THESIS FOR THE DEGREE OF DOCTOR OF PHILOSOPHY

Profiling of microRNAs in olive flounder (*Paralichthys olivaceus*) and *Epithelioma papulosum cyprini* cells following viral hemorrhagic septicemia virus infection, and functional characterization of miR-146a, miR-155 and miR-210

by
Najib Abdellaoui

Department of Aquatic Life Medicine
The Graduate School

Pukyong National University

February , 2018

Profiling of microRNAs in olive flounder (*Paralichthys olivaceus*) and *Epithelioma papulosum cyprini* cells following viral hemorrhagic septicemia virus infection, and functional characterization of miR-146a, miR-155 and miR-210

VHSV 감염에 대한 넙치와 EPC cell 의 miRNAs 발현 양상과 miR-146a, miR-155, miR-210 의 기능 분석

Advisor: Prof. Ki Hong Kim

By

Najib Abdellaoui

A thesis submitted in partial fulfillment for the requirements
for the degree of

Doctor of philosophy

in Department of Aquatic Life Medicine, The Graduate School,
Pukyong National University

February 2018

Profiling of microRNAs in olive flounder (*Paralichthys olivaceus*) and *Epithelioma papulosum cyprini* cells following viral hemorrhagic septicemia virus infection, and functional characterization of miR-146a, miR-155 and miR-210

A dissertation

by

Najib Abdellaoui

Approved by:

(Chairman) Hyun Do Jeong

(Member) Do Hyung Kim

(Member) Tae Jin Choi

(Member) Se Ryun Kwon

(Member) Ki Hong Kim

February 23, 2018

Contents

VHSV 감염에 대한 넙치와 EPC cell 의 miRNAs 발현 양상과 miR-146a, miR-155, miR-210 의 기능 분석

Najib Abdellaoui

부경대학교 대학원 수산생명의학과

요약

MicroRNAs (miRNAs) 는 19-25nt 의 small non-coding RNA 로서 인간을 비롯한 다양한 생물체에서 이미 수 천 종류 이상의 miRNA 가 밝혀져 있다. 각각의 miRNA 는 많은 수의 유전자를 조절할 수 있으며, 또한 하나의 유전자는 여러 개 miRNA 의 target 이 될 수 있다. miRNA 는 특정한 방식으로 messenger RNA (mRNA)에 결합하여 전사 후 번역을 억제함으로써 유전자 발현을 조절한다. 포유류에서는 miRNA 가 생물학적, 병리학적 과정에 미치는 영향을 기반으로 하여 miRNA 와 miRNA 의 작용기작에 대한 연구가 활발히 이루어지고 있으며, 이러한 연구들을 어류에도 적용하여 miRNA 와 miRNA 의 작용기작에 대한 이해도를 높이는 것은 어류의 질병 제어 방법의 개발에 도움이 될 것으로 여겨진다. 따라서, 본 연구에서는 전 세계적으로 양식어류에 큰 피해를 일으키고 있는 바이러스성 출혈성패혈증(VHS)의 원인체인 바이러스성 출혈성패혈증 바이러스(VHSV)를 이용하여 VHSV 의 감염이 넙치 (*Paralichthys olivaceus*)와 *Epithelioma papulosum cyprini* (EPC) 세포의 miRNA 의 발현 양상에 미치는 영향을 연구하였다.

넙치 치어를 VHSV 에 감염시킨 후 시간대 (0, 6, 12, 24, 48, 72 시간)마다 Next Generation Sequencing (NGS)를 통해 세포내 miRNA 의 발현을 분석하였다. 그 결과, 총 372 개의 mature miRNA 가 확인되었으며, 그 중 63 개의 miRNA 가 VHSV 감염에 의해 차등 발현되었다. 차등 발현된 miRNA 의 발현양이 6, 12 시간 째에 비해 24 시간 째에 크게 증가한 것으로 보아 VHSV 감염에 의한 miRNA 발현 양상의 변화는 질병의 진행과 관련이 있는 것으로 사료된다. 또한, 차등 발현된 63 개의 miRNA 의 표적 유전자 예측, GO enrichment 분석 및 KEGG 경로 분석을 통해 VHSV 의 감염에 의한 숙주의 miRNA 발현 양상 변화로 인해 다양한 생물학적 경로가 영향을 받는다는 사실을 알 수 있었다. 그리고 EPC 세포에 VHSV 를 감염 시킨 후 시간대마다 miRNA 의 발현 양상을 분석한 결과 355 개의 conserved miRNA 와 3 개의 새로운 miRNA 가 확인되었다. 그 중 103 개의 miRNA 가 차등 발현되었는데, 이들의 발현양은 3 시간, 12 시간 째에 비해 24 시간째에 크게 증가하였다. 이것은 EPC 세포가 초기 감염기에 적극적으로 반응을 하지 못한 것으로 생각되며, 이러한 현상은 바이러스가 바이러스의 유전자의 발현과 번역을 통해 감염성을 지닌 바이러스 입자를 생성하기에 충분한 시간이라고 판단된다. 차등 발현된 miRNA 중 2 개의 miRNA (miR-735, miR-738)는 어류에서만 보고가 되어 있으며, 이들의 발현도 크게 증가되었으며, 표적 유전자 예측을 통해 이들이 여러가지 면역 경로를 조절하는 것을 확인하였다. 그리고 본 연구의 결과를 통해 miR-146a, miR-155 및 miR-99 와 같은 대표적인 면역조절 miRNA 의 발현양의 증가도 확인하였다. VHSV 의 감염에 의해 차등 발현되는 miRNA 의 발현 양상의 변화를 보면, 어떠한 한 시점에서의 miRNA 의 분석은 질병의 발생 기작을 해석하기에 불충분하다고 판단된다.

본 연구의 결과를 통해서 VHSV 의 감염과 관련된 넙치와 EPC 세포의 miRNA 의 기초적인 정보를 알 수 있게 되었다. 생물학적 변화에 다양한 영향을 미치는 miRNA 의 특성을 고려하였을 때, 본 연구의 결과는 VHSV 의 병원성의 발생 기작에 대한 정보와, VHSV 의 제어 방법에 대한 정보를 제공할 수 있다고 판단된다.

넙치와 EPC 세포에서 VHSV 의 감염에 의해 발현이 증가한 miRNA 중에서 발현양이 가장 크게 증가한 2 가지 miRNA (miR-146a, miR-155)를 선정하여 본 연구에 사용하였다. 포유류에서 miR-146a 는 Tumor necrosis factor receptor associated factor 6(TRAF6)를 포함한 몇몇 유전자를 표적으로 하여 NF-kb 의 활성을 조절한다고 알려져 있다. 본 연구에서는 miR-146a 를 발현하는 vector 와 miR-146a 의 mimics 의 형질주입을 통한 miR-146a 의 과발현이 TRAF6 유전자의 발현과 VHSV 의 증식에 미치는 영향을 분석하였다. 또한, 생물정보학적 분석과 분자생물학적 기술을 이용하여 miR-155 의 기능을 분석하였다. 마지막으로, 본 연구에서는 빈산소 상태에 놓인 넙치의 혈중 miR-210 의 농도가 증가하는 것을 확인했으며, 빈산소 상태의 정상 EPC 세포와 HIF-1 α 가 knock-out 된 EPC 세포에서 miR-210 프로모터에 의해 조절되는 luciferase 의 활성을 분석하였다.

List of tables

List of figures

General introduction

The miRNAs (miRNAs) are small non-coding RNAs, first discovered by Lee et al. (., 1993). They found a small RNA molecule (Lin-4) with a length of 22 nt capable of downregulating the LIN-14 expression in *Caenorhabditis elegans* through a complementary of sequences in the 3'UTR of the gene. Later, several orthologs were found in other species (Pasquinelli et al., 2000; Lagos-Quintana et al., 2001; Lim et al., 2003). Until today, thousands of miRNAs were found in vertebrates, invertebrates, plants, and viruses (Kozomara et al., 2014). An online database called miRBase was established to collect the discovered miRNAs which contain over 35,000 mature miRNAs from 223 species (http://www.mirbase.org/). The miRNAs can bind to their targets without perfect complementarity, and each miRNA can target several genes (Bartel, 2009; Friedman et al., 2009). Furthermore, each type of cell expresses different pattern of miRNAs. Based on this evidence and diversity of miRNAs, miRNAs can be the coordinators of most physiological and pathological processes.

The miRNAs represent 1 % of the genome, and around 50 % of miRNAs are in intergenic position. The remaining miRNAs have a positions either within introns or exons (O'Carroll et al., 2013). Mainly, intergenic miRNAs possess their promoter and enhancer. On the other hand, intronic miRNAs and miRNAs embedded in exons are believed to be tightly regulated under the control of the transcription of genes (O'Carroll et al., 2013; Ha et al., 2014).

Most of the miRNAs are transcribed in the nucleus by RNA polymerase II. This transcription generates a long primary transcript with a length ranging from a hundred to several kilobases (Lee et al., 2004; Borchert et al., 2006). It contains a local hairpin structure in which miRNA is embedded. Typically, primary miRNAs (pri-miRNAs) are composed of a 33-35 stem, a terminal loop and flanking single-stranded RNA on 5' and 3' ends. The pri-miRNAs can encode a single miRNA or several miRNAs. The latter is called cluster which forms complex structures containing several hairpin structures (O'Carroll et al., 2013). The pri-miRNAs have similar features to mRNA such as a cap at 5' end and a polyadenine tail at 3' end when transcribed by RNA polymerase II (Cai et al., 2004). The

first step of biogenesis of mature miRNA, the pri-miRNA is recognized by a nuclear microprocessor that includes two proteins Drosha and DiGeorge syndrome critical region 8 (DGCR8). The DGCR8 attach to the stem region of pri-miRNA which allows recruitment of Drosha that bears an RNase activity and crops the pri-miRNA to release a small hairpin RNA called precursor miRNA (pre-miRNA) (Lee et al., 2003). The product is a small RNA molecule with a length of 65-100 nt and has a characteristic of a 3' 2nt overhang and a 5' phosphate group.

Following cleavage, the pre-miRNA is transported from nucleus to cytoplasm by a protein called Exportin 5 through binding with its cofactor GTP-binding nuclear protein RAN•GTP. Pre-miRNA is released into the cytoplasm through hydrolysis of GTP (Bohnsack et al., 2004) where it binds to RNase III enzyme called Dicer and its cofactor TAR RNA-binding protein (TRBP). The pre-miRNA binds by its 3' 2n overhangs to the PAZ domain of Dicer and is excised at a fixed distance typically 21-25 nt (MacRae et al., 2006; Park et al., 2011). The cleavage of pre-miRNA releases a duplex RNA which is loaded into the Ago protein to form the RNA-induced silencing complex (RISC) (Hammond et al., 2001). The RISC is composed of Ago protein, which contains two domains PAZ, and PIWI. The PAZ domains interact with 2nt overhangs of miRNA and PIWI have a slicer activity to cleave targets mRNAs using the guide miRNA (Lingel et al., 2003; Okamura et al., 2004; Wang et al., 2008). Generally, after loading the duplex miRNA into the Ago protein, it is unwound to keep one strand to function as mature miRNA and releases the remaining one to be degraded (Pasquinelli, 2012). Following the integration into the RISC complex, the miRNA will play the role of guide to target mRNA harboring complementary.

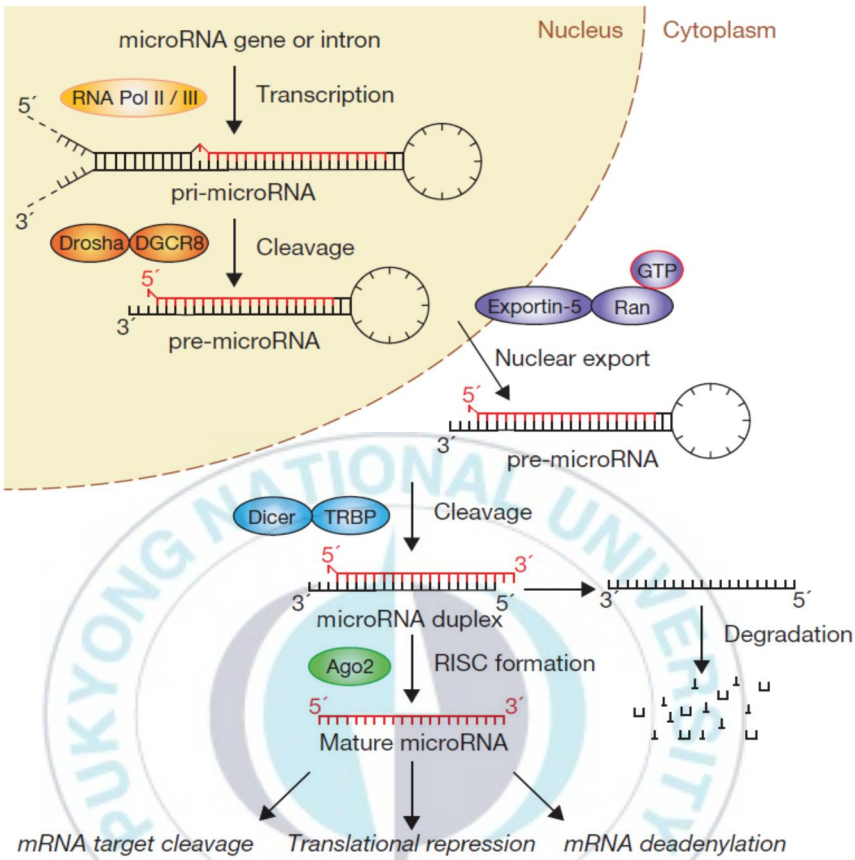

Figure 1. Canonical pathway of miRNA processing. Adapted from (Winter et al., 2009). The pri-miRNAs are transcribed by RNA polymerase II and processed to pre-miRNA by Drosha and its cofactor DGCR8. The pre-miRNA is transported to the cytoplasm by protein Exporting-5 in GTP dependent manner. In the cytoplasm, the pre-miRNA is cleaved by Dicer and its cofactor TRBP. This produces a small RNA duplex of 22 nt in length which integrates the RISC complex including Argonaute protein. The guide strand is associated with Argonaute, and the passenger is degraded.

The mature miRNA can bind to the potential target in different positions (5'UTR, CDS, and 3'UTR), although almost all miRNAs mainly target the 3'UTR region (Miranda et al., 2006; Hafner et al., 2010; Schnall-Levin et al., 2010; Hausser et al., 2013). The binding between miRNA and the target region is established through a seed region localized between 2-8 nucleotide from 5'end of miRNA (Enright et al., 2003; Lewis et al., 2003). Once the complex miRNA-RISC bounds the mRNA, it influences its expression through different mechanisms such as translation repression or degradation of mRNA (Behm-Ansmant et al., 2006; Valencia-Sanchez et al., 2006; Wakiyama et al., 2007).

The miRNAs play various roles in different biological and pathological processes. The miRNA can regulate the development (Gao, 2010), the immune system (Androulidaki et al., 2009; Curtis et al., 2015), erythropoiesis (Felli et al., 2005; Patrick et al., 2010), and so on. For example, miR-451 plays an important role in erythropoiesis (Patrick et al., 2010). The miR-155 can regulate the differentiation of T helper cells and the germinal center reaction (Thai et al., 2007). The transcription factors (Nanog, Oct4, and Sox2) that are responsible for the production of induced pluripotent stem cells (IPSC) are targets for miR-134, miR-296, and miR-470 (Tay et al., 2008). Several miRNAs have been found to be associated with cancer, such as the miR-15 and miR-16 that target B cell lymphoma 2 (Bcl2) involved into the chronic lymphocytic leukemia (Cimmino et al., 2005). Furthermore, miRNAs are the regulators of microbiological processes. MiR-214 downregulate inflammatory response mediated by NF-κb through targeting Myd88 in miiuy croaker during bacterial infection by *Vibro harveyi* (Chu et al., 2017). MiR-192 target interleukin I receptor type I during bacterial infection (Chu et al., 2016).

Also, miRNAs have an essential role in viral infection. MiR-155 have multiple functions in immunity and hematopoiesis (Masaki et al., 2007). MiR-155 can inhibit replication of Japanese encephalitis virus and downregulate NF-κb response (Pareek et al., 2014). Moreover, miR-155 can target the suppressor of cytokine signaling 1 (SOCS1), Which enhances type I interferon response expression leading to the suppression of viral replication during vesicular stomatitis virus (VSV) infection (Wang et al., 2010). On the other hand, the virus can take advantage of miRNA machinery to enhance its replication or inhibit antiviral immunity. VSV induces miR-146a during infection that targets several

genes such as IL-1 receptor-associated kinase 1 (IRAK1), IRAK2, and tumor necrosis factor (TNF) receptor-associated factor 6 (TRAF6) which suppresses type I interferon response, thereby enhance viral replication (Hou et al., 2009). MiR-9041 and miR-9850 are upregulated during white spot syndrome virus infection which inhibits JAK/STAT inducing low expression of interferon response genes (Huang et al., 2016). Besides, miR-731 enhances viral replication of Megalocytivirus in olive flounder through suppression of interferon regulatory factor 7 (IRF7) and tumor antigen p53 by binding to their 3'untranslated region (Zhang et al., 2016). Furthermore, taking advantage of host miRNA machinery, several viruses encode their miRNA in their genomes (Feldman et al., 2014; Riaz et al., 2014; Guo et al., 2015). The viral-encoded miRNAs have different roles such as human cytomegalovirus that escape CD8+ T cells through targeting aminopeptidase endoplasmic reticulum aminopeptidase 1 (ERAP) by producing a miRNA called miR-US4-1 (Kim et al., 2011).

