	0.115
hsa-miR-3651	1.7	0.364	
hsa-miR-3652	0.4	0.154	
hsa-miR-3653-3p	1.9	-0.265	
hsa-miR-3653-5p	10.7	-0.349	0.840
hsa-miR-3654	0.3	0.244	
hsa-miR-3656	0.2	0.244	
hsa-miR-3657	0.6	-0.640	
hsa-miR-3659	0.4	-0.345	
hsa-miR-365a-3p	220.6	-0.193	0.778
hsa-miR-365a-5p	3.5	-0.820	0.663
hsa-miR-365b-3p	220.9	-0.195	0.775
hsa-miR-365b-5p	1.7	0.098	
hsa-miR-3661	7.8	-0.631	0.723
hsa-miR-3662	12.3	0.810	0.483
hsa-miR-3663-3p	5.4	0.868	0.595

hsa-miR-3158-5p	0.1	-0.010	
hsa-miR-3159	0.3	0.244	
hsa-miR-3160-3p	1.6	0.681	
hsa-miR-3160-5p	1.6	0.681	
hsa-miR-3161	0.4	-0.309	
hsa-miR-3162-3p	0.3	0.114	
hsa-miR-3162-5p	0.3	0.114	
hsa-miR-3163	0.1	-0.010	
hsa-miR-3164	0.4	-0.344	
hsa-miR-3165	0.1	-0.010	
hsa-miR-3166	0.1	-0.010	
hsa-miR-3168	0.7	-0.331	
hsa-miR-3173-3p	0.5	0.355	
hsa-miR-3173-5p	3.9	-0.851	0.625
hsa-miR-3174	2.4	-1.557	0.272
hsa-miR-3175	6.0	0.141	0.957
hsa-miR-3176	37.4	-3.226	0.000
hsa-miR-3177-3p	3.8	-1.412	0.316
hsa-miR-3177-5p	0.9	-0.455	
hsa-miR-3178	0.2	0.244	
hsa-miR-3179	0.6	0.425	
hsa-miR-3180	7.0	-0.383	0.840
hsa-miR-3180-3p	6.9	-0.344	0.855
hsa-miR-3180-5p	0.5	0.288	
hsa-miR-3181	0.6	-0.221	
hsa-miR-3182	0.6	0.508	
hsa-miR-3183	0.6	-0.222	
hsa-miR-3184-3p	1.1	0.506	
hsa-miR-3184-5p	0.9	0.701	
hsa-miR-3187-3p	27.9	-1.468	0.012
hsa-miR-3187-5p	1.1	-0.218	
hsa-miR-3188	11.3	0.102	0.960
hsa-miR-3190-3p	1.2	-0.059	
hsa-miR-3190-5p	0.5	0.010	
hsa-miR-3191-3p	0.1	-0.010	
hsa-miR-3191-5p	0.5	0.010	
hsa-miR-3192-5p	0.5	-0.455	
hsa-miR-3193	0.7	0.248	
hsa-miR-3194-3p	0.2	0.244	
hsa-miR-3194-5p	0.4	-0.029	
hsa-miR-3195	0.5	0.538	
hsa-miR-3196	0.8	0.366	
hsa-miR-3197	0.5	0.400	
hsa-miR-3198	0.3	-0.179	
hsa-miR-3199	0.7	0.098	
hsa-miR-32-3p	36.9	-1.759	0.000
hsa-miR-32-5p	306.6	-1.383	0.000
hsa-miR-3200-3p	35.5	0.432	0.620
hsa-miR-3200-5p	1.3	0.008	
hsa-miR-3201	0.1	-0.010	
hsa-miR-3202	0.3	-0.153	
hsa-miR-320a	26674.2	0.718	0.003
hsa-miR-320b	1048.0	0.668	0.010
hsa-miR-320c	463.7	0.694	0.015
hsa-miR-320d	265.3	0.668	0.043
hsa-miR-320e	51.1	0.547	0.506
hsa-miR-323a-3p	0.1	-0.010	
hsa-miR-324-3p	248.2	0.110	0.857
hsa-miR-324-5p	443.5	0.200	0.736
hsa-miR-326	19.5	-0.506	0.663
hsa-miR-328-3p	114.3	-0.043	0.961
hsa-miR-328-5p	3.3	0.054	0.986
hsa-miR-330-3p	65.9	-0.624	0.239
hsa-miR-330-5p	43.7	-0.566	0.413
hsa-miR-331-3p	259.4	-0.106	0.874
hsa-miR-331-5p	26.2	0.332	0.781
hsa-miR-335-3p	1.4	-0.618	
hsa-miR-335-5p	4.0	0.435	0.840
hsa-miR-338-3p	70.2	-0.312	0.812
hsa-miR-338-5p	7.3	0.210	0.912
hsa-miR-339-3p	62.9	-0.419	0.552
hsa-miR-339-5p	474.5	-0.613	0.043

hsa-miR-6823-5p	0.5	0.509	
hsa-miR-6824-3p	2.1	-0.062	
hsa-miR-6824-5p	0.2	0.244	
hsa-miR-6825-3p	0.6	-0.167	
hsa-miR-6825-5p	2.3	0.846	0.663
hsa-miR-6826-3p	0.3	0.136	
hsa-miR-6826-5p	1.1	0.906	
hsa-miR-6827-3p	0.7	0.627	
hsa-miR-6827-5p	0.4	0.010	
hsa-miR-6829-3p	0.8	0.051	
hsa-miR-6829-5p	0.5	0.400	
hsa-miR-6830-3p	1.2	-0.029	
hsa-miR-6830-5p	0.1	-0.010	
hsa-miR-6831-3p	0.5	0.010	
hsa-miR-6831-5p	0.3	0.365	
hsa-miR-6832-3p	10.6	0.507	0.748
hsa-miR-6832-5p	3.8	0.353	0.877
hsa-miR-6833-3p	6.3	0.367	0.857
hsa-miR-6833-5p	0.5	0.356	
hsa-miR-6834-3p	2.3	0.667	0.765
hsa-miR-6834-5p	0.1	-0.010	
hsa-miR-6836-3p	0.9	0.457	
hsa-miR-6836-5p	0.1	-0.010	
hsa-miR-6837-3p	2.2	1.133	0.489
hsa-miR-7109-5p	4.0	0.399	0.855
hsa-miR-7110-3p	6.6	0.394	0.840
hsa-miR-7110-5p	0.4	-0.316	
hsa-miR-7111-3p	49.1	0.528	0.424
hsa-miR-7111-5p	4.7	0.223	0.916
hsa-miR-7112-3p	4.2	0.852	0.622
hsa-miR-7112-5p	1.9	0.175	
hsa-miR-7113-3p	2.0	0.281	
hsa-miR-7113-5p	4.4	0.393	0.855
hsa-miR-7114-3p	7.6	0.473	0.793
hsa-miR-7114-5p	6.8	0.256	0.896
hsa-miR-7151-3p	0.1	-0.010	
hsa-miR-7152-3p	1.6	1.254	
hsa-miR-7152-5p	1.6	1.254	
hsa-miR-7155-3p	0.3	0.244	
hsa-miR-7155-5p	0.1	-0.010	
hsa-miR-7159-3p	0.6	-0.063	
hsa-miR-7159-5p	0.6	-0.063	
hsa-miR-7160-3p	1.1	-0.364	
hsa-miR-7160-5p	0.4	-0.344	
hsa-miR-7162-3p	0.1	-0.010	
hsa-miR-7162-5p	0.1	-0.010	
hsa-miR-718	0.6	-0.150	
hsa-miR-744-3p	11.9	-0.964	0.421
hsa-miR-744-5p	476.7	-1.135	0.000
hsa-miR-759	0.3	-0.153	
hsa-miR-760	131.4	1.322	0.000
hsa-miR-7641	3.5	0.333	0.886
hsa-miR-765	2.8	0.364	0.877
hsa-miR-766-3p	36.5	-0.705	0.300
hsa-miR-766-5p	5.6	-0.218	0.916
hsa-miR-767-3p	0.1	-0.010	
hsa-miR-767-5p	0.2	-0.126	
hsa-miR-769-3p	43.3	-0.884	0.094
hsa-miR-769-5p	186.8	-0.800	0.012
hsa-miR-7703	5.8	-0.327	0.874
hsa-miR-7704	3.9	0.011	0.997
hsa-miR-7705	8.8	0.903	0.473
hsa-miR-7706	244.1	0.613	0.089
hsa-miR-7845-5p	0.6	-0.222	
hsa-miR-7846-3p	0.5	0.010	
hsa-miR-7848-3p	0.2	0.244	
hsa-miR-7850-5p	1.2	-0.744	
hsa-miR-7851-3p	1.0	-0.662	
hsa-miR-7854-3p	1.5	-0.438	
hsa-miR-7973	0.0		
hsa-miR-7974	127.3	0.192	0.810
hsa-miR-7975	2.1	0.051	0.988

Table 6.3 (continued from the previous page)

hsa-miR-3663-5p	2.2	1.236	0.427
hsa-miR-3664-3p	0.1	-0.010	
hsa-miR-3664-5p	0.1	-0.010	
hsa-miR-3666	0.1	-0.010	
hsa-miR-3667-5p	0.1	-0.010	
hsa-miR-3668	0.5	0.509	
hsa-miR-3677-3p	3.2	-1.024	0.552
hsa-miR-3677-5p	1.1	-0.555	
hsa-miR-3679-3p	0.3	-0.153	
hsa-miR-3679-5p	1.1	-0.724	
hsa-miR-3680-5p	0.1	-0.010	
hsa-miR-3682-5p	0.1	-0.010	
hsa-miR-3684	1.2	-0.423	
hsa-miR-3685	0.4	0.127	
hsa-miR-3687	27.4	0.440	0.770
hsa-miR-3688-3p	0.1	-0.010	
hsa-miR-3689a-3p	0.1	-0.010	
hsa-miR-3689a-5p	0.1	-0.010	
hsa-miR-3689b-3p	0.1	-0.010	
hsa-miR-3689b-5p	0.1	-0.010	
hsa-miR-3689c	0.1	-0.010	
hsa-miR-3689d	0.1	-0.010	
hsa-miR-3689e	0.1	-0.010	
hsa-miR-3689f	0.1	-0.010	
hsa-miR-369-3p	2.1	1.012	0.564
hsa-miR-3690	0.1	-0.010	
hsa-miR-3691-3p	0.5	0.009	
hsa-miR-3691-5p	0.6	-0.640	
hsa-miR-3692-3p	0.4	-0.272	
hsa-miR-3692-5p	0.4	-0.257	
hsa-miR-3713	0.4	0.127	
hsa-miR-371a-5p	0.1	-0.010	
hsa-miR-374a-3p	53.4	-2.824	0.000
hsa-miR-374a-5p	1234.3	-2.411	0.000
hsa-miR-374b-3p	31.5	-1.812	0.001
hsa-miR-374b-5p	826.5	-1.643	0.000
hsa-miR-374c-5p	18.3	-1.661	0.015
hsa-miR-375	54.2	-0.437	0.608
hsa-miR-376a-2-5p	0.2	0.244	
hsa-miR-376a-5p	0.1	-0.010	
hsa-miR-378a-3p	1144.0	-0.679	0.004
hsa-miR-378a-5p	51.3	-0.912	0.046
hsa-miR-378b	0.2	0.244	
hsa-miR-378c	48.7	-0.575	0.376
hsa-miR-378d	15.6	-0.379	0.810
hsa-miR-378e	0.2	-0.126	
hsa-miR-378g	3.8	0.871	0.616
hsa-miR-382-5p	0.2	0.244	
hsa-miR-383-3p	0.1	-0.010	
hsa-miR-383-5p	1.1	-0.669	
hsa-miR-3908	0.5	0.356	
hsa-miR-3909	2.3	-0.736	0.736
hsa-miR-3910	0.2	0.244	
hsa-miR-3911	1.1	0.028	
hsa-miR-3912-3p	15.3	0.818	0.421
hsa-miR-3912-5p	2.3	0.282	0.905
hsa-miR-3913-3p	2.8	0.630	0.774
hsa-miR-3913-5p	5.0	0.127	0.960
hsa-miR-3914	0.2	-0.126	
hsa-miR-3916	0.9	0.401	
hsa-miR-3917	0.4	0.127	
hsa-miR-3922-3p	0.4	-0.273	
hsa-miR-3922-5p	0.1	-0.010	
hsa-miR-3923	0.1	-0.010	
hsa-miR-3926	0.6	0.711	
hsa-miR-3928-3p	17.6	0.554	0.620
hsa-miR-450b-5p	45.0	-1.302	0.005
hsa-miR-4511	3.0	-0.214	0.928
hsa-miR-4512	0.8	0.304	
hsa-miR-4514	0.3	0.244	
hsa-miR-4515	0.6	0.508	
hsa-miR-4516	0.6	-0.031	

hsa-miR-33a-3p	27.4	-0.143	0.912
hsa-miR-33a-5p	169.6	0.073	0.979
hsa-miR-33b-3p	7.6	-0.391	0.840
hsa-miR-33b-5p	22.7	-0.161	0.913
hsa-miR-340-3p	26.6	-1.515	0.009
hsa-miR-340-5p	187.3	-1.652	0.000
hsa-miR-342-3p	503.9	0.046	0.949
hsa-miR-3928-5p	0.6	0.378	
hsa-miR-3929	5.4	0.002	0.999
hsa-miR-3934-3p	0.1	-0.010	
hsa-miR-3934-5p	0.9	-0.088	
hsa-miR-3935	0.2	0.244	
hsa-miR-3936	0.1	-0.010	
hsa-miR-3938	0.1	-0.010	
hsa-miR-3939	2.5	-0.115	0.969
hsa-miR-3940-3p	7.1	0.056	0.986
hsa-miR-3940-5p	1.0	0.212	
hsa-miR-3941	0.1	-0.010	
hsa-miR-3942-3p	0.1	-0.010	
hsa-miR-3942-5p	0.3	0.244	
hsa-miR-3943	2.6	-0.490	0.838
hsa-miR-3944-3p	4.2	0.442	0.840
hsa-miR-3944-5p	0.8	0.295	
hsa-miR-3945	0.4	0.127	
hsa-miR-3960	0.4	0.143	
hsa-miR-411-3p	0.1	-0.010	
hsa-miR-412-5p	0.1	-0.010	
hsa-miR-421	227.0	-1.682	0.000
hsa-miR-423-3p	2302.8	0.264	0.558
hsa-miR-423-5p	831.0	0.453	0.293
hsa-miR-424-3p	31.0	0.556	0.533
hsa-miR-424-5p	335.5	0.181	0.788
hsa-miR-425-3p	89.4	-0.236	0.774
hsa-miR-425-5p	823.8	-0.253	0.542
hsa-miR-4251	0.1	-0.010	
hsa-miR-4254	0.5	-0.484	
hsa-miR-4255	0.1	-0.010	
hsa-miR-4257	0.1	-0.010	
hsa-miR-4258	0.5	0.538	
hsa-miR-4265	0.1	-0.010	
hsa-miR-4266	1.0	0.895	
hsa-miR-4269	0.3	-0.153	
hsa-miR-4282	0.1	-0.010	
hsa-miR-4284	1.0	-0.108	
hsa-miR-4286	578.9	0.323	0.506
hsa-miR-429	4.8	0.264	0.903
hsa-miR-4290	0.9	-0.914	
hsa-miR-4292	0.5	0.509	
hsa-miR-4293	0.1	-0.010	
hsa-miR-4295	0.2	0.244	
hsa-miR-4296	0.1	-0.010	
hsa-miR-4298	1.3	0.622	
hsa-miR-4304	0.2	0.244	
hsa-miR-4306	0.2	-0.126	
hsa-miR-4314	2.6	-0.032	0.992
hsa-miR-4316	0.4	-0.316	
hsa-miR-432-5p	0.1	-0.010	
hsa-miR-4322	0.1	-0.010	
hsa-miR-4325	0.1	-0.010	
hsa-miR-4326	20.2	-3.246	0.000
hsa-miR-4417	0.8	0.579	
hsa-miR-4418	0.2	0.244	
hsa-miR-4419b	0.7	0.886	
hsa-miR-4421	4.6	1.010	0.506
hsa-miR-4422	0.1	-0.010	
hsa-miR-4423-5p	0.8	0.451	
hsa-miR-4424	0.2	0.244	
hsa-miR-4425	0.4	0.127	
hsa-miR-4426	0.1	-0.010	
hsa-miR-4428	0.2	0.244	
hsa-miR-4429	4.3	0.294	0.896
hsa-miR-4432	0.2	0.244	

hsa-miR-7976	1.6	-0.626	
hsa-miR-7977	10.7	0.912	0.428
hsa-miR-802	0.1	-0.010	
hsa-miR-8064	0.1	-0.010	
hsa-miR-8071	0.2	0.244	
hsa-miR-8072	0.9	0.058	
hsa-miR-8073	0.8	0.839	
hsa-miR-8075	0.1	-0.010	
hsa-miR-8077	0.2	0.244	
hsa-miR-8089	1.9	-0.501	
hsa-miR-6750-3p	4.8	-0.220	0.917
hsa-miR-6750-5p	0.6	-0.560	
hsa-miR-6751-3p	1.7	-0.255	
hsa-miR-6751-5p	1.5	-0.208	
hsa-miR-6752-3p	0.9	0.827	
hsa-miR-6752-5p	0.8	0.988	
hsa-miR-6753-3p	0.8	-0.301	
hsa-miR-6753-5p	0.2	-0.126	
hsa-miR-6754-3p	1.0	0.571	
hsa-miR-6754-5p	0.6	0.234	
hsa-miR-6755-3p	0.5	-0.427	
hsa-miR-6755-5p	1.5	-0.429	
hsa-miR-6757-3p	0.2	0.244	
hsa-miR-6757-5p	1.0	0.858	
hsa-miR-6758-3p	6.8	-0.050	0.986
hsa-miR-6758-5p	2.5	0.346	0.886
hsa-miR-6759-3p	4.2	1.819	0.109
hsa-miR-6759-5p	2.3	0.275	0.908
hsa-miR-676-3p	4.7	-1.481	0.255
hsa-miR-676-5p	0.1	-0.010	
hsa-miR-6760-3p	0.4	0.127	
hsa-miR-6760-5p	0.4	0.127	
hsa-miR-6761-3p	1.1	-0.773	
hsa-miR-6761-5p	0.8	0.579	
hsa-miR-6762-3p	5.2	0.902	0.552
hsa-miR-6762-5p	0.4	0.142	
hsa-miR-6763-3p	1.1	0.553	
hsa-miR-6763-5p	7.3	0.696	0.641
hsa-miR-6764-3p	6.4	0.570	0.765
hsa-miR-6764-5p	6.8	0.143	0.956
hsa-miR-6765-3p	6.0	-0.324	0.877
hsa-miR-6765-5p	0.6	-0.137	
hsa-miR-6766-3p	2.3	0.282	0.907
hsa-miR-6766-5p	0.5	0.355	
hsa-miR-6767-3p	46.6	0.434	0.598
hsa-miR-6767-5p	47.3	0.452	0.569
hsa-miR-6768-3p	49.5	0.447	0.569
hsa-miR-6768-5p	54.7	0.485	0.498
hsa-miR-6769a-3p	2.1	-0.364	0.886
hsa-miR-6769a-5p	1.8	-0.174	
hsa-miR-6769b-3p	1.1	-0.606	
hsa-miR-6769b-5p	0.7	0.428	
hsa-miR-6770-3p	5.4	0.721	0.679
hsa-miR-6770-5p	9.5	0.527	0.753
hsa-miR-6771-3p	0.1	-0.010	
hsa-miR-6771-5p	0.1	-0.010	
hsa-miR-6772-3p	0.4	0.331	
hsa-miR-6774-3p	0.4	-0.272	
hsa-miR-6837-5p	0.4	-0.344	
hsa-miR-6838-3p	2.0	0.228	
hsa-miR-6838-5p	0.5	-0.427	
hsa-miR-6839-3p	0.1	-0.010	
hsa-miR-6839-5p	0.1	-0.010	
hsa-miR-6840-3p	0.5	-0.427	
hsa-miR-6840-5p	0.3	0.124	
hsa-miR-6841-3p	1.1	-0.397	
hsa-miR-6841-5p	1.5	0.577	
hsa-miR-6842-3p	2.0	1.133	
hsa-miR-6842-5p	0.5	0.509	
hsa-miR-6843-3p	3.9	-0.126	0.961
hsa-miR-6844	20.5	0.253	0.891
hsa-miR-6845-3p	1.0	0.682	

Table 6.3 (continued from the previous page)

hsa-miR-4517	47.5	1.428	0.001
hsa-miR-4518	0.4	0.463	
hsa-miR-4519	1.4	0.885	
hsa-miR-451a	2.3	0.244	0.916
hsa-miR-452-3p	0.4	-0.344	
hsa-miR-452-5p	2.8	-1.076	0.542
hsa-miR-4521	5091.2	1.204	0.000
hsa-miR-4522	1.0	0.178	
hsa-miR-4523	10.9	-0.439	0.781
hsa-miR-4525	2.0	0.367	
hsa-miR-4532	0.2	0.244	
hsa-miR-4533	5.9	0.382	0.848
hsa-miR-4534	0.2	0.244	
hsa-miR-4536-3p	1.1	0.990	
hsa-miR-454-3p	537.7	-0.855	0.001
hsa-miR-454-5p	19.8	-0.966	0.219
hsa-miR-4540	0.1	-0.010	
hsa-miR-455-3p	77.1	0.080	0.929
hsa-miR-455-5p	21.3	-0.050	0.983
hsa-miR-4632-3p	0.5	0.010	
hsa-miR-4632-5p	0.5	0.010	
hsa-miR-4634	0.2	0.244	
hsa-miR-4638-3p	3.0	0.042	0.989
hsa-miR-4638-5p	1.1	0.028	
hsa-miR-4639-3p	2.0	1.083	
hsa-miR-4639-5p	1.5	1.114	
hsa-miR-4640-3p	1.5	0.530	
hsa-miR-4640-5p	1.0	-0.156	
hsa-miR-4641	0.6	-0.031	
hsa-miR-4644	0.5	-0.455	
hsa-miR-4645-3p	0.8	-0.126	
hsa-miR-4646-3p	4.1	0.387	0.855
hsa-miR-4647	0.4	0.009	
hsa-miR-4648	0.4	-0.344	
hsa-miR-4651	0.9	1.155	
hsa-miR-4652-3p	1.4	-1.345	
hsa-miR-4652-5p	1.1	-0.667	
hsa-miR-4654	0.3	-0.179	
hsa-miR-4655-3p	0.4	-0.272	
hsa-miR-4655-5p	0.9	-0.414	
hsa-miR-4656	0.6	-0.200	
hsa-miR-4657	0.3	0.244	
hsa-miR-4658	0.3	0.365	
hsa-miR-4659a-3p	0.1	-0.010	
hsa-miR-4660	0.7	0.248	
hsa-miR-4661-5p	0.5	-0.430	
hsa-miR-4662a-3p	0.1	-0.010	
hsa-miR-4664-3p	1.5	-0.492	
hsa-miR-4664-5p	7.9	-1.779	0.066
hsa-miR-4665-3p	0.2	0.244	
hsa-miR-4665-5p	3.6	-0.809	0.663
hsa-miR-4666a-5p	0.3	0.244	
hsa-miR-4667-3p	4.5	0.555	0.793
hsa-miR-4667-5p	1.2	-0.030	
hsa-miR-4668-3p	1.8	0.406	
hsa-miR-4668-5p	1.4	0.449	
hsa-miR-4669	9.1	0.767	0.552
hsa-miR-4670-3p	0.1	-0.010	
hsa-miR-4671-3p	0.1	-0.010	
hsa-miR-4672	0.2	-0.126	
hsa-miR-4673	0.1	-0.010	
hsa-miR-4674	0.7	-0.157	
hsa-miR-4676-3p	0.4	-0.309	
hsa-miR-4676-5p	0.3	-0.179	
hsa-miR-4677-3p	3.2	-2.301	0.031
hsa-miR-4677-5p	1.3	-1.117	
hsa-miR-4680-3p	0.1	-0.010	
hsa-miR-4683	6.9	1.342	0.231
hsa-miR-4685-3p	6.7	0.158	0.942
hsa-miR-4685-5p	0.8	0.254	
hsa-miR-4686	0.7	0.412	
hsa-miR-4687-3p	1.5	0.648	

hsa-miR-4433b-5p	0.3	0.124	
hsa-miR-4435	2.1	0.580	
hsa-miR-4440	1.7	-0.687	
hsa-miR-4441	0.3	0.124	
hsa-miR-4442	0.3	-0.179	
hsa-miR-4443	135.3	0.413	0.421
hsa-miR-4444	0.5	0.009	
hsa-miR-4446-3p	2.4	0.024	0.994
hsa-miR-4446-5p	0.7	0.388	
hsa-miR-4448	8.6	0.571	0.765
hsa-miR-4449	5.4	0.391	0.848
hsa-miR-4451	2.3	0.663	0.765
hsa-miR-4453	0.3	0.114	
hsa-miR-4454	99.3	0.260	0.770
hsa-miR-4455	0.4	0.433	
hsa-miR-4457	7.7	0.239	0.902
hsa-miR-4458	23.1	0.547	0.731
hsa-miR-4460	0.1	-0.010	
hsa-miR-4461	3.4	-0.259	0.911
hsa-miR-4466	10.7	0.738	0.558
hsa-miR-4467	2.6	-0.892	0.626
hsa-miR-4469	0.3	-0.179	
hsa-miR-4470	5.3	0.631	0.745
hsa-miR-4472	0.5	0.355	
hsa-miR-4473	1.9	-1.658	
hsa-miR-4474-3p	0.4	-0.344	
hsa-miR-4475	0.5	-0.031	
hsa-miR-4476	0.1	-0.010	
hsa-miR-4477b	0.7	0.250	
hsa-miR-4479	5.9	-0.322	0.881
hsa-miR-4482-3p	0.1	-0.010	
hsa-miR-4483	2.9	-0.316	0.896
hsa-miR-4484	15.5	0.765	0.524
hsa-miR-4485-3p	20.8	-0.001	0.999
hsa-miR-4485-5p	36.7	0.813	0.203
hsa-miR-4488	2.1	-0.520	
hsa-miR-4489	0.1	-0.010	
hsa-miR-4491	0.3	0.244	
hsa-miR-4492	0.3	0.124	
hsa-miR-4497	0.8	0.095	
hsa-miR-4498	5.1	0.834	0.620
hsa-miR-449a	16.3	-0.195	0.905
hsa-miR-449b-3p	0.7	-0.642	
hsa-miR-449b-5p	2.9	-0.024	0.994
hsa-miR-449c-3p	0.9	0.251	
hsa-miR-449c-5p	9.6	-0.479	0.776
hsa-miR-4500	0.3	-0.179	
hsa-miR-4501	0.4	-0.309	
hsa-miR-4502	0.4	0.463	
hsa-miR-450a-1-3p	3.8	-0.147	0.957
hsa-miR-450a-2-3p	2.1	-0.600	
hsa-miR-450a-5p	74.9	-0.868	0.029
hsa-miR-450b-3p	0.2	0.244	
hsa-miR-4732-5p	0.1	-0.010	
hsa-miR-4733-3p	0.6	-0.032	
hsa-miR-4733-5p	0.9	0.058	
hsa-miR-4734	7.0	0.651	0.709
hsa-miR-4738-3p	4.5	-0.050	0.986
hsa-miR-4738-5p	0.1	-0.010	
hsa-miR-4739	0.2	0.244	
hsa-miR-4741	18.9	0.389	0.770
hsa-miR-4742-3p	32.0	0.570	0.466
hsa-miR-4742-5p	15.8	0.415	0.770
hsa-miR-4743-3p	0.9	-0.088	
hsa-miR-4743-5p	1.5	-0.438	
hsa-miR-4745-3p	10.6	0.457	0.775
hsa-miR-4745-5p	6.6	0.553	0.765
hsa-miR-4746-3p	2.1	-0.564	
hsa-miR-4746-5p	6.1	-1.835	0.082
hsa-miR-4747-3p	2.9	-0.461	0.840
hsa-miR-4747-5p	5.9	0.280	0.894
hsa-miR-4748	0.5	-0.058	

hsa-miR-6846-3p	0.6	-0.032	
hsa-miR-6846-5p	0.6	-0.032	
hsa-miR-6847-3p	1.9	-0.021	
hsa-miR-6847-5p	4.1	-0.017	0.994
hsa-miR-6848-3p	1.7	0.409	
hsa-miR-6848-5p	1.5	0.648	
hsa-miR-6849-3p	2.3	-0.011	0.997
hsa-miR-6850-3p	2.8	1.226	0.427
hsa-miR-6850-5p	5.5	1.232	0.326
hsa-miR-6851-3p	0.8	-0.460	
hsa-miR-6851-5p	2.6	0.544	0.810
hsa-miR-6852-3p	0.1	-0.010	
hsa-miR-6852-5p	1.0	0.241	
hsa-miR-6853-3p	1.6	0.313	
hsa-miR-6853-5p	0.1	-0.010	
hsa-miR-6854-3p	0.1	-0.010	
hsa-miR-6854-5p	0.1	-0.010	
hsa-miR-6855-3p	6.6	0.287	0.886
hsa-miR-6855-5p	1.8	0.116	
hsa-miR-6856-3p	0.2	0.244	
hsa-miR-6856-5p	0.2	0.244	
hsa-miR-6857-3p	8.9	0.678	0.640
hsa-miR-6857-5p	1.9	-0.208	
hsa-miR-6858-3p	7.7	0.622	0.709
hsa-miR-6858-5p	0.7	0.336	
hsa-miR-6859-3p	1.8	1.884	
hsa-miR-6859-5p	1.2	-0.079	
hsa-miR-6860	0.3	0.244	
hsa-miR-6861-3p	6.0	0.756	0.626
hsa-miR-6861-5p	0.8	0.254	
hsa-miR-6862-3p	2.7	0.061	0.986
hsa-miR-6862-5p	4.5	0.548	0.782
hsa-miR-6863	0.6	-0.199	
hsa-miR-6864-5p	0.9	0.410	
hsa-miR-6865-3p	0.5	-0.058	
hsa-miR-6865-5p	1.4	-0.171	
hsa-miR-6866-3p	3.8	0.908	0.595
hsa-miR-6866-5p	7.4	0.925	0.498
hsa-miR-6867-3p	0.9	0.760	
hsa-miR-6867-5p	0.2	0.244	
hsa-miR-6868-3p	2.2	-0.686	0.765
hsa-miR-6869-3p	0.1	-0.010	
hsa-miR-6869-5p	1.8	0.604	
hsa-miR-6870-3p	1.0	0.273	
hsa-miR-6870-5p	0.2	0.244	
hsa-miR-6871-3p	1.6	0.278	
hsa-miR-6871-5p	1.6	0.046	
hsa-miR-6872-3p	1.0	-0.046	
hsa-miR-6872-5p	0.3	-0.153	
hsa-miR-6873-3p	2.3	0.307	0.896
hsa-miR-6873-5p	0.4	0.127	
hsa-miR-6874-3p	1.8	-0.025	
hsa-miR-6874-5p	0.4	0.463	
hsa-miR-6875-3p	0.2	0.244	
hsa-miR-6875-5p	1.8	0.399	
hsa-miR-6876-3p	0.5	-0.427	
hsa-miR-6876-5p	1.5	-0.150	
hsa-miR-6877-3p	3.4	0.056	0.986
hsa-miR-6877-5p	16.8	0.305	0.838
hsa-miR-6878-3p	1.1	-0.176	
hsa-miR-6878-5p	1.3	-0.054	
hsa-miR-6879-3p	3.9	-0.024	0.994
hsa-miR-6880-3p	1.9	0.880	
hsa-miR-6880-5p	0.7	0.296	
hsa-miR-6881-3p	0.7	0.413	
hsa-miR-6881-5p	0.4	0.127	
hsa-miR-6882-3p	2.0	0.341	
hsa-miR-6882-5p	6.0	0.283	0.893
hsa-miR-6883-3p	2.2	-0.055	0.986
hsa-miR-6883-5p	1.1	-0.217	
hsa-miR-6884-3p	1.4	0.572	
hsa-miR-6884-5p	1.0	0.530	