Viral hemorrhagic septicemia virus (VHSV) is a single negative-stranded RNA virus belonging to the genus *Novirhabdovirus* (King et al., 2012) that includes virus causing severe disease in aquatic hosts (Tadashi et al., 2001). The VHSV genome encodes several proteins, nucleocapsid protein (N), phosphor-protein (P), matrix protein (M), glycoprotein (G), large RNA-dependent RNA polymerase (L), and a non-virion (NV) protein. The NV protein is implicated in promoting viral replication through recruitment of protein phosphatase, Mg2+/Mn2+-dependent, 1Bb (PPM1Bb) leading to inhibition of RIG-I- and TBK1-dependent interferon (IFN) and IFN-stimulated gene promoter induction (Biacchesi et al., 2017). VHSV causes a disease in at least over 50 species of marine and freshwater fish (Skall et al., 2005) and results in high mortality with a substantial economic loss (Kim et al., 2009).

In the present study, we aimed to study the effect of VHSV on miRNAs expression in olive flounder and EPC cells. Furthermore, we focused on specific miRNAs related to immunity such as miR-146a, miR-155 or related to hypoxia such as miR-210.

Chapter I. Changes in miRNAs expression profile of olive flounder (*Paralichthys olivaceus*) in response to viral hemorrhagic septicemia virus (VHSV)

Introduction

Viral hemorrhagic septicemia virus (VHSV), a single-stranded RNA virus belonging to the genus *Novirhabdovirus* in the family Rhabdoviridae, is a highly pathogenic virus causing high mortality in different species of fish and substantial economic losses in aquaculture sector (Meyers et al., 1995; Skall et al., 2005). The genome of *Novirhabdovirus* harbor six genes expressing a nucleoprotein N, a phosphoprotein P, a matrix protein M, a glycoprotein G, a non-virion protein NV, and a large RNA-dependent RNA polymerase L (King et al., 2012).

MiRNAs are a class of highly conserved small non-coding RNA that interact with mRNA molecules by binding to their 3'untranslated regions which cause an inhibition of translation or degradation of mRNA (Bartel, 2004). miRNA has been studied in the last decade because of their significant role in various biological processes such development, cell proliferation, cell differentiation, and apoptosis (Carrington et al., 2003; Lima et al., 2011). Likewise, they play an intricate role during pathological processes such as tumorigenesis, viral and bacterial infections(Ding et al., 2007; Budhu et al., 2008; Wang et al., 2012; Cai et al., 2015).

In fish as well as in mammals, viral infections can alter expression of host miRNAs and recently, the interaction between cellular miRNA and RNA virus has been extensively studied in mammals (Shi et al., 2014; Trobaugh et al., 2014). Nevertheless, the fish virus has been poorly investigated regarding the profile of miRNAs during viral infection especially RNA virus. Wu et al.(Wu et al., 2015) have reported differentially expressed cellular miRNAs in EPC cells during infection with spring viremia of carp virus (SVCV), which is a rhabdovirus of genus *Vesiculovirus*. For VHSV, few studies were done concerning miRNAs expression except two papers which described the upregulation of miR-462 and miR-731 in rainbow trout during infection with VHSV or through immunization with DNA vaccine expression glycoprotein against VHSV (Bela-ong et al., 2015; Schyth et al., 2015)

Lately, several reports have proven the importance and involvement of miRNA in the regulation of human genes expression (Cameron et al., 2008; Zhang et al., 2014; Cai

et al., 2015). Furthermore, miRNA can play essential roles during viral infection leading to the spread of the virus or defends host through activation of immunity defenses. Therefore, investigation and study of miRNA profile during viral infection can be a robust tool to elucidate and understand the mechanisms concerning viral pathogenesis.

Olive flounder (*Paralichthys olivaceus*) is a highly appreciated fish in Korea and has been the most important cultured fish in Korea. However, VHSV causes high mortality in olive flounder leading to enormous economic loss (Kim et al., 2009). Recently, Zhang et al. (2014) explored the change of cellular miRNAs expression profiles in olive flounder during viral infection by megalocytivirus which is a DNA virus belonging to the family of *iridoviridae*. However, until now no information is available on the change of miRNAs expression profile by the infection of RNA viruses in olive flounder.

In this study, we infected olive flounder fish with VHSV and extracted RNA from their head kidney at different points time (0, 6, 12, 24. 48, 72 hours post infection), and submitted to next-generation sequencing analysis. Based on NGS, we could determine different miRNAs altered by a viral infection which were reported to have a tight relation with the immune system.

Materials and methods

1. Fish

Olive flounder fingerlings weighing approximately 2.5 g were obtained from a local olive flounder hatchery. Fish were acclimated for two weeks, during which water temperature was gradually down to 14°C. Before the experiment, free from pathogens including VHSV was verified by the examination of the liver, head kidney, and spleen from randomly sampled ten fish. The animal experiment was carried out according to the guidelines of Animal Research and Ethics Committees of Pukyong National University.

2. Viral infection

VHSV KJ2008 (Kim et al., 2011) was cultured in *Epithelioma papulosum cyprini* (EPC) cells at 15°C in the presence of 2% fetal bovine serum (FBS, Sigma). Cultures displaying extensive cytopathic effect (CPE) were harvested and centrifuged at 4,000 g for 10 min at 4°C, and the supernatants were stored at −80°C. Fish were intramuscularly injected with the virus at a dose of 10^3 plaque-forming units (pfu)/fish. At 0, 6, 12, 24, 48, and 72 h postinfection (h.p.i), five fish were randomly sampled, and the head kidney was isolated and stored at −80°C. The head kidneys of 5 fish were pooled, and total RNA was extracted using Hybrid-RTM miRNA kit (GeneAll, Korea) according to manufacturer's instructions.

3. Small RNA libraries constructions and sequencing

Macrogen, Korea conducted the construction of small RNA libraries and sequencing. The RNA quality and concentration were analyzed with an Agilent 2100 Bioanalyzer. Small RNA libraries were constructed using a TruSeq Small RNA Library Prep Kit (Illumina) according to the manufacturer's protocol. The generated libraries were sequenced using the HiSeq 2500 (Illumina).

4. Next-generation sequencing and data analysis

The quality of raw data was analyzed using FastQC (Babraham Bioinformatics, UK) (Andrews, 2010). Raw sequences were trimmed and clustered; then the sequences were aligned against zebrafish genome, which was retrieved from UCSC genome browser (Kent et al., 2002), due to the absence of reference genome for *Paralichthys olivaceus* using miRDeep2 software algorithm (Friedländer et al., 2012). To eliminate the non-miRNAs, the sequences were mapped to Rfam 9.1 database which includes the sequences of rRNA, tRNA, small nuclear RNA (snRNA) and small nucleolar RNA (snoRNA) (Nawrocki et al., 2015). After that, the retained sequences were blasted against miRBase v21.0 (Griffiths-Jones et al., 2006) (http://www.mirbase.org/) to determine the conserved miRNAs between zebrafish and olive flounder. The sequence was considered as miRNA only if they have 100% of identical sequence and possesses the whole length miRNA compare to the ones on the miRBase database. Unmatched miRNA sequences were analyzed using RNAfold algorithm through miRDeep2 software to predict novel miRNAs.

5. Differential miRNA expression analysis

Raw data were normalized by read per million (RPM, miRNA counts / total counts of each sample x 1 million). The miRNAs with at least one zeroed RPM were excluded. The RPM values were log transformed after addition of 1 to their value. The log-transformed data were normalized using Quantile normalization method (Bolstad, 2003). The differential miRNA expression was calculated based on fold change between the control group (0 h) and VHSV infected groups (6, 12, 24, 48, and 72 h) with a default cut-off of ±1.5. The analysis was done using preprocessCore R library.

6. qPCR of differentially expressed miRNAs

RNA was reverse-transcribed using miScript II RT Kit (Qiagen) following manufacturer's instructions. Briefly, one µg of RNA was added to 4 µl of 5x miScript HiSpec Buffer, two µl of 10x miScript Nucleics Mix and two µl miScript Reverse Transcriptase Mix. RNase free water was added to get a volume of 20 µl. The mix was

incubated at 37 °C for 60 min, then at 95°C for 5 min to inactivate the reverse transcriptase. The cDNA was diluted using RNase free water. The detection of mature miRNAs was done using miScript SYBR Green PCR Kit (Qiagen). The qPCR was performed using the mature sequence of miRNAs forward primers with the universal primer from the miScript SYBR Green PCR Kit. The reaction was carried out in Roche Light Cycler 480 (Roche, Germany) in a 20 µl reaction volume containing two µl of cDNA, ten µl of 2x QuantiTect SYBR Green PCR Master Mix, two µl of forward primer, two µl of universal primer and four µl of water. The mix was incubated at 95°C for 15 min, followed by 45 cycles of 94°C for 15 s, 55°C for 30 s, and 70°C for 30 s. The data analysis was done using the $2^{-\Delta\Delta Ct}$ method.

7. Target prediction and enrichment of differentially expressed miRNAs

The target prediction was done using the putative 3'untranslated regions (3'UTR) of olive flounder mRNAs which were extracted from NCBI database. The prediction was made using miRanda (Betel et al., 2010) and RNA22 (https://cm.jefferson.edu/rna22/) (Miranda et al., 2006). miRanda was used to match the entire miRNA sequence, and RNA22 was used for identification of miRNA binding sites based on pattern method. The parameters for miRanda were a score >120 and a free energy <-20 kcal/mol, and for RNA22 the free energy was <-20 kcal/mol. The predicted results by the two tools were combined. Enrichment analysis of target genes of miRNA was done using Blast2Go version 3.1 (https://www.blast2go.com/) (Conesa et al., 2005). First, the predicted target genes were blasted against the NCBI non-redundant protein database to search for sequence homology (E-value of 1.0E-3, maximum 15 hits). The best hits were mapped, annotated and the functional annotations were analyzed. For KEGG pathways, the target genes sequences were uploaded to the KEGG Automatic Annotation Server (KAAS, http://www.genome.jp/tools/kaas/) (Moriya et al., 2007). The functional annotation of target genes was done by BLAST against the KEGG database.

Table 1- 1 Primers used for Quantitative real-time PCR

Primers	Forward primer Sequence 5'-3'	Reverse primer sequence 5'-3'
pol-miR-107b	AGCAGCATTGTACAGGGCTTT	Qiagen universal primer
pol-miR-122	TGGAGTGTGACAATGGTGTTTG	-
pol-miR-146a	GCTGAGAACTGAATTCCATAGATGG	-
pol-miR-155	GCTTAATGCTAATCGTGATAGGGG	-
U6 snRNA	CGCAAGGATGACACGCAAATT	-

Results

1. Identification of miRNAs in olive flounder

To know the effect of VHSV infection on the miRNA expression profile of olive flounder, fish were infected with the virus, and cellular miRNAs expression was analyzed at 0 (control), 6, 12, 24, 48 and 72 h postinfection. Six small RNA libraries were generated and sequenced by NGS. After removing reads without adaptor, low quality reads and reads with a length ≤ 17 nt, approximately 24,000,000-25,000,000 clean reads from each small RNA library were obtained (Table 1-2). The length distribution analysis showed that the major part of reads was distributed between 20-24 nt ranges with the dominance of 22 nt (Fig. 1). The trimmed reads were blasted first to the Rfam database, then against the zebrafish genome because of lack of olive flounder genome data. More than 80% of reads mapped perfectly to zebrafish genome (Table 1-3), and the remaining reads were mapped to rRNA, tRNA, snoRNA, snRNA, or unknown.

To identify conserved miRNAs, the small RNA reads were blasted against the miRNAs of zebrafish retrieved from the miRBase database (Release 21.0). A total of 350 mature miRNAs were perfectly matched to miRNAs of zebrafish. The novel miRNAs were predicted from mature, star and loop sequence according to the RNAfold algorithm using miRDeep2.

Table 1- 2 Mapped reads to zebrafish genome

Sample	Total reads	Clustered read	Mapped reads	%	Clustered read	Unmapped reads	%	Clustered read
0 h.p.i	24484878	571357	20517671	3.80%	144572	3967207	6.20%	387944
6 h.p.i	24617636	616679	20439316	3.00%	148463	4178320	7.00%	421547
12 h.p.i	24445479	538996	20769244	5.00%	129811	3676235	5.00%	371094
24 h.p.i	25508468	706840	21433450	4.00%	146844	4075018	6.00%	519328
48 h.p.i	24871451	666721	20711514	3.30%	154564	4159937	6.70%	457346
72 h.p.i	24418077	750530	20101273	2.30%	175674	4316804	7.70%	515270

Table 1- 3 Mapped reads to miRNAs of zebrafish

Sample	Total reads	Clustered read	Mapped reads	%	Clustered read	Unmapped reads	%	Clustered read
0 h.p.i	24484878	571357	19904990	1.30%	28423	4579888	8.70%	542934
6 h.p.i	24617636	616679	19939728	1.00%	28058	4677908	9.00%	588621
12 h.p.i	24445479	538996	20073520	2.10%	28401	4371959	7.90%	510595
24 h.p.i	25508468	706840	20772470	1.40%	28856	4735998	8.60%	677984
48 h.p.i	24871451	666721	20070301	0.70%	28794	4801150	9.30%	637927
72 h.p.i	24418077	750530	19413294	9.50%	29629	5004783	0.50%	720901

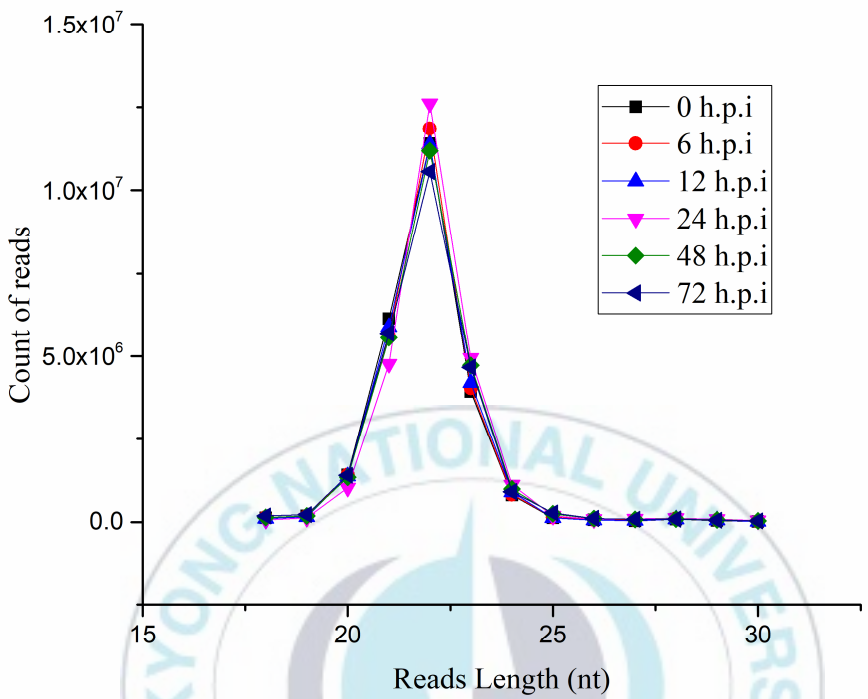

Figure 2. Reads distribution in function of length of sequence.

2. Differential expression of miRNAs during viral infection by VHSV

To investigate differentially expressed miRNAs by VHSV infection, the fold change (F.C) of miRNAs between the control group (0 h.p.i) and the infected groups (6, 12, 24, 48, and 72 h.p.i) was calculated with a threshold of ≥1.5 times (|F.C|≥1.5). The expression of 63 miRNAs was altered by VHSV infection (Fig. 2). At 6 and 12 h.p.i., less than ten miRNAs showed altered expression compared to the control group (0 h.p.i.), then, after 24 h.p.i. the responding miRNA numbers were substantially increased. Until 48 h.p.i., the number of upregulated miRNAs was higher than that of down-regulated miRNAs. However, at 72 h.p.i., the number of down-regulated miRNAs surpassed the number of upregulated miRNAs (Fig. 2). A heat map was generated to show the changes of each

miRNA expression according to time lapse after VHSV infection (Fig. 3), and miRNAs are showing similar expression pattern were grouped by clustering analysis (Fig. 4).

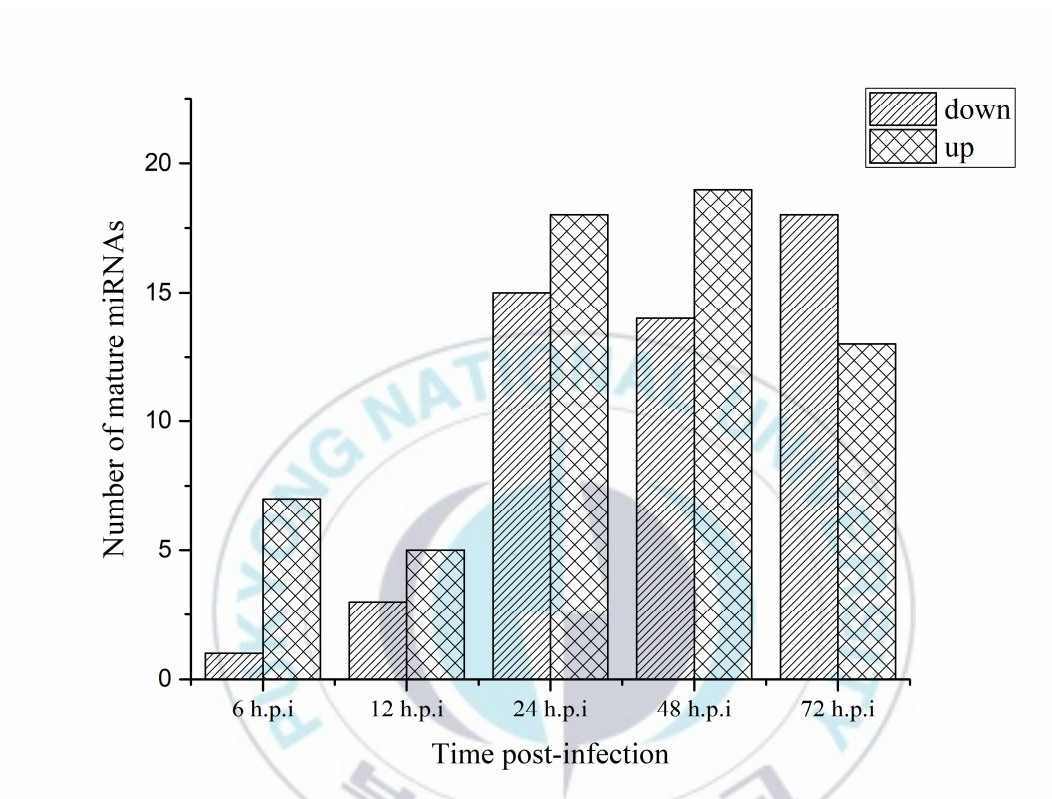

Figure 3. Differentially expressed miRNAs following the course of infection

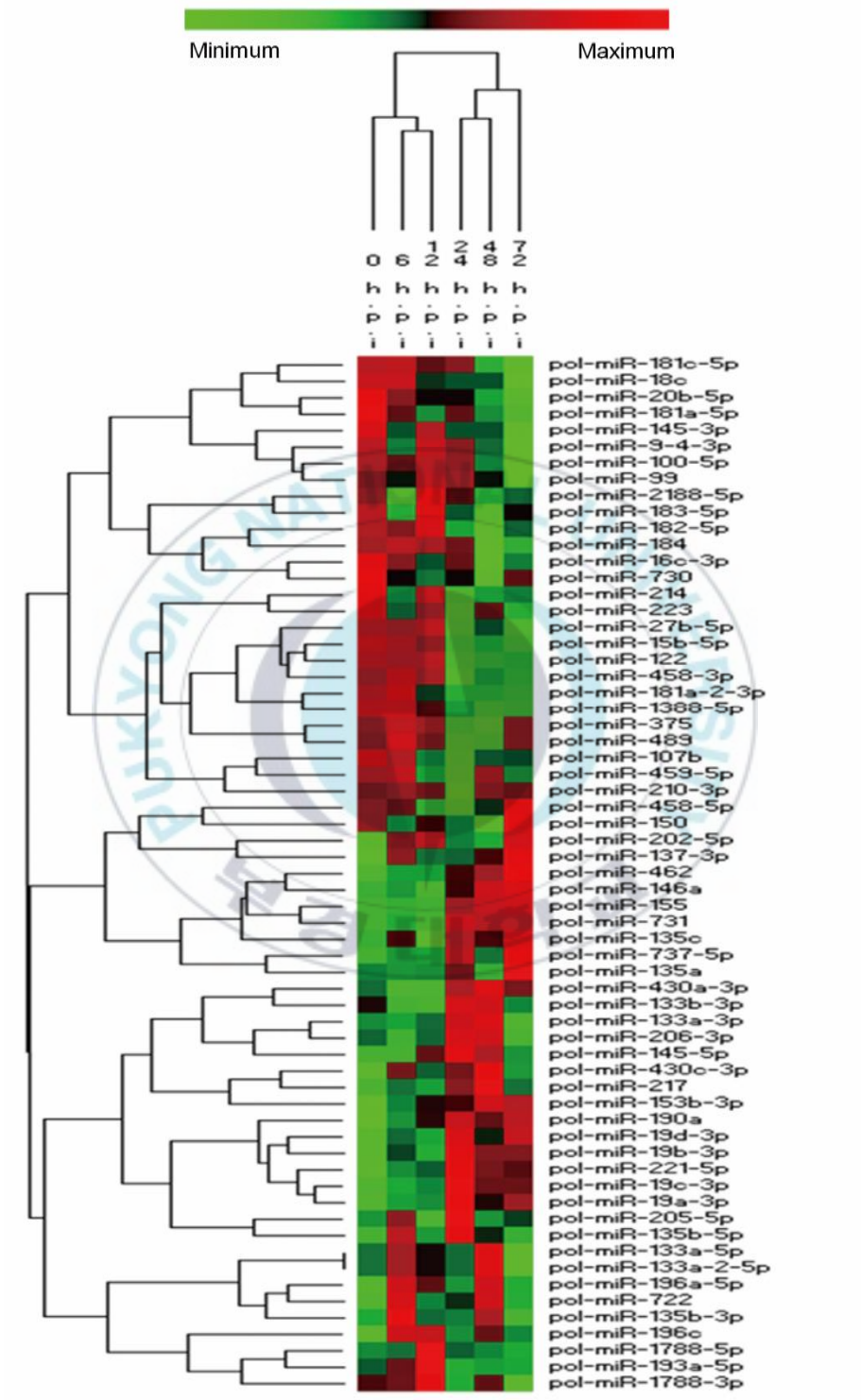
Minimum
Maximum
0 h.p.i
6 h.p.i
12 h.p.i
24 h.p.i
48 h.p.i
72 h.p.i
pol-miR-181c-5p
pol-miR-18c
pol-miR-20b-5p
pol-miR-181a-5p
pol-miR-145-3p
pol-miR-9-4-3p
pol-miR-100-5p
pol-miR-99
pol-miR-2188-5p
pol-miR-183-5p
pol-miR-182-5p
pol-miR-184
pol-miR-16c-3p
pol-miR-730
pol-miR-214
pol-miR-223
pol-miR-27b-5p
pol-miR-15b-5p
pol-miR-122
pol-miR-458-3p
pol-miR-181a-2-3p
pol-miR-1388-5p
pol-miR-375
pol-miR-489
pol-miR-107b
pol-miR-459-5p
pol-miR-210-3p
pol-miR-458-5p
pol-miR-150
pol-miR-202-5p
pol-miR-137-3p
pol-miR-462
pol-miR-146a
pol-miR-155
pol-miR-731
pol-miR-135c
pol-miR-737-5p
pol-miR-135a
pol-miR-430a-3p
pol-miR-133b-3p
pol-miR-133a-3p
pol-miR-206-3p
pol-miR-145-5p
pol-miR-430c-3p
pol-miR-217
pol-miR-153b-3p
pol-miR-190a
pol-miR-19d-3p
pol-miR-19b-3p
pol-miR-221-5p
pol-miR-19c-3p
pol-miR-19a-3p
pol-miR-205-5p
pol-miR-135b-5p
pol-miR-133a-5p
pol-miR-133a-2-5p
pol-miR-196a-5p
pol-miR-722
pol-miR-135b-3p
pol-miR-196c
pol-miR-1788-5p
pol-miR-193a-5p
pol-miR-1788-3p

Figure 4. Cluster analysis of differentially expressed miRNAs in olive flounder after experimental infection with VHSV.The expression level of differentially expressed miRNAs at different time points (0 to 72 h.p.i) is shown in different colors. Each row represents a miRNA. Up-regulated miRNAs are shown with red of increasing intensity, and down-regulated miRNAs are indicated with green of increasing intensity. The clustering was done using PermutMatrix hierarchical clustering software, and the linkage between different miRNAs was done based on McQuitty's method.

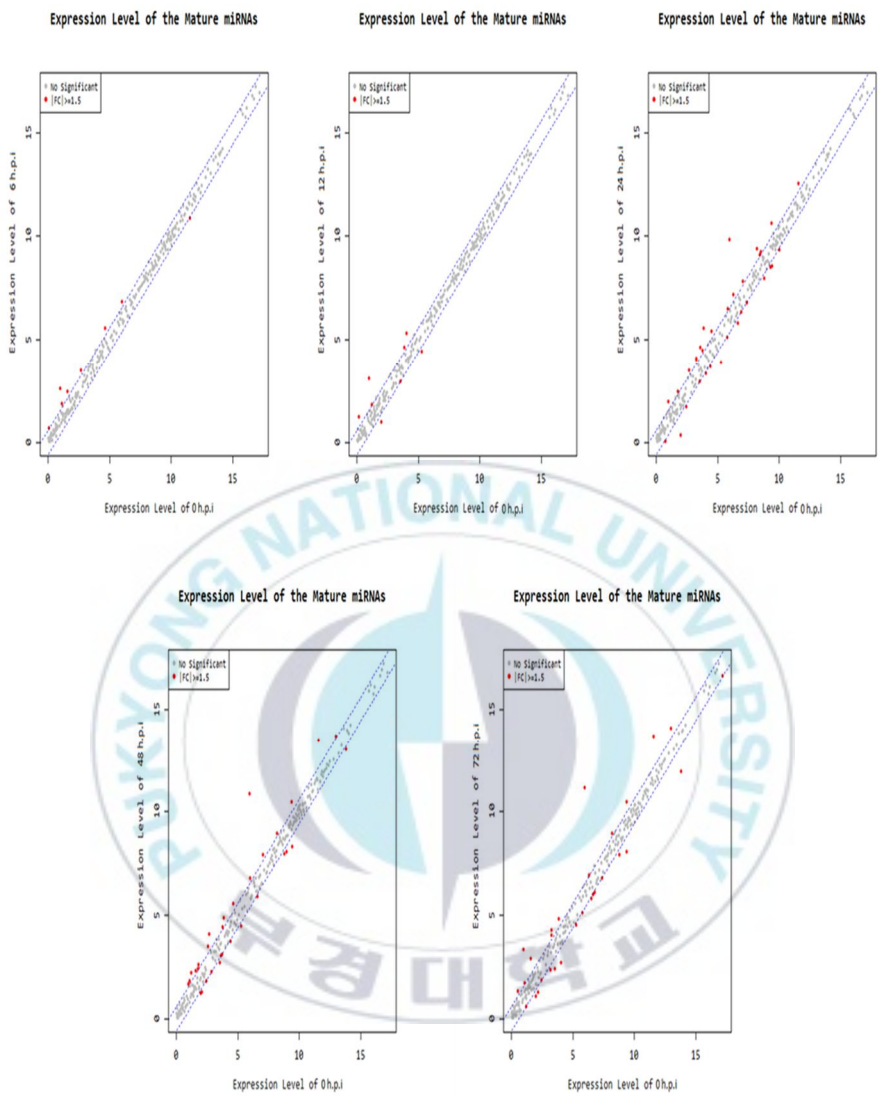

Figure 5. Effect of viral hemorrhagic septicemia virus on miRNA profile of olive flounder

3. qPCR of differentially expressed miRNAs

To validate the differential expression of miRNAs, four miRNAs were selected, and poly (T) RT-PCR was conducted to examine the expression of the chosen miRNAs. The RT-PCR results showed similar results to the results obtained from high throughput sequencing (Fig. 5).

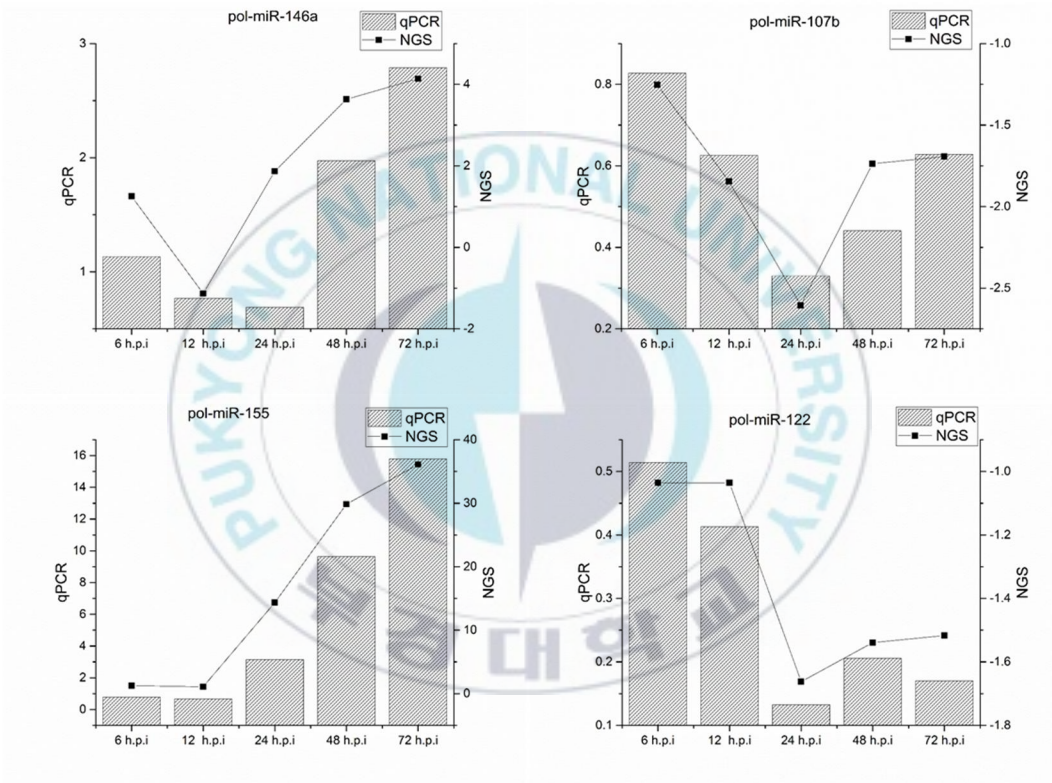

Figure 6. Expression of miRNAs during the viral infection

4. Target prediction and enrichment of differentially expressed miRNAs

The target prediction for the 63 differentially expressed miRNAs showed that there are 1346 putative targets sites in the 314 genes of olive flounder (supplement 3). The target genes of miRNA have a different function, especially the genes related to immunity (supplement 3). Immune-related genes such toll-like receptor 9 (TLR9) targeted by pol-miR-135-5p, toll-like receptor 14 (TLR14) targeted by pol-miR-181a-5p, Macrophage stimulating-1 protein (MST) targeted by pol-miR-107b, pol-miR-122, pol-miR-133a-3p, and pol-miR-133b-3p.

The gene ontology analysis based on biological processes has shown that the 314 predicted target genes of olive flounder could be clustered into 353 GO terms (supplement 4). The top 10 GO terms are regulation of regulation of transcription (DNA-templated), proteolysis, G-protein coupled receptor signaling pathway, immune response, inflammatory response, lipid catabolic process, steroid hormone mediated signaling pathway, oxidation-reduction process, defense response to bacterium, and intracellular signal transduction (Fig. 7).

Furthermore, the KEGG analysis of predicted target genes of olive flounder showed that they were involved in 69 pathways (supplement 5). Among them the top 10 pathways: Ras signaling pathway, Neuroactive ligand-receptor interaction, Cytokine-cytokine receptor interaction, Rap1 signaling pathway, cAMP signaling pathway, PI3K-Akt signaling pathway, NF-kappa B signaling pathway, TNF signaling pathway, HIF-1 signaling pathway, FoxO signaling pathway (Fig. 8).

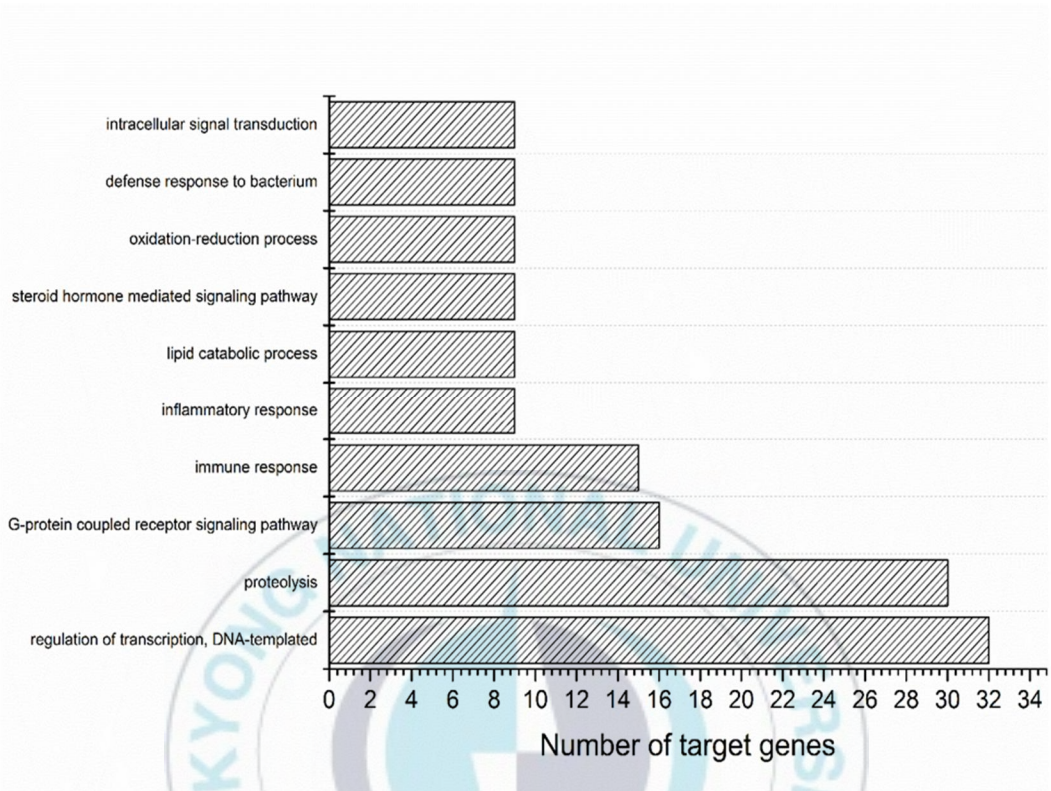

Figure 7. Top ten GO terms of biological process of target genes of olive flounder