Table 6.3 (continued from the previous page)

hsa-miR-4687-5p	0.1	-0.010	
hsa-miR-4688	1.6	-0.227	
hsa-miR-4689	0.2	-0.126	
hsa-miR-4690-3p	2.0	0.221	
hsa-miR-4690-5p	0.6	0.440	
hsa-miR-4691-3p	0.7	-0.670	
hsa-miR-4691-5p	0.2	-0.126	
hsa-miR-4695-3p	0.3	0.114	
hsa-miR-4695-5p	0.1	-0.010	
hsa-miR-4700-3p	0.4	0.154	
hsa-miR-4700-5p	0.7	0.428	
hsa-miR-4701-3p	5.0	0.244	0.908
hsa-miR-4701-5p	4.9	0.277	0.896
hsa-miR-4706	1.0	-0.898	
hsa-miR-4707-3p	0.3	0.365	
hsa-miR-4707-5p	0.4	0.127	
hsa-miR-4709-3p	0.2	0.244	
hsa-miR-4712-3p	0.4	0.127	
hsa-miR-4712-5p	0.2	0.244	
hsa-miR-4713-3p	0.2	0.244	
hsa-miR-4713-5p	4.4	-0.604	0.770
hsa-miR-4714-3p	0.2	0.244	
hsa-miR-4716-3p	0.2	0.244	
hsa-miR-4716-5p	0.1	-0.010	
hsa-miR-4717-3p	1.5	-0.342	
hsa-miR-4717-5p	0.4	0.143	
hsa-miR-4721	0.4	0.433	
hsa-miR-4722-3p	0.9	0.237	
hsa-miR-4722-5p	1.4	-1.370	
hsa-miR-4723-3p	5.7	0.022	0.994
hsa-miR-4723-5p	1.2	0.215	
hsa-miR-4725-3p	1.0	-0.571	
hsa-miR-4725-5p	0.8	-0.854	
hsa-miR-4726-3p	1.8	-0.080	
hsa-miR-4726-5p	3.9	0.510	0.817
hsa-miR-4727-3p	0.7	0.590	
hsa-miR-4727-5p	0.2	0.244	
hsa-miR-4728-3p	11.4	0.405	0.798
hsa-miR-4728-5p	1.7	-0.206	
hsa-miR-4732-3p	0.1	-0.010	
hsa-miR-509-3p	0.2	-0.126	
hsa-miR-5090	2.7	0.215	0.929
hsa-miR-5091	0.1	-0.010	
hsa-miR-5092	0.5	-0.162	
hsa-miR-5093	0.1	-0.010	
hsa-miR-5094	20.1	0.293	0.838
hsa-miR-5095	0.1	-0.010	
hsa-miR-5100	89.4	0.451	0.421
hsa-miR-511-3p	0.2	-0.126	
hsa-miR-511-5p	0.1	-0.010	
hsa-miR-513a-5p	0.2	0.244	
hsa-miR-514a-3p	0.3	0.114	
hsa-miR-515-3p	0.1	-0.010	
hsa-miR-515-5p	0.1	-0.010	
hsa-miR-517a-3p	0.3	0.244	
hsa-miR-517b-3p	0.3	0.244	
hsa-miR-517c-3p	0.2	-0.126	
hsa-miR-5187-3p	3.7	-1.051	0.524
hsa-miR-5187-5p	8.3	0.434	0.810
hsa-miR-5188	4.7	0.300	0.896
hsa-miR-5189-3p	0.4	0.127	
hsa-miR-5189-5p	0.3	-0.153	
hsa-miR-518a-3p	0.2	0.244	
hsa-miR-518f-3p	0.1	-0.010	
hsa-miR-5193	0.9	-0.459	
hsa-miR-519a-3p	0.1	-0.010	
hsa-miR-520b	0.1	-0.010	
hsa-miR-520c-3p	0.1	-0.010	
hsa-miR-520f-3p	0.1	-0.010	
hsa-miR-532-3p	29.2	-0.414	0.688
hsa-miR-532-5p	105.7	0.100	0.901
hsa-miR-542-3p	47.5	-0.797	0.141

hsa-miR-4749-3p	2.8	-0.280	0.905
hsa-miR-4749-5p	10.0	0.403	0.810
hsa-miR-4750-5p	1.2	-1.196	
hsa-miR-4752	0.3	0.365	
hsa-miR-4753-3p	0.2	-0.126	
hsa-miR-4754	1.0	0.537	
hsa-miR-4757-3p	0.2	0.244	
hsa-miR-4757-5p	0.4	0.463	
hsa-miR-4758-3p	1.1	0.399	
hsa-miR-4758-5p	0.1	-0.010	
hsa-miR-4762-3p	1.0	-0.574	
hsa-miR-4762-5p	1.0	-0.574	
hsa-miR-4763-3p	0.6	0.440	
hsa-miR-4763-5p	0.6	-0.063	
hsa-miR-4764-3p	0.2	0.244	
hsa-miR-4766-3p	1.4	-0.401	
hsa-miR-4766-5p	0.7	-0.396	
hsa-miR-4767	1.5	0.101	
hsa-miR-4768-5p	0.2	-0.126	
hsa-miR-4769-3p	0.2	0.244	
hsa-miR-4771	0.4	0.142	
hsa-miR-4775	3.8	0.772	0.673
hsa-miR-4778-3p	0.6	0.378	
hsa-miR-4778-5p	0.2	-0.126	
hsa-miR-4781-3p	2.4	0.701	0.753
hsa-miR-4781-5p	0.2	0.244	
hsa-miR-4783-3p	2.8	0.017	0.994
hsa-miR-4783-5p	0.4	0.127	
hsa-miR-4784	0.1	-0.010	
hsa-miR-4785	12.7	0.226	0.893
hsa-miR-4786-3p	2.6	0.609	0.780
hsa-miR-4786-5p	1.1	0.247	
hsa-miR-4787-3p	33.7	1.369	0.014
hsa-miR-4787-5p	1.3	0.311	
hsa-miR-4791	5.4	0.643	0.733
hsa-miR-4795-3p	2.9	0.001	0.999
hsa-miR-4795-5p	0.3	0.124	
hsa-miR-4797-3p	0.3	0.136	
hsa-miR-4798-3p	0.6	0.083	
hsa-miR-4798-5p	0.6	-0.160	
hsa-miR-4799-5p	0.7	-0.606	
hsa-miR-4800-3p	0.1	-0.010	
hsa-miR-4802-3p	0.2	0.244	
hsa-miR-4802-5p	0.5	-0.427	
hsa-miR-4804-5p	0.1	-0.010	
hsa-miR-483-3p	21.8	-0.758	0.413
hsa-miR-483-5p	8.6	0.081	0.974
hsa-miR-484	5661.3	0.536	0.038
hsa-miR-486-3p	9.8	-1.173	0.305
hsa-miR-486-5p	98.0	-1.723	0.000
hsa-miR-487b-3p	0.1	-0.010	
hsa-miR-488-3p	3.4	-0.420	0.850
hsa-miR-488-5p	0.4	-0.272	
hsa-miR-489-3p	2.0	-1.706	
hsa-miR-490-5p	0.1	-0.010	
hsa-miR-491-3p	5.3	-1.659	0.170
hsa-miR-491-5p	28.6	-2.643	0.000
hsa-miR-494-3p	0.4	0.127	
hsa-miR-496	0.1	-0.010	
hsa-miR-497-3p	1.5	-0.132	
hsa-miR-497-5p	47.3	-0.176	0.886
hsa-miR-4999-3p	0.6	0.377	
hsa-miR-4999-5p	0.3	0.365	
hsa-miR-499a-3p	0.2	-0.126	
hsa-miR-499a-5p	5.4	-0.185	0.929
hsa-miR-499b-3p	0.1	-0.010	
hsa-miR-5000-3p	0.5	-0.162	
hsa-miR-5000-5p	0.7	-0.642	
hsa-miR-5001-3p	12.8	1.637	0.029
hsa-miR-5001-5p	0.7	0.627	
hsa-miR-5002-3p	0.4	0.127	
hsa-miR-5002-5p	1.6	0.313	

hsa-miR-6885-3p	5.8	0.744	0.648
hsa-miR-6885-5p	2.8	0.603	0.780
hsa-miR-6886-3p	3.9	1.442	0.263
hsa-miR-6886-5p	18.7	0.186	0.901
hsa-miR-6887-3p	0.5	0.289	
hsa-miR-6887-5p	0.5	0.289	
hsa-miR-6888-3p	0.9	0.330	
hsa-miR-6889-3p	2.9	0.285	0.903
hsa-miR-6889-5p	2.9	-0.047	0.988
hsa-miR-6890-3p	1.6	-0.103	
hsa-miR-6890-5p	0.8	-0.359	
hsa-miR-6891-5p	3.8	0.070	0.983
hsa-miR-6892-3p	1.6	0.175	
hsa-miR-6892-5p	0.4	0.154	
hsa-miR-6893-3p	0.9	0.526	
hsa-miR-6893-5p	0.2	0.244	
hsa-miR-6894-3p	7.9	-0.648	0.676
hsa-miR-6894-5p	3.4	0.924	0.595
hsa-miR-6895-3p	9.7	0.189	0.924
hsa-miR-6895-5p	1.0	0.278	
hsa-miR-7-1-3p	55.9	-0.180	0.860
hsa-miR-7-2-3p	0.1	-0.010	
hsa-miR-7-5p	1496.9	-0.256	0.525
hsa-miR-708-3p	4.2	-0.210	0.924
hsa-miR-708-5p	42.5	-0.173	0.886
hsa-miR-7106-3p	1.1	0.624	
hsa-miR-7106-5p	2.2	-0.105	0.974
hsa-miR-7107-3p	0.1	-0.010	
hsa-miR-7107-5p	0.1	-0.010	
hsa-miR-7108-3p	3.1	0.857	0.626
hsa-miR-7108-5p	3.3	-0.143	0.960
hsa-miR-7109-3p	3.5	0.491	0.831
hsa-miR-873-3p	0.2	0.244	
hsa-miR-873-5p	1.0	-0.477	
hsa-miR-874-3p	79.2	-0.069	0.949
hsa-miR-874-5p	6.7	-0.394	0.840
hsa-miR-876-3p	0.2	-0.126	
hsa-miR-876-5p	0.6	-0.145	
hsa-miR-877-3p	484.3	0.466	0.279
hsa-miR-877-5p	1909.5	0.760	0.001
hsa-miR-885-3p	0.1	-0.010	
hsa-miR-885-5p	0.7	-0.144	
hsa-miR-887-3p	36.6	-0.203	0.850
hsa-miR-887-5p	1.1	0.032	
hsa-miR-888-5p	0.2	0.244	
hsa-miR-889-3p	0.1	-0.010	
hsa-miR-891a-5p	0.3	-0.153	
hsa-miR-892b	0.1	-0.010	
hsa-miR-892c-3p	0.1	-0.010	
hsa-miR-9-3p	120.8	0.134	0.874
hsa-miR-9-5p	400.2	0.050	0.961
hsa-miR-924	0.3	0.114	
hsa-miR-92a-1-5p	82.3	0.132	0.886
hsa-miR-92a-3p	10815.0	-0.032	0.961
hsa-miR-92b-3p	717.1	0.303	0.426
hsa-miR-92b-5p	52.8	0.506	0.470
hsa-miR-93-3p	282.3	0.174	0.770
hsa-miR-93-5p	6733.6	0.136	0.775
hsa-miR-933	8.2	0.589	0.733
hsa-miR-935	73.0	-0.962	0.027
hsa-miR-936	0.2	0.244	
hsa-miR-937-3p	16.1	0.566	0.626
hsa-miR-937-5p	1.7	0.643	
hsa-miR-938	0.6	-0.149	
hsa-miR-939-3p	8.7	0.214	0.908
hsa-miR-939-5p	12.1	0.279	0.857
hsa-miR-940	117.5	-0.227	0.774
hsa-miR-941	489.6	2.434	0.000
hsa-miR-942-3p	2.9	-0.635	0.775
hsa-miR-942-5p	22.7	-1.274	0.050
hsa-miR-943	7.0	-0.045	0.986
hsa-miR-95-3p	37.3	-0.046	0.974

Table 6.3 (continued from the previous page)

hsa-miR-542-5p	11.7	-0.969	0.405
hsa-miR-545-3p	3.2	-1.537	0.290
hsa-miR-545-5p	10.9	-1.376	0.119
hsa-miR-548a-3p	14.4	1.341	0.076
hsa-miR-548a-5p	4.5	0.454	0.840
hsa-miR-548ab	0.2	-0.126	
hsa-miR-548ag	2.9	0.259	0.911
hsa-miR-548ai	0.9	-0.824	
hsa-miR-548al	1.3	-0.456	
hsa-miR-548am-5p	0.1	-0.010	
hsa-miR-548an	1.3	-1.153	
hsa-miR-548ao-3p	0.1	-0.010	
hsa-miR-548ao-5p	0.1	-0.010	
hsa-miR-548ap-3p	0.2	0.244	
hsa-miR-548ap-5p	0.9	-0.531	
hsa-miR-548aq-5p	1.1	0.033	
hsa-miR-548ar-3p	0.2	-0.126	
hsa-miR-548as-3p	1.6	-1.513	
hsa-miR-548at-3p	0.2	0.244	
hsa-miR-548at-5p	0.2	0.244	
hsa-miR-548aw	5.1	1.067	0.466
hsa-miR-548ay-3p	0.6	-0.570	
hsa-miR-548b-3p	32.6	-3.925	0.000
hsa-miR-548b-5p	0.1	-0.010	
hsa-miR-548ba	0.2	0.244	
hsa-miR-548d-3p	1.0	-1.036	
hsa-miR-548e-3p	6.7	-2.221	0.034
hsa-miR-548e-5p	2.6	-1.635	0.231
hsa-miR-548f-3p	5.2	0.252	0.905
hsa-miR-548h-5p	2.3	-0.166	0.956
hsa-miR-548j-3p	0.7	0.428	
hsa-miR-548j-5p	2.0	-0.946	
hsa-miR-548k	5.6	-2.245	0.049
hsa-miR-548l	1.1	-1.090	
hsa-miR-548n	1.0	-0.621	
hsa-miR-548o-3p	0.1	-0.010	
hsa-miR-548q	0.8	-0.421	
hsa-miR-548s	0.5	0.010	
hsa-miR-548t-5p	0.1	-0.010	
hsa-miR-548u	0.2	-0.126	
hsa-miR-548v	0.8	-0.421	
hsa-miR-548z	0.3	0.244	
hsa-miR-550a-3-5p	3.3	-0.808	0.665
hsa-miR-550a-3p	95.9	-2.020	0.000
hsa-miR-550a-5p	11.6	-1.442	0.095
hsa-miR-550b-2-5p	0.2	0.244	
hsa-miR-550b-3p	0.7	-0.157	
hsa-miR-551a	1.9	-0.930	
hsa-miR-551b-3p	165.9	-0.298	0.735
hsa-miR-551b-5p	15.9	-0.058	0.979
hsa-miR-552-5p	1.1	-0.971	
hsa-miR-556-3p	9.7	-1.645	0.081
hsa-miR-556-5p	3.2	-0.960	0.595
hsa-miR-5579-3p	0.1	-0.010	
hsa-miR-5579-5p	0.3	-0.179	
hsa-miR-5580-5p	0.1	-0.010	
hsa-miR-5581-3p	0.7	-0.718	
hsa-miR-5582-3p	1.5	-0.142	
hsa-miR-5583-3p	0.3	-0.153	
hsa-miR-5583-5p	0.5	0.011	
hsa-miR-5584-3p	0.1	-0.010	
hsa-miR-5584-5p	1.3	-0.696	
hsa-miR-5586-5p	0.1	-0.010	
hsa-miR-5587-3p	2.2	-1.441	0.324
hsa-miR-5587-5p	4.0	-2.139	0.061
hsa-miR-5588-3p	0.2	0.244	
hsa-miR-5588-5p	0.3	-0.153	
hsa-miR-5589-3p	0.1	-0.010	
hsa-miR-5589-5p	0.1	-0.010	
hsa-miR-561-3p	0.5	-0.409	
hsa-miR-561-5p	4.4	-2.137	0.055
hsa-miR-5680	0.5	0.509	
hsa-miR-5006-3p	0.6	-0.032	
hsa-miR-5008-3p	1.0	-0.431	
hsa-miR-5008-5p	0.9	-0.371	
hsa-miR-5009-3p	0.1	-0.010	
hsa-miR-5009-5p	0.1	-0.010	
hsa-miR-500a-3p	46.0	-0.662	0.289
hsa-miR-500a-5p	35.4	-0.387	0.667
hsa-miR-500b-3p	1.2	-0.078	
hsa-miR-500b-5p	35.4	-0.387	0.667
hsa-miR-501-3p	24.1	-0.543	0.595
hsa-miR-501-5p	39.2	-0.091	0.942
hsa-miR-5010-3p	38.2	0.515	0.524
hsa-miR-5010-5p	3.7	0.710	0.736
hsa-miR-502-3p	37.2	-1.136	0.026
hsa-miR-502-5p	7.2	-0.182	0.926
hsa-miR-503-3p	2.7	0.782	0.705
hsa-miR-503-5p	267.7	-0.156	0.840
hsa-miR-504-5p	0.9	0.404	
hsa-miR-5047	2.7	0.662	0.765
hsa-miR-505-3p	233.6	-0.884	0.003
hsa-miR-505-5p	15.5	-0.210	0.896
hsa-miR-508-3p	0.1	-0.010	
hsa-miR-5087	0.6	0.233	
hsa-miR-5088-3p	6.3	0.382	0.848
hsa-miR-6720-3p	2.7	-1.045	0.555
hsa-miR-6720-5p	12.8	-1.076	0.273
hsa-miR-6721-5p	8.5	0.680	0.626
hsa-miR-6722-3p	0.3	0.244	
hsa-miR-6722-5p	0.3	0.244	
hsa-miR-6723-5p	14.8	0.457	0.765
hsa-miR-6724-5p	58.4	0.809	0.077
hsa-miR-6726-3p	8.1	0.764	0.595
hsa-miR-6726-5p	0.7	-0.606	
hsa-miR-6727-3p	1.0	0.212	
hsa-miR-6727-5p	1.0	-0.433	
hsa-miR-6728-3p	4.8	0.430	0.840
hsa-miR-6728-5p	2.1	-0.348	0.887
hsa-miR-6729-3p	4.4	0.157	0.955
hsa-miR-6729-5p	0.3	0.136	
hsa-miR-6730-3p	0.5	0.509	
hsa-miR-6730-5p	2.1	0.615	0.781
hsa-miR-6731-3p	0.1	-0.010	
hsa-miR-6732-3p	2.6	-0.678	0.765
hsa-miR-6732-5p	0.7	0.540	
hsa-miR-6733-3p	1.6	0.775	
hsa-miR-6733-5p	3.1	0.511	0.823
hsa-miR-6734-3p	2.5	1.034	0.546
hsa-miR-6734-5p	2.1	0.106	
hsa-miR-6735-3p	3.3	0.379	0.873
hsa-miR-6735-5p	4.6	0.415	0.840
hsa-miR-6736-3p	1.2	0.273	
hsa-miR-6736-5p	1.6	-0.008	
hsa-miR-6737-3p	5.5	0.379	0.855
hsa-miR-6737-5p	0.3	0.114	
hsa-miR-6738-3p	4.0	0.416	0.848
hsa-miR-6738-5p	1.2	0.355	
hsa-miR-6739-3p	2.2	0.443	0.848
hsa-miR-6739-5p	0.2	0.244	
hsa-miR-6740-3p	5.4	-0.318	0.886
hsa-miR-6740-5p	1.0	0.579	
hsa-miR-6741-3p	15.0	0.516	0.690
hsa-miR-6741-5p	1.8	0.578	
hsa-miR-6742-3p	5.4	0.136	0.957
hsa-miR-6742-5p	2.6	0.290	0.903
hsa-miR-6743-3p	6.5	-0.046	0.986
hsa-miR-6743-5p	0.5	-0.058	
hsa-miR-6745	0.7	0.886	
hsa-miR-6746-3p	1.0	-0.156	
hsa-miR-6746-5p	0.3	0.365	
hsa-miR-6747-3p	45.4	-0.093	0.942
hsa-miR-6747-5p	0.8	0.839	
hsa-miR-6748-3p	1.2	0.097	
hsa-miR-95-5p	0.1	-0.010	
hsa-miR-9500	0.5	0.010	
hsa-miR-96-3p	5.6	0.604	0.758
hsa-miR-96-5p	157.8	-0.239	0.765
hsa-miR-98-3p	2.5	0.076	0.983
hsa-miR-98-5p	35.4	0.337	0.751
hsa-miR-99a-3p	20.9	-0.725	0.534
hsa-miR-99a-5p	688.5	-0.716	0.004
hsa-miR-99b-3p	80.8	-0.791	0.059
hsa-miR-99b-5p	820.9	-0.790	0.014
hsa-miR-663a	5.0	0.264	0.902
hsa-miR-663b	4.2	0.423	0.840
hsa-miR-664a-3p	198.4	0.403	0.421
hsa-miR-664a-5p	22.2	0.504	0.640
hsa-miR-664b-3p	32.2	0.295	0.793
hsa-miR-664b-5p	7.1	0.602	0.733
hsa-miR-670-3p	0.1	-0.010	
hsa-miR-671-3p	25.0	0.039	0.983
hsa-miR-671-5p	279.0	0.626	0.189
hsa-miR-6715b-3p	0.1	-0.010	
hsa-miR-6716-3p	2.3	-0.097	0.977
hsa-miR-6716-5p	0.5	0.010	
hsa-miR-6717-5p	0.1	-0.010	
hsa-miR-6719-3p	0.2	0.244	
hsa-miR-5682	3.3	-0.531	0.810
hsa-miR-5683	3.1	-0.036	0.991
hsa-miR-5684	0.5	0.509	
hsa-miR-5687	0.1	-0.010	
hsa-miR-5689	0.3	0.365	
hsa-miR-5690	0.8	0.295	
hsa-miR-5692a	0.1	-0.010	
hsa-miR-5692b	0.7	0.413	
hsa-miR-5692c	2.4	0.526	0.812
hsa-miR-5693	0.7	-0.210	
hsa-miR-5695	1.1	-0.218	
hsa-miR-5696	1.9	0.684	
hsa-miR-5697	1.0	1.076	
hsa-miR-5699-3p	2.9	-2.068	0.059
hsa-miR-659-5p	5.2	1.145	0.412
hsa-miR-660-3p	3.7	-0.413	0.850
hsa-miR-660-5p	156.4	0.002	0.999
hsa-miR-662	0.1	-0.010	
hsa-miR-6748-5p	0.5	0.010	
hsa-miR-6749-3p	1.5	0.483	
hsa-miR-675-3p	0.1	-0.010	
hsa-miR-675-5p	1.3	-0.783	
spk_3	711.1	0.473	0.248
spk_4	653.6	0.564	0.062
spk_6	784.0	0.578	0.033
spk_7	790.4	0.410	0.316
spk_11	904.5	0.655	0.029
spk_13	1363.6	0.393	0.326
spk_14	890.3	0.649	0.007
spk_15	649.6	1.082	0.000
spk_17	410.5	0.608	0.047
spk_19	966.0	0.832	0.002
spk_21	1135.9	0.705	0.016
spk_24	2108.6	0.975	0.001
spk_25	476.7	0.406	0.316
spk_28	1736.3	0.641	0.036
spk_29	1526.1	-0.093	0.916

Table 6.4 DESeq2 output from small RNA sequencing conducted using HCT116 grown with 0.1% or 9.1% FBS.

mature	baseMean	log2FC	padj
hsa-let-7a-2-3p	470.7	0.606	0.001
hsa-let-7a-3p	1745.3	0.196	0.303
hsa-let-7a-5p	107685.6	0.731	0.000
hsa-let-7b-3p	1045.7	0.988	0.002
hsa-let-7b-5p	32680.7	0.948	0.000
hsa-let-7c-3p	3.7	0.234	0.422
hsa-let-7c-5p	1437.8	1.070	0.000
hsa-let-7d-3p	1326.7	-0.230	0.252
hsa-let-7d-5p	16560.6	0.041	0.848
hsa-let-7e-3p	123.7	0.296	0.363
hsa-let-7e-5p	6129.5	0.816	0.000
hsa-let-7f-1-3p	359.8	-0.293	0.225
hsa-let-7f-2-3p	234.0	0.657	0.007
hsa-let-7f-5p	49136.4	0.387	0.008
hsa-let-7g-3p	251.5	0.705	0.013
hsa-let-7g-5p	28454.2	0.384	0.016
hsa-let-7i-3p	819.6	0.118	0.691
hsa-let-7i-5p	23053.9	0.145	0.554
hsa-miR-100-3p	369.0	0.826	0.012
hsa-miR-100-5p	65992.2	0.947	0.000
hsa-miR-101-3p	11842.0	0.726	0.003
hsa-miR-101-5p	53.1	1.503	0.000
hsa-miR-103a-2-5p	98.7	0.178	0.644
hsa-miR-103a-3p	35771.0	0.599	0.000
hsa-miR-103b	0.1	0.026	NA
hsa-miR-105-5p	3.1	0.136	NA
hsa-miR-106a-3p	1.4	0.072	NA
hsa-miR-106a-5p	2687.6	-0.058	0.824
hsa-miR-106b-3p	1904.0	0.086	0.692
hsa-miR-106b-5p	17441.4	0.238	0.392
hsa-miR-107	10342.1	1.069	0.000
hsa-miR-10a-3p	159.9	0.850	0.000
hsa-miR-10a-5p	7767.3	1.014	0.000
hsa-miR-10b-3p	35.1	0.568	0.155
hsa-miR-10b-5p	1764.8	0.925	0.000
hsa-miR-1179	5.0	0.100	0.784
hsa-miR-1180-3p	1407.2	0.201	0.482
hsa-miR-1180-5p	46.8	-0.451	0.215
hsa-miR-1181	2.3	0.067	NA
hsa-miR-1184	0.1	0.027	NA
hsa-miR-1185-1-3p	18.8	-0.086	0.848
hsa-miR-1185-2-3p	8.5	0.211	0.615
hsa-miR-1185-5p	3.2	-0.179	NA
hsa-miR-1193	0.2	-0.041	NA
hsa-miR-1197	2.9	-0.112	NA
hsa-miR-1199-3p	0.5	0.003	NA
hsa-miR-1199-5p	0.5	0.003	NA
hsa-miR-122-3p	0.2	-0.042	NA
hsa-miR-122-5p	1.8	0.058	NA
hsa-miR-1224-3p	10.8	-0.005	0.988
hsa-miR-1224-5p	23.9	0.625	0.140
hsa-miR-1225-3p	2.1	-0.141	NA
hsa-miR-1225-5p	2.1	-0.140	NA
hsa-miR-1226-3p	70.5	-0.791	0.010
hsa-miR-1226-5p	19.4	-2.153	0.000
hsa-miR-1227-3p	6.5	-0.688	0.140
hsa-miR-1228-3p	9.1	0.181	0.657
hsa-miR-138-2-3p	0.2	-0.041	NA
hsa-miR-138-5p	14.3	-0.006	0.986
hsa-miR-139-3p	27.0	0.217	0.618
hsa-miR-139-5p	364.7	0.318	0.196
hsa-miR-140-3p	1533.8	0.419	0.056
hsa-miR-140-5p	799.3	0.555	0.027
hsa-miR-141-3p	39632.4	0.577	0.034
hsa-miR-141-5p	442.7	0.625	0.003
hsa-miR-142-3p	151.6	1.874	0.000
hsa-miR-142-5p	75.4	1.703	0.000
hsa-miR-143-3p	83.1	2.040	0.000
hsa-miR-143-5p	1.4	0.008	NA
hsa-miR-144-3p	3.9	0.298	0.333
hsa-miR-144-5p	1.8	0.162	NA
hsa-miR-145-3p	244.3	-0.564	0.009
hsa-miR-145-5p	3953.1	0.081	0.746
hsa-miR-1468-5p	11.6	1.113	0.063
hsa-miR-1469	0.2	-0.041	NA
hsa-miR-146a-5p	13.0	1.492	0.014

mature	baseMean	log2FC	padj
hsa-miR-1228-5p	0.5	-0.065	NA
hsa-miR-1229-3p	33.1	-0.435	0.292
hsa-miR-1229-5p	0.3	0.036	NA
hsa-miR-1233-3p	1.7	0.067	NA
hsa-miR-1234-3p	7.3	0.004	0.991
hsa-miR-1236-3p	5.6	-0.185	0.562
hsa-miR-1236-5p	0.8	0.041	NA
hsa-miR-1237-3p	15.8	-0.153	0.746
hsa-miR-1237-5p	2.1	-0.141	NA
hsa-miR-1238-3p	0.6	0.075	NA
hsa-miR-1238-5p	0.4	0.041	NA
hsa-miR-124-3p	8.9	1.375	0.051
hsa-miR-124-5p	0.4	0.041	NA
hsa-miR-1243	1.3	-0.065	NA
hsa-miR-1244	0.5	0.003	NA
hsa-miR-1246	45.0	-0.937	0.020
hsa-miR-1247-3p	4.0	-0.314	0.353
hsa-miR-1247-5p	124.5	-0.248	0.447
hsa-miR-1248	14.7	0.516	0.252
hsa-miR-1249-3p	81.6	-0.784	0.013
hsa-miR-1249-5p	2.1	-0.274	NA
hsa-miR-1250-3p	2.8	0.238	NA
hsa-miR-1250-5p	3.4	0.342	0.285
hsa-miR-1251-5p	1.1	-0.095	NA
hsa-miR-1252-3p	9.3	0.145	0.755
hsa-miR-1252-5p	15.9	0.254	0.556
hsa-miR-1253	0.6	0.075	NA
hsa-miR-1254	108.5	-0.201	0.546
hsa-miR-1255a	53.5	0.581	0.145
hsa-miR-1256	5.4	0.126	0.761
hsa-miR-1257	4.7	-0.376	0.318
hsa-miR-1258	3.6	-0.007	0.980
hsa-miR-125a-3p	142.5	0.671	0.025
hsa-miR-125a-5p	5463.3	0.869	0.000
hsa-miR-125b-1-3p	965.5	0.620	0.001
hsa-miR-125b-2-3p	2.4	0.088	NA
hsa-miR-125b-5p	41390.8	1.102	0.000
hsa-miR-126-3p	2645.0	0.539	0.003
hsa-miR-126-5p	1191.3	0.617	0.001
hsa-miR-1260a	11.6	1.125	0.053
hsa-miR-1260b	782.2	0.434	0.065
hsa-miR-1262	31.3	-0.057	0.897
hsa-miR-1266-3p	1.6	-0.028	NA
hsa-miR-1266-5p	17.5	-0.167	0.717
hsa-miR-1268a	0.3	0.036	NA
hsa-miR-1268b	34.8	-0.412	0.293
hsa-miR-127-3p	1.8	-0.052	NA
hsa-miR-127-5p	0.5	0.059	NA
hsa-miR-1271-3p	1.5	0.019	NA
hsa-miR-1271-5p	0.5	0.003	NA
hsa-miR-1272	1.8	-0.248	NA
hsa-miR-1273a	0.2	-0.041	NA
hsa-miR-1273c	8.8	-0.051	0.901
hsa-miR-1273d	7.3	-0.380	0.352
hsa-miR-1273e	1.5	-0.047	NA
hsa-miR-1275	69.8	-0.421	0.197
hsa-miR-1276	4.0	-0.422	0.217
hsa-miR-1277-3p	86.5	0.290	0.508
hsa-miR-1277-5p	354.9	0.247	0.546
hsa-miR-1278	25.0	-0.039	0.935
hsa-miR-128-1-5p	56.0	-0.812	0.017
hsa-miR-128-3p	5917.0	-0.156	0.377
hsa-miR-1281	0.3	0.036	NA
hsa-miR-1283	0.7	-0.036	NA
hsa-miR-1284	3.7	-0.233	0.434
hsa-miR-1285-3p	37.9	-0.088	0.837
hsa-miR-1285-5p	0.2	-0.041	NA
hsa-miR-1286	6.6	0.062	0.866
hsa-miR-1287-3p	25.4	1.357	0.004
hsa-miR-1287-5p	133.9	0.771	0.024
hsa-miR-1288-3p	0.5	0.003	NA
hsa-miR-1289	2.0	0.164	NA
hsa-miR-129-1-3p	3.9	2.040	0.039
hsa-miR-129-2-3p	0.2	-0.041	NA
hsa-miR-129-5p	2.7	0.329	NA
hsa-miR-1290	0.9	0.003	NA

mature	baseMean	log2FC	padj
hsa-miR-6732-5p	1.1	0.124	NA
hsa-miR-6733-3p	1.5	0.097	NA
hsa-miR-6733-5p	2.1	-0.026	NA
hsa-miR-6734-3p	1.8	-0.056	NA
hsa-miR-6734-5p	4.0	-0.238	0.506
hsa-miR-6735-3p	2.1	-0.013	NA
hsa-miR-6735-5p	1.5	0.114	NA
hsa-miR-6736-3p	0.5	0.059	NA
hsa-miR-6799-3p	10.1	-0.279	0.508
hsa-miR-6799-5p	2.6	-0.137	NA
hsa-miR-6800-3p	7.8	-0.206	0.614
hsa-miR-6800-5p	1.3	0.061	NA
hsa-miR-6801-3p	3.4	-0.155	0.614
hsa-miR-6801-5p	1.8	-0.236	NA
hsa-miR-6802-3p	3.5	0.510	0.148
hsa-miR-6802-5p	0.4	-0.001	NA
hsa-miR-6803-3p	17.1	0.281	0.524
hsa-miR-6803-5p	0.2	-0.041	NA
hsa-miR-6804-3p	1.1	0.027	NA
hsa-miR-6804-5p	4.9	-0.099	0.782
hsa-miR-6805-3p	4.2	-0.134	0.657
hsa-miR-6805-5p	5.5	-0.049	0.896
hsa-miR-6806-3p	0.7	-0.029	NA
hsa-miR-6807-3p	5.8	-0.063	0.866
hsa-miR-6807-5p	3.3	-0.163	0.596
hsa-miR-6808-3p	1.3	0.055	NA
hsa-miR-6808-5p	0.2	-0.041	NA
hsa-miR-6809-3p	0.2	-0.041	NA
hsa-miR-6809-5p	0.2	-0.041	NA
hsa-miR-6810-3p	1.7	0.140	NA
hsa-miR-6810-5p	1.7	0.149	NA
hsa-miR-6811-5p	0.4	0.000	NA
hsa-miR-6812-3p	6.3	-0.039	0.919
hsa-miR-6812-5p	1.7	-0.007	NA
hsa-miR-6813-3p	0.8	-0.010	NA
hsa-miR-6813-5p	1.8	-0.068	NA
hsa-miR-6814-3p	0.7	-0.028	NA
hsa-miR-6815-3p	3.6	-0.073	0.839
hsa-miR-6815-5p	2.5	0.027	NA
hsa-miR-6816-3p	8.1	0.217	0.573
hsa-miR-6816-5p	0.7	-0.029	NA
hsa-miR-6817-3p	2.6	-0.087	NA
hsa-miR-6817-5p	0.7	-0.035	NA
hsa-miR-6818-3p	3.4	0.181	0.591
hsa-miR-6818-5p	0.6	0.072	NA
hsa-miR-6819-3p	2.1	-0.081	NA
hsa-miR-6819-5p	0.5	-0.065	NA
hsa-miR-6820-3p	7.9	-0.021	0.967
hsa-miR-6820-5p	2.3	-0.033	NA
hsa-miR-6821-3p	1.6	-0.274	NA
hsa-miR-6821-5p	1.8	-0.145	NA
hsa-miR-6822-5p	0.7	0.037	NA
hsa-miR-6823-3p	0.4	-0.001	NA
hsa-miR-6823-5p	0.9	-0.068	NA
hsa-miR-6824-3p	3.7	0.217	0.518
hsa-miR-6824-5p	1.1	-0.119	NA
hsa-miR-6825-3p	0.9	0.045	NA
hsa-miR-6825-5p	1.3	-0.158	NA
hsa-miR-6826-3p	0.9	-0.001	NA
hsa-miR-6826-5p	0.7	0.037	NA
hsa-miR-6827-3p	0.2	-0.041	NA
hsa-miR-6827-5p	0.2	-0.042	NA
hsa-miR-6829-3p	1.0	0.019	NA
hsa-miR-6829-5p	0.2	0.035	NA
hsa-miR-6830-3p	0.4	-0.001	NA
hsa-miR-6832-3p	1.6	0.145	NA
hsa-miR-6832-5p	0.4	0.043	NA
hsa-miR-6833-3p	3.5	0.086	0.784
hsa-miR-6833-5p	0.6	0.017	NA
hsa-miR-6834-3p	2.7	-0.129	NA
hsa-miR-6834-5p	0.3	0.036	NA
hsa-miR-6835-3p	0.2	-0.041	NA
hsa-miR-6835-5p	0.4	0.041	NA
hsa-miR-6836-3p	1.9	0.161	NA
hsa-miR-6836-5p	0.8	0.052	NA
hsa-miR-6837-3p	0.5	-0.066	NA

Table 6.4 (continued from the previous page)

hsa-miR-146b-3p	6.0	0.602	0.172
hsa-miR-146b-5p	441.5	1.419	0.000
hsa-miR-1471	0.4	0.041	NA
hsa-miR-147a	0.2	0.035	NA
hsa-miR-147b	31.2	0.175	0.689
hsa-miR-148a-3p	3150.4	0.874	0.000
hsa-miR-148a-5p	32.0	0.263	0.533
hsa-miR-148b-3p	6009.2	-0.006	0.981
hsa-miR-148b-5p	159.4	-0.498	0.139
hsa-miR-149-3p	23.7	-1.211	0.007
hsa-miR-149-5p	1542.7	-0.457	0.019
hsa-miR-150-3p	0.6	0.017	NA
hsa-miR-150-5p	12.7	-0.401	0.350
hsa-miR-151a-3p	7213.2	0.267	0.138
hsa-miR-151a-5p	12723.2	0.658	0.000
hsa-miR-151b	1626.0	1.163	0.000
hsa-miR-152-3p	106.3	1.283	0.000
hsa-miR-152-5p	0.2	-0.041	NA
hsa-miR-153-3p	1338.9	0.107	0.722
hsa-miR-153-5p	47.8	0.434	0.268
hsa-miR-1537-3p	14.5	0.068	0.869
hsa-miR-1537-5p	2.0	-0.086	NA
hsa-miR-1538	7.3	-0.210	0.596
hsa-miR-1539	0.5	-0.065	NA
hsa-miR-154-3p	39.0	-0.463	0.206
hsa-miR-154-5p	9.4	-0.108	0.806
hsa-miR-155-5p	0.2	-0.041	NA
hsa-miR-1587	0.2	-0.041	NA
hsa-miR-15a-3p	49.7	-0.694	0.100
hsa-miR-15a-5p	5388.6	-0.097	0.804
hsa-miR-15b-3p	809.1	-0.874	0.000
hsa-miR-15b-5p	9124.3	-0.564	0.000
hsa-miR-16-1-3p	93.4	-0.254	0.555
hsa-miR-16-2-3p	999.9	-0.358	0.038
hsa-miR-16-5p	38170.5	0.017	0.949
hsa-miR-17-3p	1902.6	0.002	0.997
hsa-miR-17-5p	34363.7	-0.103	0.703
hsa-miR-181a-2-3p	98.2	0.749	0.004
hsa-miR-181a-3p	484.9	0.901	0.000
hsa-miR-181a-5p	15014.7	1.099	0.000
hsa-miR-181b-2-3p	2.8	0.082	NA
hsa-miR-181b-3p	37.2	-0.303	0.445
hsa-miR-181b-5p	4202.4	0.115	0.588
hsa-miR-181c-3p	18.7	0.263	0.547
hsa-miR-181c-5p	267.7	0.998	0.000
hsa-miR-181d-3p	0.7	-0.036	NA
hsa-miR-181d-5p	87.7	-0.010	0.980
hsa-miR-182-3p	54.5	0.396	0.312
hsa-miR-182-5p	8467.7	0.727	0.000
hsa-miR-1825	0.2	-0.042	NA
hsa-miR-183-3p	190.8	0.266	0.293
hsa-miR-183-5p	4228.1	0.212	0.333
hsa-miR-184	2.8	0.222	NA
hsa-miR-185-3p	115.2	0.590	0.037
hsa-miR-185-5p	3776.6	0.267	0.103
hsa-miR-186-3p	107.1	-0.025	0.963
hsa-miR-186-5p	8542.8	0.056	0.789
hsa-miR-187-3p	12.4	0.123	0.790
hsa-miR-188-3p	10.8	-0.078	0.852
hsa-miR-188-5p	366.5	-0.282	0.281
hsa-miR-18a-3p	584.4	-0.319	0.106
hsa-miR-18a-5p	7650.0	-0.395	0.151
hsa-miR-18b-3p	1.2	0.035	NA
hsa-miR-18b-5p	385.3	-0.012	0.979
hsa-miR-1908-3p	11.5	-0.917	0.083
hsa-miR-1908-5p	9.5	0.109	0.806
hsa-miR-1909-3p	2.7	-0.109	NA
hsa-miR-1909-5p	1.8	0.008	NA
hsa-miR-190a-3p	18.7	0.819	0.098
hsa-miR-190a-5p	315.5	1.340	0.000
hsa-miR-190b	23.0	0.243	0.570
hsa-miR-191-3p	260.9	0.429	0.080
hsa-miR-191-5p	27659.4	0.927	0.000
hsa-miR-1910-3p	27.9	-0.995	0.016
hsa-miR-1910-5p	42.1	-1.382	0.000
hsa-miR-1913	0.8	-0.012	NA
hsa-miR-1914-3p	30.7	-1.994	0.000

hsa-miR-1291	3.1	-0.016	NA
hsa-miR-1292-3p	5.1	-0.691	0.131
hsa-miR-1292-5p	106.0	-0.328	0.333
hsa-miR-1293	45.3	-1.317	0.001
hsa-miR-1294	13.5	-0.306	0.482
hsa-miR-1295a	7.9	-0.133	0.758
hsa-miR-1296-3p	32.1	0.171	0.715
hsa-miR-1296-5p	1897.7	-0.148	0.515
hsa-miR-1297	3.3	0.265	0.266
hsa-miR-1298-5p	0.2	-0.041	NA
hsa-miR-1301-3p	503.9	-0.558	0.004
hsa-miR-1301-5p	8.8	-0.521	0.242
hsa-miR-1302	0.6	0.017	NA
hsa-miR-1304-3p	0.2	-0.042	NA
hsa-miR-1304-5p	208.5	-0.563	0.012
hsa-miR-1305	3.7	-0.122	0.598
hsa-miR-1306-3p	22.1	-1.604	0.001
hsa-miR-1306-5p	98.6	-1.252	0.000
hsa-miR-1307-3p	7170.3	-0.174	0.525
hsa-miR-1307-5p	6121.7	0.346	0.172
hsa-miR-130a-3p	2906.3	0.465	0.135
hsa-miR-130a-5p	62.8	0.131	0.758
hsa-miR-130b-3p	2450.7	0.252	0.301
hsa-miR-130b-5p	1107.1	0.010	0.970
hsa-miR-132-3p	1282.7	0.859	0.000
hsa-miR-132-5p	74.9	1.067	0.001
hsa-miR-1323	0.2	-0.041	NA
hsa-miR-133a-3p	0.2	-0.041	NA
hsa-miR-133a-5p	0.2	0.035	NA
hsa-miR-134-5p	11.7	-0.251	0.562
hsa-miR-1343-3p	22.4	0.511	0.238
hsa-miR-1343-5p	29.6	-0.238	0.588
hsa-miR-135a-5p	11.4	0.311	0.473
hsa-miR-135b-3p	62.7	0.120	0.766
hsa-miR-135b-5p	2108.9	0.578	0.020
hsa-miR-136-3p	0.7	-0.036	NA
hsa-miR-136-5p	0.2	-0.041	NA
hsa-miR-137	0.2	0.035	NA
hsa-miR-138-1-3p	0.2	-0.041	NA
hsa-miR-1976	12.0	-0.018	0.970
hsa-miR-199a-3p	104.1	0.626	0.018
hsa-miR-199a-5p	2.5	0.357	NA
hsa-miR-199b-3p	77.2	0.568	0.051
hsa-miR-199b-5p	64.8	0.658	0.056
hsa-miR-19a-3p	21887.0	-0.374	0.080
hsa-miR-19a-5p	85.3	-0.573	0.188
hsa-miR-19b-1-5p	424.5	-0.518	0.025
hsa-miR-19b-2-5p	3.1	-0.068	NA
hsa-miR-19b-3p	34784.0	-0.129	0.556
hsa-miR-200a-3p	15475.4	1.067	0.000
hsa-miR-200a-5p	458.6	0.681	0.000
hsa-miR-200b-3p	14709.4	0.726	0.000
hsa-miR-200b-5p	606.3	0.318	0.122
hsa-miR-200c-3p	64277.2	0.660	0.000
hsa-miR-200c-5p	404.5	0.229	0.301
hsa-miR-202-3p	0.4	0.041	NA
hsa-miR-202-5p	1.5	0.211	NA
hsa-miR-203a-3p	1581.5	-0.262	0.168
hsa-miR-203a-5p	21.3	-0.115	0.804
hsa-miR-203b-3p	54.9	-0.247	0.507
hsa-miR-203b-5p	2.0	-0.112	NA
hsa-miR-204-5p	4.6	0.302	0.349
hsa-miR-205-3p	0.9	0.065	NA
hsa-miR-205-5p	196.8	3.825	0.000
hsa-miR-2053	0.2	-0.042	NA
hsa-miR-208a-3p	0.2	-0.042	NA
hsa-miR-208a-5p	0.2	-0.042	NA
hsa-miR-208b-3p	0.2	-0.042	NA
hsa-miR-208b-5p	0.2	-0.042	NA
hsa-miR-20a-3p	546.0	0.067	0.809
hsa-miR-20a-5p	32649.3	0.009	0.979
hsa-miR-20b-3p	1.2	0.035	NA
hsa-miR-20b-5p	6.4	0.223	0.549
hsa-miR-21-3p	5753.7	0.357	0.190
hsa-miR-21-5p	514949.6	0.439	0.014
hsa-miR-210-3p	1873.0	1.138	0.001
hsa-miR-210-5p	11.2	0.889	0.092

hsa-miR-6838-3p	1.3	0.054	NA
hsa-miR-6838-5p	1.7	0.144	NA
hsa-miR-6839-3p	1.0	0.020	NA
hsa-miR-6839-5p	0.6	0.072	NA
hsa-miR-6840-3p	1.4	-0.045	NA
hsa-miR-6840-5p	2.0	-0.033	NA
hsa-miR-6842-3p	2.6	-0.010	NA
hsa-miR-6842-5p	0.2	-0.042	NA
hsa-miR-6843-3p	0.2	-0.041	NA
hsa-miR-6844	5.9	-0.340	0.380
hsa-miR-6845-3p	2.4	0.101	NA
hsa-miR-6845-5p	1.8	0.067	NA
hsa-miR-6846-3p	2.3	0.000	NA
hsa-miR-6846-5p	1.1	0.084	NA
hsa-miR-6847-3p	2.1	-0.194	NA
hsa-miR-6847-5p	2.3	-0.315	NA
hsa-miR-6848-3p	0.4	-0.001	NA
hsa-miR-6848-5p	1.8	-0.082	NA
hsa-miR-6849-3p	1.5	0.023	NA
hsa-miR-6849-5p	0.2	-0.042	NA
hsa-miR-6850-3p	8.4	-0.395	0.345
hsa-miR-6850-5p	16.3	-0.033	0.946
hsa-miR-6851-3p	0.9	0.004	NA
hsa-miR-6851-5p	1.8	0.007	NA
hsa-miR-6852-3p	0.2	-0.041	NA
hsa-miR-6852-5p	0.3	0.036	NA
hsa-miR-6853-3p	1.4	0.112	NA
hsa-miR-6853-5p	0.5	0.045	NA
hsa-miR-6854-3p	0.4	-0.001	NA
hsa-miR-6854-5p	0.2	-0.041	NA
hsa-miR-6855-3p	1.4	0.008	NA
hsa-miR-6855-5p	0.3	0.036	NA
hsa-miR-6856-3p	0.7	-0.121	NA
hsa-miR-6857-3p	0.9	-0.116	NA
hsa-miR-6857-5p	0.5	-0.066	NA
hsa-miR-6858-3p	2.0	0.030	NA
hsa-miR-6858-5p	1.3	-0.065	NA
hsa-miR-6859-3p	0.7	-0.092	NA
hsa-miR-6859-5p	1.1	-0.200	NA
hsa-miR-6860	0.2	0.035	NA
hsa-miR-6861-3p	1.4	0.073	NA
hsa-miR-6861-5p	0.3	0.036	NA
hsa-miR-6862-3p	1.5	-0.218	NA
hsa-miR-6862-5p	2.6	0.040	NA
hsa-miR-6864-3p	0.8	0.041	NA
hsa-miR-6865-3p	0.9	-0.060	NA
hsa-miR-6865-5p	0.2	-0.041	NA
hsa-miR-6866-3p	0.9	0.003	NA
hsa-miR-7976	45.4	-0.438	0.225
hsa-miR-7977	1.9	0.217	NA
hsa-miR-8059	0.6	0.017	NA
hsa-miR-8071	0.3	0.036	NA
hsa-miR-8072	6.3	0.328	0.402
hsa-miR-8074	0.6	0.053	NA
hsa-miR-8077	0.2	-0.042	NA
hsa-miR-8080	0.3	0.036	NA
hsa-miR-8087	0.2	-0.041	NA
hsa-miR-8088	0.4	0.041	NA
hsa-miR-8089	0.7	0.082	NA
hsa-miR-873-3p	0.3	0.036	NA
hsa-miR-874-3p	6.5	0.604	0.181
hsa-miR-875-5p	0.4	0.043	NA
hsa-miR-877-3p	170.1	-0.786	0.003
hsa-miR-877-5p	1037.4	-0.263	0.395
hsa-miR-885-3p	1.1	0.027	NA
hsa-miR-885-5p	13.4	2.297	0.001
hsa-miR-887-3p	0.2	-0.041	NA
hsa-miR-888-5p	0.3	0.036	NA
hsa-miR-889-3p	7.6	-0.214	0.596
hsa-miR-892c-3p	0.8	0.041	NA
hsa-miR-9-3p	1894.9	-0.249	0.156
hsa-miR-9-5p	4468.0	0.133	0.750
hsa-miR-922	0.4	0.041	NA
hsa-miR-924	1.5	0.030	NA
hsa-miR-92a-1-5p	216.3	-0.831	0.000
hsa-miR-92a-2-5p	0.7	0.037	NA
hsa-miR-92a-3p	48460.4	-0.251	0.242

Table 6.4 (continued from the previous page)

hsa-miR-1914-5p	5.7	-3.640	0.004
hsa-miR-1915-3p	15.1	-0.527	0.236
hsa-miR-1915-5p	9.4	-0.133	0.760
hsa-miR-192-3p	6.6	0.298	0.455
hsa-miR-192-5p	268.4	1.528	0.000
hsa-miR-193a-3p	131.2	0.250	0.547
hsa-miR-193a-5p	96.8	0.190	0.549
hsa-miR-193b-3p	964.2	0.609	0.001
hsa-miR-193b-5p	93.0	-0.026	0.956
hsa-miR-194-3p	4.4	0.248	0.476
hsa-miR-194-5p	555.7	2.060	0.000
hsa-miR-195-3p	5.0	-0.306	0.413
hsa-miR-195-5p	145.7	0.929	0.001
hsa-miR-196a-3p	3.2	0.161	0.627
hsa-miR-196a-5p	1996.9	-0.210	0.292
hsa-miR-196b-3p	75.2	-0.148	0.715
hsa-miR-196b-5p	4628.2	-0.113	0.556
hsa-miR-197-3p	2087.6	0.350	0.176
hsa-miR-197-5p	11.9	-0.110	0.806
hsa-miR-1973	11.8	-0.162	0.720
hsa-miR-29c-3p	1757.5	-0.077	0.848
hsa-miR-29c-5p	114.1	-0.460	0.095
hsa-miR-301a-3p	3416.0	-0.400	0.043
hsa-miR-301a-5p	119.1	-1.132	0.000
hsa-miR-301b-3p	784.7	0.010	0.979
hsa-miR-301b-5p	51.5	-1.699	0.000
hsa-miR-302a-3p	4.9	-0.304	0.397
hsa-miR-302a-5p	2.3	-0.295	NA
hsa-miR-302b-3p	10.3	-1.752	0.009
hsa-miR-302b-5p	0.2	-0.041	NA
hsa-miR-302c-3p	4.3	-5.898	0.001
hsa-miR-302c-5p	0.4	-0.065	NA
hsa-miR-302d-3p	3.6	-0.068	0.847
hsa-miR-3064-3p	9.1	0.118	0.793
hsa-miR-3064-5p	4.0	-0.144	0.697
hsa-miR-3065-3p	31.0	2.053	0.000
hsa-miR-3065-5p	123.0	1.492	0.000
hsa-miR-3074-3p	4.9	-0.123	0.750
hsa-miR-3074-5p	5.5	-0.047	0.904
hsa-miR-30a-3p	36.4	-0.629	0.095
hsa-miR-30a-5p	262.0	-0.729	0.001
hsa-miR-30b-3p	64.3	-0.050	0.902
hsa-miR-30b-5p	8736.8	0.453	0.003
hsa-miR-30c-1-3p	68.4	0.581	0.063
hsa-miR-30c-2-3p	2.1	-0.260	NA
hsa-miR-30c-5p	15571.2	0.654	0.000
hsa-miR-30d-3p	122.6	-0.413	0.116
hsa-miR-30d-5p	10020.4	0.391	0.012
hsa-miR-30e-3p	1392.3	0.251	0.135
hsa-miR-30e-5p	11971.0	0.668	0.000
hsa-miR-31-3p	13355.2	0.827	0.000
hsa-miR-31-5p	137326.4	0.876	0.000
hsa-miR-3115	14.7	-0.524	0.240
hsa-miR-3116	3.8	-0.028	0.936
hsa-miR-3120-3p	4.9	-0.133	0.738
hsa-miR-3120-5p	0.2	0.035	NA
hsa-miR-3121-3p	0.5	0.003	NA
hsa-miR-3121-5p	0.6	0.016	NA
hsa-miR-3122	0.2	-0.042	NA
hsa-miR-3124-3p	0.9	-0.001	NA
hsa-miR-3124-5p	1.9	-0.042	NA
hsa-miR-3126-3p	0.7	-0.030	NA
hsa-miR-3126-5p	1.5	-0.047	NA
hsa-miR-3127-3p	9.5	-0.095	0.823
hsa-miR-3127-5p	8.2	0.067	0.875
hsa-miR-3128	3.7	0.087	0.809
hsa-miR-3129-3p	7.9	-0.273	0.517
hsa-miR-3129-5p	1.7	0.047	NA
hsa-miR-3130-3p	17.3	0.266	0.546
hsa-miR-3130-5p	50.7	-0.187	0.637
hsa-miR-3131	2.9	0.263	NA
hsa-miR-3132	5.8	-0.736	0.126
hsa-miR-3133	10.0	-0.215	0.616
hsa-miR-3134	1.8	0.117	NA
hsa-miR-3136-3p	1.3	-0.006	NA
hsa-miR-3136-5p	16.6	0.114	0.806
hsa-miR-3137	1.2	-0.027	NA

hsa-miR-211-3p	1.1	-0.031	NA
hsa-miR-211-5p	3.2	0.081	0.808
hsa-miR-2110	261.6	-0.292	0.310
hsa-miR-2113	7.1	0.045	0.919
hsa-miR-2114-3p	0.8	0.095	NA
hsa-miR-2114-5p	4.1	0.140	0.714
hsa-miR-2115-3p	0.4	-0.001	NA
hsa-miR-2115-5p	0.8	0.052	NA
hsa-miR-2116-3p	23.4	0.377	0.367
hsa-miR-2116-5p	11.7	-0.101	0.820
hsa-miR-2117	0.2	-0.041	NA
hsa-miR-212-3p	12.7	-0.033	0.946
hsa-miR-212-5p	3.3	-0.040	0.895
hsa-miR-215-3p	0.9	0.004	NA
hsa-miR-215-5p	7.6	1.069	0.075
hsa-miR-216a-5p	1.1	-0.119	NA
hsa-miR-216b-5p	0.7	-0.035	NA
hsa-miR-217	0.2	0.035	NA
hsa-miR-218-1-3p	5.1	0.275	0.448
hsa-miR-218-2-3p	0.3	0.036	NA
hsa-miR-218-5p	95.8	1.045	0.004
hsa-miR-219a-1-3p	47.0	-0.133	0.755
hsa-miR-219a-5p	330.9	0.215	0.609
hsa-miR-219b-3p	1.6	-0.195	NA
hsa-miR-219b-5p	15.9	-0.480	0.278
hsa-miR-22-3p	8978.4	-0.270	0.145
hsa-miR-22-5p	417.0	-0.196	0.376
hsa-miR-221-3p	220804.5	0.232	0.125
hsa-miR-221-5p	2855.9	0.114	0.624
hsa-miR-222-3p	337313.1	0.396	0.015
hsa-miR-222-5p	10256.0	-0.464	0.002
hsa-miR-223-3p	9.1	-0.876	0.096
hsa-miR-223-5p	0.2	-0.041	NA
hsa-miR-224-3p	14.6	-0.228	0.596
hsa-miR-224-5p	648.0	-0.694	0.000
hsa-miR-2276-3p	16.7	-0.426	0.328
hsa-miR-2276-5p	2.5	-0.026	NA
hsa-miR-2277-3p	58.9	0.341	0.378
hsa-miR-2277-5p	54.2	0.334	0.357
hsa-miR-2278	31.1	-0.420	0.284
hsa-miR-2355-3p	15.5	-0.576	0.199
hsa-miR-2355-5p	10.5	-0.124	0.784
hsa-miR-23a-3p	46692.4	0.293	0.231
hsa-miR-23a-5p	297.1	0.141	0.740
hsa-miR-23b-3p	8759.4	0.483	0.014
hsa-miR-23b-5p	56.1	0.012	0.979
hsa-miR-23c	56.0	0.723	0.099
hsa-miR-24-1-5p	98.0	0.311	0.304
hsa-miR-24-2-5p	557.8	0.047	0.848
hsa-miR-24-3p	36383.5	0.156	0.361
hsa-miR-2467-3p	1.5	-0.040	NA
hsa-miR-2467-5p	4.2	-0.274	0.445
hsa-miR-25-3p	30017.9	0.394	0.006
hsa-miR-25-5p	368.9	-0.223	0.397
hsa-miR-2681-3p	0.7	-0.023	NA
hsa-miR-2681-5p	0.7	-0.023	NA
hsa-miR-26a-1-3p	23.1	-0.020	0.969
hsa-miR-26a-2-3p	67.4	1.308	0.000
hsa-miR-26a-5p	25479.4	1.337	0.000
hsa-miR-26b-3p	139.4	0.008	0.981
hsa-miR-26b-5p	12596.9	0.382	0.025
hsa-miR-27a-3p	46617.7	0.491	0.004
hsa-miR-27a-5p	525.2	0.644	0.000
hsa-miR-27b-3p	8812.6	0.471	0.015
hsa-miR-27b-5p	123.7	-0.386	0.207
hsa-miR-28-3p	1914.0	0.831	0.000
hsa-miR-28-5p	2387.3	0.792	0.000
hsa-miR-2909	0.2	-0.041	NA
hsa-miR-296-3p	17.3	1.116	0.033
hsa-miR-296-5p	36.9	0.512	0.188
hsa-miR-298	0.6	0.017	NA
hsa-miR-299-3p	4.7	-0.102	0.786
hsa-miR-299-5p	4.9	-0.196	0.535
hsa-miR-29a-3p	76608.5	0.788	0.000
hsa-miR-29a-5p	1339.3	0.607	0.060
hsa-miR-29b-1-5p	1453.7	0.406	0.014
hsa-miR-29b-2-5p	79.8	-0.436	0.180

hsa-miR-92b-3p	4605.5	-0.393	0.050
hsa-miR-92b-5p	208.7	-1.393	0.000
hsa-miR-93-3p	1210.4	0.029	0.916
hsa-miR-93-5p	32214.7	0.131	0.525
hsa-miR-933	3.0	0.405	NA
hsa-miR-934	4.7	4.856	0.002
hsa-miR-935	153.5	1.240	0.000
hsa-miR-936	0.8	0.056	NA
hsa-miR-937-3p	35.1	0.307	0.440
hsa-miR-937-5p	8.1	-0.055	0.895
hsa-miR-938	0.9	-0.122	NA
hsa-miR-939-3p	14.0	0.092	0.842
hsa-miR-96-3p	52.0	-0.010	0.980
hsa-miR-96-5p	2323.8	0.689	0.000
hsa-miR-98-3p	431.5	0.082	0.782
hsa-miR-98-5p	6143.1	0.206	0.350
hsa-miR-99a-3p	0.4	0.041	NA
hsa-miR-99a-5p	53.2	1.145	0.003
hsa-miR-99b-3p	303.6	0.226	0.350
hsa-miR-6764-3p	2.1	0.088	NA
hsa-miR-6764-5p	2.7	0.068	NA
hsa-miR-6765-3p	14.7	-1.063	0.060
hsa-miR-6765-5p	0.2	-0.042	NA
hsa-miR-6766-3p	2.4	-0.205	NA
hsa-miR-6767-3p	14.2	-0.186	0.657
hsa-miR-6767-5p	13.9	-0.169	0.694
hsa-miR-6768-3p	16.0	-0.112	0.804
hsa-miR-6768-5p	21.6	-0.634	0.169
hsa-miR-6769a-3p	1.5	0.087	NA
hsa-miR-6769a-5p	1.0	0.022	NA
hsa-miR-6769b-3p	1.3	-0.159	NA
hsa-miR-6770-3p	4.0	0.088	0.784
hsa-miR-6770-5p	7.3	0.329	0.422
hsa-miR-6771-5p	0.9	-0.074	NA
hsa-miR-6772-3p	0.4	-0.048	NA
hsa-miR-6772-5p	0.2	-0.041	NA
hsa-miR-6773-5p	0.2	-0.041	NA
hsa-miR-6775-3p	5.1	0.124	0.750
hsa-miR-6775-5p	0.2	-0.042	NA
hsa-miR-6776-3p	1.6	0.077	NA
hsa-miR-6776-5p	0.6	0.075	NA
hsa-miR-6777-3p	25.8	0.900	0.042
hsa-miR-6777-5p	7.2	0.516	0.240
hsa-miR-6778-3p	0.9	0.055	NA
hsa-miR-6778-5p	0.5	0.003	NA
hsa-miR-6779-3p	1.6	0.031	NA
hsa-miR-6779-5p	2.0	0.117	NA
hsa-miR-6780a-3p	0.4	-0.001	NA
hsa-miR-6780a-5p	1.5	0.098	NA
hsa-miR-6780b-3p	4.3	0.035	0.932
hsa-miR-6780b-5p	1.2	-0.111	NA
hsa-miR-6781-3p	1.3	0.055	NA
hsa-miR-6781-5p	1.3	0.061	NA
hsa-miR-6782-3p	1.0	0.018	NA
hsa-miR-6782-5p	0.2	-0.041	NA
hsa-miR-6783-3p	1.8	-0.147	NA
hsa-miR-6783-5p	4.4	-0.086	0.819
hsa-miR-6784-3p	6.1	0.167	0.648
hsa-miR-6784-5p	1.1	-0.032	NA
hsa-miR-6785-3p	0.9	-0.157	NA
hsa-miR-6785-5p	0.5	-0.065	NA
hsa-miR-6786-3p	7.1	-0.440	0.293
hsa-miR-6786-5p	4.8	-0.248	0.456
hsa-miR-6787-3p	8.0	0.046	0.919
hsa-miR-6787-5p	0.5	0.003	NA
hsa-miR-6789-3p	0.9	-0.158	NA
hsa-miR-6789-5p	3.3	-0.200	0.549
hsa-miR-6790-3p	0.2	-0.042	NA
hsa-miR-6790-5p	0.4	0.041	NA
hsa-miR-6791-3p	2.9	0.244	NA
hsa-miR-6791-5p	1.1	0.022	NA
hsa-miR-6792-3p	2.1	0.151	NA
hsa-miR-6792-5p	0.5	0.045	NA
hsa-miR-6793-3p	2.9	0.023	NA
hsa-miR-6793-5p	2.1	-0.021	NA
hsa-miR-6794-3p	9.2	0.130	0.781
hsa-miR-6794-5p	2.0	0.080	NA