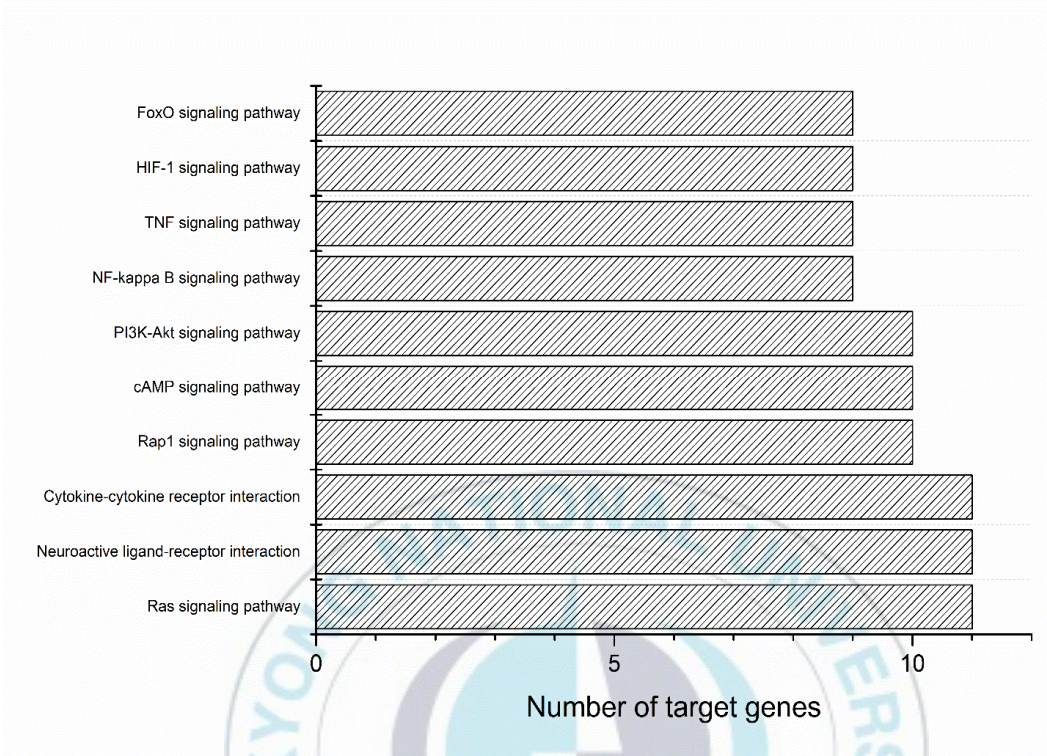

Figure 8. Top 10 abundant KEGG pathways of the target genes from olive flounder

Discussion

Competition between host cells and viruses to regulate cellular miRNAs expression can lead to favorable or detrimental results for host cells. To know the effect of VHSV infection on the cellular miRNA expression profile in olive flounder, fish were infected with VHSV and cellular miRNAs expression at different time points was analyzed by the high-throughput sequencing. A total of 350 mature miRNAs were found, and, among them, 63 miRNAs were differentially expressed during VHSV infection. Compared to the results of Wu et al. (., 2015) in which 14 miRNAs (including one novel miRNA) were differentially expressed in EPC cells by SVCV infection. Five miRNAs (miR-181a-5p, -19b-3p, -722, -214, -20b) with the same sequences and 3 miRNAs (miR-15, -181, -16) with nearly identical sequences were overlapped. This indicates that the cellular miRNAs expressions between olive flounder and EPC cells in response to rhabdoviral infection (SVCV and VHSV) were similar each other. Furthermore, two miRNAs, miR-462 and miR-731, that were up-regulated by VHSV infection in rainbow trout (Schyth et al., 2015), were also up-regulated in this study, suggesting that the cellular miRNAs between rainbow trout and olive flounder might similarly respond to VHSV infection.

The differentially expressed miRNA number was greatly increased from 24 h.p.i. compared to the number at 6 and 12 h.p.i., suggesting that the alteration of miRNAs expression by VHSV infection may be closely related to the increase of the viral titers. Furthermore, many differentially expressed miRNAs were either upregulated or down-regulated from the time point of 24 h.p.i., suggesting that the time around 24 h.p.i. would be a furious phase that can determine the progression of the viral disease.

Based on target prediction analysis, the 63 differentially expressed miRNAs target 314 genes of olive flounder. These genes play various role in different biological processes such as regulation of transcription, proteolysis and immune response which prove that the miRNA have an impact on the different level of host biology. The GO enrichment analysis and the KEGG pathway analysis of predicted target genes of differentially expressed miRNAs provided us with information about the different pathways affected by the viral infection through the downregulation or upregulation of host miRNAs. Among the

analyzed pathways and GO (supplement 4, 5), we find the immune response and the inflammatory response beside the apoptosis pathway which play a crucial role as innate defense against the viral infection (Everett et al., 1999).

Among the differentially expressed miRNAs, the most strikingly increased miRNA during VHSV infection was miR-155 that was up-regulated to 14.4 times at 24 h.p.i. and to 36.1 times at 72 h.p.i. compared to the uninfected fish. The predicted target genes for miR-155 were the complement component C9, the heat shock protein 90 (HSP90)-α and -ß. In mammals, miR-155 is known to have various functions in immune, hematopoiesis, and inflammation processes and Wang et al.(., 2010) reported that the overexpression of miR-155 by vesicular stomatitis virus infection led to a positive regulation of IFN production. The HSP90 acts as a molecular chaperone and is essential not only for host cells to promote correct folding of target proteins but also for the replication of various viruses including vesicular stomatitis virus (VSV) and influenza virus (Connor et al., 2007; Chase et al., 2008). Thus, the present high up-regulation of HSP90-targeting miRNAs can be detrimental or favorable to fish, and further researches are needed to know the role of HSP90 and HSP90-regulated pathways in VHSV replication. In this study, pol-miR-146a was one of the most highly upregulated miRNAs from 24 h.p.i, and the predicted target gene was phospholipase C beta 1. The phospholipase C beta 1 hydrolyze phosphatidyl inositol- bisphosphate (PIP2) into inositol triphosphate (IP3) and diacylglycerol (DAG) that activates protein kinase C (PKC) which plays a crucial role in immune cell signaling (TAN et al., 2003). In human, the miR-146a is known to have various roles in immune and disease processes. The miR-146a targets the IRAK1, TRAF6 genes causing an attenuation of TLR4 signaling in monocytes (Taganov et al., 2006). Also, it down-regulates the inflammatory reaction in lung epithelial cells (Perry et al., 2008). The miR-146a was overexpressed during infection with VSV, which inhibited the immune response through impairing TRAF6, IRAK1, and IRAK2 genes and triggering the down-regulation of IFN production (Hou et al., 2009). Thus, the present increase of pol-miR-146a can be favorable for VHSV replication. Besides these major differentially expressed miRNAs, we observed an upregulation of several miRNAs, such as miR-202 which plays a crucial role in tumor suppression through inhibition of lipoprotein receptor-related

protein 6 expression (Zhang et al., 2014), or miR-221 which is an oncogenic miRNA (Chun-zhi et al., 2010; Rommer et al., 2013; Bae et al., 2015). Furthermore, we observed upregulation of miR-19b, a member of the miR-19 family, additionally to its anti-thrombotic role (Li et al., 2014), the miR-19b inhibit the replication of hepatitis B (Jung et al., 2013).

On the other hand, VHSV infection caused downregulation of multiple miRNAs, including miR-107b and miR-122. In mammals, the miR-122 is abundant in liver and play a crucial role in liver development and differentiation. Furthermore, the miR-122 trigger the IFN type I expression by inhibition of suppressor of cytokine signaling 1 (Li et al., 2013). In case of hepatitis B infection, the virus downregulates the miR-122 to favorite the replication and persistence of virus (Wang et al., 2012). In our study, we observed the downregulation of miR-122 6 hours after infection, but it was significant after 24 hours of infection. The miR-107b, a member of the miR-103 family, play various role in the different type of tumors (Yang et al., 2014; Zhang et al., 2014; Zhang et al., 2015). Additionally, the miR-107b have an inhibitory role in TNF production through downregulation of Cyclin-dependent Kinase 6 (Hennessy et al., 2011).

Additionally, there was downregulation of several miRNAs such miR-100 which is categorized as oncomiR (Varnholt et al., 2008; Chen et al., 2014; Morais et al., 2014). Furthermore, the miR-100 favorite the viral infection of White spot syndrome virus in shrimp through inhibition of trypsin which is a pro-apoptosis protein (Yang et al., 2014). Also, there was downregulation of miR-20b, a member of miR-20 family and a member of oncomiR group (Lei et al., 2009; Cascio et al., 2010; Ahmad et al., 2015), which play an essential role as antiviral against human immunodeficiency virus by targeting cellular histone acetyl transferase, co-factor to Tat-activated transcription, causing an inhibition of viral replication (Triboulet et al., 2007).

This study is the first report about the expression of miRNA of olive flounder challenged with a viral infection. In this study, we reported the dynamic of viral hemorrhagic septicemia infection in vivo using as a model the olive flounder and based on high-throughput sequencing technology; we could determine the variation of miRNA profile through time. Additionally, we could determine new miRNAs for olive flounder.

Chapter II. Viral hemorrhagic septicemia virus (VHSV) infection-mediated sequential changes in miRNAs profile of *Epithelioma papulosum cyprini* (EPC) cells

Introduction

MiRNAs are small non-coding RNA molecules that were discovered first time in *Caenorhabditis elegans* (Lee et al., 1993), and play a critical role in the regulation of lots of genes expression. MiRNAs of animals are usually transcribed from independent genes or introns of other genes and matured through being processed in the nucleus and cytoplasm by Drosha and Dicer, respectively. Mature miRNAs are 20-24 nt in length and inhibit the expression of their target genes through guiding the RNA-induced silencing complex (RISC) to 3′UTR of target mRNAs (Djuranovic et al., 2011). Bioinformatics and next-generation sequencing (NGS) technologies allow us to systemically analyze the complicated role of miRNAs in various biological processes including host-pathogen interactions (Carrington et al., 2003; Ding et al., 2007; Lima et al., 2011). In viral infections, host miRNAs can either inhibit viral replication(Pan et al., 2014; Trobaugh et al., 2014) or be used as a tool to facilitate viral replication (Pedersen et al., 2007; Guo et al., 2013). Therefore, investigation on the host miRNAs profile changes in response to viral infection can help to understand the mechanism of host immune responses, which can provide information needed to develop appropriate control measures against viral infections.

Viral hemorrhagic septicemia virus (VHSV) is notorious for causing mass mortalities in a broad range of cultured fish worldwide (Gomez-Casado et al., 2011), and has been the primary cause of economic loss in olive flounder (Paralichthys olivaceus) culture in Korea (Kim et al., 2009). VHSV is a member of the genus *Novirhabdovirus* in the family Rhabdoviridae. The genome of VHSV is approximately 11 kb that encodes six proteins: nucleoprotein (N), phosphoprotein (P), matrix protein (M), glycoprotein (G), non-virion protein (NV), and RNA-dependent RNA polymerase (L). There are many reports on the role of each protein of VHSV in relation to viral infection and replication and on the development of prophylactic vaccines against VHSV. However, the interaction between the host miRNAs and VHSV infection is poorly investigated. Schyth et al. (2015) (Schyth et al., 2015) reported the up-regulation of two miRNAs (miR-462 and miR-731) in rainbow trout by VHSV infection, and lately, we reported the changes of miRNA profiles in olive flounder by VHSV infection according to time lapse (Abdellaoui et al., 2016).

The study of the interaction between host immune system and the viral infection can lead to a better understanding of viral pathogenesis and a better control of the disease. In the present study, we analyzed the effect of VHSV infection on the miRNAs expression in *Epithelioma papulosum cyprini* (EPC) cells at different time points using the next generation sequencing.

Materials and methods

1. Cell culture and virus

EPC cells were grown on Leibovitz medium (L-15, Sigma) supplemented with 10% of fetal bovine serum (FBS, BI) and 1% penicillin/streptomycin (Gibco). VHSV KJ2008 stock (Kim et al., 2011) was prepared using EPC cells, which were grown at 15°C in L-15 with 2% FBS and the antibiotics. For VHSV infection, approximately 1×10^6 EPC cells were plated on a 35-mm dish and incubated overnight at 28°C. When the confluence of cells was over 80%, the dishes were moved to 20°C and incubated overnight. Cells were infected with VHSV at a multiplicity of infection (MOI) 1 and incubated at 15°C. The cells were collected at 0, 3, 12, 24, and 48 hours post-infection (h.p.i) and stored at -80°C until use.

2. RNA extraction and small RNA library construction and sequencing

The RNA from collected cells at each time point was extracted using Hybrid-RTM miRNA kit (GeneAll, Korea) according to the manufacturer's instructions. The small RNA library construction and sequencing were done using Macrogen (Korea) services. Briefly, analysis of RNA quality and concentration were conducted using Agilent 2100 Bioanalyzer, and small RNA library construction was done using a TruSeq Small RNA Library Prep Kit (Illumina) according to the manufacturer's protocol. The generated libraries were sequenced using the HiSeq 2500 (Illumina).

3. High-through sequencing and data analysis

Quality of generated data was analyzed using FastQC (Babraham Bioinformatics, UK). The raw data were filtered by removing 3' adapter sequence, and low-quality reads was calculated, then the clean reads were mapped to zebrafish genome due to lack of EPC cell genome. To eliminate non-miRNAs, the sequences were mapped to Rfam 9.1 database which includes sequences of rRNA, tRNA, small nuclear RNA (snRNA) and small nucleolar RNA (snoRNA).

Furthermore, the reads were also mapped to VHSV genome. Conserved miRNAs were identified by aligning to zebrafish miRNAs retrieved from miRBase version 210 (http://www.mirbase.org/), and aligned sequences were considered as miRNAs only when they have 100% identical sequence and possess the whole length of miRNA compared to the ones on the miRBase database. The remaining sequences were mapped to other vertebrate miRNAs, and unmatched ones were analyzed using miRdeep2 for prediction of possible novel miRNAs.

4. Analysis of differentially expressed miRNAs

Normalization of data was done using RPM method (read per million) where the raw data were miRNA counts / total counts of each sample x 1 million. MiRNAs with at least one zeroed RPM were excluded. RPM values were log transformed after addition of 1 to their value. Log-transformed data were normalized using quantile normalization method [14]. The fold change was calculated between the control group (0 h.p.i) and the VHSV infected cells (3, 12, 24, 48 h.p.i) with a cut-off of ±1.5. The analysis was done using the R package and the preprocessCore R library.

5. qPCR of differentially expressed miRNA

RNA was reverse-transcribed using miScript II RT Kit (Qiagen) following manufacturer's instructions. Briefly, one µg of RNA was added to 4 µl of 5x miScript HiSpec Buffer, two µl of 10x miScript Nucleics Mix and two µl miScript Reverse Transcriptase Mix. RNase free water was added to get a volume of 20 µl. The mix was incubated at 37 °C for 60 min, then at 95°C for 5 min to inactivate the reverse transcriptase. The cDNA was diluted using RNase free water. Detection of mature miRNAs was done using miScript SYBR Green PCR Kit (Qiagen). QPCR was performed using the mature sequence of miRNA as forward primers with the universal primer from the miScript SYBR Green PCR Kit. The reaction was carried out in Roche Light Cycler 480 (Roche) in a 20 µl reaction volume containing two µl of cDNA, ten µl of 2x QuantiTect SYBR Green PCR Master Mix, two µl of forward primer, two µl of universal primer and four µl of water. The

mixture was incubated at 95°C for 15 min, followed by 45 cycles of 94°C for 15 s, 55°C for 30 s, and 70°C for 30 s. The data analysis was done using the $2^{-\Delta\Delta Ct}$ method. The primers used for the qPCR are listed in Table 1.

6. Target prediction of differentially expressed miRNAs and gene ontology

Target prediction of miRNAs was done using the assembled expressed tag sequences (EST) of fathead minnow retrieved from NCBI database. Briefly, around 200.000 EST sequences were retrieved from NCBI database and assembled using EGassembler (Masoudi-Nejad et al., 2006) into 19.754 contigs and 29.279 singletons. All the contigs were annotated with OrfPredictor (Min et al., 2005) and the 3'UTR sequences were retrieved. The target prediction was performed using the sRNAtoolbox (Rueda et al., 2015) through use of three miRNA target prediction programs for animals (PITA, miRanda, and TargetSpy). The predicted ORF were blasted against the nr database through TRUFA (Kornobis et al., 2015). The GO and KEGG pathways annotations were done using Blast2Go (Conesa et al., 2005).

Table 2- 1 Primers used for qPCR

miRNA	Forward primer 5'-3'	Reverse primer 5'-3'
miR-92a-5p	GGTTGGGATTGGTAGCAATGCT	Qiagen universal primer
miR-738	GCTACGGCCCGCGTCGGGACCTC	-
miR-735-5p	GGCTGGTCCGAAGGCGGT	-
U6	GCTTCGGCAGCACATATACTA	-

Results

1. Identification of miRNAs in EPC cells

After cleaning the raw data, the different libraries generated clean reads between 18,000,000 and 24,000,000. The length distribution of reads showed that the major reads length is located between 20-24 nt (Fig. 9).

Identification of candidate miRNAs was done by blasting the small RNA against zebrafish miRNAs retrieved from the miRBase database (Release 21.0). A total of 350 mature miRNAs were perfectly matched to miRNAs of zebrafish. The remaining miRNA sequences were blasted against the vertebrate miRNAs, which permit to identify five mature miRNAs, and the unmatched sequences were considered as novel miRNAs (Supplement 1).

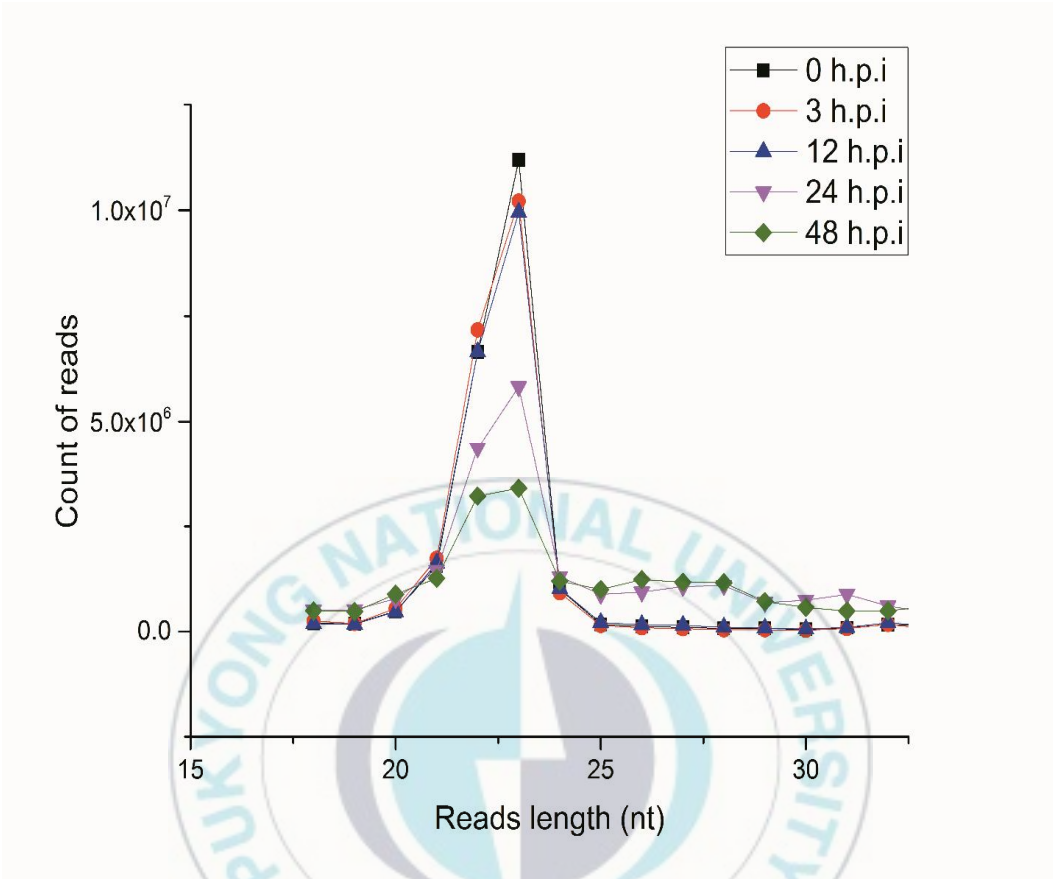

Figure 9. Size distribution of small RNAs after discarding junk reads, trimming the adapter sequence, removing reads <17 or >30 nt, and mapping to Rfam database.

2. Differentially expressed miRNAs

To determine the effect of VHSV infection on the expression of miRNAs, the fold change (F.C) between the control group (0 h.p.i) and the infected groups (3, 12, 24, 48 h.p.i) was calculated with a threshold of F.C≥1.5 (supplement 2).

The viral infection caused alteration of 102 miRNAs. In early hours of infection (3, 12 h.p.i), the number of altered miRNAs was less than 10, then the number of responding miRNAs was steeply increased (Fig. 10). Until 12 h.p.i, the downregulated miRNAs were higher than the upregulated ones. However, after 24 of infection, the number of up-regulated miRNAs was higher than that of down-regulated ones (Fig. 10). The

altered miRNAs were clustered into a heat map to show the temporal change of each miRNA at different points of time after the viral infection (Fig. 11).

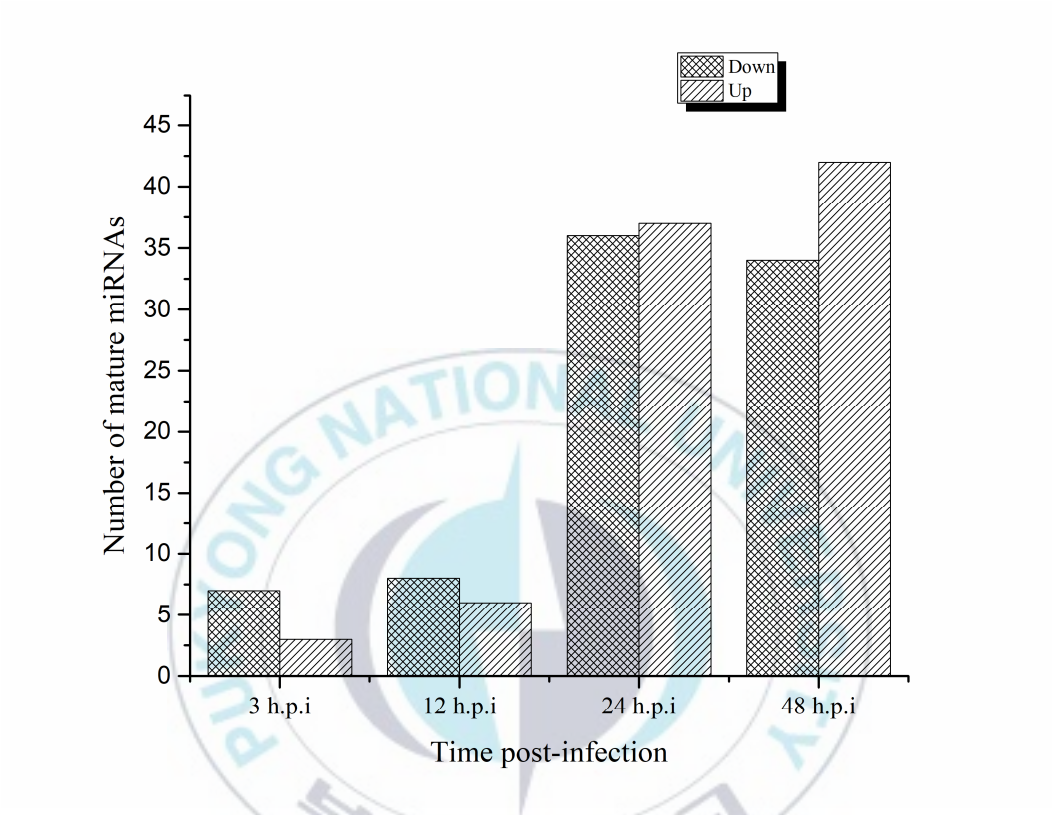

Figure 10. Number of deregulated miRNAs during the viral infection in EPC cell line at different points of time (3, 12, 24, 48 h.p.i) based on their trend (upregulated and downregulated).

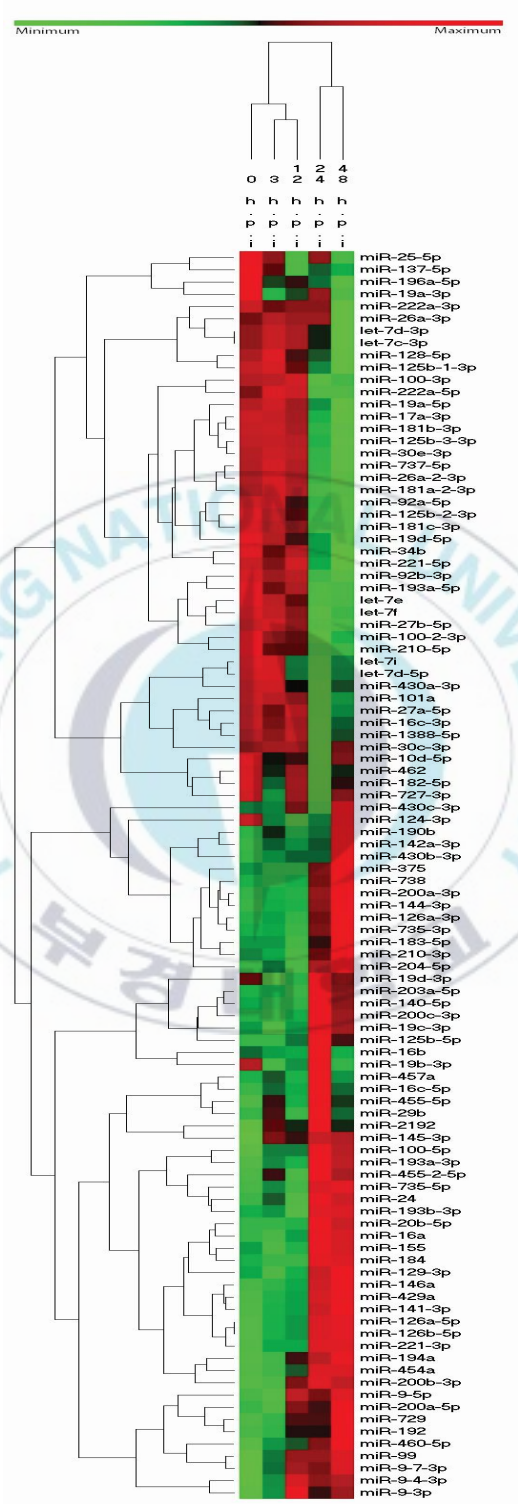

Figure 11. Hierarchical cluster analysis of differentially expressed miRNAs following the chronology of viral infection at different points of time (0 to 48 h.p.i). Each row represents a miRNA. Up-regulated miRNAs are shown with red of increasing intensity, and down-regulated miRNAs are indicated with green of increasing intensity. The clustering was done using PermutMatrix hierarchical clustering software, and the linkage between different miRNAs was done based on McQuitty's method

3. Real-time PCR of differentially expressed miRNAs

To confirm the high throughput sequencing results, three miRNAs were chosen, and a real-time PCR was done to study their expression. The real-time PCR data showed similar patterns to the results from the next generation sequencing data (Fig. 12).

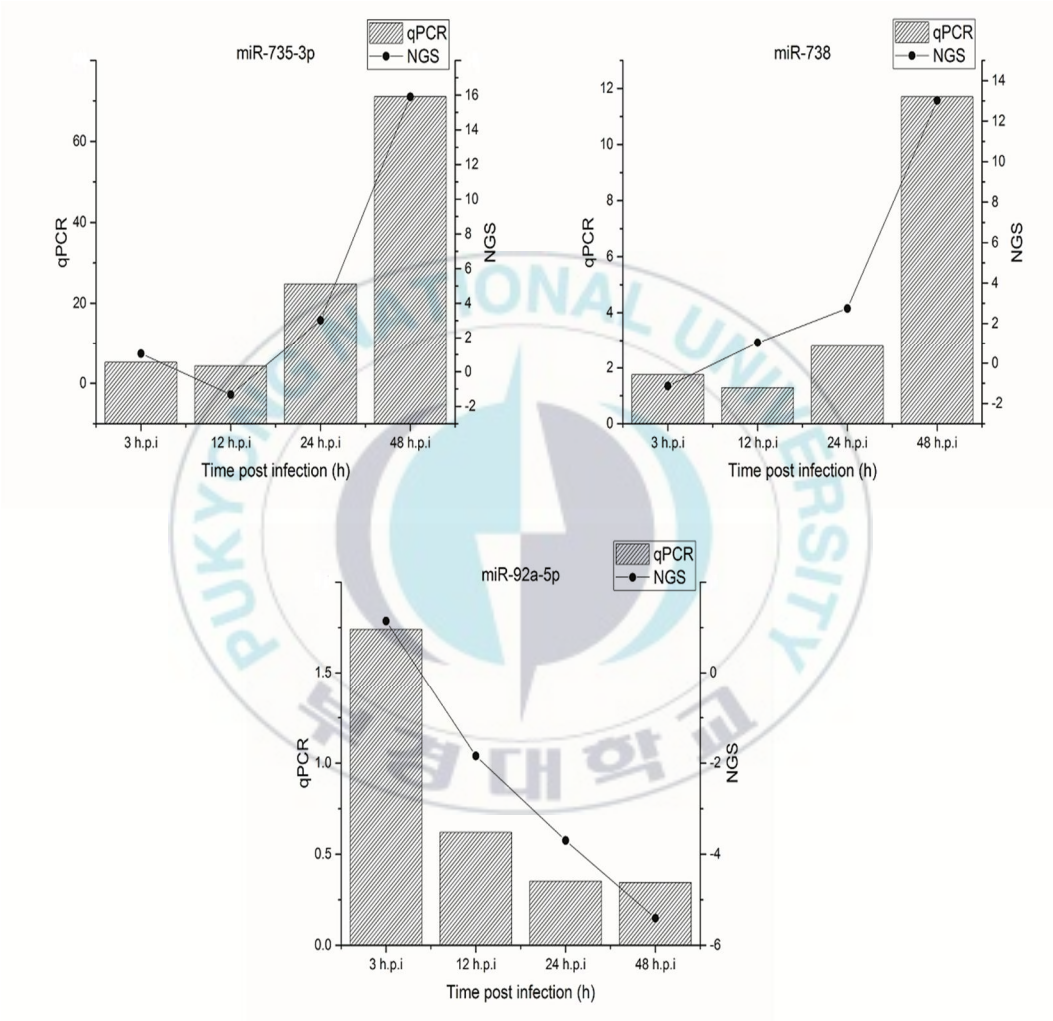

Figure 12. Confirmation of miRNAs expression during the infection based on RT-qPCR.The expression of different miRNAs was measured using the RT-qPCR. The relative expression of miRNA was calculated based on $2^{-\Delta\Delta Ct,}$ and the normalization was done through the use of small nuclear RNA U6.

4. Target prediction and gene ontology of differentially expressed miRNAs

The sRNAtoolbox could predict over 40.000 putative target sites in the 15.000 contigs of fathead minnow. The predicted target genes have a broad range of different functions, especially, including genes related to immune responses such as complement C3, interferon regulatory factor 5, and MHC class II, and Cathepsin S precursor (Supplement 3).

The gene ontology analysis of predicted target genes based on biological process showed that the 15.000 target genes were clustered into 27 GO terms of level 2 (Fig. 13), and there were around 356 genes related to the immune system process. The KEGG pathway analysis grouped the predicted target genes into 20 pathways (Fig. 14).

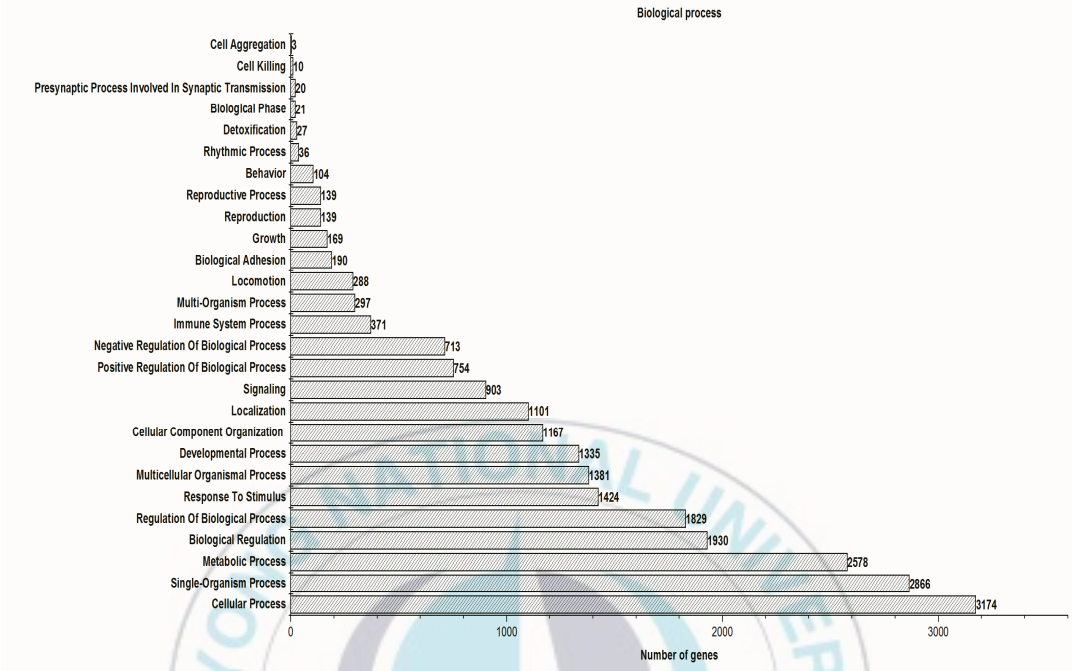

Figure 13. Gene ontology terms of target genes of differentially expressed miRNAs. The target genes of deregulated miRNAs were blasted, annotated using the Blast2GO software with default parameters.

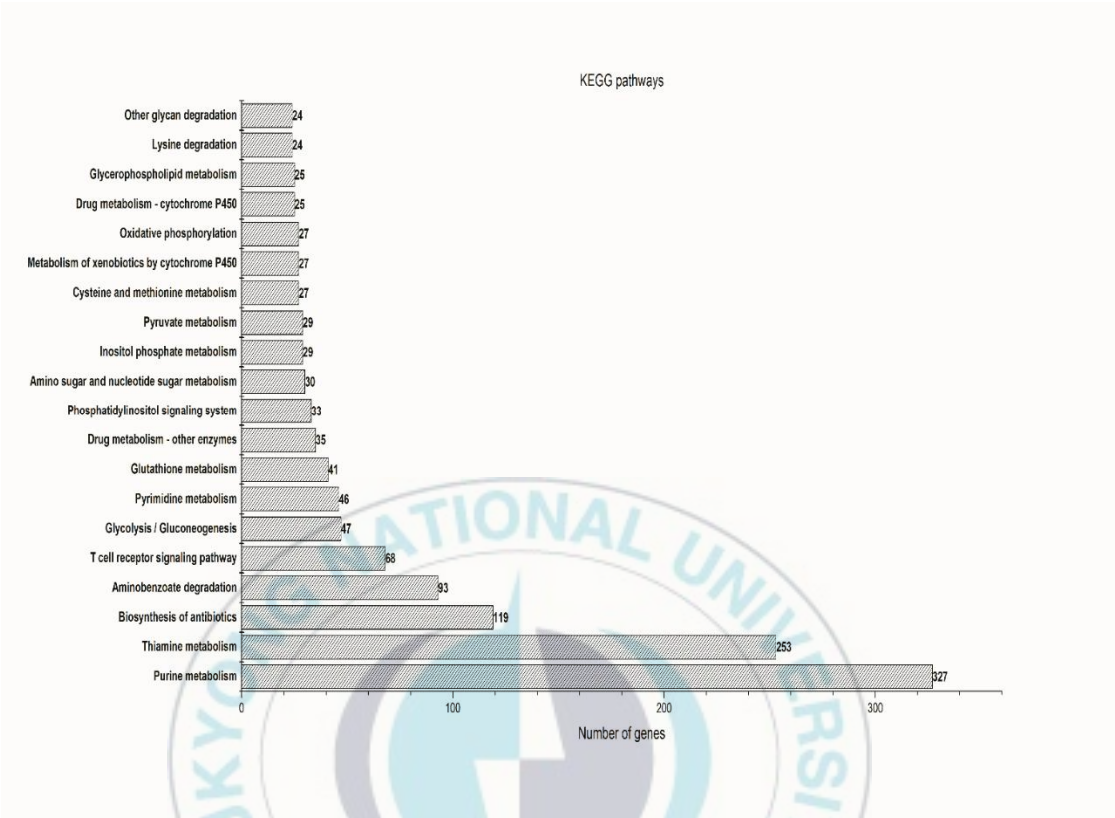

Figure 14. KEGG pathways of target genes of deregulated miRNAs in EPC cell line during the viral infection with VHSV. The KEGG pathways analysis was done using the KEGG Automatic Annotation Server.