Table 6.4 (continued from the previous page)

hsa-miR-3138	26.7	-0.781	0.052
hsa-miR-3139	1.1	-0.094	NA
hsa-miR-3140-3p	12.5	-0.702	0.137
hsa-miR-3140-5p	3.4	-0.112	0.758
hsa-miR-3141	1.5	0.178	NA
hsa-miR-3143	19.9	-0.649	0.146
hsa-miR-3144-3p	2.0	0.032	NA
hsa-miR-3144-5p	0.6	0.017	NA
hsa-miR-3145-3p	5.5	-0.045	0.910
hsa-miR-3145-5p	6.8	-0.521	0.227
hsa-miR-3146	3.3	0.073	0.819
hsa-miR-3147	0.3	0.036	NA
hsa-miR-3148	1.3	-0.152	NA
hsa-miR-3149	1.8	0.003	NA
hsa-miR-3150a-3p	9.6	-0.515	0.249
hsa-miR-3150a-5p	19.9	-0.463	0.276
hsa-miR-3150b-3p	0.5	0.059	NA
hsa-miR-3150b-5p	0.5	0.059	NA
hsa-miR-3153	1.6	-0.282	NA
hsa-miR-3155a	4.9	-1.519	0.044
hsa-miR-3156-3p	0.2	-0.041	NA
hsa-miR-3157-3p	4.4	0.166	0.641
hsa-miR-3157-5p	29.9	-0.517	0.190
hsa-miR-3158-3p	164.9	-0.885	0.000
hsa-miR-3158-5p	46.9	-0.756	0.069
hsa-miR-3159	11.5	0.221	0.614
hsa-miR-3160-3p	1.6	0.039	NA
hsa-miR-3160-5p	1.7	0.049	NA
hsa-miR-3162-3p	1.3	0.072	NA
hsa-miR-3162-5p	2.1	0.029	NA
hsa-miR-3163	1.3	0.144	NA
hsa-miR-3164	7.7	-0.391	0.346
hsa-miR-3165	1.8	-0.218	NA
hsa-miR-3166	0.9	-0.081	NA
hsa-miR-3168	5.9	-0.388	0.333
hsa-miR-3169	0.7	-0.066	NA
hsa-miR-3170	2.1	0.041	NA
hsa-miR-3173-3p	7.5	-0.179	0.652
hsa-miR-3173-5p	50.9	-0.807	0.017
hsa-miR-3174	2.9	-0.124	NA
hsa-miR-3175	18.2	-0.453	0.296
hsa-miR-3176	63.9	-1.154	0.000
hsa-miR-3177-3p	19.0	-1.140	0.018
hsa-miR-3177-5p	3.3	-0.119	0.746
hsa-miR-3178	1.2	0.105	NA
hsa-miR-3179	21.4	-0.749	0.083
hsa-miR-3180	12.7	0.449	0.290
hsa-miR-3180-3p	12.9	0.401	0.332
hsa-miR-3180-5p	3.1	0.035	NA
hsa-miR-3181	4.6	-0.118	0.766
hsa-miR-3182	1.7	-0.153	NA
hsa-miR-3183	1.8	-0.234	NA
hsa-miR-3184-3p	0.7	-0.092	NA
hsa-miR-3184-5p	0.7	-0.094	NA
hsa-miR-3185	1.0	0.053	NA
hsa-miR-3187-3p	131.4	-1.564	0.000
hsa-miR-3187-5p	3.1	-0.162	NA
hsa-miR-3188	2.6	0.047	NA
hsa-miR-3189-3p	11.2	1.254	0.047
hsa-miR-3663-5p	1.3	-0.127	NA
hsa-miR-3664-3p	8.5	-0.263	0.524
hsa-miR-3664-5p	3.8	-0.114	0.766
hsa-miR-3665	0.2	-0.041	NA
hsa-miR-3667-3p	83.9	-0.069	0.848
hsa-miR-3667-5p	50.3	-0.005	0.986
hsa-miR-3668	0.2	0.035	NA
hsa-miR-367-3p	1.6	-0.300	NA
hsa-miR-3670	0.2	-0.042	NA
hsa-miR-3672	0.9	0.003	NA
hsa-miR-3674	0.4	0.041	NA
hsa-miR-3677-3p	3.1	-0.342	NA
hsa-miR-3677-5p	1.6	-0.205	NA
hsa-miR-3678-3p	0.7	-0.028	NA
hsa-miR-3678-5p	0.5	-0.048	NA
hsa-miR-3679-3p	3.7	-0.156	0.625
hsa-miR-3679-5p	28.9	-1.106	0.010
hsa-miR-3680-3p	3.4	-0.149	0.629

hsa-miR-29b-3p	29009.3	0.743	0.038
hsa-miR-3189-5p	8.8	0.402	0.347
hsa-miR-3190-3p	3.3	-0.112	0.755
hsa-miR-3190-5p	0.9	-0.002	NA
hsa-miR-3191-3p	1.8	0.131	NA
hsa-miR-3191-5p	1.3	0.148	NA
hsa-miR-3192-5p	1.9	0.238	NA
hsa-miR-3193	5.0	0.330	0.350
hsa-miR-3194-3p	8.4	-0.015	0.973
hsa-miR-3194-5p	22.4	0.152	0.750
hsa-miR-3196	0.8	-0.011	NA
hsa-miR-3198	2.2	-0.051	NA
hsa-miR-3199	1.2	-0.029	NA
hsa-miR-32-3p	212.8	-0.221	0.411
hsa-miR-32-5p	2543.6	0.310	0.364
hsa-miR-3200-3p	475.4	-0.494	0.010
hsa-miR-3200-5p	61.0	-0.471	0.141
hsa-miR-3201	1.9	-0.114	NA
hsa-miR-3202	1.3	0.050	NA
hsa-miR-320a	27828.6	0.806	0.000
hsa-miR-320b	2321.6	0.748	0.002
hsa-miR-320c	1012.0	0.649	0.017
hsa-miR-320d	571.4	0.915	0.005
hsa-miR-320e	84.9	1.299	0.004
hsa-miR-323a-3p	25.8	-0.145	0.753
hsa-miR-323a-5p	0.9	-0.157	NA
hsa-miR-323b-3p	2.3	-0.143	NA
hsa-miR-324-3p	2279.8	1.014	0.000
hsa-miR-324-5p	2897.4	1.003	0.000
hsa-miR-326	243.2	0.477	0.040
hsa-miR-328-3p	167.0	2.381	0.000
hsa-miR-328-5p	2.0	-0.050	NA
hsa-miR-329-3p	40.3	-0.365	0.336
hsa-miR-329-5p	0.4	0.000	NA
hsa-miR-330-3p	901.1	0.092	0.778
hsa-miR-330-5p	546.8	0.147	0.508
hsa-miR-331-3p	2514.0	0.330	0.131
hsa-miR-331-5p	168.7	-0.207	0.448
hsa-miR-335-3p	917.5	-1.404	0.000
hsa-miR-335-5p	1074.8	-0.457	0.007
hsa-miR-337-3p	0.2	-0.041	NA
hsa-miR-337-5p	0.3	0.036	NA
hsa-miR-338-3p	18.7	3.142	0.000
hsa-miR-338-5p	3.6	0.304	0.353
hsa-miR-339-3p	849.4	0.053	0.818
hsa-miR-339-5p	4115.4	0.009	0.979
hsa-miR-33a-3p	229.3	1.098	0.000
hsa-miR-33a-5p	1973.3	0.996	0.068
hsa-miR-33b-3p	349.2	-0.664	0.000
hsa-miR-33b-5p	1100.1	0.498	0.265
hsa-miR-340-3p	139.2	0.035	0.919
hsa-miR-340-5p	943.3	0.496	0.008
hsa-miR-342-3p	985.8	0.182	0.458
hsa-miR-342-5p	36.4	0.099	0.823
hsa-miR-345-3p	9.4	-0.016	0.973
hsa-miR-345-5p	1829.8	0.579	0.000
hsa-miR-346	41.0	-0.665	0.069
hsa-miR-34a-3p	344.7	1.128	0.000
hsa-miR-34a-5p	8597.7	1.611	0.000
hsa-miR-34b-3p	3.5	0.191	0.556
hsa-miR-34b-5p	8.6	2.945	0.003
hsa-miR-34c-3p	3.0	0.402	NA
hsa-miR-34c-5p	27.2	3.107	0.000
hsa-miR-3529-5p	0.2	-0.041	NA
hsa-miR-3591-5p	0.7	-0.092	NA
hsa-miR-3605-3p	39.4	0.324	0.397
hsa-miR-3605-5p	8.7	0.308	0.465
hsa-miR-3607-3p	7.8	-0.086	0.841
hsa-miR-3607-5p	3.9	-0.072	0.824
hsa-miR-3609	1.4	0.007	NA
hsa-miR-361-3p	563.1	1.020	0.000
hsa-miR-361-5p	2332.1	0.824	0.000
hsa-miR-3610	0.4	0.041	NA
hsa-miR-3611	51.1	0.012	0.980
hsa-miR-3612	0.2	-0.042	NA
hsa-miR-3613-3p	39.6	-0.419	0.304
hsa-miR-3613-5p	178.4	-0.026	0.935

hsa-miR-6795-3p	1.1	-0.035	NA
hsa-miR-6795-5p	0.5	-0.065	NA
hsa-miR-6796-3p	1.3	-0.012	NA
hsa-miR-6796-5p	0.3	0.036	NA
hsa-miR-6797-3p	12.4	0.273	0.535
hsa-miR-6797-5p	2.9	0.268	NA
hsa-miR-6798-3p	3.4	-0.032	0.925
hsa-miR-6798-5p	0.3	0.036	NA
hsa-miR-6866-5p	1.6	0.077	NA
hsa-miR-6868-3p	3.1	0.148	NA
hsa-miR-6869-3p	0.7	-0.030	NA
hsa-miR-6869-5p	2.3	-0.242	NA
hsa-miR-6870-3p	1.2	0.095	NA
hsa-miR-6871-3p	1.6	0.099	NA
hsa-miR-6871-5p	0.7	0.037	NA
hsa-miR-6872-3p	0.7	0.037	NA
hsa-miR-6872-5p	0.7	0.037	NA
hsa-miR-6873-3p	4.4	0.181	0.616
hsa-miR-6873-5p	0.2	-0.041	NA
hsa-miR-6874-3p	1.1	-0.119	NA
hsa-miR-6875-3p	1.3	-0.007	NA
hsa-miR-6875-5p	1.5	0.026	NA
hsa-miR-6876-3p	0.2	-0.042	NA
hsa-miR-6876-5p	1.2	0.030	NA
hsa-miR-6877-3p	1.4	-0.065	NA
hsa-miR-6877-5p	5.2	0.098	0.806
hsa-miR-6878-3p	0.6	0.016	NA
hsa-miR-6878-5p	0.5	-0.065	NA
hsa-miR-6879-3p	1.5	0.086	NA
hsa-miR-6879-5p	0.2	-0.042	NA
hsa-miR-6880-3p	2.3	0.065	NA
hsa-miR-6881-3p	11.6	-0.851	0.099
hsa-miR-6881-5p	2.7	-0.230	NA
hsa-miR-6882-3p	0.8	0.056	NA
hsa-miR-6882-5p	1.3	0.072	NA
hsa-miR-6883-3p	2.5	0.034	NA
hsa-miR-6883-5p	0.7	-0.093	NA
hsa-miR-6884-3p	0.9	-0.001	NA
hsa-miR-6884-5p	0.9	-0.081	NA
hsa-miR-6885-3p	4.0	0.109	0.761
hsa-miR-6885-5p	3.6	0.000	0.997
hsa-miR-6886-3p	10.0	0.430	0.326
hsa-miR-6886-5p	17.7	-0.017	0.973
hsa-miR-6887-3p	1.3	0.056	NA
hsa-miR-6887-5p	1.1	0.081	NA
hsa-miR-6888-3p	0.2	-0.041	NA
hsa-miR-6888-5p	0.4	-0.065	NA
hsa-miR-6889-3p	1.6	-0.186	NA
hsa-miR-6889-5p	1.6	-0.078	NA
hsa-miR-6890-3p	0.4	-0.001	NA
hsa-miR-6890-5p	1.1	0.032	NA
hsa-miR-6891-3p	0.9	-0.122	NA
hsa-miR-6891-5p	2.4	0.026	NA
hsa-miR-6892-3p	0.4	-0.065	NA
hsa-miR-6892-5p	0.8	-0.009	NA
hsa-miR-6893-3p	2.7	-0.305	NA
hsa-miR-6893-5p	1.8	-0.347	NA
hsa-miR-6894-3p	3.0	0.044	NA
hsa-miR-6894-5p	0.4	-0.001	NA
hsa-miR-6895-3p	1.5	0.111	NA
hsa-miR-6895-5p	0.3	0.036	NA
hsa-miR-7-1-3p	1728.6	0.069	0.766
hsa-miR-7-2-3p	3.0	0.240	NA
hsa-miR-7-5p	40419.0	-0.137	0.593
hsa-miR-708-3p	0.3	0.036	NA
hsa-miR-708-5p	1.6	0.145	NA
hsa-miR-7106-5p	1.3	-0.082	NA
hsa-miR-7108-3p	2.0	0.027	NA
hsa-miR-7108-5p	5.3	-0.368	0.318
hsa-miR-7109-3p	1.1	-0.086	NA
hsa-miR-7109-5p	2.0	0.273	NA
hsa-miR-711	0.4	-0.001	NA
hsa-miR-7110-3p	6.7	-0.062	0.878
hsa-miR-7111-3p	38.6	-1.299	0.001
hsa-miR-7111-5p	4.9	-0.566	0.168
hsa-miR-7112-3p	4.1	-0.895	0.066
hsa-miR-7112-5p	1.8	-0.222	NA

Table 6.4 (continued from the previous page)

hsa-miR-3680-5p	3.2	-0.053	0.863
hsa-miR-3682-3p	1.6	-0.116	NA
hsa-miR-3682-5p	0.2	0.035	NA
hsa-miR-3684	11.4	-0.121	0.789
hsa-miR-3685	0.2	-0.041	NA
hsa-miR-3687	30.5	-0.634	0.119
hsa-miR-3688-3p	2.5	0.183	NA
hsa-miR-3688-5p	0.2	0.035	NA
hsa-miR-3689a-3p	0.2	-0.041	NA
hsa-miR-3689a-5p	0.5	0.003	NA
hsa-miR-3689b-5p	0.5	0.003	NA
hsa-miR-3689c	0.2	-0.041	NA
hsa-miR-3689e	0.5	0.003	NA
hsa-miR-369-3p	48.1	-0.080	0.852
hsa-miR-369-5p	9.2	-0.188	0.657
hsa-miR-3691-3p	8.3	-0.254	0.515
hsa-miR-3691-5p	28.6	-0.655	0.112
hsa-miR-3692-3p	0.6	0.016	NA
hsa-miR-3692-5p	0.8	-0.011	NA
hsa-miR-370-3p	0.5	-0.048	NA
hsa-miR-3713	0.4	-0.048	NA
hsa-miR-371a-3p	1.0	-0.048	NA
hsa-miR-371a-5p	2.6	-0.313	NA
hsa-miR-372-3p	3.3	-0.313	0.339
hsa-miR-372-5p	0.2	-0.041	NA
hsa-miR-373-3p	1.3	-0.158	NA
hsa-miR-373-5p	0.4	-0.065	NA
hsa-miR-374a-3p	458.1	0.884	0.000
hsa-miR-374a-5p	12734.1	0.979	0.000
hsa-miR-374b-3p	114.6	-0.114	0.775
hsa-miR-374b-5p	4750.9	0.713	0.000
hsa-miR-374c-3p	1.3	-0.066	NA
hsa-miR-374c-5p	171.2	0.397	0.190
hsa-miR-375	547.3	0.445	0.016
hsa-miR-376a-2-5p	2.8	0.353	NA
hsa-miR-376a-3p	70.2	-0.195	0.591
hsa-miR-376a-5p	7.0	-0.021	0.965
hsa-miR-376b-3p	20.7	0.098	0.823
hsa-miR-376b-5p	6.7	0.158	0.703
hsa-miR-376c-3p	65.3	-0.040	0.919
hsa-miR-376c-5p	6.9	0.124	0.772
hsa-miR-377-3p	24.4	-0.279	0.521
hsa-miR-377-5p	1.5	-0.032	NA
hsa-miR-378a-3p	6287.8	-0.285	0.077
hsa-miR-378a-5p	377.8	-0.280	0.225
hsa-miR-378b	0.2	0.035	NA
hsa-miR-378c	637.8	-0.202	0.350
hsa-miR-378d	293.8	-0.274	0.201
hsa-miR-378e	1.7	-0.065	NA
hsa-miR-378f	0.2	0.035	NA
hsa-miR-378g	9.7	0.025	0.964
hsa-miR-378i	0.7	0.037	NA
hsa-miR-379-3p	3.7	-0.238	0.347
hsa-miR-379-5p	18.2	-0.129	0.784
hsa-miR-380-3p	2.4	-0.263	NA
hsa-miR-380-5p	0.4	0.041	NA
hsa-miR-381-3p	49.1	-0.213	0.613
hsa-miR-381-5p	1.6	0.098	NA
hsa-miR-382-3p	7.8	0.065	0.875
hsa-miR-382-5p	27.5	-0.347	0.382
hsa-miR-3909	35.4	-0.306	0.445
hsa-miR-3910	1.6	-0.205	NA
hsa-miR-3911	2.8	0.067	NA
hsa-miR-3912-3p	2.7	-0.098	NA
hsa-miR-3912-5p	1.5	0.183	NA
hsa-miR-3913-3p	0.7	-0.035	NA
hsa-miR-3913-5p	2.5	0.335	NA
hsa-miR-3916	0.6	0.017	NA
hsa-miR-3917	0.5	0.003	NA
hsa-miR-3918	0.9	-0.158	NA
hsa-miR-3919	0.2	-0.042	NA
hsa-miR-3922-3p	3.5	-0.205	0.517
hsa-miR-3922-5p	1.5	0.112	NA
hsa-miR-3923	0.2	-0.041	NA
hsa-miR-3925-3p	0.4	-0.048	NA
hsa-miR-3925-5p	0.2	-0.041	NA
hsa-miR-3928-3p	32.6	0.503	0.239

hsa-miR-3614-3p	71.7	1.844	0.000
hsa-miR-3614-5p	70.7	1.913	0.000
hsa-miR-3615	674.4	0.574	0.010
hsa-miR-3616-3p	0.3	0.036	NA
hsa-miR-3616-5p	0.3	0.036	NA
hsa-miR-3617-3p	1.5	-0.047	NA
hsa-miR-3617-5p	17.1	-0.297	0.499
hsa-miR-3618	0.7	-0.031	NA
hsa-miR-3619-3p	10.3	-1.592	0.015
hsa-miR-3619-5p	37.0	-1.155	0.003
hsa-miR-362-3p	424.3	-0.145	0.596
hsa-miR-362-5p	362.0	-0.271	0.302
hsa-miR-3620-3p	7.6	-1.552	0.027
hsa-miR-3620-5p	1.8	-0.359	NA
hsa-miR-3621	5.6	0.157	0.700
hsa-miR-3622a-3p	1.4	0.066	NA
hsa-miR-3622a-5p	3.1	0.041	NA
hsa-miR-3622b-3p	0.2	0.035	NA
hsa-miR-3622b-5p	0.4	-0.001	NA
hsa-miR-363-3p	0.7	0.037	NA
hsa-miR-363-5p	0.5	0.003	NA
hsa-miR-3646	0.7	0.025	NA
hsa-miR-3648	17.7	-0.740	0.119
hsa-miR-3649	0.2	-0.042	NA
hsa-miR-3651	0.9	0.056	NA
hsa-miR-3652	0.7	0.024	NA
hsa-miR-3653-3p	1.1	-0.037	NA
hsa-miR-3653-5p	4.6	0.142	0.715
hsa-miR-3654	0.6	0.075	NA
hsa-miR-3656	0.3	0.036	NA
hsa-miR-3657	42.7	-0.414	0.326
hsa-miR-3658	0.4	0.043	NA
hsa-miR-3659	31.7	-0.470	0.242
hsa-miR-365a-3p	1799.5	-0.050	0.855
hsa-miR-365a-5p	17.5	-0.557	0.215
hsa-miR-365b-3p	1799.3	-0.050	0.855
hsa-miR-365b-5p	1.5	-0.047	NA
hsa-miR-3661	0.7	-0.093	NA
hsa-miR-3662	7.5	-0.114	0.784
hsa-miR-3663-3p	10.4	-0.098	0.823
hsa-miR-411-3p	4.5	-0.068	0.850
hsa-miR-411-5p	12.7	0.101	0.823
hsa-miR-412-3p	0.2	-0.041	NA
hsa-miR-412-5p	1.6	-0.026	NA
hsa-miR-421	428.2	-0.696	0.000
hsa-miR-422a	0.4	0.041	NA
hsa-miR-423-3p	10753.4	0.129	0.660
hsa-miR-423-5p	4521.9	0.176	0.586
hsa-miR-424-3p	38.3	-0.613	0.099
hsa-miR-424-5p	574.4	-0.272	0.330
hsa-miR-425-3p	723.3	0.891	0.000
hsa-miR-425-5p	10660.0	1.125	0.000
hsa-miR-4251	0.4	-0.048	NA
hsa-miR-4254	3.8	-0.165	0.616
hsa-miR-4257	0.2	-0.042	NA
hsa-miR-4258	0.4	0.041	NA
hsa-miR-4260	0.3	0.036	NA
hsa-miR-4261	1.8	0.057	NA
hsa-miR-4265	1.1	-0.200	NA
hsa-miR-4266	10.2	-0.472	0.276
hsa-miR-4269	0.2	0.035	NA
hsa-miR-4276	0.2	-0.041	NA
hsa-miR-4277	0.7	0.031	NA
hsa-miR-4281	0.2	-0.041	NA
hsa-miR-4283	0.2	0.035	NA
hsa-miR-4284	16.2	0.366	0.397
hsa-miR-4285	0.4	-0.001	NA
hsa-miR-4286	99.0	1.358	0.000
hsa-miR-4287	0.2	-0.041	NA
hsa-miR-4289	0.7	0.056	NA
hsa-miR-429	5426.7	0.604	0.000
hsa-miR-4290	3.5	0.073	0.806
hsa-miR-4291	0.4	0.000	NA
hsa-miR-4292	0.4	-0.048	NA
hsa-miR-4296	0.4	-0.048	NA
hsa-miR-4298	0.4	-0.001	NA
hsa-miR-4303	0.2	-0.041	NA

hsa-miR-7113-3p	1.1	-0.096	NA
hsa-miR-7113-5p	2.0	-0.123	NA
hsa-miR-7114-3p	4.3	0.088	0.806
hsa-miR-7114-5p	3.3	-0.094	0.782
hsa-miR-7150	1.4	-0.239	NA
hsa-miR-7152-3p	1.4	0.113	NA
hsa-miR-7152-5p	1.4	0.113	NA
hsa-miR-7154-3p	0.2	-0.041	NA
hsa-miR-7154-5p	0.2	-0.041	NA
hsa-miR-7155-3p	2.4	-0.043	NA
hsa-miR-7155-5p	1.4	0.066	NA
hsa-miR-7159-3p	0.2	-0.041	NA
hsa-miR-7159-5p	0.2	-0.041	NA
hsa-miR-7160-3p	0.4	0.000	NA
hsa-miR-7160-5p	0.4	0.000	NA
hsa-miR-718	0.2	-0.041	NA
hsa-miR-744-3p	139.0	0.025	0.946
hsa-miR-744-5p	4107.4	-0.105	0.715
hsa-miR-758-3p	4.5	-0.445	0.241
hsa-miR-758-5p	0.2	-0.042	NA
hsa-miR-760	59.3	-1.043	0.001
hsa-miR-761	0.2	-0.041	NA
hsa-miR-762	0.2	-0.041	NA
hsa-miR-7641	18.6	-0.774	0.103
hsa-miR-765	0.8	0.063	NA
hsa-miR-766-3p	95.9	0.260	0.448
hsa-miR-766-5p	13.1	0.362	0.403
hsa-miR-767-3p	0.2	-0.041	NA
hsa-miR-767-5p	2.3	0.244	NA
hsa-miR-769-3p	261.5	-0.256	0.293
hsa-miR-769-5p	1077.9	0.500	0.002
hsa-miR-7703	2.8	0.154	NA
hsa-miR-7704	8.6	0.447	0.301
hsa-miR-7705	11.0	0.277	0.524
hsa-miR-7706	61.4	0.347	0.328
hsa-miR-7844-5p	0.2	0.035	NA
hsa-miR-7845-5p	0.2	-0.041	NA
hsa-miR-7846-3p	0.4	0.041	NA
hsa-miR-7847-3p	0.9	-0.117	NA
hsa-miR-7848-3p	1.0	0.023	NA
hsa-miR-7850-5p	0.2	-0.041	NA
hsa-miR-7851-3p	39.7	-0.194	0.642
hsa-miR-7853-5p	0.4	-0.065	NA
hsa-miR-7854-3p	28.5	-0.859	0.033
hsa-miR-7855-5p	0.2	-0.041	NA
hsa-miR-7974	212.2	-1.357	0.000
hsa-miR-7975	0.9	0.055	NA
hsa-miR-99b-5p	5645.4	0.162	0.507
hsa-miR-939-5p	26.1	-0.227	0.588
hsa-miR-940	276.8	0.299	0.171
hsa-miR-941	398.7	-0.343	0.107
hsa-miR-942-3p	27.7	-3.347	0.000
hsa-miR-942-5p	372.2	-1.138	0.000
hsa-miR-943	1.8	0.234	NA
hsa-miR-944	0.2	0.035	NA
hsa-miR-95-3p	316.1	2.732	0.000
hsa-miR-95-5p	6.3	0.757	0.129
hsa-miR-9500	0.2	-0.041	NA
hsa-miR-4755-3p	0.9	-0.048	NA
hsa-miR-4755-5p	4.6	-0.078	0.809
hsa-miR-4756-3p	0.2	-0.041	NA
hsa-miR-4756-5p	0.2	-0.041	NA
hsa-miR-4757-5p	0.5	0.059	NA
hsa-miR-4758-3p	4.9	0.056	0.877
hsa-miR-4758-5p	1.5	-0.031	NA
hsa-miR-4761-3p	2.9	0.492	NA
hsa-miR-4761-5p	3.2	-0.047	0.875
hsa-miR-4762-3p	1.3	0.213	NA
hsa-miR-4762-5p	3.5	0.058	0.869
hsa-miR-4763-3p	3.5	0.116	0.746
hsa-miR-4763-5p	6.4	0.013	0.979
hsa-miR-4765	0.5	-0.066	NA
hsa-miR-4766-3p	16.8	-0.238	0.588
hsa-miR-4766-5p	1.5	-0.025	NA
hsa-miR-4767	1.4	0.120	NA
hsa-miR-4768-3p	0.4	-0.001	NA
hsa-miR-4768-5p	0.7	0.031	NA