Discussion

The chronological analysis of miRNAs expression in EPC cells infected with VHSV showed that the number of differentially expressed miRNAs was highly increased at 24 h.p.i compared to 3 h.p.i and 12 h.p.i. This miRNA expression pattern in response to VHSV infection was similar to the pattern from our previous in vivo experiment with olive flounder (Abdellaoui et al., 2016), suggesting that EPC cells, as well as olive flounder, might not actively respond to VHSV infection at an early infection period, which can allow viruses to transcribe and translate their genes enough to produce viral particles that can infect to another cell.

Recently, Wu et al. (., 2015) reported the effect of spring viremia of carp virus (SVCV) infection on miRNAs expression in EPC cells, in which ten conserved and four novel miRNAs were differentially expressed in EPC cells at 36 h.p.i. with SVCV. Among the ten conserved miRNAs, the change of miR-124, miR-16a, and miR-19c expressions by virus infection was similar to those of the present study. Considering the vital role of miR-16-1 in viral infection (Wang et al., 2013), and miR-19 in the regulation of the inflammation during viral infection through the modulation of RING finger protein 11 (Ashraf et al., 2016) This similarity suggests the possible common involvement of these miRNAs in rhabdoviral infections in fish. The differences in the number of differentially expressed miRNAs between Wu et al. (., 2015) and the present study might be caused by differences in viral species, viral virulence and/or viral infection intensity (MOI 0.1 in Wu et al. (., 2015) and MOI 1 in this study).

The let-7 family of miRNAs is functionally conserved across different phyla and has a relation with cell proliferation and differentiation (Johnson et al., 2007). In fish, let-7 miRNA was downregulated during the bacterial infection in tilapia (Schulte et al., 2011; Wang et al., 2016). Similarly, let-7 miRNAs were downregulated by VHSV infection in this study, suggesting that let-7 miRNAs might have an identical function to viral and to bacterial infections. Among downregulated miRNAs by VHSV infection, there is the miR-125 known to be involved in the regulation of host immune defense(Potenza et al., 2011; Rajaram et al., 2011; Willimott et al., 2012). MiR-125 targets several immune genes, such as C-C chemokine receptor type 9-like, CD209 antigen, and immunoglobulin light chain.

Furthermore, in mammals, miR-125 targets the IFN regulatory factor 4 (IRF4), and the increase of miR-125 elevates the responsiveness of macrophages to IFN-γ which leads to upregulate macrophages activity (Chaudhuri et al., 2011). Thus, in this study, VHSV infection could cause a downregulation of miR-125 to potentiate the viral replication.

Among upregulated miRNAs by VHSV infection, miR-735-3p, miR-735-5p, and miR-738 were the most highly increased miRNAs with 15, 6, and 13 folds changes, respectively. MiR-738 has been identified only in fish species and was detected in the commune immune organ such the spleen of common carp (Wang a et al., 2010; Li et al., 2014). The miR-735 was also found only in fish species until now, and based on the present target prediction, it could regulate several immune genes (Supplement 3) as well as ubiquitin-conjugating enzyme E2 D3 that is involved in different immune processes such as the toll-like receptor 3 (TLR3) signaling pathway and the MyD88-independent TLR signaling pathway. Furthermore, the present results showed upregulation of representative immune regulating miRNAs such as miR-146a, miR-155, and miR-99. The role of miR-146a has been extensively studied, and its different functions are well characterized. MiR-146a plays a key regulator in immune responses through modulation of the TLRs and cytokine signaling (Liu et al., 2010; Schulte et al., 2013). It has been reported that the viral infection could cause an overexpression of miR-146a which lead to negative feedback of the interferon response pathway (Cameron et al., 2008; Hou et al., 2009). Like previous studies, miR-146a was upregulated following the progression of VHSV infection in this study. Based on target prediction, miR-146a targets several immune genes which involved in different process such as inflammatory response, complement activation, positive regulation of type I interferon production through regulation of catenin beta-1 and complement C3 (Supplement 3). Besides miR-146a, there was upregulation of miR-155 during VHSV infection. As known, miR-155 has several roles in inflammatory response and host immunity. The overexpression of miR-155 has a positive feedback on regulation of TLR3/TLR4 signaling pathways (Li et al., 2013). Furthermore, miR-155 is crucial in the activation and development of lymphocytes B and T through modulation of T-cell-receptor and B-cell-receptor (Rodriguez et al., 2007). Also, miR-155 has several targets, among which there was the C-C chemokine receptor type 9-like (Supplement 3) that is

involved in a neutrophil activation process and several pathways, such as cytokine-cytokine receptor interaction and chemokine signaling. Besides these two miRNAs, there was upregulation of miR-99 known to be an oncogene miRNA (Li et al., 2011). It was reported that miR-99 enhanced the replication of hepatitis B virus through the modulation of the phosphoinositide 3-kinase/Akt/mTOR signaling pathway (Lin et al., 2015). In our study, the miR-99 has two target genes: kinase C alpha type and complement factor B. The kinase C alpha type is involved in several processes including positive regulation of macrophage differentiation, innate immune responses, and response to interleukin-1. The complement factor B modulates biological processes such as responses to bacterium and complement activation. Thus, upregulation of miR-99 by VHSV infection might be favorite for the viral proliferation.

In conclusion, our results showed the change of miRNAs profile in EPC cells according to the time lapse of VHSV infection. Considering the broad and complex interactions between miRNAs and genes expression, the present results would give a basis for the further understanding on the pathogenesis of VHSV and the development of new control measures against VHSV infection.

Chapter III. Effect of miR-146a on VHSV replication

Introduction

MiRNAs are a class of small non-coding RNA with a length ranging from 18-24 nt. The first miRNA was discovered in *Caenorhabditis elegans*, lin-4, which represses the expression of lin-14 gene through binding to its 3' UTR sequence. Later, findings of small RNA with similar function were discovered in several species. Until today, the miRNA registry counts more than 30,000 mature miRNAs in over 200 species. The discovery of miRNA has opened the door to a new class of small RNA besides miRNA such piwi-interacting RNA, small interfering RNA and other categories of small RNA.

The miRNA interacts with mRNA mainly through binding, through which, they can control the expression of the protein by inhibition of translation or degrading the mRNA. Furthermore, based on this binding and bioinformatics analysis, a single miRNA can regulate expression of hundreds of genes, and similarly, several miRNAs can regulate a single gene.

The miRNAs are involved in different physiological and pathologic processes. The miR-126 have shown to regulate Homeobox genes which are involved in the regulation of hematopoietic stem cells (Shen et al., 2008). Also, miR-181 was proven to be involved in natural killer cells development through enhancing Notch signaling (Cichocki et al., 2011). Furthermore, the miR-150 stimulates differentiation of megakaryocyte-erythrocyte progenitor into megakaryocyte by downregulation of MYB (Lu et al., 2008). In addition to their physiological role, the miRNAs can be double-edged swords in pathological processes. Following infection, the miRNA can enhance immunity by upregulating immune genes cells involved into immunity such as miR-155 which enhance IFN type I response through binding to suppressor of cytokine signaling 1 resulting in the degradation of mRNA of the latter (Wang et al., 2010). Also, the miR-32 downregulates viral replication of retrovirus primate foamy virus type1 through binding to its 3' untranslated region (UTR) (Lecellier et al., 2005).

On the other hand, miRNAs can create a favorable environment for viral replication by inhibiting host defense. The miR-122 enhances replication of hepatitis C virus through binding to the 5'UTR of the virus (Jopling et al., 2005). Furthermore, miR-132 downregulates p300 transcriptional co activator that will favorize replication of

Kaposi's sarcoma-associated herpesvirus (Lagos et al., 2010). In fish, miRNAs have various roles such as in mammals. However, few reports focused on the role of miRNA in fish. Following viral infection by Megalocytivirus, the miR-731 is upregulated which inhibits type I interferon and apoptosis (Zhang et al., 2016). MiR-146a is indicated to negatively regulate immune response during infection in mammals (Hou et al., 2009; Wu et al., 2013). Furthermore, miR-146a can cause a suppression of immune response of T cells through targeting STAT1 that leads to downregulation of IFN-α signaling pathway (Wang et al., 2013). In fish, miR-146a was observed to be upregulated during bacterial infection by *Salmonella typhimurium* in zebrafish (Ordas et al., 2013). However, miR-146a function during viral infection is still unclear as we observed an upregulation of miR-146a following viral infection by VHSV in-vitro and in-vivo studies.

VHSV is a notorious virus causing a deadly disease and high mortality in aquaculture (Marianne et al., 2006; Kim et al., 2009). The VHSV is a negative single-stranded RNA virus that contains six genes coding for different proteins and belonging to genus *Novirhabdovirus* (King et al., 2012). In recent years, VHSV became a broad virus touching different species and different environments which required control action and preventive measurements such as vaccination. Most studies have focused on developing vaccines based on different molecular techniques. Yet, the molecular mechanism underlying the viral pathogenicity and its interaction with the host cells still blurred and required thorough investigation to understand these mechanisms.

Lately, through the use of next-generation technology and miRNA transcriptome analysis, we investigated the effect of VHSV infection on miRNAs expression in-vivo and in-vitro, and we could find that several miRNAs were differentially regulated following VHSV infection (Abdellaoui et al., 2016; Abdellaoui et al., 2017). Among them, there was upregulation of miR-146a after the viral infection. Still, the mechanism of action of this miRNA during viral infection and its impact on the host and viral pathogenesis of VHSV is still indefinite.

The purpose of this study was to elucidate the role of miR-146a during viral infection by VHSV, giving the significance of this miR-146a in mammalian immunity system.

Materials and methods

1. Cell culture and virus

Epithelioma papulosum cyprini (EPC) cells were grown in Leibovitz's L-15 medium (Sigma Aldrich) supplemented with 10 % of fetal bovine serum (Gibco) and 1 % of penicillin/streptomycin (Gibco). VHSV KJ2008 stock was prepared using EPC cells.

2. miRNA and plasmid construction

2.1. Precursor miRNA prediction

Based on our previous study (Abdellaoui et al., 2017), fathead minnow miR-146a sequence was 100 % identical to zebrafish miR-146a. So, the precursor mir-146a was predicted through blasting the zebrafish mir-146a against fathead minnow whole genome shotgun deposited under genebank accession number JNCD00000000, and we extracted 85 nt from the genome with a high match to zebrafish precursor. The retrieved sequences were analyzed using mFold (Zuker, 2003) with default parameters to predict secondary structure. Furthermore, the predicted hairpin structure was submitted to iMiRNA-SSF (Chen et al., 2016) which classifies pre-miRNA hairpin sequences as real or pseudo-pre-miRNA.

2.2. Prediction of miR-146a target

The TRAF6 gene was retrieved based on fathead minnow shotgun genome assembly and transcriptome shotgun assembly. First, TRAF6 of related species to fathead minnow such zebrafish, common carp were retrieved and blasted against transcriptome. The highest match was retrieved and blasted against protein database of NCBI and UniProt database. Using similar approaches, the 3'UTR of TRAF6 was retrieved, and the target prediction of miR-146a was done using miRanda, Targetscan and PITA prediction tools (Kertesz et al., 2007; Betel et al., 2010).

2.3. Construction of plasmid expressing pri-mir-146a and TRAF6-3'UTR

The plasmid expressing miR-146a was constructed using pcDNA 3.1(+) (Thermo Fisher Scientific). First, genomic DNA was extracted from EPC cells using Exgene cell SV (Geneall) following manufacturer's instructions. The primary pri-mir-146a was PCR amplified using primers ppr-mir-146a-NheI-F and ppr-mir-146a-NotI-R which generated a fragment of 222 bp that was run on an agarose gel (0.9%) and visualized using Ultraview (KoreaLabTech). The amplified fragment was purified using Expin Gel SV (Geneall), subcloned into pGEM-T easy vector (Promega) and several clones were sequenced. After confirmation of sequence, the T-vector was digested with corresponding enzymes, and ligated into pcDNA3.1 (+). The constructed plasmid was designated as pc-pri-mir-146a.

Also, the 3'UTR of TRAF6 was cloned in the same way. First, *Metridia* luciferase gene was first amplified from pNFkb-MetLuc2-reporter vector (Clontech) using Metluc-NheI-F and Metluc-BamHI-R primers, visualized on agarose and purified using Expin Gel SV kit. The purified fragment was cloned into pGEM-T easy vector, and several clones were sequenced. The confirmed clone was digested and subcloned into pcDNA3.1(+) vector and designated as pc-Metluc. Then, 3'UTR of TRAF6 was cloned from genomic DNA of EPC cells using primers TRAF6-3UTR-BamHI-F and TRAF6-3UTR-ApaI-R. The amplified fragment was inserted into pGEM-T easy and subcloned into pc-Metluc vector through ligation using the respective enzymes, and the ligated vector was nominated as pc-Metluc-TRAF6-3UTR.

MiR-146a binding site on TRAF6-3UTR was predicted using, as previously stated, miRanda and PITA. The binding site was mutated on seed region to abolish interaction of miR-146a with it. Mutation of binding site was done using site-directed mutagenesis technique and a pair of primers (TRAF6-3UTR-SDM-F and TRAF6-3UTR-SDM-R). The generated plasmid was designated as pc-Metluc-TRAF6-3UTR-SDM.

3. Construction of sponge miRNA for miR-146a

Sponge miRNA are RNA molecules bearing complementary binding sites concerning a specific miRNA to be studied through loss of function. Usually, sponge miRNA construct contains around four to 10 binding sites, transcribed by a strong

promoter such as CMV promoter and are linked to a reporter gene such as EGFP or luciferase gene.

Sponge miRNA against miR-146a was designed as perfectly complementary to miRNA or with a bulged between 9-12 nt of miRNA. We generated six binding sites for each type of sponge (perfect or bulged) using Macrogen service, and they were inserted into pUC19 flanked with two enzymes sites (BamHI, XbaI). Using enzyme digestion, the sponges were inserted into the pc-Meluc vector using the respective enzyme, and they were labeled as pc-Metluc-146a-sp and pc-Metluc-146a-sb.

4. Transfection of cells and generation of stable cells expressing miR-146a, sponge miRNA, TRAF6-3UTR, and TRAF6-3UTR-SDM

EPC cells were seeded into T-25 flasks and incubated at 28 °C in L-15 medium supplemented with 10 % of FBS and 1 % of penicillin/streptomycin. When confluency reached 80-90%, cells were transfected using Neon system following manufacturer's instructions. Briefly, cells were trypsinized, centrifuged, and counted using trypan blue. For transfection, we used $3x10^6$ cells and washed them with PBS (without Ca2+ and Mg2+) by centrifugation for 5 min at 3000 rpm and resuspended the cells using buffer R. After that; we added plasmid expressing sponge miRNA or expressing miR-146a to cells and electroplated them with optimized pulse conditions. Then, we plated transfected cells onto 35-mm dishes. The cells were incubated at 28 °C overnight. After two days, selection of cells harboring the vector stared by adding G-418 (400 μg/ml, Sigma) antibiotic to culture medium and it was done for one month.

After one-month, stable cells expressing miR-146a or sponge miRNA were generated, and stocks were made and stored at -150 °C for future use. Similarly, cells expressing TRAF6-3UTR or TRAF6-3UTR-SDM were made and keep it at -150 °C until use.

5. Knockout of TRAF6 in EPC cells using clustered regularly interspaced short palindromic repeats (CRISPR) RNA-guided Cas9 nucleases technique

5.1. Construction of vector expressing Cas9 and gRNA

First, we constructed a Cas9 expressing vector with selection marker geneticin (G418). Briefly, vector CAS740G-1(System Biosciences, Korea) was mutated using a pair of primers (Kan-SDM-NotI-F and Kan-SDM-NotI-R) to insert restriction enzyme site NotI. After confirmation of mutation by sequencing, kanamycin resistance cassette was cloned from the pFC-MCS-pA-SV40-Neo vector (System Biosciences, Korea) and inserted into the mutated vector using NotI and NdeI enzymes. Generated vector was sequenced and designated as pCAS9-Kan.

Guide RNA (gRNA) targeting TRAF6 gene was designed using CHOPCHOP web tool (Montague et al., 2014). First, the sequence of TRAF6 gene was submitted to the tool, then gRNA with non-off-target effect was selected.

The gRNA was generated using overlap- PCR. First, gRNA was generated using primers TRAF6-gRNA-F1 and gRNA-HDV-ApaI-R, and plasmid KHV-TKgRNA-Cas9 was used as template. Then a second PCR was done using PCR product and a pair of specific primers (TRAF6-gRNA-F2 and gRNA-HDV-ApaI-R). Finally, using a pair of primers TRAF6-gRNA-NheI and gRNA-HDV-ApaI-R, gRNA and gRNA scaffold were generated, cloned into pGEM-T vector and sequenced for confirmation. After enzyme digestion with NheI and ApaI, gRNA and gRNA scaffold were inserted into pc-DNA 3.1(+) vector and confirmed by sequencing. The fragment harboring CMV promoter, gRNA, gRNA scaffold, and bovine growth hormone polyadenylation signal was amplified using a pair of primers (pc-CMV-AgeI-F and BgH-pA-EcoRI-R), cloned into pGEM-T vector and sequenced for confirmation. After digestion of vector with AgeI and EcoRI enzymes, the fragment was inserted into pCAS9-Kan vector, confirmation was done using sequencing, and the constructed plasmid was designated as pCAS9-TRAF6.