Table 6.4 (continued from the previous page)

hsa-miR-3928-5p	1.9	0.319	NA
hsa-miR-3929	6.7	0.172	0.678
hsa-miR-3934-3p	5.9	-0.232	0.546
hsa-miR-3934-5p	34.9	-0.514	0.182
hsa-miR-3935	0.2	-0.041	NA
hsa-miR-3936	1.7	-0.139	NA
hsa-miR-3939	1.5	-0.053	NA
hsa-miR-3940-3p	26.6	-0.168	0.715
hsa-miR-3940-5p	4.4	-0.238	0.448
hsa-miR-3941	1.1	-0.119	NA
hsa-miR-3942-3p	5.6	-0.156	0.639
hsa-miR-3942-5p	4.9	0.001	0.997
hsa-miR-3943	7.4	0.022	0.967
hsa-miR-3944-3p	9.4	-0.224	0.598
hsa-miR-3944-5p	4.7	-0.395	0.304
hsa-miR-3945	0.2	-0.041	NA
hsa-miR-3973	0.5	0.003	NA
hsa-miR-3978	0.3	0.036	NA
hsa-miR-409-3p	39.1	-0.128	0.777
hsa-miR-409-5p	6.0	0.068	0.855
hsa-miR-410-3p	16.6	-0.377	0.373
hsa-miR-4500	26.2	0.554	0.203
hsa-miR-4501	0.7	-0.092	NA
hsa-miR-4502	2.7	-0.128	NA
hsa-miR-4504	6.2	-0.075	0.852
hsa-miR-4507	2.0	-0.038	NA
hsa-miR-4508	0.4	0.041	NA
hsa-miR-4509	0.1	0.026	NA
hsa-miR-450a-1-3p	6.5	-0.021	0.963
hsa-miR-450a-2-3p	4.4	0.054	0.883
hsa-miR-450a-5p	168.0	-0.447	0.071
hsa-miR-450b-3p	0.9	-0.067	NA
hsa-miR-450b-5p	49.9	-1.122	0.002
hsa-miR-4510	0.4	0.000	NA
hsa-miR-4511	5.5	-0.051	0.898
hsa-miR-4512	4.9	-0.006	0.983
hsa-miR-4515	0.8	-0.011	NA
hsa-miR-4516	1.3	-0.055	NA
hsa-miR-4517	40.4	-0.092	0.824
hsa-miR-4519	0.5	-0.066	NA
hsa-miR-451a	12.2	0.840	0.106
hsa-miR-452-3p	41.8	-0.707	0.078
hsa-miR-452-5p	111.2	-0.699	0.011
hsa-miR-4520-2-3p	0.2	-0.041	NA
hsa-miR-4520-3p	0.9	-0.045	NA
hsa-miR-4520-5p	0.2	-0.041	NA
hsa-miR-4521	2634.5	-1.787	0.000
hsa-miR-4522	0.2	-0.041	NA
hsa-miR-4523	18.1	-0.576	0.200
hsa-miR-4524a-3p	0.2	-0.041	NA
hsa-miR-4524a-5p	0.8	0.041	NA
hsa-miR-4525	2.3	0.010	NA
hsa-miR-4526	0.6	0.016	NA
hsa-miR-4532	5.2	1.346	0.065
hsa-miR-4533	1.1	0.026	NA
hsa-miR-4534	0.6	0.072	NA
hsa-miR-454-3p	1708.8	-0.379	0.024
hsa-miR-454-5p	75.1	-0.898	0.004
hsa-miR-455-3p	1329.6	-0.059	0.819
hsa-miR-455-5p	381.8	0.217	0.507
hsa-miR-4632-3p	0.4	0.041	NA
hsa-miR-4632-5p	0.4	0.041	NA
hsa-miR-4634	0.2	-0.042	NA
hsa-miR-4635	2.7	-0.007	NA
hsa-miR-4637	0.3	0.036	NA
hsa-miR-4638-3p	3.7	0.330	0.333
hsa-miR-4638-5p	2.1	0.085	NA
hsa-miR-4639-3p	0.6	0.017	NA
hsa-miR-4639-5p	0.2	0.035	NA
hsa-miR-4640-3p	3.1	-0.002	NA
hsa-miR-4640-5p	4.4	0.105	0.782
hsa-miR-4642	0.5	-0.066	NA
hsa-miR-4643	0.2	-0.041	NA
hsa-miR-4644	0.9	-0.158	NA
hsa-miR-4645-3p	2.9	0.111	NA
hsa-miR-4645-5p	0.3	0.036	NA
hsa-miR-4646-3p	2.9	-0.035	NA

hsa-miR-4306	3.2	0.137	NA
hsa-miR-4309	0.5	-0.066	NA
hsa-miR-431-5p	0.5	-0.066	NA
hsa-miR-4312	0.2	-0.042	NA
hsa-miR-4313	0.6	0.017	NA
hsa-miR-4314	4.1	0.226	0.527
hsa-miR-4315	0.2	-0.041	NA
hsa-miR-4316	0.9	0.101	NA
hsa-miR-4317	0.2	0.035	NA
hsa-miR-432-5p	0.2	0.035	NA
hsa-miR-4322	0.5	-0.065	NA
hsa-miR-4324	1.9	0.318	NA
hsa-miR-4325	1.5	-0.053	NA
hsa-miR-4326	100.0	-1.131	0.000
hsa-miR-4417	7.3	-0.035	0.935
hsa-miR-4419b	0.2	-0.042	NA
hsa-miR-4420	0.2	-0.041	NA
hsa-miR-4422	2.7	0.139	NA
hsa-miR-4423-3p	3.4	0.838	0.060
hsa-miR-4423-5p	8.1	0.362	0.380
hsa-miR-4424	0.7	-0.093	NA
hsa-miR-4425	2.6	0.279	NA
hsa-miR-4426	0.2	-0.042	NA
hsa-miR-4428	0.3	0.036	NA
hsa-miR-4429	6.8	0.382	0.333
hsa-miR-4431	0.6	0.017	NA
hsa-miR-4432	0.3	0.036	NA
hsa-miR-4433b-5p	0.3	0.036	NA
hsa-miR-4435	3.9	-0.907	0.070
hsa-miR-4436b-3p	8.5	-0.102	0.806
hsa-miR-4436b-5p	5.2	-0.295	0.407
hsa-miR-4437	0.2	-0.041	NA
hsa-miR-4440	7.5	-0.238	0.549
hsa-miR-4441	0.6	0.016	NA
hsa-miR-4443	32.1	1.675	0.000
hsa-miR-4444	0.8	0.133	NA
hsa-miR-4445-3p	0.2	0.035	NA
hsa-miR-4445-5p	0.7	-0.036	NA
hsa-miR-4448	7.7	0.465	0.280
hsa-miR-4449	25.3	-0.247	0.570
hsa-miR-4451	3.3	-0.094	0.782
hsa-miR-4454	45.9	0.065	0.881
hsa-miR-4455	0.3	0.036	NA
hsa-miR-4457	3.7	0.092	0.804
hsa-miR-4458	6.2	0.036	0.935
hsa-miR-4461	19.2	-0.542	0.207
hsa-miR-4463	2.3	-0.049	NA
hsa-miR-4466	32.8	-0.225	0.596
hsa-miR-4467	4.4	-2.140	0.030
hsa-miR-4469	0.8	0.052	NA
hsa-miR-4470	2.2	0.147	NA
hsa-miR-4472	0.2	-0.041	NA
hsa-miR-4473	4.5	-0.459	0.142
hsa-miR-4474-3p	2.5	-0.181	NA
hsa-miR-4474-5p	0.2	-0.041	NA
hsa-miR-4475	0.2	-0.041	NA
hsa-miR-4476	0.2	-0.041	NA
hsa-miR-4479	4.1	0.071	0.850
hsa-miR-448	0.4	0.041	NA
hsa-miR-4482-3p	2.2	-0.011	NA
hsa-miR-4482-5p	2.6	0.069	NA
hsa-miR-4483	0.6	0.016	NA
hsa-miR-4484	47.8	-0.752	0.027
hsa-miR-4485-3p	55.5	-0.039	0.929
hsa-miR-4485-5p	126.7	-0.567	0.016
hsa-miR-4486	0.2	-0.042	NA
hsa-miR-4488	5.9	-0.258	0.477
hsa-miR-4489	0.5	-0.048	NA
hsa-miR-4492	0.3	0.036	NA
hsa-miR-4493	0.3	0.036	NA
hsa-miR-4495	0.2	-0.041	NA
hsa-miR-4497	2.2	0.112	NA
hsa-miR-4498	1.1	-0.119	NA
hsa-miR-4499	0.2	-0.041	NA
hsa-miR-449a	141.2	0.144	0.745
hsa-miR-449b-3p	3.7	-0.177	0.598
hsa-miR-449b-5p	83.7	-0.254	0.499

hsa-miR-4769-3p	1.4	-0.119	NA
hsa-miR-4769-5p	0.7	-0.094	NA
hsa-miR-4771	0.2	-0.042	NA
hsa-miR-4772-3p	0.7	-0.036	NA
hsa-miR-4772-5p	0.2	-0.041	NA
hsa-miR-4774-3p	0.4	-0.065	NA
hsa-miR-4774-5p	0.7	-0.035	NA
hsa-miR-4775	2.0	-0.123	NA
hsa-miR-4777-3p	0.4	-0.001	NA
hsa-miR-4777-5p	0.2	0.035	NA
hsa-miR-4779	0.2	0.035	NA
hsa-miR-4781-3p	1.8	-0.230	NA
hsa-miR-4781-5p	1.0	0.069	NA
hsa-miR-4782-3p	0.2	-0.041	NA
hsa-miR-4782-5p	0.4	0.043	NA
hsa-miR-4783-3p	9.2	-0.476	0.280
hsa-miR-4783-5p	1.3	-0.068	NA
hsa-miR-4784	1.1	-0.095	NA
hsa-miR-4785	5.6	-0.457	0.263
hsa-miR-4786-3p	1.5	0.184	NA
hsa-miR-4786-5p	1.1	-0.147	NA
hsa-miR-4787-3p	96.1	-0.249	0.460
hsa-miR-4787-5p	3.9	-0.288	0.288
hsa-miR-4788	0.4	-0.048	NA
hsa-miR-4789-3p	0.8	0.041	NA
hsa-miR-5188	8.4	-0.726	0.132
hsa-miR-5189-3p	0.2	0.035	NA
hsa-miR-5189-5p	0.7	-0.035	NA
hsa-miR-518a-3p	0.2	-0.041	NA
hsa-miR-518a-5p	0.2	-0.041	NA
hsa-miR-518b	0.6	0.017	NA
hsa-miR-518c-3p	0.2	-0.041	NA
hsa-miR-518c-5p	0.2	-0.041	NA
hsa-miR-518d-3p	0.2	-0.041	NA
hsa-miR-518d-5p	0.5	0.003	NA
hsa-miR-518e-3p	0.2	-0.041	NA
hsa-miR-518e-5p	1.9	0.170	NA
hsa-miR-518f-5p	0.3	0.036	NA
hsa-miR-5191	0.4	0.041	NA
hsa-miR-5192	0.3	0.036	NA
hsa-miR-5193	0.4	0.041	NA
hsa-miR-519a-3p	1.9	0.020	NA
hsa-miR-519a-5p	1.9	0.170	NA
hsa-miR-519b-3p	0.2	0.035	NA
hsa-miR-519b-5p	1.7	0.201	NA
hsa-miR-519c-3p	0.2	-0.041	NA
hsa-miR-519c-5p	1.9	0.150	NA
hsa-miR-519d-3p	0.4	-0.065	NA
hsa-miR-519d-5p	0.2	-0.041	NA
hsa-miR-519e-3p	0.2	-0.041	NA
hsa-miR-519e-5p	0.2	-0.041	NA
hsa-miR-520a-3p	0.2	-0.041	NA
hsa-miR-520a-5p	0.2	-0.041	NA
hsa-miR-520c-3p	0.2	-0.041	NA
hsa-miR-520c-5p	0.5	0.003	NA
hsa-miR-520d-3p	0.2	-0.041	NA
hsa-miR-520d-5p	0.2	-0.041	NA
hsa-miR-520e	0.2	-0.041	NA
hsa-miR-520f-3p	0.2	-0.041	NA
hsa-miR-520f-5p	0.2	-0.041	NA
hsa-miR-520g-3p	0.8	0.041	NA
hsa-miR-520g-5p	0.2	-0.041	NA
hsa-miR-520h	0.8	0.041	NA
hsa-miR-521	0.7	0.037	NA
hsa-miR-522-3p	0.9	-0.117	NA
hsa-miR-522-5p	1.9	0.170	NA
hsa-miR-523-5p	1.7	0.201	NA
hsa-miR-524-3p	0.2	-0.041	NA
hsa-miR-524-5p	0.4	-0.001	NA
hsa-miR-526a	0.5	0.003	NA
hsa-miR-527	0.2	-0.041	NA
hsa-miR-532-3p	257.5	-0.215	0.502
hsa-miR-532-5p	716.6	-0.100	0.644
hsa-miR-539-3p	7.9	-0.203	0.627
hsa-miR-539-5p	4.0	-0.389	0.239
hsa-miR-541-3p	0.2	-0.042	NA
hsa-miR-541-5p	0.9	-0.067	NA

Table 6.4 (continued from the previous page)

hsa-miR-4646-5p	0.2	-0.041	NA
hsa-miR-4647	1.4	0.119	NA
hsa-miR-4648	0.2	-0.042	NA
hsa-miR-4651	2.5	0.102	NA
hsa-miR-4652-3p	6.3	-0.346	0.378
hsa-miR-4652-5p	3.8	0.165	0.570
hsa-miR-4653-3p	8.5	-0.279	0.504
hsa-miR-4653-5p	9.1	-1.145	0.057
hsa-miR-4654	4.6	-0.270	0.392
hsa-miR-4655-3p	1.3	0.060	NA
hsa-miR-4655-5p	1.8	0.121	NA
hsa-miR-4656	1.1	-0.147	NA
hsa-miR-4657	0.9	0.002	NA
hsa-miR-4659a-3p	26.5	-0.903	0.031
hsa-miR-4659a-5p	3.0	-0.173	NA
hsa-miR-4659b-3p	1.5	0.028	NA
hsa-miR-4659b-5p	0.2	-0.042	NA
hsa-miR-466	12.3	-0.328	0.447
hsa-miR-4660	9.9	-0.349	0.395
hsa-miR-4661-3p	1.0	0.080	NA
hsa-miR-4661-5p	18.2	-0.055	0.904
hsa-miR-4662a-5p	0.9	0.003	NA
hsa-miR-4662b	0.2	-0.042	NA
hsa-miR-4664-3p	16.4	0.013	0.979
hsa-miR-4664-5p	151.3	-0.052	0.867
hsa-miR-4665-3p	0.2	0.035	NA
hsa-miR-4665-5p	5.4	-0.746	0.115
hsa-miR-4666b	0.6	0.017	NA
hsa-miR-4667-3p	6.3	0.296	0.445
hsa-miR-4667-5p	2.1	0.037	NA
hsa-miR-4668-5p	0.5	-0.066	NA
hsa-miR-4669	7.2	-0.114	0.789
hsa-miR-4670-3p	0.6	0.075	NA
hsa-miR-4670-5p	0.6	0.072	NA
hsa-miR-4671-3p	5.7	-0.083	0.834
hsa-miR-4671-5p	0.5	0.045	NA
hsa-miR-4672	2.4	-0.051	NA
hsa-miR-4673	0.7	0.082	NA
hsa-miR-4674	0.7	0.082	NA
hsa-miR-4676-3p	6.1	-0.207	0.588
hsa-miR-4676-5p	6.1	-0.230	0.562
hsa-miR-4677-3p	11.7	-1.590	0.012
hsa-miR-4677-5p	9.4	-0.203	0.627
hsa-miR-4680-5p	0.3	0.036	NA
hsa-miR-4682	0.5	-0.048	NA
hsa-miR-4683	0.6	0.016	NA
hsa-miR-4684-3p	1.9	-0.047	NA
hsa-miR-4684-5p	0.7	-0.093	NA
hsa-miR-4685-3p	7.5	0.173	0.662
hsa-miR-4686	0.8	0.053	NA
hsa-miR-4687-3p	2.3	0.061	NA
hsa-miR-4687-5p	2.1	0.088	NA
hsa-miR-4688	0.5	0.003	NA
hsa-miR-4689	15.2	-0.012	0.979
hsa-miR-4690-3p	3.7	0.016	0.969
hsa-miR-4690-5p	1.6	0.099	NA
hsa-miR-4691-3p	0.9	-0.066	NA
hsa-miR-4691-5p	0.2	-0.041	NA
hsa-miR-4695-3p	1.5	-0.047	NA
hsa-miR-4695-5p	0.7	-0.024	NA
hsa-miR-4789-5p	0.2	-0.041	NA
hsa-miR-4791	5.3	0.168	0.657
hsa-miR-4793-3p	0.5	0.059	NA
hsa-miR-4793-5p	0.4	0.043	NA
hsa-miR-4794	0.6	0.075	NA
hsa-miR-4795-3p	0.9	0.066	NA
hsa-miR-4795-5p	0.2	-0.041	NA
hsa-miR-4796-3p	27.1	-0.100	0.821
hsa-miR-4796-5p	12.5	-0.321	0.457
hsa-miR-4797-3p	1.3	-0.013	NA
hsa-miR-4797-5p	2.0	-0.053	NA
hsa-miR-4799-3p	0.4	-0.065	NA
hsa-miR-4799-5p	2.9	-0.163	NA
hsa-miR-4802-3p	0.5	-0.066	NA
hsa-miR-4802-5p	1.6	-0.076	NA
hsa-miR-4803	0.8	0.096	NA
hsa-miR-4804-3p	6.7	-0.114	0.784

hsa-miR-449c-3p	4.3	-0.120	0.723
hsa-miR-449c-5p	75.0	-0.301	0.357
hsa-miR-4697-3p	9.9	0.541	0.232
hsa-miR-4697-5p	1.1	0.119	NA
hsa-miR-4700-3p	0.8	0.095	NA
hsa-miR-4700-5p	1.2	0.105	NA
hsa-miR-4701-3p	1.9	-0.126	NA
hsa-miR-4701-5p	1.7	-0.076	NA
hsa-miR-4704-3p	0.3	0.036	NA
hsa-miR-4704-5p	0.7	-0.030	NA
hsa-miR-4706	6.4	-0.431	0.264
hsa-miR-4707-3p	60.5	-0.096	0.810
hsa-miR-4707-5p	106.2	-1.855	0.000
hsa-miR-4708-3p	0.7	0.036	NA
hsa-miR-4708-5p	0.2	-0.042	NA
hsa-miR-4710	0.5	-0.048	NA
hsa-miR-4712-3p	0.7	-0.028	NA
hsa-miR-4712-5p	0.7	-0.028	NA
hsa-miR-4713-3p	3.3	0.446	0.171
hsa-miR-4713-5p	55.4	0.673	0.066
hsa-miR-4714-3p	1.8	0.059	NA
hsa-miR-4714-5p	0.5	0.059	NA
hsa-miR-4715-3p	0.3	0.036	NA
hsa-miR-4715-5p	0.3	0.036	NA
hsa-miR-4716-3p	0.2	0.035	NA
hsa-miR-4717-3p	2.4	-0.036	NA
hsa-miR-4717-5p	1.1	-0.032	NA
hsa-miR-4720-5p	0.2	-0.041	NA
hsa-miR-4721	0.5	-0.065	NA
hsa-miR-4722-3p	21.7	-2.321	0.000
hsa-miR-4722-5p	23.2	-2.051	0.000
hsa-miR-4723-3p	4.3	-0.377	0.293
hsa-miR-4723-5p	1.8	-0.054	NA
hsa-miR-4726-3p	0.7	0.037	NA
hsa-miR-4726-5p	6.6	0.118	0.766
hsa-miR-4727-3p	0.5	-0.048	NA
hsa-miR-4727-5p	0.2	-0.042	NA
hsa-miR-4728-3p	7.9	0.193	0.643
hsa-miR-4728-5p	0.8	0.133	NA
hsa-miR-4729	0.5	0.045	NA
hsa-miR-4730	2.2	-0.123	NA
hsa-miR-4731-3p	1.4	-0.113	NA
hsa-miR-4731-5p	13.2	-0.756	0.125
hsa-miR-4733-3p	0.8	-0.012	NA
hsa-miR-4733-5p	1.3	0.072	NA
hsa-miR-4734	2.0	0.017	NA
hsa-miR-4736	17.5	1.075	0.033
hsa-miR-4738-3p	3.2	-0.070	NA
hsa-miR-4738-5p	0.5	0.003	NA
hsa-miR-4739	0.9	-0.122	NA
hsa-miR-4740-3p	0.2	-0.041	NA
hsa-miR-4740-5p	0.2	-0.041	NA
hsa-miR-4741	9.3	-0.726	0.135
hsa-miR-4742-3p	4.5	-0.066	0.859
hsa-miR-4742-5p	2.7	-0.063	NA
hsa-miR-4743-3p	0.8	0.053	NA
hsa-miR-4743-5p	0.4	0.000	NA
hsa-miR-4744	0.5	-0.048	NA
hsa-miR-4745-3p	28.0	-1.327	0.002
hsa-miR-4745-5p	14.6	-3.299	0.000
hsa-miR-4746-3p	0.5	0.003	NA
hsa-miR-4746-5p	10.5	-0.121	0.784
hsa-miR-4747-3p	2.3	0.064	NA
hsa-miR-4747-5p	3.9	0.226	0.482
hsa-miR-4748	0.7	0.085	NA
hsa-miR-4749-3p	2.0	0.165	NA
hsa-miR-4749-5p	5.3	0.245	0.518
hsa-miR-4750-3p	0.2	-0.041	NA
hsa-miR-4750-5p	2.6	0.204	NA
hsa-miR-4751	0.4	-0.065	NA
hsa-miR-4752	0.7	-0.031	NA
hsa-miR-4753-3p	2.8	0.010	NA
hsa-miR-4753-5p	0.5	0.045	NA
hsa-miR-4754	0.5	-0.048	NA
hsa-miR-506-3p	0.2	0.035	NA
hsa-miR-508-3p	0.4	0.041	NA
hsa-miR-508-5p	0.2	-0.041	NA

hsa-miR-542-3p	85.6	-0.497	0.156
hsa-miR-542-5p	27.5	0.031	0.955
hsa-miR-543	42.8	-0.073	0.862
hsa-miR-544a	2.0	-0.183	NA
hsa-miR-545-3p	42.5	-0.008	0.983
hsa-miR-545-5p	37.5	-1.462	0.001
hsa-miR-548a-3p	29.9	-0.409	0.301
hsa-miR-548a-5p	9.9	-1.831	0.009
hsa-miR-548ab	9.3	0.470	0.286
hsa-miR-548ac	2.7	-0.415	NA
hsa-miR-548ad-5p	2.6	0.219	NA
hsa-miR-548ag	0.3	0.036	NA
hsa-miR-548ai	7.6	-0.107	0.799
hsa-miR-548ak	0.3	0.036	NA
hsa-miR-548al	0.4	0.000	NA
hsa-miR-548am-3p	0.8	0.133	NA
hsa-miR-548am-5p	1.0	0.054	NA
hsa-miR-548an	4.0	0.056	0.875
hsa-miR-548ap-5p	1.5	-0.045	NA
hsa-miR-548aq-5p	20.4	-1.064	0.029
hsa-miR-548ar-3p	23.9	-0.112	0.806
hsa-miR-548ar-5p	0.2	0.035	NA
hsa-miR-548as-3p	0.2	0.035	NA
hsa-miR-548as-5p	0.2	0.035	NA
hsa-miR-548at-3p	0.9	-0.119	NA
hsa-miR-548at-5p	2.9	-0.222	NA
hsa-miR-548au-3p	1.1	-0.119	NA
hsa-miR-548av-3p	0.9	-0.061	NA
hsa-miR-548av-5p	1.3	0.064	NA
hsa-miR-548aw	3.0	0.403	NA
hsa-miR-548ay-3p	12.3	-0.117	0.799
hsa-miR-548az-3p	0.7	0.037	NA
hsa-miR-548az-5p	2.1	0.294	NA
hsa-miR-548b-3p	49.2	0.954	0.016
hsa-miR-548b-5p	1.1	0.167	NA
hsa-miR-548ba	0.5	0.059	NA
hsa-miR-548c-3p	3.7	0.086	0.815
hsa-miR-548c-5p	0.4	-0.001	NA
hsa-miR-548d-3p	187.2	-1.294	0.000
hsa-miR-548d-5p	0.1	0.027	NA
hsa-miR-548e-3p	78.4	0.078	0.838
hsa-miR-548e-5p	28.3	-0.081	0.852
hsa-miR-548f-3p	0.2	-0.041	NA
hsa-miR-548g-3p	0.4	-0.065	NA
hsa-miR-548g-5p	0.4	-0.065	NA
hsa-miR-548i	12.3	0.817	0.107
hsa-miR-548j-3p	3.7	-0.173	0.602
hsa-miR-548j-5p	19.8	-0.676	0.126
hsa-miR-548k	61.3	-0.864	0.006
hsa-miR-548l	33.6	-0.556	0.190
hsa-miR-548n	20.1	-0.045	0.921
hsa-miR-548o-3p	33.9	-0.114	0.791
hsa-miR-548o-5p	0.2	-0.041	NA
hsa-miR-548p	3.8	0.073	0.823
hsa-miR-548q	2.7	0.432	NA
hsa-miR-548s	12.0	0.084	0.850
hsa-miR-548t-5p	1.4	-0.118	NA
hsa-miR-548u	9.1	-0.201	0.615
hsa-miR-548v	59.8	-0.039	0.929
hsa-miR-548x-3p	0.1	0.027	NA
hsa-miR-549a	1.5	0.025	NA
hsa-miR-550a-3-5p	23.6	0.169	0.716
hsa-miR-550a-3p	388.4	-0.525	0.003
hsa-miR-550a-5p	78.2	-0.818	0.008
hsa-miR-619-5p	0.5	0.003	NA
hsa-miR-624-3p	27.6	-0.264	0.546
hsa-miR-624-5p	192.3	0.090	0.784
hsa-miR-625-3p	1093.6	0.124	0.627
hsa-miR-625-5p	954.3	0.184	0.482
hsa-miR-627-3p	67.7	-0.044	0.919
hsa-miR-627-5p	180.4	0.446	0.065
hsa-miR-628-3p	31.4	0.067	0.877
hsa-miR-628-5p	39.1	0.071	0.866
hsa-miR-629-3p	155.8	-0.463	0.080
hsa-miR-629-5p	712.6	-0.262	0.166
hsa-miR-631	0.4	0.041	NA
hsa-miR-632	0.2	-0.042	NA

Table 6.4 (continued from the previous page)