5.2. Generation of TRAF6 knockout cells (ΔTRAF6)

EPC cells were seeded into 35 mm dish and incubated at 28℃ in L-15 medium supplemented with 10 % FBS and 1 % of penicillin/streptomycin. Next day, the medium was changed to transfection medium supplemented with 10% of FBS and 20 mM HEPES and cells were transfected with pCAS9-TRAF6 plasmid (1ug) using Fugene HD (Roche) according to manufacturer's instructions. Two days later, cells were transferred to a T25 flask, and the selection was done using culture medium containing G418 (400 μg/ml).

6. Luciferase assay

Cells expressing luciferase or sponge miRNA were plated on six-well at a density of $3x10^6$ and incubated at 28 °C. Luciferase expression was evaluated using Ready-To-Glow Secreted Luciferase Assay (clontech) following manufacturer's instructions. Briefly, 50 ul of the medium was added to 96 well white plate and added 0.5 ul of the substrate and 4.5 ul of buffer. We measured luciferase expression using Victor 3 (PerkinElmer) following constructor's directions.

7. RNA extraction and qPCR

RNA extraction was done using Hybrid-R RNA purification kit (Geneall, Korea) following constructer's instruction. Briefly, cells were lysed in 1 ml of Riboex and 200 μl of chloroform, then incubated at RT for 2 min. The mixture was centrifuged at 13.000 rpm for 15 min at 4°C and then transferred the aqueous phase to e-tube. Using column, the aqueous phase was passed through after mixing with RB1 and then washed using SW1 and RNW. The RNA was eluted, and genomic DNA was removed using geneall Riboclear kit (Geneall, Korea).

One μg of RNA was reverse transcribed using Hyperscript RT-PCR (Geneall, Korea). The mixture was incubated at 55 °C for 60 min, then further incubated at 95 °C for 5 min. The complementary DNA (cDNA) was diluted using DNase and RNase free water and stored at -20 ° C until use.

qPCR was performed using Roche lightcycler 480. Briefly, two µl of cDNA was added to a mixture containing 10 ul of 2xSYBR green, one µl of specific primers (5pmol), and six µl of DNase and RNase free water. PCR conditions were as follows: initial denaturation was done at 95 °C for 15 min, followed by 40 cycles of denaturation at 95 °C for 10 s, annealing at 60 °C for 10 s and then elongation at 72 °C for 20 s. Data analysis was done using $2^{-\Delta\Delta CT}$.

For small RNA, RNA extraction was done using Hybrid-R™ miRNA (geneall) following constructer's instructions. Then miRNAs were reverse transcribed and quantified using HB miR Multi Assay Kit TM system II (HeimBiotek, Korea). Briefly, synthesis of cDNA was done using a specific RT primer to the desired miR. After assembling the different components, RT-PCR was done in a thermal cycler with an initial step of 37 °C for one h followed by incubation at 95 °C for 5 min and finally held at 4 °C. The final product was stored at -20 °C until use.

Two µl of cDNA was used during real-time PCR which was performed in Roche Light Cycler 480 (Roche). Amplification was done as follow: initial activation at 95 °C for 15 min, followed by 40 cycles of denaturation at 95 °C for 10 s and annealing-extension step at 60 °C for 40 s. Small nucleolar U6 was used as reference gene. The results were analyzed using $2^{-\Delta\Delta Ct}$.

8. Plaque assay

EPC cells harboring pc-pri-mir-146, pc-luc vector, pc-Metluc-146a-sp and pc-Metluc-146a-sb were seeded in 35 mm dish (10^6 cells/dish) and incubated at 28 °C with 2 ml of L-15 medium containing 10 % FBS and antibiotics (penicillin-streptomycin). Next day, cells were incubated at 20 °C overnight. Twenty-four hours later, cells were infected with wild-type VHSV at an MOI of 0.01. The cells were incubated at 14 °C, and the supernatant was harvested at 12, 24, 4, and 72 hours post-infection. The titer of virus was determined using plaque assay.

First, EPC cells were inoculated with each supernatant that was serially diluted from 10^{-1} to 10^{-5}. After inoculation, cells were incubated at 14°C for one h; then cells were overlapped with plaquing medium composed of 0.8% agarose in L-15 medium

supplemented with 2 % FBS and antibiotics. After seven days, the layer of gel was removed, the dish washed, cells fixed with 10 % of formalin and then stained with 3 % of crystal violet for 30 min at RT. The dish was washed with distilled water, and the plaque-forming units (PFU) were counted.

Table 3- 1 Oligonucleotides used for construction of different plasmids

Primers	Sequence (5'-3')
ppr-mir-146a-NheI-F	GCTAGCACCATTTTAGTACACTTGATGGGCAAC
ppr-mir-146a-NotI-R	GCGGCCGCTGTTTTCTTGGTGTATTTTTAATACTTTTGTTGT
Metluc-NheI-F	GCTAGCGCCACCATGGACATCAAGGTGGTGTTCACC
Metluc-BamHI-R	GGATCCTCACCTGTCGCCGGCCATGC
TRAF6-3UTR-BamHI-F	GGATCCAGTTCCTACATCGCTCCTGCAT
TRAF6-3UTR-ApaI-R	GGGCCCTCGATACTCGATTCTCGATACCCAACC
TRAF6-3UTR-SDM-F	CGCTCCTGCATTCTCAAG**GGA**TCAATGACACTCTGCTG
TRAF6-3UTR-SDM-R	CAGCAGAGTGTCATTGA**TCC**CTTGAGAATGCAGGAGCG
Kan-SDM-NotI-F	CGTTGTCGGGAAGATGCG**GCCG**CTGATCCTTCAACTCAGC
Kan-SDM-NotI-R	GCTGAGTTGAAGGATCAG**CGGC**CGCATCTTCCCGACAACG
PFC-Kan-NotI-F	GCGGCCGCCGCGGAACCCCTATTTGTTTATTTTTC
PFC-Kan-NdeI-R	CATATGGAACAAACGACCCAACACCGTG
TRAF6-gRNA-F1	TGAGTGTCCTATCTGTCTAAGTTTTAGAGCTAGAAATAGCAAGTT
TRAF6-gRNA-F2	GACGAAACGAGTAAGCTCGTCTGAGTGTCCTATCTGTCTAAGTTT
gRNA-TRAF6-NheI-F	GCTAGCCACTCACTGATGAGTCCGTGAGG
gRNA-HDV-ApaI-R	GGGCCCGTCCCATTCGCCATGCCGAA
pc-cmv-AgeI-F	ACCGGTGACATTGATTATTGACTAGTTATTA
BgH-pA-EcoRI-R	GAATTCCCATAGAGCCCACCGCATCC

Restriction enzymes are underlined, and mutation sites are bolded.

Table 3- 2 Primers used for real-time RT-PCR

Primers	Sequences (5'-3')
EPC-BA-real-time-F	AAGGAGAAGCTCTGCTATGTGGCT
EPC-BA-real-time-R	AAGGTGGTCTCATGGATACCGCAA
EPC-ISG15-realtime-291F	TGATGCAAATGAGACCGTAGAT
EPC-ISG15-realtime-391R	CAGTTGTCTGCCGTTGTAAATC
EPC-MX-qPCR-F	TGGAGGAACCTGCCTTAAATA
EPC-MX-qPCR-R	GTCTTTGCTGTTGTCAGAAGATTAG

Results

1. Prediction of primary miRNA 146 a (pri-mir-146a)

The blast of mature zebrafish miR-146a against the genome of fathead minnow gave two hits with 100 % homology to zebrafish miR-146a. The blast results were aligned with miR-146a of other fish, and they showed a high conservation among fish (Fig.15). Then, the secondary structure of precursor mir-146a was predicted using mFold software (Fig.16).

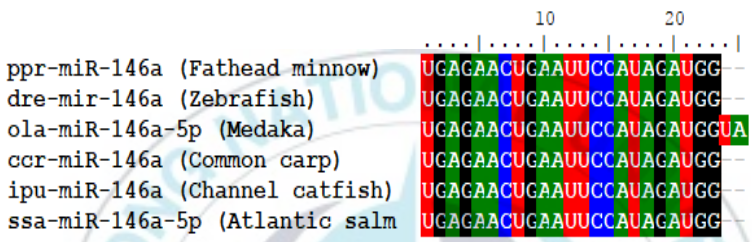

Figure 15. Conservation of miR-146a among different species of fish.

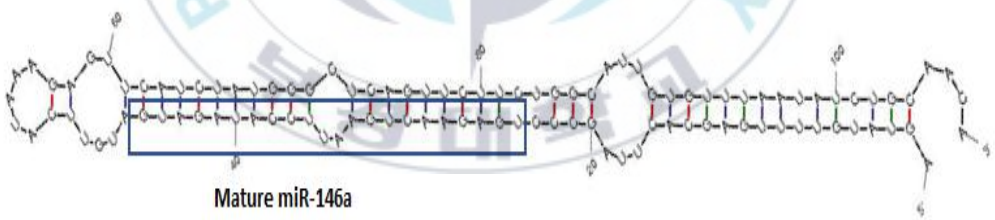

Figure 16. Predicted secondary structure of precursor mir-146a (mFold). Mature miR-146a is highlighted with blue box.

2. Construction of plasmid pc-pri-mir-146a

Plasmid-harboring primary mir-146a was constructed (Fig.17). The EPC cells transfected with the plasmid showed over 14 folds of overexpression at 72 hours-post transfection and around six folds 92 hours-post-transfection compared to control group (Fig.18).

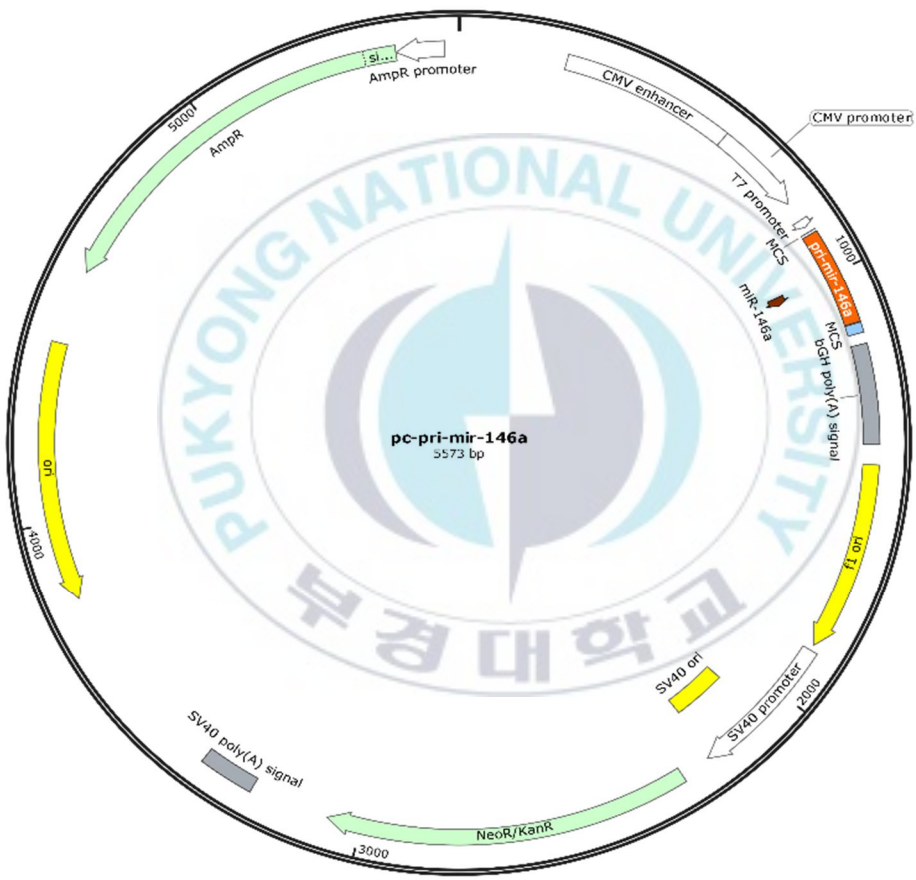

Figure 17. Map of plasmid pc-pri-mir-146a, primary mir-14a is expressed by constitutive promoter CMV.

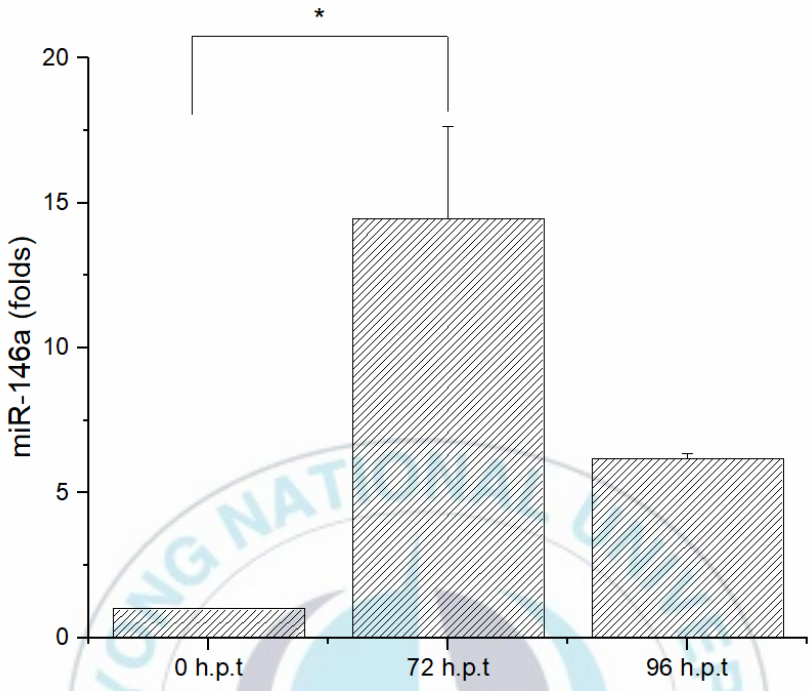

Figure 18. Quantification of miR-146a in *Epithelioma papulosum cyprini* (EPC) cells using real-time RT-PCR. Relative expression of miR-146a in EPC cells transfected with the plasmid expressing miR-146a was compared to mock control cells using Ct method. Fold changes (means ± SD based on triplicate assay) were represented in histograms. The U6 gene was used as internal control. Significant differences from the control group were analyzed using Student's t-test. The asterisk represents a significant difference at $P<0.05$.

3. Validation of sponge miRNA efficiency

EPC cells were transfected with pc-Metluc, pc-Metluc-146a-sb, pc-Metluc-146a-sp and selected with G418 for one month. The cells were infected with VHSV at different MOI, and miR-146a expression was analyzed based on luciferase expression. As results, cells expressing perfect sponge miRNA against miR-146a showed a statically significant decrease of luciferase activity compared to cells expressing luciferase or bulged sponge

against miR-146a (Fig.19). Furthermore, independently of MOI, we observed the same pattern of decrease for cells harboring perfect sponge miRNA.

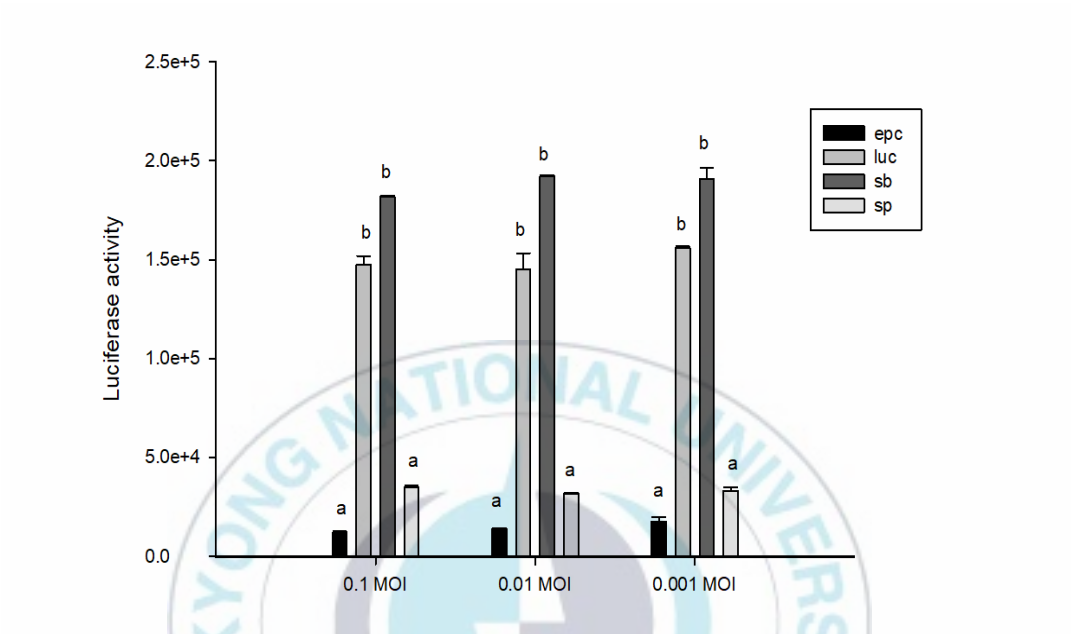

Figure 19. Analysis of luciferase expression in *Epithelioma papulosum cyprini* (EPC) cells harboring luciferase expressing vector (luc) or harboring perfect sponge miRNA (sp) expressing vector or harboring vector expressing bulged sponge miRNA (sb).Cells were infected with wild-type VHSV at different MOI (0.1,0.01, and 0.001) and luciferase activity was analyzed 24 hours post-infection. Different letters on the bars indicate significantly different at $P<0.05$.

4. Effect of sponge miRNA targeting miR-146a and miR-146a expressing vector on replication of VHSV

To investigate the role of miR-146a in viral infection with VHSV, we infected EPC cells expressing luciferase, cells expressing perfect or bulged miRNA against miR-146a, and cells harboring vector expressing miR-146a with VHSV at MOI of 0.01. Cells transfected with the vector expressing perfect sponge miR-146a had the lowest virus titer compared to control group at 72 h.p.i (Fig. 20). Furthermore, cells harboring vector

expressing miR-146a showed the highest virus titer compared to control group at 48, and 72 h.p.i. On the other hand, cells expressing bulged sponge miRNA did not have any effect on viral titer compared to control group.