hsa-miR-4804-5p	12.7	-1.027	0.065
hsa-miR-483-3p	136.0	0.066	0.859
hsa-miR-483-5p	45.3	0.131	0.777
hsa-miR-484	3143.2	-0.153	0.559
hsa-miR-485-3p	39.1	-0.890	0.011
hsa-miR-485-5p	4.0	-0.147	0.691
hsa-miR-486-3p	27.9	3.382	0.000
hsa-miR-486-5p	160.2	3.309	0.000
hsa-miR-487a-3p	16.2	-0.323	0.454
hsa-miR-487a-5p	4.2	-0.180	0.602
hsa-miR-487b-3p	43.7	-0.261	0.502
hsa-miR-487b-5p	0.9	-0.066	NA
hsa-miR-488-3p	1.5	-0.053	NA
hsa-miR-488-5p	0.5	-0.065	NA
hsa-miR-489-3p	25.3	0.558	0.196
hsa-miR-489-5p	2.7	0.191	NA
hsa-miR-491-3p	34.0	-0.174	0.694
hsa-miR-491-5p	269.3	0.499	0.030
hsa-miR-492	1.3	0.145	NA
hsa-miR-493-3p	0.2	0.035	NA
hsa-miR-493-5p	1.0	-0.048	NA
hsa-miR-494-3p	17.3	-0.131	0.782
hsa-miR-495-3p	55.7	-0.110	0.784
hsa-miR-495-5p	0.4	-0.001	NA
hsa-miR-496	1.5	0.030	NA
hsa-miR-497-3p	6.4	0.223	0.555
hsa-miR-497-5p	91.9	1.149	0.000
hsa-miR-498	0.6	0.017	NA
hsa-miR-4999-3p	2.1	-0.013	NA
hsa-miR-4999-5p	4.4	0.042	0.914
hsa-miR-499a-3p	3.4	0.173	0.599
hsa-miR-499a-5p	29.2	0.938	0.036
hsa-miR-499b-3p	0.2	0.035	NA
hsa-miR-499b-5p	0.4	-0.001	NA
hsa-miR-5000-3p	2.5	0.099	NA
hsa-miR-5000-5p	0.9	-0.066	NA
hsa-miR-5001-3p	156.4	0.313	0.246
hsa-miR-5001-5p	9.3	-0.177	0.683
hsa-miR-5002-5p	0.2	0.035	NA
hsa-miR-5003-3p	0.2	-0.042	NA
hsa-miR-5003-5p	1.1	-0.097	NA
hsa-miR-5004-3p	0.2	-0.042	NA
hsa-miR-5006-3p	2.5	-0.293	NA
hsa-miR-5006-5p	0.5	-0.048	NA
hsa-miR-5008-3p	36.7	-0.987	0.009
hsa-miR-5008-5p	27.9	-0.766	0.098
hsa-miR-5009-3p	0.4	-0.001	NA
hsa-miR-5009-5p	2.5	-0.131	NA
hsa-miR-500a-3p	277.8	-0.263	0.322
hsa-miR-500a-5p	233.3	-0.629	0.003
hsa-miR-500b-3p	2.2	-0.189	NA
hsa-miR-500b-5p	233.5	-0.631	0.003
hsa-miR-501-3p	205.9	-0.707	0.005
hsa-miR-501-5p	196.9	-0.998	0.000
hsa-miR-5010-3p	38.0	0.217	0.596
hsa-miR-5010-5p	4.8	-0.348	0.305
hsa-miR-502-3p	360.2	-0.418	0.046
hsa-miR-502-5p	61.7	-0.472	0.167
hsa-miR-503-3p	3.8	-0.816	0.075
hsa-miR-503-5p	256.0	-1.666	0.000
hsa-miR-504-5p	1.1	0.107	NA
hsa-miR-5047	1.5	-0.047	NA
hsa-miR-505-3p	1501.1	0.329	0.061
hsa-miR-505-5p	102.6	0.135	0.745
hsa-miR-561-5p	155.6	0.253	0.556
hsa-miR-566	0.4	0.000	NA
hsa-miR-568	0.4	0.041	NA
hsa-miR-5681b	0.5	0.003	NA
hsa-miR-5683	4.5	0.277	0.441
hsa-miR-5684	1.6	-0.028	NA
hsa-miR-5688	1.1	0.087	NA
hsa-miR-5690	15.4	-0.205	0.642
hsa-miR-5692b	0.4	0.041	NA
hsa-miR-5692c	0.6	0.072	NA
hsa-miR-5693	0.5	-0.065	NA
hsa-miR-5695	1.6	-0.025	NA
hsa-miR-5696	0.9	0.003	NA
hsa-miR-5087	1.6	0.025	NA
hsa-miR-5088-3p	3.9	-0.021	0.963
hsa-miR-5088-5p	0.4	-0.048	NA
hsa-miR-5089-3p	1.0	0.068	NA
hsa-miR-5089-5p	2.2	0.071	NA
hsa-miR-509-3p	0.9	0.056	NA
hsa-miR-5090	3.9	-0.012	0.973
hsa-miR-5091	1.3	0.148	NA
hsa-miR-5092	5.9	-0.459	0.252
hsa-miR-5093	0.7	-0.068	NA
hsa-miR-5094	20.8	-0.289	0.502
hsa-miR-5096	0.5	-0.065	NA
hsa-miR-5100	23.0	0.395	0.348
hsa-miR-511-3p	0.7	-0.027	NA
hsa-miR-511-5p	0.9	-0.061	NA
hsa-miR-512-3p	0.2	-0.041	NA
hsa-miR-512-5p	0.4	-0.048	NA
hsa-miR-513a-5p	0.2	-0.041	NA
hsa-miR-514a-3p	0.3	0.036	NA
hsa-miR-514b-5p	0.2	0.035	NA
hsa-miR-515-3p	0.2	-0.041	NA
hsa-miR-515-5p	0.2	-0.041	NA
hsa-miR-516a-3p	0.2	-0.041	NA
hsa-miR-516a-5p	2.0	0.200	NA
hsa-miR-516b-3p	0.2	-0.041	NA
hsa-miR-516b-5p	0.2	-0.041	NA
hsa-miR-517-5p	0.2	-0.041	NA
hsa-miR-517a-3p	0.2	-0.041	NA
hsa-miR-517b-3p	0.2	-0.041	NA
hsa-miR-517c-3p	0.6	0.017	NA
hsa-miR-5187-3p	1.4	-0.076	NA
hsa-miR-5187-5p	2.7	0.145	NA
hsa-miR-550b-2-5p	3.9	-0.154	0.649
hsa-miR-550b-3p	4.6	-0.121	0.760
hsa-miR-551a	433.6	0.082	0.790
hsa-miR-551b-3p	24.1	0.370	0.383
hsa-miR-551b-5p	0.5	0.003	NA
hsa-miR-552-3p	0.2	0.035	NA
hsa-miR-552-5p	0.2	0.035	NA
hsa-miR-553	0.2	0.035	NA
hsa-miR-555	0.4	-0.048	NA
hsa-miR-556-3p	159.0	0.208	0.452
hsa-miR-556-5p	99.7	-0.037	0.920
hsa-miR-5571-3p	0.3	0.036	NA
hsa-miR-5571-5p	0.3	0.036	NA
hsa-miR-5572	0.4	0.041	NA
hsa-miR-5580-3p	8.1	-0.185	0.662
hsa-miR-5580-5p	6.4	-0.095	0.809
hsa-miR-5581-3p	11.0	-0.495	0.265
hsa-miR-5581-5p	0.7	0.025	NA
hsa-miR-5582-3p	55.8	-0.611	0.057
hsa-miR-5582-5p	0.4	0.041	NA
hsa-miR-5583-3p	10.5	-0.702	0.143
hsa-miR-5583-5p	7.7	-0.144	0.738
hsa-miR-5584-3p	0.2	-0.041	NA
hsa-miR-5584-5p	1.3	0.054	NA
hsa-miR-5585-5p	0.5	0.003	NA
hsa-miR-5587-3p	1.4	0.067	NA
hsa-miR-5587-5p	1.6	-0.028	NA
hsa-miR-5588-5p	0.4	-0.048	NA
hsa-miR-5589-3p	1.7	-0.017	NA
hsa-miR-5589-5p	1.7	-0.017	NA
hsa-miR-559	11.8	-0.433	0.320
hsa-miR-561-3p	41.6	0.027	0.963
hsa-miR-609	4.3	0.227	0.516
hsa-miR-610	5.4	-0.234	0.530
hsa-miR-611	0.8	0.133	NA
hsa-miR-6124	0.5	0.059	NA
hsa-miR-6125	0.6	0.072	NA
hsa-miR-6126	0.2	-0.041	NA
hsa-miR-6127	0.2	0.035	NA
hsa-miR-6128	0.8	-0.012	NA
hsa-miR-6129	0.2	0.035	NA
hsa-miR-6132	0.2	0.035	NA
hsa-miR-615-3p	401.6	0.165	0.574
hsa-miR-615-5p	9.6	-0.133	0.766
hsa-miR-616-3p	13.3	0.329	0.447
hsa-miR-636	35.7	-0.769	0.062
hsa-miR-637	0.9	0.099	NA
hsa-miR-638	0.2	0.035	NA
hsa-miR-639	1.6	0.134	NA
hsa-miR-641	177.6	0.038	0.904
hsa-miR-642a-3p	61.6	1.821	0.000
hsa-miR-642a-5p	263.0	0.934	0.000
hsa-miR-642b-3p	3.5	0.122	0.740
hsa-miR-642b-5p	25.1	1.473	0.003
hsa-miR-643	49.1	-0.075	0.850
hsa-miR-644a	0.2	-0.041	NA
hsa-miR-645	0.2	-0.041	NA
hsa-miR-646	1.1	0.026	NA
hsa-miR-647	0.2	-0.042	NA
hsa-miR-6501-3p	0.9	-0.066	NA
hsa-miR-6501-5p	3.9	0.094	0.792
hsa-miR-6503-3p	1.0	0.116	NA
hsa-miR-6503-5p	0.4	0.041	NA
hsa-miR-6504-3p	0.4	-0.001	NA
hsa-miR-6504-5p	0.4	-0.001	NA
hsa-miR-6505-3p	3.3	-0.050	0.881
hsa-miR-6505-5p	1.8	0.070	NA
hsa-miR-6506-3p	0.4	0.041	NA
hsa-miR-6506-5p	0.4	0.041	NA
hsa-miR-6508-3p	0.2	-0.042	NA
hsa-miR-6508-5p	0.2	-0.042	NA
hsa-miR-6509-3p	3.9	0.253	0.452
hsa-miR-6509-5p	1.0	0.068	NA
hsa-miR-651-3p	8.1	-1.181	0.059
hsa-miR-651-5p	206.7	0.273	0.314
hsa-miR-6510-3p	4.7	0.223	0.543
hsa-miR-6510-5p	0.2	-0.041	NA
hsa-miR-6511a-3p	45.7	-0.244	0.547
hsa-miR-6511a-5p	16.9	-0.020	0.969
hsa-miR-6511b-3p	30.5	0.211	0.616
hsa-miR-6511b-5p	16.9	-0.020	0.969
hsa-miR-6512-3p	0.5	0.059	NA
hsa-miR-6512-5p	0.5	0.059	NA
hsa-miR-6513-3p	1.8	0.219	NA
hsa-miR-6513-5p	1.2	0.130	NA
hsa-miR-6514-3p	2.3	0.011	NA
hsa-miR-6514-5p	3.5	-0.019	0.965
hsa-miR-6515-3p	8.8	0.070	0.867
hsa-miR-6515-5p	2.3	0.065	NA
hsa-miR-6516-3p	7.9	0.343	0.405
hsa-miR-6516-5p	10.5	0.687	0.154
hsa-miR-652-3p	1690.3	0.555	0.001
hsa-miR-652-5p	168.6	0.689	0.003
hsa-miR-653-3p	12.0	0.738	0.135
hsa-miR-653-5p	13.3	0.111	0.806
hsa-miR-654-3p	29.7	-0.319	0.425
hsa-miR-654-5p	4.5	-0.200	0.576
hsa-miR-655-3p	26.2	-0.174	0.692
hsa-miR-655-5p	0.2	-0.041	NA
hsa-miR-656-3p	2.4	0.028	NA
hsa-miR-657	3.0	0.190	NA
hsa-miR-658	0.7	-0.092	NA
hsa-miR-659-3p	2.9	0.110	NA
hsa-miR-659-5p	5.0	0.007	0.983
hsa-miR-660-3p	79.2	-0.124	0.758
hsa-miR-660-5p	997.5	-0.080	0.755
hsa-miR-661	0.2	-0.042	NA
hsa-miR-662	8.8	-0.192	0.648
hsa-miR-663a	11.1	-0.185	0.669
hsa-miR-663b	11.5	-0.389	0.361
hsa-miR-664a-3p	102.5	0.661	0.020
hsa-miR-664a-5p	15.2	1.045	0.044
hsa-miR-664b-3p	18.4	0.790	0.095
hsa-miR-664b-5p	1.8	-0.005	NA
hsa-miR-668-3p	0.7	-0.023	NA
hsa-miR-671-3p	187.1	0.100	0.772
hsa-miR-671-5p	2321.9	-0.089	0.740
hsa-miR-6715a-3p	0.7	-0.092	NA
hsa-miR-6715b-3p	2.6	-0.018	NA
hsa-miR-6715b-5p	0.2	0.035	NA
hsa-miR-6716-3p	2.5	0.277	NA
hsa-miR-6716-5p	0.2	-0.041	NA

Table 6.4 (continued from the previous page)

hsa-miR-5697	4.0	-0.074	0.842
hsa-miR-5698	1.7	-0.080	NA
hsa-miR-5699-3p	35.1	-0.151	0.746
hsa-miR-5699-5p	26.7	-0.346	0.405
hsa-miR-570-3p	64.2	-0.228	0.546
hsa-miR-570-5p	7.2	-0.115	0.784
hsa-miR-5701	0.2	0.035	NA
hsa-miR-5702	2.4	0.155	NA
hsa-miR-5703	0.5	0.059	NA
hsa-miR-5704	0.2	0.035	NA
hsa-miR-5706	0.4	-0.065	NA
hsa-miR-572	1.1	0.027	NA
hsa-miR-573	30.3	-3.489	0.000
hsa-miR-574-3p	408.9	0.895	0.000
hsa-miR-574-5p	0.9	0.003	NA
hsa-miR-576-3p	89.1	-0.218	0.497
hsa-miR-576-5p	952.9	-0.200	0.318
hsa-miR-577	285.6	-0.591	0.003
hsa-miR-578	0.8	-0.011	NA
hsa-miR-5787	0.4	0.000	NA
hsa-miR-579-3p	43.1	-0.285	0.478
hsa-miR-579-5p	37.4	-0.618	0.122
hsa-miR-580-3p	7.6	0.048	0.916
hsa-miR-580-5p	0.7	-0.036	NA
hsa-miR-581	1.1	-0.031	NA
hsa-miR-582-3p	0.5	0.045	NA
hsa-miR-582-5p	1.3	0.051	NA
hsa-miR-584-3p	76.5	0.082	0.827
hsa-miR-584-5p	1232.7	0.308	0.095
hsa-miR-586	0.7	0.024	NA
hsa-miR-588	1.6	-0.095	NA
hsa-miR-589-3p	36.3	-0.702	0.067
hsa-miR-589-5p	86.9	-0.717	0.014
hsa-miR-590-3p	1872.2	-0.090	0.782
hsa-miR-590-5p	1058.5	-0.303	0.378
hsa-miR-592	1.4	-0.154	NA
hsa-miR-596	0.4	0.041	NA
hsa-miR-597-3p	12.1	-0.466	0.288
hsa-miR-597-5p	56.2	-0.369	0.322
hsa-miR-598-3p	0.9	0.099	NA
hsa-miR-598-5p	0.6	0.053	NA
hsa-miR-600	1.3	0.000	NA
hsa-miR-601	1.6	-0.283	NA
hsa-miR-602	6.0	-0.256	0.521
hsa-miR-605-3p	1.0	0.068	NA
hsa-miR-605-5p	0.9	-0.068	NA
hsa-miR-6069	0.6	0.072	NA
hsa-miR-607	0.5	0.003	NA
hsa-miR-6075	0.3	0.036	NA
hsa-miR-6076	0.2	-0.041	NA
hsa-miR-6077	0.3	0.036	NA
hsa-miR-6080	0.2	-0.041	NA
hsa-miR-6086	0.2	0.035	NA
hsa-miR-6087	18.0	0.701	0.123
hsa-miR-616-5p	44.6	0.184	0.644
hsa-miR-617	0.3	0.036	NA
hsa-miR-618	29.2	0.078	0.856
hsa-miR-619-3p	0.5	0.003	NA
hsa-miR-6736-5p	0.5	0.003	NA
hsa-miR-6737-3p	3.2	0.129	NA
hsa-miR-6737-5p	0.4	0.041	NA
hsa-miR-6738-3p	0.6	0.072	NA
hsa-miR-6739-3p	0.7	-0.121	NA
hsa-miR-6739-5p	0.2	-0.042	NA
hsa-miR-6740-3p	2.7	0.064	NA
hsa-miR-6741-3p	6.4	-0.089	0.818
hsa-miR-6741-5p	1.1	0.038	NA
hsa-miR-6742-3p	0.9	0.056	NA
hsa-miR-6742-5p	1.5	0.023	NA
hsa-miR-6743-3p	2.2	0.061	NA
hsa-miR-6743-5p	0.9	-0.117	NA
hsa-miR-6745	0.2	0.035	NA
hsa-miR-6746-3p	1.5	-0.038	NA
hsa-miR-6746-5p	0.9	0.103	NA
hsa-miR-6747-3p	20.5	-0.020	0.969
hsa-miR-6747-5p	0.5	0.045	NA
hsa-miR-6748-3p	2.0	0.029	NA
hsa-miR-6748-5p	0.3	0.036	NA
hsa-miR-6749-3p	3.3	0.349	0.285
hsa-miR-6749-5p	0.2	0.035	NA
hsa-miR-675-3p	5.0	-0.186	0.616
hsa-miR-675-5p	11.3	-1.155	0.051
hsa-miR-6750-3p	2.0	0.168	NA
hsa-miR-6750-5p	1.6	-0.029	NA
hsa-miR-6751-3p	2.2	0.089	NA
hsa-miR-6751-5p	3.0	0.038	NA
hsa-miR-6752-3p	0.4	0.000	NA
hsa-miR-6753-3p	0.4	0.000	NA
hsa-miR-6753-5p	0.2	0.035	NA
hsa-miR-6754-3p	0.8	0.052	NA
hsa-miR-6754-5p	1.0	0.018	NA
hsa-miR-6755-3p	1.0	0.018	NA
hsa-miR-6755-5p	1.4	0.072	NA
hsa-miR-6756-3p	1.7	-0.011	NA
hsa-miR-6757-3p	0.4	-0.001	NA
hsa-miR-6757-5p	0.7	-0.035	NA
hsa-miR-6758-3p	3.4	0.032	0.934
hsa-miR-6758-5p	0.4	0.041	NA
hsa-miR-6759-3p	0.7	-0.035	NA
hsa-miR-6759-5p	0.8	0.053	NA
hsa-miR-676-3p	12.6	-0.393	0.357
hsa-miR-676-5p	1.1	-0.029	NA
hsa-miR-6761-3p	0.4	0.041	NA
hsa-miR-6761-5p	0.4	0.041	NA
hsa-miR-6762-3p	2.5	0.103	NA
hsa-miR-6762-5p	0.2	-0.041	NA
hsa-miR-6763-3p	1.3	0.073	NA
hsa-miR-6763-5p	6.9	0.183	0.649
hsa-miR-6719-3p	1.1	0.015	NA
hsa-miR-6721-5p	3.5	-0.061	0.850
hsa-miR-6722-3p	0.7	-0.066	NA
hsa-miR-6722-5p	0.7	-0.066	NA
hsa-miR-6723-5p	56.7	-0.685	0.041
hsa-miR-6724-5p	75.2	-0.555	0.149
hsa-miR-6726-3p	4.2	0.019	0.965
hsa-miR-6726-5p	1.3	-0.066	NA
hsa-miR-6727-3p	1.5	-0.052	NA
hsa-miR-6727-5p	1.3	-0.127	NA
hsa-miR-6728-3p	1.3	-0.068	NA
hsa-miR-6728-5p	1.0	-0.048	NA
hsa-miR-6729-3p	2.8	0.019	NA
hsa-miR-6729-5p	1.1	0.021	NA
hsa-miR-6730-5p	1.3	0.143	NA
hsa-miR-6731-3p	2.0	0.022	NA
hsa-miR-6731-5p	0.5	0.003	NA
hsa-miR-6732-3p	3.3	0.021	0.963
spk_12	3486.3	-0.949	0.000
spk_13	2125.5	-0.648	0.037
spk_16	2448.1	-0.895	0.001
spk_17	1317.1	-0.957	0.000
spk_22	1300.3	-0.599	0.044
spk_23	2061.0	-0.931	0.000
spk_27	46.5	-0.700	0.077
spk_3	2405.0	-0.822	0.000
spk_30	1562.1	-0.218	0.614
spk_5	1422.6	-0.881	0.000

Table 6.5 N termini of DROSHA from various species.

Species (common name)	Protein ID	Total length (a.a)	N-term. length (a.a)	C-term. length (a.a)	N-term. sequence	P proportion
C. teleta (Polychaete worm)	R7TLJ0	1087	24	1063	MRDELSTLLDKDEPENEVEIDLTQ	0.041666667
S. purpuratus (Purple sea urchin)	W4YAL1	1237	38	1199	MIRQITDPSKTCQRWNDLERELREEELEENDEDKDPLE	0.052631579
C. elegans (Roundworm)	O01326	1086	122	964	MSDEKISMTLNFPKHKRARRKKYQKEYQERHKEEMMQQLGRRFQNQPSTSSAPPDTVE KIPLPTESTSALPFGDSPRLTEKDYETNYMIDPPVVSTHSAELIKSNRVVIKAEEAEKYMMIK A	0.081967213
A. aegypti (Yellow fever mosquito)	Q16YA9	1374	230	1144	MSYYRPKSSYSGSYYAGRSSKGEENGNPRSSHSSSRDPPPPGTSADSYLLAEATNFSVP PPVIPPVRPVSLPPAQHGAMPGSGNGVSSRYHSSGSQPYYGQYASTSSRYYSSSGSRT NERREGSEAYSDHSKRSSYSRSRSSPPPGSYSYRSGRSHSVPTRDHDRRPKSRDRERD RDRSTRSSTRTEHTRRTDSASGDSKERPPRVSRFKVDSEREAILSKWRKNFCETP	0.104347826
I. scapularis (Deer tick)	A0A6P7VW02	1312	277	1035	MNPSNLNLTARPGCGTGALVGQPGLPAYCTAALVPCTAQGPLVGGPQGPLVAGSAWTT AVPGGAAQYRPAGSYGAVAAHGYGAGVLASQGQLTLHAASAQWSSASCVSVMPLTPLS GPYTYPGPALQQFAPQPYPGCTSVLPGWRPEATHVTGSSSSERDRDRGSRRCRDRSR EGRRSREGRSPRRSSRERHGHSSRSRSGHSGRSRPRHRERLRSPGPQRRRRSRGSGER GSVSPDERPLPPARPRERPSQERRREGCARRTPKGPSRDASPPQPEGD	0.126353791
D. melanogaster (Fruit fly)	Q7KNF1	1327	247	1080	MYQPPLPPPPVQPAPPPPPPPPEEDLSPPGVGVPSHNYSSNESHSQSSKSLDYVYPETP APYASSVPSYDPYQQPPAYGYEGYAYNEQAQKYGGQESHYQYQYPASGSSFLYESYKY PDRYPAYSSNYRPPSERQRYTSNSSSQGYHHYPGYSSGRRYEQRHDQEHRQIQDSRYA HEPRHGHYAHRQAKGSQHGYYGSAARNQVSDDYSPRGHHERERNETLEKTRAKPKVE TERDRLLRQIWCSNFC	0.137651822
D. rerio (Zebrafish)	F1QKS5	1289	306	983	MSFHAGRGCPRGRLPAPGQIYHPASPRYHYDPSAAPGPVYNPQGGSSYMPPHPDFMSF HFPPPSQASNTLPQCPIRPPVFTEPPPFPPPPPHSSDGSTPMPIQNSYPYMMPNIPPPPLP PMPPSVPPTMPYPPTYPMSYPPQPQLPPPPSFNPAYGQPSGSFKPERSRPPLHYKTDSC SRSPERLRHHDDHRHRGHSYSEYGSRHNREFGGEKRDRGCSSERRRSDSPRRCKSDY DRGRVSSRHRSRERYRHRDDPGSPSSDRHRKHARNRSGSRERKRRRVEEDKERRTDG SSSSRERSVNSSRS	0.199346405
X. tropicalis (Western clawed frog)	F6YT85	1317	346	971	MSLHSGRGGPQARGGPGAPLQPFRPQNLRPAQPQSSGQYCYDPQSTPPPPTFSNMPN TNYVPRPDYMSYPPPATPATQSAINQCLPRPPFPVRQSYPMPPCFPPAPPASAPGNPP AVVTPVGQCPYPYMMPPVMPPPPIMPPPLPHVPYQPPYSAGYPPQPFPPPPPSPQPTPS FNSYQQAAPSFQGNNHYRHASHGGYQTEKSQTDHRVQERGKHYEDHRRREYSHSDRH RSEKHSDRRERGRSSERSRRLDGSRHRSDYEYRRGPSRGRTPSRHPSYERSSSRERHR HRESRRSTSTERSYRKRPKSPSPSSREHKRSRWEEDNESLSESSSAKEKSSISFKEK	0.196531792
G. gallus (Red junglefowl)	R4GIX1	1336	351	985	MSFHSGRGCPRGQGGPGARTSAQTYRPQNLRQLHPQQPSVQYQYDQQAAPAATYSNP SATSYMPPRPDFVPYPPPVPPSTQNPINQCPMRPPFPNHQMRQSFPVPPCFPPAPPPVP APSNAPVPATATGQSTFPYMMPPPAVPHPPPPPPVIPQQVNYQPVYSTGYSQQSFPPPNF NSYQHNSGSFQSSTTNSSSSGSSHFRHTGQYQGEKSQSDRRSPERSKHYDEHRHREHS HIHGDRHRSNNHGDRRDRGRSPDRRRQESSRHRTEYDRGRMSPHHRSYERSRERER DRHRHRDSRRSPSPDRSYKKDYKRAGSRSPSRERKRPRWEEERERWSESQSANKEKN YTSIKD	0.156695157
T. guttata (Zebra finch)	H0YUQ6	1336	351	985	MSFHSGRGCPRGQGGPGARTSTQTYRPQNLRQLHPQQPSVQYQYEQQTAPPTTYSNP PASGYMPPRPDFVPYPPPVPPSTQNPISQCPMRPPFPNHQMRQSFPVPPCFPPTPPPVP NPSNTPVPGTPAGQSTFPYMMPPPTVPHPPPPPPVMPQQVSYQPVYSAGYSQQSFPPPPS FSSYQHSSGSFPSSTAGSSASSSHFRHTGQYQGEKSQSDRRSPDRSKHYDEHRHREH GHIHGDRHRSANHGDRRDRGRSPDRRRQESSRHRTDYERGRISPHHRSYERNRERER ERHRHRDSRRSPSPDRSYKKDYKRAGSRSPSRERKRTRWEEDRERWSENQSSSKEKN YTAVKD	0.165242165
B. taurus (Cattle)	A0A3Q1MXH2	1338	353	985	MQGSACHRMSFHPGGPRCPRGRGGHGARPSSAPAFRPQNLRLLHPQQPPVQYQYEP PSAPSTTFSNSPAPNFLPPRPDFVPFPPPMMPPSAQGPLPPCPIRPPFPNHQMRPFPVPP CFPPMPPPLPCPNNPPVPGAPPGQGAFPFMMPPPSLPHPPPPPVVPQQVNYQYPPGYS HHSFPPPNFNSFQNSPSSFPPSASNSSSPHFRHLPPYPLPKAPSERRSPERLKHYDDHR HRDHSHGRGERHRSLERRERGRSPDRRRQDSRYRSDHERGRTPSRHRSYERSRERE RERHRHRDSRRSPSLERSYKKEYKRSGSRSPSREKKRGRWEEEKDRWSDIPGSGKEK NYTSIKE	0.220963173
C. familiaris (Dog)	J9NRX6	1398	414	984	MPVLFFLSPSAYIPCGRCDISRHRVTMQGNTCHRMSFHPGRGCPRGRGGHGARPSAPA FRPQNLRLLHPQQPPVQYQYEPPSAPSTTFSNSPAPNFLPPRPDFVPFPPPMPPSAQGP LPPCPIRPPFPNHQMRPPFPVPPCFPPMPPPMPCPNNPPVPGAPPGQQGTFPFMMPPPS MPHPPPPPPVMPQQVNYQYPPGYSHHNFPPPPNFNSFQNNPSSFPPSANNSTSPHFRHLP PYPLPKAPSERRSPERLKHYEDHRHRDHSHGRGERHRSLDRRERGRSPDRRRQDSRY RSDYDRGRTPSRHRSYERSRERERERHRHRDSRRSPSLERSYKKEYKRSGRSYGLPVV PEPAGCTPELPGEIIKNTDSWAPPPETVNHHSPSREKKRARWEEEKDRWSDSQSTGKEK NYTSIKE	0.210144928
O. cuniculus (Rabbit)	G1SD58	1365	380	985	MSVYILFFLSCRAYSSCGRCDVSGQYVMMQGSTCHRMSFHPGRGCPRGRGGHGARPS APTFRPQNLRLLHPQQPPAQYQYEPPSAPATTFSSSPAPSFLPPRTDFVPFPPPMPPSAQ GPLPPCPIRPPFPSHQMRHPFPVPPCFPPVPPPVPCASTPPVPGAPPGQGAFPFMVPPP SVPQPPPPPTLPQQVSYQCPPGYAHHSFPPPPSFNGFQSSPSAFPPSAGTGGGPHFRH LPPYPLPKAPSERRSPERLKHYDGHRHRDHSHGRGERHRSLDRRERGRSPDRRRPDS RYRSDYDRGRTPSRHRSYERGRERERERHRHRDNRRSPSLERSYKKEYKRSGSRSPS REKKRARWEEEKDRWNDNQSSGKEKNYTSIKE	0.197368421
M. musculus (Mouse)	Q5HZJ0	1373	388	985	MQGNTCHRMSYHPGRGCPRGRGGHGARPSAPAFRPQNLRLLHPQQPPAQYQYEPPS APSSSYSNSQAPSFMPPRPDFVPYPPPAAPSAQGPLPPCPVRPPYPNHQMRHPFPVPP CFPPMPPPMPCPNNPPAGAPPGQGTFPFMMPPPSMPHPPPPPVMPQQVNYQYPPGY SHSFPPPGFNSYQNNSSSFPPSANSSSTPHFRHLPPYSLPKAQNERRSPERLKHYDDHR HRDHSHGRGERHRSLERRERGRSPERRRPESRYRSDYDRGRTPPPRHRSYERSRERD RERHRHREARRSPSLERSYKKEYKRSGRSYALPVAPEPAGCTPELPGEMIKTTESWAPP PENVNHRSPSREKKRARWEEEKDRWSDSQGSGKEKNYTSIKE	0.206185567
H. sapiens (Human)	Q9NRR4	1374	389	985	MMQGNTCHRMSFHPGRGCPRGRGGHGARPSAPSFRPQNLRLLHPQQPPVQYQYEPP SAPSTTFSNSPAPNFLPPRPDFVPFPPPMPPSAQGPLPPCPIRPPFPNHQMRHPFPVPP CFPPMPPPMPCPNNPPVPGAPPGQGTFPFMMPPPSMPHPPPPPVMPQQVNYQYPPGY SHHNFPPPSFNSFQNNPSSFLPSANNSSSPHFRHLPPYPLPKAPSERRSPERLKHYDDH RHRDHSHGRGERHRSLDRRERGRSPDRRRQDSRYRSDYDRGRTPSRHRSYERSRER ERERHRHRDNRRSPSLERSYKKEYKRSGRSYGLSVVPEPAGCTPELPGEIIKNTDSWAP PLEIVNHRSPSREKKRARWEEEKDRWSDNQSSGKDKNYTSIKE	0.205655527

Table 6.6 DEP output from IP-MS experiment to screen potential interactors of p140m or FLm.

ID	padj	log2FC	ID	padj	log2FC	ID	padj	log2FC
Q9NRG9	0.697	-1.69	Q8WYP5	0.893	-0.304	O00203	0.905	-0.306
P49588	0.775	-0.4	P23526	0.895	0.145	O14617	0.904	0.184
P28288	0.927	-0.0475	O43865	0.0144	2.22	Q9Y2T2	0.921	0.0934
P61221	0.865	0.221	O95433	0.918	-0.0786	P27695	0.871	-0.316
Q8NE71	0.21	1.61	Q9BQI0	0.171	-1.59	Q8NCW5	0.895	0.539
Q9UG63	0.924	-0.0555	O95831	0.876	0.279	P07741	0.914	-0.301
Q9NUQ8	0.917	-0.0745	Q9BRQ8	0.0255	-1.24	O60306	0.822	0.618
Q9NUJ1	0.0269	-1.38	Q12904	0.911	-0.0978	P10398	0.927	0.0585
O14639	0.192	-1.04	Q13155	0.893	-0.144	P84077	3.65E-13	-2.92
P09110	0.659	-1.82	P54819	0.896	0.456	P18085	0.894	-0.233
Q13085	0.894	0.567	P27144	0.873	0.448	P84085	0.825	-0.98
Q9H845	0.463	-0.76	Q02952	0.818	-0.418	Q8IWW6	0.913	-0.177
P11310	0.871	0.53	Q9ULX6	0.423	-2.38	Q9P227	0.878	-0.29
P49748	0.9	0.335	Q96B36	0.345	-0.727	P52565	0.927	0.0403
Q15027	0.928	0.0385	P54886	0.901	-0.119	Q92888	0.924	-0.0909
P24752	0.782	0.421	P05091	0.902	0.16	Q92974	0.884	-0.658
Q9BWD1	0.873	1.16	P51648	0.902	0.2	Q14155	0.895	0.253
P53396	0.785	0.384	P49419	0.924	0.19	P40616	0.93	-0.00609
Q99798	0.663	2.15	P49189	0.909	-0.42	Q66PJ3	0.908	-0.191
Q9NPJ3	0.884	-0.449	P04075	0.827	0.487	Q9NVJ2	0.735	-0.626
O00154	0.819	-0.76	P09972	0.931	0.000217	Q8IUR7	0.869	0.328
Q9Y305	0.78	0.472	Q86V81	0.376	1.05	Q9H993	0.709	-0.992
Q15067	0.725	1.1	P17707	0.747	-0.638	O15143	0.818	-1.07
P24666	0.881	0.208	Q9UJX3	0.888	0.45	O15144	0.771	-0.572
O95573	0.636	0.789	Q9NU02	0.84	-1.39	O15145	0.794	-0.978
O60488	0.71	0.965	Q8IWZ3	0.647	-0.704	P59998	0.377	-0.832
P12814	0.891	-0.185	Q9NQW6	0.239	1.11	O15511	0.441	-1.31
O43707	0.377	-0.661	P39687	0.844	1	Q9BPX5	0.929	-0.0588
Q9NZ32	0.655	-0.527	Q92688	0.927	-0.144	Q9Y294	0.9	0.228
P42025	0.77	-0.438	O43423	0.825	-1.93	O95671	0.272	-1.03
P61160	0.865	-0.366	Q9BTT0	0.92	-0.0579	P08243	0.924	-0.0663
P61158	0.25	-0.736	P04083	0.875	0.297	Q12797	0.899	0.17
Q15847	0.0606	-1.77	P50995	0.2	-0.899	Q9NVI7	0.897	-0.273
Q9H2P0	0.908	0.468	P12429	0.0531	-1.22	Q9NT62	0.89	0.297
Q16186	0.662	-0.98	P08758	0.928	0.0277	P31939	0.923	-0.192
P30566	0.888	0.343	P08133	0.602	0.516	Q6DD88	0.901	-0.366
P30520	0.924	-0.0349	P20073	0.892	-0.257	O00244	0.025	1.56
Q9Y4W6	0.835	-0.396	O43747	0.926	0.101	P05023	0.511	-0.571
Q53H12	0.368	-1.38	Q9BXS5	0.791	-0.802	P05026	0.918	-0.183
Q9UKV8	0.724	-0.464	O95782	0.913	-0.143	P54709	0.874	-1.04
Q53EU6	0.872	-0.395	P63010	0.924	-0.0548	P16615	0.823	-0.302
O00116	0.488	2.02	Q96CW1	0.922	-0.0564	P25705	0.904	-0.111
Q5TZA2	0.749	-0.459	Q9NV06	0.869	-0.701	Q9UNQ2	0.793	0.453
O75718	0.792	-0.529	P61962	0.922	-0.0831	O60832	0.5	0.765
P10515	0.909	0.118	P24534	0.831	-0.291	O94905	0.827	0.451
P09622	0.903	0.237	P29692	0.748	0.411	Q96HE7	0.249	1.48
P36957	0.782	0.554	O43324	0.797	-0.412	P30040	0.604	1.04
Q9NPF5	0.759	0.589	P26641	0.842	-0.25	Q9BS26	0.883	-0.614
Q86Y56	0.115	-0.928	P13639	0.928	-0.0137	P10768	0.922	-0.056
O60884	0.785	-0.415	Q96C19	0.223	-1.08	Q9H6T0	0.0613	-1.49
Q96EY1	0.687	-0.738	Q15029	0.54	0.526	Q9BSJ8	0.908	-0.358
P25685	0.893	-0.171	P00533	0.903	0.205	A0FGR8	0.796	-0.696
Q9UBS4	0.916	-0.0957	Q9H223	0.755	-0.534	P62495	0.817	0.96
Q9UDY4	0.902	0.518	P41567	0.917	-0.122	P13804	0.869	-0.985
Q99615	0.73	-0.982	P47813	0.799	-1.27	P38117	0.863	-0.27
O75937	0.928	0.053	P19525	0.724	-0.659	O95571	0.925	0.046
Q8WXX5	0.799	-1.02	Q9NR50	0.875	-0.308	Q9Y3B2	0.579	-1.39
Q6XZF7	0.923	-0.0584	Q14152	0.923	-0.0411	Q01780	0.924	-0.0596
P26358	0.873	0.592	P55884	0.914	-0.09	Q9NQT5	0.879	0.844
Q9ULA0	0.922	0.12	Q99613	0.907	-0.108	Q9NPD3	0.903	-0.131
O43598	0.627	2.06	P60228	0.792	-0.45	Q5RKV6	0.433	-0.662
Q5QJE6	0.918	-0.0993	O75821	0.917	-0.0767	Q15024	0.913	0.319
Q96N67	0.918	0.095	Q13347	0.897	-0.193	Q96B26	0.597	-2.18
Q9BU89	0.89	-0.672	O75822	0.919	-0.0871	Q06265	0.821	-0.526
O60762	0.653	-0.813	Q9UBQ5	0.891	0.213	P15311	0.69	-0.56
Q9UHL4	0.3	-0.876	Q9Y262	0.906	-0.117	Q01469	0.866	0.241
Q16555	0.901	0.159	Q7L2H7	0.908	0.255	Q96CS3	0.813	-0.402
Q9Y295	0.868	-0.73	P06730	0.857	-0.273	Q6P587	0.916	0.116
Q9NRR4	0.0132	-2.8	Q15056	0.924	-0.0615	Q96GK7	0.916	0.293
Q08554	0.924	-0.109	P55010	0.813	-0.321	Q9NZB2	0.633	-1.08
Q14126	0.899	0.342	P63241	0.927	-0.0313	Q9NUQ9	0.93	-0.0123
P60981	0.878	-0.248	O60841	0.845	0.956	Q14320	0.899	-0.208
Q13115	0.759	-0.607	P56537	0.913	0.102	Q8NCA5	0.85	0.305
P33316	0.92	-0.088	Q9BQ52	0.9	-0.333	Q9Y285	0.339	-1.25
O14641	0.896	-0.187	Q15006	0.906	0.641	Q9NSD9	0.483	0.602
Q9Y6G9	0.484	-0.96	P50402	0.866	-0.404	Q14517	0.857	-0.968
Q8NCM8	0.908	-0.241	Q92979	0.894	-0.296	P62861	0.908	0.238
Q9NP97	0.824	-0.881	P09104	0.897	0.444	P22087	0.863	0.428
Q96AV8	0.00283	2.6	Q9UHY7	0.523	-1.02	A6NHQ2	0.538	-0.7
Q9UH73	0.8	0.379	Q9NPA8	0.916	-0.118	Q8NEZ5	0.903	-0.197
Q99848	0.886	0.4	O43491	0.845	0.319	P14324	0.617	1.78
Q13011	0.917	-0.314	P29317	0.00848	-1.64	P22570	0.00184	-3.05
P30084	0.913	0.193	P58107	0.917	-0.169	Q9BQL6	0.341	-1.19

ID	padj	log2FC	ID	padj	log2FC	ID	padj	log2FC
P06576	0.807	-0.396	Q9Y224	0.806	0.313	O60508	0.917	0.193
P36542	0.92	-0.0683	Q96S19	0.208	-0.822	P60953	0.804	-0.81
P30049	0.905	-0.199	Q53F19	0.679	1.07	Q9Y5S2	0.848	-0.924
Q5VTU8	0.872	-0.252	Q07021	0.908	0.151	Q99459	0.805	0.325
P24539	0.249	-0.836	Q9NWY4	0.855	-0.415	Q6P1J9	0.842	0.409
O75947	0.668	-0.47	P27708	0.921	-0.0603	Q9H5V8	0.603	-0.812
P56134	0.908	0.134	Q13137	0.584	2.69	P06493	0.818	-0.446
O75964	0.882	0.236	Q05682	0.433	1.8	P21127	0.887	0.247
P48047	0.903	-0.118	P27797	0.913	-0.283	P24941	0.901	0.173
P38606	0.713	0.692	O43852	0.737	0.869	P11802	0.0865	-0.851
P21281	0.592	0.874	Q13557	0.296	-2	Q00535	0.926	-0.0421
P21283	0.802	-0.836	Q13555	0.916	-0.163	Q96JB5	0.925	-0.0465
Q9Y5K8	0.815	0.944	Q9P1Y5	0.566	0.698	Q00534	0.883	0.368
P36543	0.715	-1.28	Q86VP6	0.708	0.791	P50750	0.892	-0.399
O75348	0.816	1.25	P27824	0.284	-0.747	P42771	0.914	0.224
Q9UII2	0.836	-0.582	P40123	0.76	0.484	Q7Z7K6	0.865	-0.387
Q9UII2	0.849	3.07	P07384	0.622	-1.21	Q96G23	0.878	-0.657
Q9UBB4	0.924	-0.0907	P17655	0.271	0.763	Q9Y6A4	0.919	-0.209
Q8WWM7	0.893	-0.197	P04632	0.853	0.565	Q9Y281	0.919	-0.0992
O95817	0.901	0.161	Q14444	0.911	0.13	Q96JM3	0.693	-1.63
Q9UQB8	0.25	-0.816	P52907	0.76	-0.693	Q8IWX8	0.0313	-1.31
O75531	0.922	-0.156	P47755	0.425	-0.808	Q9HD42	0.924	0.251
O75934	0.834	0.305	P47756	0.0814	-1.12	Q9UHD1	0.915	0.0965
Q9P287	0.923	-0.0929	Q9Y2V2	0.852	1.1	Q99653	0.876	-0.306
Q13867	0.926	0.0597	Q86X55	0.78	-0.886	Q9Y3Y2	0.73	1.87
Q14692	0.86	0.404	P49589	0.881	-0.436	O76071	0.915	0.124
Q8NFC6	0.896	0.38	P31944	0.781	1.73	Q6FI81	0.595	-1.07
Q9Y3E2	0.881	-0.409	P55210	0.69	0.795	Q969X6	0.915	-0.112
Q9H3K6	0.731	-0.364	P20810	0.863	0.73	Q9NZ45	0.238	-1.07
Q14137	0.884	-0.395	P04040	0.361	0.819	Q07065	0.768	-0.903
O95861	0.395	-0.906	Q13951	0.893	-0.174	P12277	0.925	-0.142
Q12830	0.919	-0.124	P45973	0.91	-0.239	O00299	0.903	-0.126
Q8TDN6	0.914	0.151	Q8IX12	0.263	1.4	Q9Y696	0.87	-0.657
P35613	0.0769	-0.904	Q8WUD4	0.907	0.273	P54105	0.749	-1.46
P20290	0.902	0.277	Q96CT7	0.672	1.72	O96005	0.53	-0.922
O43684	0.888	0.175	Q96A33	0.86	-0.369	O76031	0.842	-0.446
P41223	0.769	0.586	Q16204	0.843	0.431	P09496	0.919	-0.0725
Q13895	0.834	-0.839	P24385	0.826	-0.837	Q00610	0.801	-0.326
Q7L1Q6	0.926	-0.0693	Q9Y5K6	0.0183	1.54	O75153	0.865	0.286
Q9BUA3	0.929	-0.0184	O95400	0.895	0.207	Q8NFW8	0.873	0.209
Q9HB07	0.897	-0.305	Q12834	0.863	-0.91	P30085	0.818	-0.769
Q7Z3D6	0.868	-0.428	Q16543	0.706	-0.434	P62633	0.92	0.119
Q96KP4	0.9	0.476	Q08257	0.862	-0.443	Q96PD2	0.862	0.647
Q15417	0.798	0.455	O75390	0.929	0.0209	P81605	0.718	0.794
A5YKK6	0.906	0.152	O75534	0.927	0.0269	P27707	0.86	0.745
P09543	0.846	-0.452	P48729	0.924	0.0378	Q96C86	0.906	0.167
Q9Y2B0	0.93	0.0143	P48730	0.924	0.0577	Q14203	0.918	0.0793
Q8NBJ5	0.929	-0.0242	P68400	0.919	-0.0578	O75935	0.908	-0.228
P21964	0.858	-0.679	P19784	0.93	-0.0129	Q9UJW0	0.585	-0.503
P53621	0.872	-0.203	P67870	0.691	0.532	Q9BTE1	0.754	-0.561
P53618	0.904	-0.131	P21291	0.824	-0.662	O00399	0.508	-1.39
O14579	0.925	0.127	Q16527	0.316	-0.634	Q9H773	0.877	0.326
Q9Y678	0.819	-0.348	P04080	0.92	0.066	Q7Z4W1	0.929	0.0127
Q9UBF2	0.887	0.232	Q13363	0.671	-0.807	Q16531	0.75	0.385
P61201	0.614	1.36	P56545	0.864	-0.299	Q5TDH0	0.883	-0.517
Q9UNS2	0.911	-0.396	P32929	0.885	-0.523	P39656	0.0988	-0.873
Q92905	0.923	0.0942	P35222	0.903	0.131	P30046	0.32	2.26
Q7L5N1	0.928	-0.039	O60716	0.854	-0.521	Q92499	0.93	-0.00701
Q99627	0.892	-0.645	P17812	0.924	-0.0728	Q9NVP1	0.914	-0.301
Q9BR76	0.402	-0.873	Q6PD62	0.91	0.187	Q9UHI6	0.899	0.293
Q9ULV4	0.649	-0.507	P07858	0.92	-0.084	Q9BUQ8	0.0622	0.99
P20674	0.93	-0.0347	P07339	0.884	-0.4	Q9GZR7	0.851	0.438
P10606	0.908	-0.585	Q14247	0.895	-0.167	Q9UJV9	0.886	-0.479
P12074	0.918	0.176	Q13616	0.913	-0.121	Q7L014	0.872	0.258
P14406	0.378	-0.684	Q13617	0.849	-0.433	Q9H0S4	0.925	0.0552
Q99829	0.829	-0.406	Q13620	0.0293	-2.17	Q9Y6V7	0.669	-0.677
O75131	0.909	-0.113	O60888	0.93	0.0375	P26196	0.888	-0.218
Q9UBL6	0.385	1.73	Q9HCG8	0.808	0.343	Q16698	0.891	0.174
P36551	0.723	0.463	Q9NXE8	0.911	-0.161	Q9BUN8	0.916	0.344
P31327	0.927	-0.16	Q6UX04	0.354	2.24	Q9GZP9	0.0329	-1.27
Q10570	0.864	-0.24	Q9H5V9	0.876	-0.305	O00273	0.378	1.36
Q9P2I0	0.88	-0.308	O43169	0.691	3.19	Q8WYQ5	0.0749	-1.2
Q9UKF6	0.906	-0.221	P00387	0.919	-0.311	Q15392	0.906	-0.14
O95639	0.242	-1.58	P08574	0.065	-1.08	P00374	0.681	-1.39
Q16630	0.875	-0.255	P99999	0.839	0.698	O43143	0.798	0.362
Q8N684	0.612	-1.02	Q7L576	0.79	-0.662	O60231	0.888	0.193
P50416	0.816	-0.648	P51398	0.93	-0.0064	Q7L2E3	0.803	-0.311
P16220	0.821	-0.92	P14868	0.884	-0.172	Q9H2U1	0.93	-0.00889
P50238	0.876	-0.623	Q6PI48	0.792	-0.598	Q92620	0.924	-0.0985
P46109	0.805	0.699	Q96EP5	0.401	-0.711	Q14562	0.829	0.633
Q8IUI8	0.852	-0.483	Q16643	0.173	-1.25	O60610	0.853	-1.11
Q9BZJ0	0.837	0.345	Q9UK59	0.906	0.165	Q9UPY3	0.415	0.668
P42126	0.897	0.754	Q9H6S3	0.344	-1.42	P07954	0.919	0.233

Table 6.6 (continued from the previous page)

Q5VYK3	0.898	-0.339	O75616	0.853	-0.477	Q14192	0.792	-0.499
Q6P2E9	0.846	-0.282	O75477	0.819	0.821	Q6UN15	0.895	0.18
Q96AY3	0.884	0.485	Q9NWU2	0.75	0.47	P09211	0.928	-0.0161
Q02790	0.888	-0.233	Q9Y2X7	0.884	0.502	P29084	0.762	-1.22
Q13451	0.859	0.327	Q92896	0.376	-0.923	P35269	0.861	-0.271
FLAG	0.909	-0.221	Q92990	0.891	-0.227	P13984	0.816	0.552
Q13045	0.902	-0.136	Q04760	0.926	0.227	Q12789	0.878	1.08
P21333	0.893	0.169	Q9HC38	0.93	-0.009	Q9UKN8	0.665	-0.644
O75369	0.247	0.769	O76003	0.903	-0.244	O00178	0.93	0.016
Q14315	0.486	0.794	O94925	0.861	-0.244	Q9BZE4	0.929	0.02
O75955	0.926	0.0421	P00367	0.907	-0.102	P13807	0.901	-0.369
Q96CP2	0.000169	-1.98	P15104	0.0808	2.09	P07305	0.18	-1.03
Q06787	0.74	0.594	Q49A26	0.921	-0.0986	O75367	0.928	0.0772
P49354	0.912	-0.245	P60983	0.915	-0.189	P84243	0.772	1.02
Q14331	0.846	0.389	P29992	0.64	-0.907	Q9P035	0.663	0.7
Q16658	0.468	-0.819	P04899	0.00195	-2.33	Q16836	0.927	-0.0995
P02794	0.585	0.934	P08754	0.2	-1.89	P40939	0.828	0.271
Q9C0B1	0.914	-0.326	P63092	0.842	-0.594	P55084	0.921	-0.0627
Q8IY81	0.797	-0.915	P62873	0.808	-1.25	P12081	0.752	-0.767
P51114	0.708	0.506	P62879	0.575	-0.615	O14929	0.873	-0.228
P51116	0.347	1.21	P63244	0.339	-0.713	Q9Y450	0.894	-0.178
P11413	0.0476	-0.928	Q9BVP2	0.87	0.334	Q7Z4H3	0.918	0.139
Q8TAE8	0.81	-0.368	Q9HD26	0.558	1.99	P51858	0.78	0.558
O14976	0.908	0.247	P17174	0.927	0.108	Q7Z4V5	0.652	1.1
P51570	0.753	-1.52	P00505	0.918	0.149	Q9H0R4	0.857	0.245
Q14697	0.849	0.771	P43304	0.866	0.213	Q9H583	0.922	0.0883
P04406	0.91	-0.107	Q9NQX3	0.0284	1.07	Q9NRZ9	0.599	-0.585
Q9NY12	0.929	-0.0145	P06744	0.923	-0.227	O94992	0.931	0.00138
P41250	0.922	-0.0423	Q92917	0.884	0.56	O14964	0.91	-0.183
P22102	0.916	0.0887	Q8NFJ5	0.327	-1.82	Q6NVY1	0.771	0.385
O75323	0.707	-0.942	Q13098	0.856	-0.893	P49773	0.859	0.678
Q04446	0.927	0.0457	P07203	0.471	-0.71	Q9BX68	0.887	0.527
Q92538	0.911	-0.143	P62993	0.897	-0.37	P68431	0.762	0.914
P48507	0.778	-0.424	Q9UBQ7	0.925	-0.0464	P62805	0.92	0.108
Q92616	0.803	-0.452	Q9HAV7	0.476	-0.565	Q71DI3	0.848	0.773
P31150	0.752	-0.855	Q12849	0.902	-0.327	Q5TEC6	0.916	0.104
P50395	0.902	-0.271	Q9BQ67	0.913	-0.265	P19367	0.846	-0.642
P57678	0.401	-1.1	P49840	0.86	-0.563	P52789	0.874	-0.428
Q8TEQ6	0.749	-1.14	P06396	0.61	0.526	P04439	0.919	0.0896
Q7L5D6	0.926	0.0402	P15170	0.737	0.388	P01889	0.855	-0.519
Q96RP9	0.922	-0.0928	Q8IYD1	0.903	0.521	P10321	0.799	-0.485
Q06210	0.897	0.139	P00390	0.907	0.123	Q8TCT9	0.254	-1.61
O75223	0.77	0.696	Q9Y2Q3	0.871	-0.413	P17096	0.903	-0.174
Q92820	0.92	0.146	P78417	0.925	-0.132	P52926	4.7E-09	4.49
P09429	0.808	0.427	P11717	0.428	0.843	O60684	0.902	0.331
P26583	0.748	1.01	P01859	0.902	-0.218	P01116	0.564	-0.623
O15347	0.0405	-2.42	A2NJV5	0.785	-1.12	Q8N9T8	0.576	1.19
P35914	0.913	-0.305	A0A075B6	0.925	-0.06	Q86UP2	0.319	1.36
Q9H910	0.77	0.464	Q13123	0.898	-0.216	O00515	0.712	-0.637
Q13151	0.69	-0.499	Q12906	0.204	-0.723	P11279	0.851	-0.312
P22626	0.819	-0.284	Q13418	0.912	0.168	P13473	0.895	-0.646
P51991	0.9	-0.162	Q16891	0.799	-0.379	Q9NS86	0.0756	0.975
Q99729	0.914	-0.197	P20839	0.452	-1.13	P28838	0.923	0.235
P07910	0.352	-0.608	P12268	0.000127	-1.59	Q6PKG0	0.834	-1.04
Q14103	0.35	-0.665	P49441	0.667	-0.669	Q71RC2	0.902	-0.208
O14979	0.364	-0.631	Q9BT40	0.918	-0.0815	Q92615	0.909	-0.224
Q9BUJ2	0.777	-0.845	Q8TEX9	0.882	-0.616	Q14847	0.398	-0.754
Q1KMD3	0.419	-0.564	O95373	0.895	-0.446	Q14739	0.909	0.466
Q5SSJ5	0.923	0.0562	O15397	0.764	0.736	Q86VQ0	0.778	1.49
P00492	0.923	0.0557	Q96P70	0.846	-0.776	P00338	0.29	0.891
Q99714	0.495	0.729	Q86U28	0.876	0.25	P07195	0.814	0.569
Q53GQ0	0.882	-0.707	P05161	7.47E-07	-2.18	Q96PV6	0.885	-0.275
P51659	0.854	-0.646	Q9NPH2	0.539	0.58	O95202	0.906	0.291
Q6YN16	0.909	0.143	P17301	0.865	0.494	P09382	0.842	-0.361
Q0VDF9	0.713	0.507	P26006	4.09E-12	-2.4	P17931	0.874	-0.695
P34932	0.849	0.579	P23229	0.834	-1.43	Q08380	0.373	-0.917
O95757	0.895	0.478	P05556	0.868	0.289	Q99538	0.534	1.26
P38646	0.914	0.0824	P16144	6.38E-13	-4.93	P18858	0.928	-0.0279
Q9NZL4	0.925	0.0433	Q9Y6Y0	0.31	1.19	Q9UHB6	0.904	-0.157
P61604	0.877	-0.291	P23458	0.686	1.09	P49257	0.741	-1.75
Q92598	0.908	0.123	Q6NYC1	0.924	-0.133	Q12907	0.924	0.288
O43719	0.449	-0.942	P14923	0.675	1.09	Q9H0V9	0.462	-0.69
Q9Y4L1	0.867	-0.511	Q15046	0.685	-0.64	Q8WWI1	0.778	0.82
Q9NX55	0.906	-0.471	Q8IYT4	0.818	-1.72	P36776	0.902	-0.135
P41252	0.927	0.0199	Q7LBC6	0.906	-0.158	Q8NF37	0.895	-0.306
Q9NSE4	0.382	1.49	Q14145	0.687	-0.499	Q93052	0.817	1.13
Q5T440	0.82	0.427	Q92945	1.23E-09	-2.09	P42704	0.813	-0.309
Q14197	0.808	-0.905	Q15397	0.819	1	Q96AG4	0.926	-0.0467
P14735	0.916	-0.152	Q69YN4	0.788	-0.8	Q9UFC0	0.903	-0.27
O75874	0.761	1.24	A0MZ66	0.0155	1.49	Q9H089	0.807	-1.34
P48735	0.923	-0.148	Q14807	0.76	0.443	Q3MHD2	0.921	-0.0599
P50213	0.928	0.0326	Q02241	0.921	0.135	Q8ND56	0.918	0.15
O43837	0.726	-0.993	Q99661	0.922	0.0808	P62310	0.859	0.883
P51553	0.888	0.891	P33176	0.916	0.103	Q9Y4Z0	0.877	0.385

Q9Y6M1	0.915	-0.0853	Q07866	0.889	-0.251	Q9Y4Y9	0.903	-0.388
O00425	0.793	-1.55	O00505	0.878	0.237	O95777	0.913	0.176
Q9NX58	0.808	-1.42	Q9Y3A3	0.914	-0.114	Q92552	0.519	0.543
O95372	0.872	-0.601	Q13724	0.82	1.1	Q9Y2Q9	0.548	0.532
P61626	0.921	-0.104	Q9HCE1	0.448	0.923	Q9NP92	0.632	-0.736
Q9UPN3	0.321	0.976	O75352	0.888	0.232	Q92665	0.884	0.304
Q9BQ69	0.891	0.25	Q99547	0.697	-0.979	P82930	0.93	-0.00512
O15479	0.921	0.0852	Q6WCQ1	0.582	-1.45	P82673	0.828	-1.39
Q96A72	0.164	2.14	P25325	0.797	-0.648	P82932	0.921	-0.0706
Q9BXY0	0.87	-0.586	Q9Y605	0.000105	-2.64	Q9Y2R9	0.921	0.0865
P27816	0.872	0.213	Q9NV56	0.882	-0.222	P82933	0.876	0.569
P28482	0.349	0.785	Q9BYD6	0.923	0.0839	Q9UKD2	0.703	1.22
Q8TD08	0.761	1.28	Q9Y3B7	0.827	-0.834	P43246	0.906	-0.185
Q8NDC0	0.542	1.63	P52815	0.883	0.293	P52701	0.927	0.0235
Q9P0L2	0.902	0.958	Q9BYD1	0.859	-1.26	Q96DH6	0.849	-0.32
P56192	0.857	0.354	Q6P1L8	0.903	-0.174	P26038	0.911	0.097
P31153	0.696	0.464	Q9P015	0.834	-0.304	Q13126	0.764	-0.472
Q9NZL9	0.875	0.27	Q9NRX2	0.889	-0.187	P00846	0.869	-0.243
O95983	0.587	-0.679	Q9H0U6	0.835	-0.836	Q9Y6C9	0.895	-0.233
Q9NR56	0.883	-0.445	P49406	0.763	0.615	P00403	0.861	-1.03
P49736	0.285	-0.803	Q5T653	0.61	-1.44	P11586	0.897	-0.187
P25205	0.929	0.0121	Q16540	0.928	-0.0529	Q6UB35	0.817	0.362
P33991	0.448	-0.604	Q96A35	0.818	-0.949	P13995	0.88	-0.247
P33992	0.922	0.0564	Q13084	0.922	-0.118	Q8NCE2	0.725	-0.422
Q14566	0.314	-0.702	P09001	0.903	0.333	P58546	0.895	0.25
P33993	0.626	-0.477	O75394	0.831	-0.474	O75431	0.646	-0.999
Q9BTE3	0.867	0.225	Q9BZE1	0.668	-1.28	Q8WXI7	0.875	-1.6
Q14676	0.841	0.952	Q96DV4	0.926	-0.0497	P22033	0.0293	-1.04
P40925	0.93	0.0134	Q9NYK5	0.851	-0.287	P53602	0.809	0.453
P40926	0.904	-0.203	Q9BYD3	0.636	-0.533	Q14764	0.429	-2.92
P23368	0.927	-0.0819	Q9NQ50	0.855	-0.698	P35580	0.875	0.468
P53582	0.911	-0.104	Q9H9J2	0.829	-0.282	Q7Z406	0.89	-0.24
P55081	0.887	0.346	Q9BRJ2	0.928	-0.0332	P35579	0.759	0.416
Q8IWI9	0.702	0.668	Q96GC5	0.899	-0.317	P05976	0.872	-0.974
O60502	0.622	-0.697	Q13405	0.893	0.328	P19105	0.884	0.249
Q9BQP7	0.869	-0.717	Q8N5N7	0.395	-1.27	Q15746	0.931	-0.00303
P14174	0.905	0.406	Q96EL3	0.843	1.17	O43795	0.718	0.503
P46013	0.891	-0.196	Q9BYD2	0.894	0.396	O00159	0.849	-0.319
Q9UL63	0.813	-0.415	P82664	0.849	0.519	O94832	0.845	0.298
Q96T76	0.911	-0.246	Q9Y3D3	0.901	-0.14	Q9ULV0	1.71E-11	2.58
Q9BU76	0.917	0.223	Q9Y2R5	0.921	0.0655	Q9NQX4	0.85	-0.745
P51948	0.807	-1.27	Q9Y399	0.898	-0.188	Q9UM54	0.921	0.0982
Q8NEH6	0.637	-0.724	P82650	0.925	0.043	Q13459	0.924	0.111
Q70IA6	0.878	0.32	Q9Y3D9	0.882	0.197	Q9NZM1	3.19E-06	-4.66
P41227	0.917	-0.0753	Q00653	0.913	0.385	Q9BRJ7	0.0201	-1.51
Q9BXJ9	0.923	-0.0582	Q8NBF2	0.767	1.07	O43809	0.91	-0.122
Q96AH0	0.434	0.812	Q9NX24	0.866	0.744	Q9UKK9	0.89	-0.364
P43490	0.902	-0.28	P55769	0.922	-0.0593	Q7Z417	0.863	-0.404
Q9NR45	0.794	0.955	Q9BYG3	0.888	-0.451	P57740	0.923	0.0664
P55209	0.914	-0.131	Q9BPW8	0.82	0.702	Q8WUM0	0.862	0.225
Q99733	0.898	-0.133	O15226	0.423	-1.41	P49790	0.874	-0.3
O43776	0.123	0.963	P30414	0.00523	2	O75694	0.648	0.491
P49321	0.842	0.335	Q9NVX2	0.921	0.194	Q12769	0.7	0.569
Q9H0A0	0.825	-0.887	Q96D46	0.841	0.671	Q92621	0.875	-0.457
Q9BPX3	0.875	-0.414	P15531	0.931	0.00112	Q8TEM1	0.898	0.258
Q09161	0.205	1.29	P22392	0.908	0.107	Q8NFH5	0.846	-0.485
P52298	0.414	0.773	P30419	0.92	-0.194	Q99567	0.909	-0.166
Q9Y2A7	0.891	-0.406	Q9ULX3	0.306	-0.64	Q8N1F7	0.823	-0.417
P19338	0.863	0.261	Q9Y3T9	0.845	-0.996	P52948	0.65	-0.567
Q969V3	0.468	-0.601	Q9BVI4	0.516	-1.09	P61970	0.853	0.713
Q9HCD5	0.728	0.999	Q9H8H0	0.83	-0.638	Q9UBU9	0.907	0.328
Q92597	0.849	-0.857	Q9H6R4	0.88	-0.428	Q9Y6K5	0.907	-0.135
O95299	0.841	-0.694	Q5SY16	0.818	0.312	P04181	0.855	0.361
Q9P0J0	0.285	-1.25	Q14978	0.927	0.0329	Q9NX40	0.876	-0.308
O00483	0.92	0.0783	P46087	0.861	-0.327	Q5SWX8	0.873	-0.258
Q16718	0.906	0.432	O00567	0.91	0.133	Q02218	0.924	0.0796
P51970	0.833	-0.445	Q9Y2X3	0.922	0.0629	Q8N543	0.00502	-1.72
Q16795	0.539	-0.598	Q9Y314	0.642	-0.537	Q9NZT2	0.819	-0.545
O14561	0.818	0.468	P55786	0.826	-0.36	Q9NTK5	0.885	0.411
O96000	0.728	-0.635	O75607	0.869	0.514	O60313	0.538	0.724
O95168	0.0341	-1.18	P15559	9.53E-05	-3.98	P22059	0.929	-0.0185
O43674	0.484	-0.9	P24468	0.321	-0.939	Q9BZF1	0.698	-0.621
Q9Y6M9	0.468	-0.783	Q15738	0.913	-0.195	Q9NRP0	0.597	-0.637
P28331	0.781	-0.953	P46459	0.902	-0.16	Q96FW1	0.83	-0.438
O75306	0.851	-0.517	Q9H0G5	0.0404	1.27	P55809	0.816	1.05
O75489	0.117	-1.26	Q08J23	0.839	-0.949	O95747	0.86	-0.35
O43920	0.841	-0.81	Q96P11	0.496	-1.1	P0DP25	0.867	0.257
O75380	0.0845	-1.08	P49902	0.584	0.725	P0DPI2	0.797	1.47
O75251	0.00233	-1.46	Q5TFE4	0.893	-0.403	P13674	0.857	-0.761
O00217	0.762	-1.06	Q9BV86	0.923	0.331	O15460	0.902	-0.294
P49821	0.908	-0.227	Q9BSD7	0.908	-0.16	P07237	0.916	0.0775
P19404	0.756	-0.565	P53384	0.819	0.484	Q9UQ80	0.889	0.174
Q15843	0.809	-1.57	Q9Y5Y2	0.917	0.102	Q13310	0.569	0.499
Q8TD19	0.857	-0.753	Q02818	0.727	-1.3	Q86U42	0.867	0.243

Table 6.6 (continued from the previous page)

P28074	0.893	-0.509	Q6WKZ4	0.873	-2.15	Q14257	0.925	0.0601
P28072	0.891	0.23	P61106	0.793	0.637	P35241	0.607	0.798
P46063	0.905	0.17	P62888	0.922	0.0535	P42677	0.888	1.48
Q04206	0.503	-1.17	P62899	0.285	0.758	Q71UM5	0.917	0.361
P40937	0.778	-0.675	P62910	0.931	-0.00179	P23396	0.888	-0.158
P61586	0.754	-1.88	P49207	0.853	-0.28	P61247	0.929	-0.0114
P08134	0.83	-0.914	P42766	0.873	0.206	P62701	0.883	0.175
Q9HBH0	0.794	-0.375	P18077	0.903	-0.124	P46782	0.701	-0.433
P84095	0.633	-1.5	Q9Y3U8	0.922	0.0656	P62753	0.906	0.132
Q8IXI2	0.462	-1.66	P61513	0.894	0.455	P62081	0.569	-0.744
Q06587	0.0342	-1.91	P63173	0.894	-0.187	P62241	0.908	-0.101
Q99496	0.815	0.479	Q59GN2	0.824	0.668	P46781	0.907	0.113
Q5VTR2	0.875	-0.716	P36578	0.901	0.149	P08865	0.922	0.0471
Q63HN8	0.585	-0.642	P46777	0.922	0.0453	P10301	0.906	-0.238
O75150	0.811	0.595	Q02878	0.894	0.166	Q9P2E9	0.83	0.36
P13489	0.904	-0.126	P18124	0.897	0.169	P23921	0.917	0.109
O43148	0.668	0.485	P62424	0.907	0.125	P31350	0.058	-1
Q9HC36	0.218	-1.16	P62917	0.923	0.0546	P56182	0.829	-1.07
Q9H4A4	0.917	-0.251	P32969	0.522	-0.629	Q5JTH9	0.824	0.792
Q13464	0.837	0.366	P05388	0.905	-0.114	Q9Y3B9	0.91	-0.169
Q9H6T3	0.92	-0.234	P05386	0.831	0.69	O43818	0.892	-0.305
Q9H7B2	0.844	-0.462	P04843	0.466	-0.584	Q15050	0.915	-0.184
P27635	0.82	0.646	P04844	0.894	-0.212	O00442	0.827	0.393
P62906	0.918	0.0701	P78346	0.695	0.838	Q9Y3I0	0.68	0.495
P62913	0.915	-0.0846	Q96P16	0.929	0.0122	Q9BY42	0.683	-0.786
P30050	0.732	-0.38	Q9NQG5	0.897	-0.321	Q9NQC3	0.907	0.169
P26373	0.917	0.0848	P46783	0.695	-0.495	P60903	0.588	1.04
P40429	0.918	-0.0777	P62280	0.925	0.031	P06702	0.845	1.51
P50914	0.905	-0.144	P25398	0.814	-0.344	P25815	0.93	-0.0304
P61313	0.874	0.218	P62277	0.904	0.129	Q96ER3	0.902	-0.187
P18621	0.854	0.286	P62263	0.907	0.135	Q9NTJ5	0.924	-0.0975
Q07020	0.922	-0.0515	P62841	0.731	2.37	Q9UBE0	0.928	-0.0661
Q02543	0.852	-0.272	P62244	0.891	0.165	Q15424	0.336	0.94
P84098	0.918	-0.0753	P62249	0.877	0.209	Q9Y512	0.696	-1.12
P46778	0.75	0.54	P08708	0.906	0.232	O00422	0.0612	1.19
P35268	0.875	0.359	P62269	0.928	0.0224	Q9NR31	0.88	0.514
Q6P5R6	0.906	-0.158	P39019	0.763	-0.456	P82979	0.741	1.3
P62750	0.907	0.144	P15880	0.913	-0.0859	P49591	0.92	-0.132
P83731	0.908	0.169	P60866	0.931	0.000767	Q9NP81	0.00649	1.77
P61353	0.921	-0.0727	P63220	0.776	-0.369	O43290	0.749	1.12
P46776	0.919	-0.0724	P62266	0.87	0.27	Q15020	0.389	-1.71
P46779	0.913	-0.128	P62847	0.917	0.106	Q9Y3A5	0.909	0.142
P47914	0.586	0.719	P62851	0.926	-0.0352	Q99590	0.825	0.518
P39023	0.875	0.222	P62854	0.928	0.0242	O14828	0.808	-0.923
O00767	0.918	-0.243	P34897	0.924	-0.0409	P62318	0.89	0.184
P22307	0.923	-0.111	Q96BD8	0.352	1.09	P62304	0.843	0.373
Q14160	0.284	-0.873	Q9P270	0.913	0.134	P62306	0.922	0.108
Q96KG9	0.815	-0.89	Q14493	0.844	-0.499	P62308	0.874	0.267
Q9BRK5	0.81	1.21	P53985	0.152	-2.86	P63162	0.878	0.257
P31040	0.913	0.159	Q15758	0.86	-0.233	Q13425	0.903	-0.365
P21912	0.862	-0.273	P53007	0.923	0.16	Q13573	0.676	0.479
Q96GA7	0.796	-1.23	Q9UBX3	0.366	-0.687	Q13596	0.928	0.0208
P67812	0.924	-0.0687	Q02978	0.864	-1.37	Q96L92	0.868	-0.358
O15027	0.808	1.05	Q6NUK1	0.914	0.194	Q9UNH7	0.914	-0.116
O75396	0.911	0.514	Q00325	0.919	-0.0633	P35610	0.847	-0.999
Q15436	0.866	-1.2	P12235	0.807	-1.14	P00441	0.787	1.19
Q15437	0.928	-0.0156	P05141	0.902	-0.128	P18583	0.68	0.803
Q9Y6Y8	0.751	-0.352	P12236	0.874	0.313	Q00796	0.919	0.0946
O94979	0.9	0.275	P11166	0.915	-0.111	P23497	0.898	-0.235
P61619	0.825	-1.01	P11169	0.615	0.928	Q02447	0.823	0.944
Q9UBV2	0.593	-1.94	Q15043	0.277	-1.12	Q8NB90	0.473	-1.48
O60613	0.91	-0.211	P08195	0.913	-0.331	Q15005	0.887	-0.506
Q9NVA2	0.769	-0.526	Q9BWU0	0.917	0.0969	P61009	0.895	-0.299
Q15019	0.923	0.0449	Q01650	0.907	-0.632	Q96T58	0.879	0.584
Q16181	0.916	0.168	Q9GZT3	0.927	0.0238	Q56A73	0.883	-0.545
Q9UHD8	0.929	0.0109	P51532	0.864	0.419	Q5W111	0.602	1.28
Q8NC51	0.873	0.267	O60264	0.884	-0.467	O15269	0.762	-1.01
P30740	0.826	-0.921	Q9H4L7	0.853	0.411	Q13501	0.93	0.00779
P35237	0.733	0.815	Q12824	0.635	-1.29	Q8WXA9	0.646	0.711
P50453	0.715	0.656	A6NHR9	0.892	0.401	O75044	0.896	0.322
P50454	0.73	-0.372	Q6IN85	0.892	-0.202	P19623	0.56	-0.636
Q01105	0.775	1.16	O75940	0.836	-0.957	P61011	0.867	-0.282
Q15459	0.915	-0.204	P52788	0.695	0.633	Q9UHB9	0.553	0.687
Q15428	0.927	-0.0243	P53814	0.913	0.353	O76094	0.914	-0.116
Q12874	0.884	-0.245	Q2TAY7	0.853	0.245	P49458	0.857	-0.353
O75533	0.93	-0.00911	Q9HAU4	0.285	2.26	Q96SB4	1.82E-13	4.48
Q13435	0.907	-0.107	Q6GMV2	0.853	0.344	P78362	0.00436	2.73
Q15393	0.884	0.259	O00161	0.192	-0.761	P08240	0.716	0.918
Q15427	0.884	0.187	Q7KZF4	0.928	0.03	Q9Y5M8	0.912	-0.1
Q9Y3B4	0.931	0.00123	Q8TAD8	0.747	1.11	Q8IYB3	0.288	1.03
Q9H9B4	0.897	0.157	O75643	0.81	0.323	Q9BXP5	0.842	0.297
Q9BWM7	0.893	-0.202	Q96DI7	0.581	0.522	Q13243	0.337	0.816
O95470	0.841	1.1	P08621	0.324	0.815	Q13242	0.677	0.518
Q99961	0.751	0.364	P09012	0.836	0.451	P05455	0.848	0.645

Q8IXH7	0.715	-0.683	Q9Y266	0.921	-0.077	Q9UKS6	0.896	-0.298
P18615	0.798	-0.629	Q96RS6	0.754	0.515	Q8N7H5	0.79	-0.815
P43034	0.755	0.65	O15212	0.892	-0.24	Q8TF01	0.92	-0.0993
P68402	0.926	0.108	Q16875	0.9	-0.161	Q9H307	2.42E-07	1.94
Q15102	0.755	-0.814	P17858	0.927	-0.0736	Q9NRX1	0.896	0.532
P22234	0.908	0.116	P08237	0.833	-0.778	Q9NVS9	0.765	-1.53
Q9H074	0.925	0.0553	Q01813	0.909	-0.116	Q8TCS8	0.74	-0.58
Q13177	0.616	1.65	P07737	0.91	0.259	Q14181	0.392	-0.753
Q8WX93	1.8E-06	-2.73	P35080	0.875	0.246	P28340	0.834	-0.366
Q9Y3D7	0.928	-0.042	P18669	0.724	1.31	Q9BY77	0.0652	1.82
P51003	0.797	-0.366	Q96HS1	0.878	-0.23	P24928	0.874	0.529
O43252	0.849	0.434	P52209	0.895	-0.159	P30876	0.856	-0.433
Q99497	0.923	0.135	P00558	0.861	0.334	P19387	0.88	0.502
O95453	0.869	1.03	O95336	0.871	-0.915	P19388	0.719	-0.422
Q9UKK3	0.6	-1.06	P36871	0.894	-0.488	P52434	0.912	-0.152
Q96IZ0	0.872	0.339	O95394	0.781	0.685	P62875	0.831	-0.777
Q9BVG4	0.915	0.143	A6NDG6	0.879	-0.551	Q99575	0.88	-0.442
Q96KB5	0.785	1	O00264	0.913	-0.288	P16435	0.711	-1.36
P61457	0.912	0.186	P35232	0.8	-0.418	P0CG39	0.864	-1.37
Q16822	0.925	-0.0869	Q99623	0.86	-0.253	Q15181	0.899	-0.125
P22061	0.902	0.119	Q8IXK0	0.906	-0.37	Q9H2U2	0.643	0.676
P12004	0.92	0.0735	Q7RTV0	0.866	0.944	Q06203	0.833	0.322
P49585	0.516	1.5	Q8IWS0	0.746	-0.751	Q86W92	0.000157	-2.04
Q13442	0.91	0.188	Q53GA4	0.232	-0.886	Q8NEY8	0.844	0.385
Q14690	0.88	-0.641	Q9NRX4	0.792	-1.36	P23284	0.901	-0.376
Q6L8Q7	0.916	-0.0919	Q92643	0.885	-0.334	Q08752	0.9	-0.141
P08559	0.894	0.154	P12273	0.86	0.31	Q9UNP9	0.862	0.336
P11177	0.63	-0.546	Q8TBX8	0.908	-0.422	Q13427	0.427	1.2
O00330	0.591	1.94	O00625	0.834	-0.325	O43447	0.93	-0.00881
P30101	0.896	0.192	Q9GZP4	0.794	0.485	Q9Y3C6	0.77	0.659
P13667	0.902	-0.238	P48739	0.799	-1.2	Q8WUA2	0.541	0.673
O00151	0.45	2.04	Q16513	0.882	-0.328	P35813	0.155	1.11
Q96HC4	0.0364	-1.4	Q9Y263	0.875	0.555	O75688	0.842	0.377
Q9NR12	0.783	-0.537	Q01970	0.879	-0.277	O15355	0.618	-1.4
Q9P0J1	0.409	-1.31	Q8N3E9	0.0339	-1.63	Q9Y570	0.854	-0.483
Q9NUG6	0.93	-0.0053	Q15149	0.63	-0.598	Q96QC0	0.856	-0.615
O00764	0.879	-0.4	P53350	0.911	-0.22	O14974	0.91	0.18
P30086	0.906	0.77	Q02809	0.905	-0.36	Q12972	0.922	-0.0628
P12955	0.921	0.117	O60568	0.923	-0.0762	Q96SB3	0.228	-1.15
O00541	0.887	-0.196	O43660	0.702	2	P63151	0.914	0.102
O15067	0.885	0.514	P13797	0.899	-0.14	Q14738	0.903	-0.28
Q9UHV9	0.928	-0.021	O15305	0.267	-1.17	Q08209	0.848	-0.64
Q9NQP4	0.891	-0.42	Q10713	0.914	0.398	P53041	0.916	0.0868
Q99471	0.915	-0.107	O75439	0.882	-0.266	O00743	0.838	0.413
Q5H9R7	0.869	0.566	Q99436	0.861	-0.741	Q9NP72	0.687	-0.735
O43663	0.446	-0.661	P62191	0.828	-0.295	Q9H0U4	0.752	-0.684
P32119	0.921	0.0569	P35998	0.783	-0.431	Q9UL25	0.834	-0.794
P30048	0.819	0.376	P43686	0.877	-0.255	P61019	0.86	-0.44
Q13162	0.84	0.345	P62195	0.847	-0.26	Q15286	0.92	0.231
P30044	0.905	-0.122	Q99460	0.879	0.386	P20339	0.432	-1.22
P48147	0.927	-0.043	O75832	0.817	-1.11	P51148	0.913	0.174
P54619	0.93	-0.0106	O00231	0.703	-0.504	P20340	0.63	-0.592
P10644	0.817	-0.421	Q9UNM6	0.284	-0.679	P51149	0.785	-1.43
P14314	0.817	-1.46	O00487	0.856	-0.37	Q5HYI8	0.931	0.00185
P78527	0.883	-0.168	Q13200	0.865	-0.218	P54727	0.93	0.0296
O75569	0.928	-0.0236	O43242	0.486	-0.688	P78406	0.818	-0.689
O60678	0.899	-0.209	Q16401	0.858	-0.721	P11233	0.776	-0.638
O94903	0.88	-0.191	Q15008	0.411	-0.829	Q9UKM9	0.619	-0.48
Q9UMS4	0.876	0.195	P51665	0.924	0.0784	P43487	0.915	0.154
O43395	0.401	1.54	P48556	0.368	-1.55	Q6VN20	0.828	0.593
Q8NAV1	0.676	0.799	O00233	0.463	-1.68	Q9H6Z4	0.895	-0.221
Q5VTL8	0.178	1.42	O95456	0.927	-0.0255	Q96S59	0.927	-0.0346
O43172	0.913	-0.0996	Q8WXF1	0.526	-0.727	P54136	0.877	-0.183
O75400	0.741	0.436	Q96EY7	0.79	-0.606	Q7Z6E9	0.445	-0.691
Q13523	0.155	2.33	Q15185	0.927	0.0273	Q9NWB1	0.344	-0.857
O94906	0.927	0.0347	Q05397	0.835	0.313	P28749	0.784	-2.09
Q6P2Q9	0.676	0.473	P18031	0.854	-0.479	Q9NTZ6	0.506	-1.27
P11908	0.929	0.016	Q06124	0.887	0.306	Q8IXT5	0.913	0.146
Q14558	0.808	-0.526	Q6NZI2	0.576	-0.837	Q96T37	0.308	0.833
O60256	0.888	-0.468	Q9Y3E5	0.907	-0.124	Q96I25	0.419	-1.35
Q96M27	0.92	-0.11	Q03393	0.0131	-1.67	Q9NW64	0.854	-0.444
P48634	0.903	0.457	Q00577	0.827	0.731	Q5T8P6	0.745	0.827
Q9Y520	0.874	0.724	Q13610	0.912	0.149	Q9P2N5	0.816	-0.327
Q9Y617	0.93	-0.02	Q15269	0.584	-1.45	P98179	0.912	-0.34
O75475	0.912	0.552	P49023	0.904	-0.4	Q9BTD8	0.859	-0.525
P25786	0.912	0.166	P32322	0.258	-0.723	P52756	0.917	0.174
P25787	0.903	-0.736	Q96C36	0.904	-0.476	P78332	0.756	-1.25
P25788	0.903	0.502	Q53H96	0.414	-1.44	Q9Y5S9	0.178	1.29
P25789	0.901	-0.125	P11216	0.0126	-2.24	P38159	0.299	0.831
P28066	0.749	1.24	P06737	0.861	-0.895	Q96E39	0.134	0.86
P60900	0.925	0.07	Q2TAL8	0.291	-0.833	P18754	0.911	-0.691
O14818	0.929	0.0151	Q9H974	0.789	-0.89	Q9P258	0.331	0.668
P20618	0.752	1.5	P61026	0.859	-0.488	Q9Y2P8	0.881	0.205
P49721	0.668	1.68	Q15907	0.258	-1.17	Q15293	0.723	0.54

Table 6.6 (continued from the previous page)

Q96B97	0.000417	1.7	P09661	0.895	0.263	Q04837	0.914	0.138	P22695	0.0343	-1.8	Q9H7D7	0.591	0.673	O95218	0.87	0.321
Q8TBC3	0.908	-0.482	P09234	0.853	-0.251	P28290	0.735	-0.548	P47985	0.795	-0.668	Q9UNX4	0.798	-1.05	O43264	0.743	-1.11
P43307	0.592	-0.493	O75347	0.905	-0.749	Q9C0C2	0.899	-0.196	Q15942	0.742	-0.503						
Q9UNL2	0.617	-1.29	Q99426	0.763	-0.698	Q92973	0.878	-0.187									
P51571	0.527	-0.565	Q9BTW9	0.902	-0.426	Q9Y5L0	0.929	-0.0181									
Q08945	0.869	-0.207	Q9UHD2	0.0909	-1.11	Q9UPQ9	1.82E-13	3									
O60232	0.924	-0.0398	Q12788	0.786	-1.64	Q9H0E2	0.755	-0.525									
Q9NP77	0.813	-0.556	Q969Z0	0.191	-0.742	Q15388	0.929	-0.00942									
P50502	0.909	0.126	P23193	0.455	-0.593	Q9NS69	0.865	-0.441									
P42224	0.0985	-1.16	Q15369	0.881	-0.766	Q15785	0.88	-0.328									
P40763	0.927	0.0782	O14776	0.154	0.788	O96008	0.79	-0.879									
O95793	0.881	-0.289	Q9BQ70	0.875	-0.84	O94826	0.891	0.194									
P31948	0.923	-0.0426	Q13428	0.751	0.934	P11387	0.919	0.0735									
P16949	0.916	0.448	Q9NZ01	0.883	0.19	Q5JTV8	0.9	-0.253									
Q9UJZ1	0.764	-1.1	Q9UGI8	0.563	0.582	Q12888	0.871	-0.725									
Q13033	0.905	0.147	Q00059	0.912	-0.511	O43399	0.89	1.17									
P46977	0.82	0.897	Q8WVM0	0.841	0.278	P60174	0.913	0.388									
Q9UNE7	0.917	0.119	Q92734	0.000381	-1.93	P09493	0.901	0.459									
Q9P2W9	0.885	0.499	P02786	0.358	-0.986	P06753	0.922	-0.0901									
Q15833	0.908	-0.235	Q8NI27	0.851	-0.623	P67936	0.862	-0.363									
P53999	0.929	0.0109	Q96J01	0.898	0.272	P13693	0.898	0.181									
Q9P2R7	0.88	-0.499	P52888	0.924	0.0498	Q9ULW0	0.74	0.628									
P53597	0.906	-0.443	Q9BV44	0.888	-0.245	Q13595	0.415	0.7									
Q96I99	0.855	0.599	Q9P016	0.0813	-1.25	P19474	0.917	0.11									
Q9Y2Z0	0.794	-0.76	Q9NQ88	0.763	-0.482	P36406	0.901	-0.173									
Q8NBJ7	0.481	-0.929	O43615	0.488	-1.62	Q14258	0.834	-0.275									
P61956	0.847	-1.45	Q3ZCQ8	0.839	-0.573	Q9C037	0.917	0.166									
O94901	0.893	0.258	Q07157	0.429	1.14	Q14669	0.143	-0.89									
Q9Y5B9	0.885	-0.166	P04183	0.811	-0.368	Q15645	0.899	0.742									
P63272	0.852	-0.662	P29401	0.883	0.273	Q15654	0.84	-0.613									
O00267	0.892	-0.282	Q99805	0.919	-0.0757	Q9NXH9	0.914	-0.153									
Q7KZ85	0.209	-1.46	Q9HD45	0.93	-0.014	Q7L0Y3	0.777	-0.736									
O15260	0.906	-0.47	Q92544	0.829	-0.391	Q9UI30	0.927	0.0204									
O95926	0.762	-1.1	Q9UM00	0.912	-0.506	Q7Z2T5	0.93	-0.012									
O60506	0.912	-0.0861	P49755	0.0594	-1.09	P10155	0.798	-0.929									
Q8NF91	0.863	-0.285	Q9Y3A6	0.0322	-1.32	P43897	0.931	-0.00337									
Q16563	0.826	0.922	Q9BVK6	0.906	-0.305	Q99816	0.904	-0.126									
Q9Y6A5	0.836	0.339	P57088	0.922	0.0723	Q15631	0.898	0.209									
Q6P1X5	0.929	-0.0254	Q9BUB7	0.00491	-1.6	Q99598	0.924	0.124									
P37837	0.587	-1.72	P28289	0.573	-0.797	Q9Y5U2	0.897	0.166									
P26639	0.896	-0.546	Q9NZR1	0.871	0.449	Q16762	0.654	-0.865									
Q8TC07	0.53	-1.07	Q9NYL9	0.626	-0.658	Q6P3X3	0.789	1.66									
Q96NH3	0.766	-0.367	Q6ZXV5	0.87	-2.03	O95801	0.829	-0.286									
O60343	0.395	1.52	Q8NFZ5	0.771	0.961	Q14166	0.79	-1.6									
Q8WZ42	0.0176	-1.71	P07919	0.866	-1.65	Q9C0J8	0.891	-0.225									
Q96CW5	0.923	0.0754	O14949	0.331	-1.95	Q8NI36	0.91	0.152									
P49411	0.927	-0.0178	Q96IX5	0.851	-0.274	Q15061	0.834	1.34									
Q12792	0.561	-0.604	Q14694	0.86	-0.299	Q5MNZ6	0.868	-0.275									
Q6IBS0	0.326	-0.78	P51784	0.806	-0.469	P61964	0.888	0.305									
Q9BRA2	0.915	0.199	P54578	0.908	-0.293	Q9NNW5	0.62	-0.787									
Q8NBS9	0.853	0.425	Q9Y4E8	0.891	0.191	Q9GZS3	0.892	-0.464									
O43396	0.921	0.0792	Q53GS9	0.877	0.342	Q8IWA0	0.726	-0.587									
Q16881	0.809	-0.528	P45974	0.795	-1.33	Q96S55	0.843	-0.616									
P04818	0.329	-0.75	Q93009	0.899	0.144	Q9HAV4	0.805	-1.04									
Q01081	0.528	-0.779	Q93008	0.55	-1.76	O43592	0.776	-0.631									
P22314	0.929	0.0147	Q9BVJ6	0.914	-0.171	P13010	0.916	0.0841									
Q9UBT2	0.869	0.839	Q9Y5J1	0.852	-0.998	Q9H0D6	0.78	-0.425									
A0AVT1	0.673	-1.26	Q9NYH9	0.877	-0.365	P54577	0.795	-1.21									
Q5T6F2	0.428	1.85	P46939	0.802	-0.49	Q9Y2Z4	0.839	-0.381									
P49459	0.876	0.825	O95399	0.907	-0.743	P67809	0.84	-0.318									
P61077	0.854	0.327	P51809	0.361	-0.819	Q96TA2	0.918	-0.176									
P63279	0.877	0.241	Q9P0L0	0.926	-0.0564	Q86U90	0.365	-1.01									
P68036	0.901	0.42	O95292	0.855	-0.657	Q96MU7	0.327	1.73									
Q9C0C9	0.00129	2.18	P26640	0.916	-0.0704	Q9Y5A9	0.868	0.867									
Q9NPD8	0.153	-1.13	P50552	0.819	-1.17	Q7Z739	0.842	-0.898									
Q13404	0.836	1	P61758	0.831	0.372	O75152	0.905	-0.241									
Q14139	0.909	0.139	P18206	0.783	0.377	Q5T200	0.461	3.39									
Q5T4S7	0.908	-0.331	P55072	0.908	0.204	Q8WU90	0.881	0.252									
Q8N806	0.875	0.287	P21796	0.898	-0.318	Q7Z2W4	0.92	-0.111									
P17480	0.804	1.06	P45880	0.822	-0.417	Q96H79	0.227	0.957									
Q04323	0.916	-0.266	Q9Y277	0.777	-1.41	Q6NZY4	0.607	-1.73									
P09936	0.849	1.85	Q9P253	0.819	-0.594	Q8TCF1	0.643	-0.6									
Q9Y5K5	0.471	-0.636	O75436	0.859	0.304	Q15911	0.895	-0.208									
Q9BZX2	0.9	-0.616	Q96QK1	0.906	-0.407	Q96KR1	0.0002	-2.28									
Q9Y3C8	0.857	0.305	Q9NRW7	0.821	-0.391	Q7Z3T8	0.772	1.51									
Q92890	0.735	-0.389	Q9UN37	0.843	-0.914	Q68DK2	0.744	-1.23									
O60701	7.01E-05	-2.55	O75351	0.917	-0.127	O75844	0.926	0.0645									
Q9NYU2	0.757	0.64	Q9NP79	0.742	0.641	O15231	5.21E-07	-3.18									
Q96T88	0.458	-0.702	Q9Y2W2	0.668	0.617	O43670	0.908	-0.164									
P11172	0.831	0.569	Q969T9	0.878	-0.538	Q5BKZ1	0.273	-2.23									
Q9H3U1	0.676	-0.451	O75717	0.905	0.168	Q969S3	0.862	1.56									
Q92900	0.839	-0.41	O75083	0.829	-0.266	Q14966	0.799	-0.481									
Q9UDW1	0.852	-0.255	Q9GZL7	0.716	0.883	Q9Y5V0	0.93	0.00759									
P31930	0.0176	-1.09	Q9BV38	0.751	0.517	Q9Y6R6	0.858	3.39									

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국문초록

인트론 마이크로RNA 프로세싱 과정에 있어 DROSHA의 비정형 proline-rich domain의 역할

마이크로RNA(microRNA or miRNA)의 생합성은 마이크로프로세서 복합체(Microprocessor complex)를 구성하는 리보핵산(RNA) 분해효소인 드로셔(DROSHA)에 의해 시작된다. DROSHA 단백질은 miRNA 1차 전구체(primary miRNA or pri-miRNA)에 결합하여 절단하는 역할을 한다. DROSHA는 수천 개의 다른 헤어핀(hairpin)들과 구별되는 pri-miRNA의 독특한 특징들을 인식하여 miRNA 생성 경로로 안내하는 역할을 한다. 그동안의 많은 연구를 통해, pri-miRNA 절단의 분자적 기전은 DROSHA의 중앙과 카르복실 말단(C-terminal) 도메인에 크게 의존한다는 것이 밝혀져 왔다. DROSHA의 구조를 갖춘 도메인의 기능은 광범위하게 연구된 반면, 아민 말단(N-terminal)에 있는 프롤린이 풍부한 비정형 도메인(disordered proline-rich domain or PRD)의 기능에 대해서는 명확하게 알려진 바가 없다.

이 논문에서 나는 PRD가 인트론(intron)에 위치한 miRNA의 생성을 촉진하는 역할을 한다는 것을 밝혔다. 나는 전장 DROSHA 단백질의 절단으로 생성된, PRD를 가지고 있지 않은 p140이라는 DROSHA 동위체(isoform)를 발견했다. 마이크로RNA 시퀀싱(sequencing)을 통해, 나는 p140이 인트로닉(intronic) miRNA의 생합성에 있어서 그 기능이 떨어지는 것을 확인하였다. 시퀀싱 결과와 일맥상통하게, 엑손(exon)과 인트론을 포함한 미니진(minigene)을 사용한 실험에서도 PRD는 인트론에 위치한 헤어핀의 절단을 향상시켰지만, 엑손에 위치한 헤어핀들에서는 그 현상이 보이지 않았다. 스플라이싱(splicing)에 중요한 요소들을 돌연변이 시켰을

때도 인트로닉 miRNA에 대한 촉진 효과는 여전히 관찰되었고, 이는 PRD가 인트론 내에 존재하는 서열과 상호작용하여 기능하지만, 스플라이싱과는 독립적으로 작용함을 의미한다. 아미노산 서열 자체의 보존도는 높지 않은 제브라피쉬(zebrafish)와 제노프스(xenopus) DROSHA의 아민 말단 지역이 인트로닉 miRNA 생성에 있어서 인간의 아민 말단 지역을 대체할 수 있는 것으로 보아, 이 부분이 기능적으로 보존되어 있음을 알 수 있다. 나는 또한 빠르게 진화하는 인트로닉 miRNA들이 보존된 miRNA들보다 일반적으로 PRD에 더 의존하는 경향성을 발견하였고, 이는 PRD의 miRNA 진화에서의 역할을 시사한다.

이 논문은 miRNA가 위치한 유전적 맥락(genomic context)을 감지하는 낮은 복잡성(low-complexity)의 비정형 도메인에 의한 miRNA 생합성 조절의 새로운 계층(layer)을 제시한다.

감 사 의 글

이 졸업논문을 끝으로 지난 7년 동안의 학위 과정을 마치게 되었습니다. 돌이켜보면 아쉬움과 부족함이 많이 남는 시간이었지만, 대학원에 입학할 당시 가졌던 '연구의 시작부터 마무리까지의 한 사이클을 경험하고 싶다'는 소망에는 충분한 시간이었던 것 같습니다. 지난 7년은 제가 연구했던 마이크로RNA와 DROSHA 단백질에 관해 탐구하는 시간이었음과 동시에, 저라는 사람에 대해 알아가는 시간이었습니다. 저에게 중요한 가치는 무엇인지, 어떻게 슬럼프를 극복하는지, 어떤 환경에서 가장 즐겁고 생산적인 사람인지 등에 대해 알아가는 시간이었고, 이를 토대로 앞으로 독립적인 연구자로 살아가며 많은 어려움을 마주했을 때 잘 이겨낼 수 있을 것이라는 용기를 내 봅니다. 또한, 건강한 삶에서 운동과 같이 몸을 움직이는 행위가 얼마나 중요한 것인지 몸소 체험했으니, 학위 과정 동안 느꼈던 많은 것들을 앞으로도 스스로 잊지 말았으면 합니다.

긴 시간 동안 많이 도와주신 김빛내리 지도교수님, 저와 인연을 맺은 연구실 선후배님들, 힘들 때 힘이 되어 준 친구들과 대학원 동기들께 지면을 빌려 감사의 마음을 전하고자 합니다. 또한, 바쁘신 와중에도 저의 박사학위 심사를 맡아주시고 아낌없는 조언을 해 주신 강찬희 교수님, 노성훈 교수님, 이현우 교수님, 김유식 교수님께도 진심으로 감사의 말씀을 드립니다.

제가 대학원에 입학했을 때부터 만나, 지금까지 한결같이 제 옆에서 저를 웃게 하는 남편 종우에게 고마움을 전합니다. 당신 덕분에 힘들고 지난한 과정에서도 '나'라는 사람을 잃어버리지 않을 수 있었습니다. 앞으로 함께 할 날이 더 많음이 저에겐

큰 기쁨이고 힘입니다. 우리가 새롭게 마주할 도전을 즐겁게 맞아봅시다. 따뜻한 애정과 믿음으로 저희 가정을 지원해 주시는 시부모님께도 또한 감사드립니다.

마지막으로, 30년 넘는 긴 세월 동안 한결같은 사랑과 믿음으로 저를 지지해 주신 엄마, 아빠, 그리고 든든한 동생 장원이에게 가장 큰 감사를 드립니다. 좌절로 가득 찼던 수많은 날의 끝에 가족이 있었기에 버틸 수 있었고, 같이 흘려준 눈물과 애정이 담긴 공감은 제가 학위 과정을 포기하지 않고 마칠 수 있게 한 견고한 버팀목이었습니다. 아빠, 엄마가 일군 울타리에서 성장할 수 있었음이 저에게는 너무나 큰 축복이었고, 여전히 큰 힘입니다. 제가 받은 사랑을 기억하고 간직하며, 저희의 가정도 잘 꾸려나가 보겠습니다. 앞으로도 건강하게 옆에서 지켜봐 주세요.