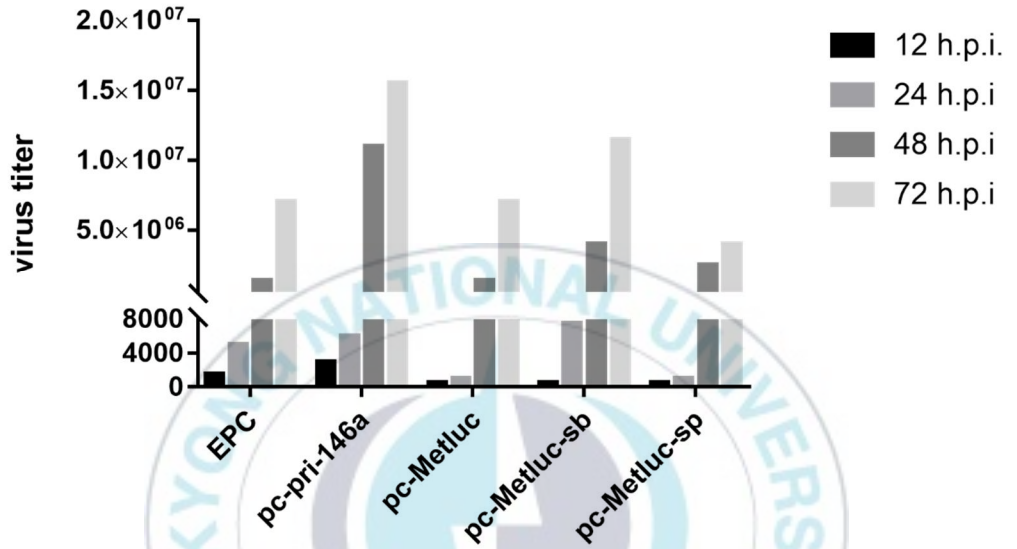

Figure 20. Virus titer of each group was measured using plaque assay.Cells were infected with wild-type VHSV at an MOI of 0.01 for 12, 24, 48, and 72 hours. The viral titers were measured using plaque assay.

5. MiR-146a regulate TRAF6 expression in EPC cells

Using miRanda, PITA and Targetscan tools, we found a binding site in the 3'UTR of TRAF6 (Fig.21).

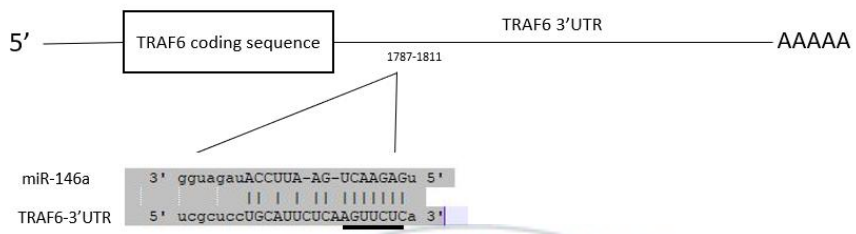

Figure 21. Schematic of the binding site of miR-146a in the TRAF6-3'UTR. Complementarities between miR-146a and target site are shown, and the seed sequence is underlined.

To validate interaction between miR-146a and putative binding site, we cloned the full length of TRAF6 3'UTR into pc-Metluc and mutated the binding site. EPC cells harboring TRAF6-3'UTR and TRAF6-3'UTR-SDM vectors were seeded into 24 wells at a concentration of 10^5 in L-15 medium containing 10 % FBS, 1% of antibiotics (penicillin-streptomycin) and incubated at 28 °C overnight. Next day, cells were transfected with mimics of miR-146a at different concentrations (25 nM, 50 nM, and 100 nM) and negative control mimics (NCM) with a final concentration of 100 nM. Luciferase activity was measured at 24 and 48 hours-post transfection (h.p.t) using Ready-To-Glow Secreted Luciferase Assay (Clontech).

Transfection of miR-146a mimics reduced luciferase activities at 24 and 48 hours in EPC cells harboring TRAF6-3'UTR vector, while transfection of negative control mimics did not alter luciferase activity (Fig.22 A). These results, indicate that miR-146a bind directly to target site in 3'UTR of TRAF6.

Furthermore, to investigate if the binding site is solely responsible for the targeting, we mutated seed region in the binding site. Introduction of mutation in 3'UTR of TRAF6

impaired the effect of miR-146a and transfection of mimics did not show any reduction of luciferase activities compared to control group (Fig. 22 B).

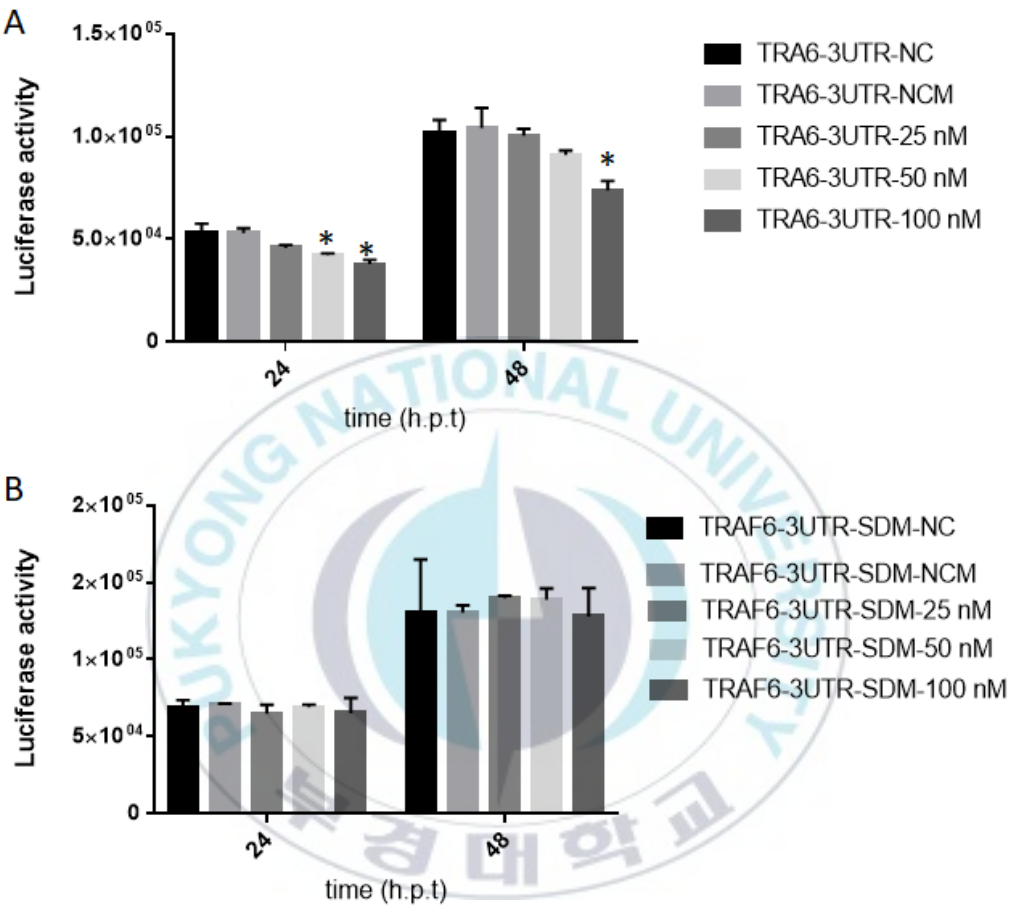

Figure 22. Luciferase activities in EPC cells harboring TRAF6-3'UTR vector or TRAF6-3'UTR-SDM vector. A. cells expressing TRAF6-3'UTR were transfected with negative control mimics (NCM) at a final concentration of 100 mM or with miR-146a mimics at a final concentration of 25, 50, and 100 nM. Luciferase activities were measured 24 hours and 48 hours-post-transfection (h.p.t). B. cells expressing TRAF6-3'UTR-SDM were transfected with negative control mimics (NCM) at a final concentration of 100 mM or with miR-146a mimics at a final concentration of 25, 50, and 100 nM. Luciferase activities were measured 24 hours and 48 hours-post-transfection (h.p.t). Data are shown as mean ± SD. Asterisk indicates significant difference at $p<0.05$.

6. TRAF6 regulates type I interferon response pathway

6.1. Knockout of TRAF6 in EPC cells

To further study the target gene of miR-146a, TRAF6 was knocked-out using CRISPR technology. EPC cells were transfected with pCAS9-TRAF6 using Fugene HD following manufacturer's instruction, and the selection was done using G418. Knockout of TRAF6 was confirmed using sequencing. Briefly, genomic DNA was extracted, and PCR amplified using specific pair of primers (TRAF6-F and TRAF6-R). Then PCR product was cloned into the pGEM-T vector and submitted to sequencing. The Cas9 system caused indels of several nucleotides or insertion of one nucleotide (Fig.23).

Figure 23. Alignment of exon 1 of TRAF6 from wild-type EPC cells with sequences of TRAF6 from ΔTRAF6-EPC cells. Guide RNA (sgRNA) indicate the target site in exon 1 of TRAF6. Sequencing results of wt-TRAF6 and ΔTRAF6 using universal primers (M13F-pUC and M13R-pUC) show mutation around the site of cleavage by the Cas9 system.

6.2. Effect of knockout of TRAF6 on type I interferon response

ISG-15 expression was significantly downregulated at 0 h.p.t in ΔTRAF6-EPC cells compared to wild-type EPC cells. After poly: IC treatment, the ISG-15 level was significantly increased in wild-type EPC cells compared with ΔTRAF6-EPC cells at six h.p.t (Fig. 24 A). Furthermore, transcription of MX1 was significantly downregulated in ΔTRAF6-EPC cells compared to wild-type EPC cells at 0 h.p.t. On the other hand, poly: IC stimulation caused a significant up-regulation of MX1 gene expression in wild-type EPC cells compared to ΔTRAF6-EPC cells at 6 and 12 h.p.t (Fig. 10 B).

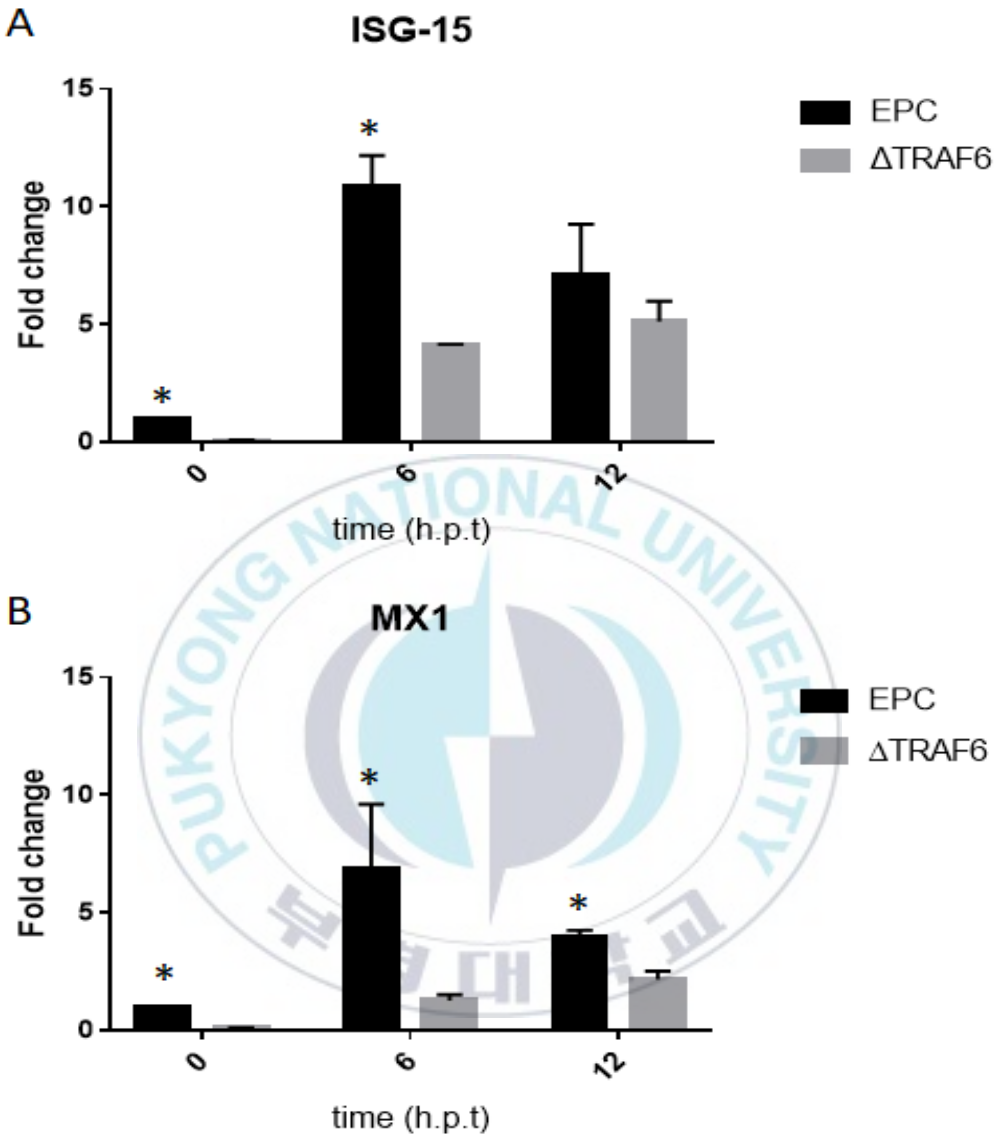

Figure 24. Real-time RT-PCR of ISG-15 and MX1 mRNA in EPC cells and ΔTRAF6-EPC.A. Relative mRNA expressions of ISG-15 gene was assessed in wild-type EPC cells and ΔTRAF6-EPC cells before and after stimulation with poly: IC at 0, 6, and 12 hours-post treatment (h.p.t). B. Relative mRNA expression of MX1 gene was assessed in wild-type EPC cells and ΔTRAF6-EPC cells before and after stimulation with poly: IC for 6 and 12 hours. Beta-actin gene was used as internal control and data is shown as mean ±SD.

Discussion

MiRNAs are post-transcription regulators that play essential roles in different physiological or pathological processes (Bartel, 2004). MiRNAs also have an important function in controlling immune system either by enhancing immunity against viral infection (Wen et al., 2013) or by having a negative effect on host immunity which boosts viral replication (Ashraf et al., 2016). Several studies have shown the upregulation of miR-146a upon viral infection (Cameron et al., 2008; Punj et al., 2010) that indicated an essential role in viral infection.

Furthermore, our previous study (Abdellaoui et al., 2017) have shown an upregulation of miR-146a expression after infection of EPC cells with VHSV. In this present study, we could prove that miR-146a helped in the establishment of favorable environment for viral replication. The viral infection with VHSV at a different MOI (0.1, 0.01, 0.001) caused a significant decrease of luciferase activity in cells transfected with perfect sponge miRNAs compared to the mock group. These results could be explained by sequestration of miR-146a through binding to sponge miRNA which led to reduced luciferase activity. Furthermore, overexpressing miR-146a in EPC cells have enhanced virus replication compared to control group. Finally, the viral replication was impaired in the presence of sponge miRNA against miR-146a. Based on that, the miR-146a could help viral replication. It has been reported that miR-146a plays a proviral role following infection with vesicular stomatitis virus (Hou et al., 2009) and following infection with dengue virus (Wu et al., 2013).

Until now, several miRNAs were investigated for their role in positively (proviral) or negatively influencing viral replication. For example, miR-122 in hepatitis chronic virus (HCV) infection has shown to play a proviral role by binding to 5'UTR of HCV RNA genome which enhances viral replication (Jopling et al., 2008). On the other hand, miR-155 has been shown to have an antiviral role against vesicular stomatitis virus by promoting type I IFN response (Wang et al., 2010). The double role of miRNA (proviral and antiviral roles) can be explained by the complexity of interaction between host's immunity and pathogens. The host's immunity produces miRNAs to defend against

pathogens. However, viruses have established several mechanisms to take advantage of miRNAs to enhance their replication.

MiR-146a has been well studied in mammals, and several target genes were discovered including TNF receptor-associated factor 6 (TRAF6), IL-1 receptor-associated kinase (IRK1), signal transducer and activator of transcription 1 (STAT1) (Taganov et al., 2006; Tang et al., 2009). In this study, using several target prediction tools, we predicted the binding site of miR-146a in 3'UTR of fathead minnow TRAF6. Furthermore, we generated cells lines harboring a vector that express luciferase protein linked to 3'UTR of fathead minnow TRAF6, and we could demonstrate that overexpression of miR-146a downregulated luciferase activity in a concentration-dependent manner. To confirm the authenticity of targeting site, we mutated binding site and generated cells lines expressing mutated 3'UTR of fathead minnow TRAF6 linked to the luciferase gene. The reporter assay did not show any significant difference between mock cells transfected with negative control mimics and cells transfected with mimics of miR-146a. These results indicate a direct interaction between miR-146a and fathead minnow TRAF6 gene. Interestingly, recent studies have shown the role of miR-146a in regulating host immunity by targeting TRAF6 such as infection with dengue virus or following infection with vesicular stomatitis virus (Hou et al., 2009; Wu et al., 2013). However, until now the role of miR-146a in viral infection in fish is still unknown except one report that showed the role of miR-146a on inhibition of NF-κb activation following Singapore grouper iridovirus infection but without identifying the target gene (Ni et al., 2017).

To investigate the role of fathead minnow TRAF6 on activation of type I interferon response, we knocked-out TRAF6 gene in *Epithelium Papulosum Cyprini* cells (EPC) using Crisp-cas9 technology. Before stimulation of EPC cells and ΔTRAF6-EPC cells with poly: IC, we observed a reduced expression of interferon-stimulated gene 15 (ISG-15) and MX1 genes in ΔTRAF6-EPC cells compared to EPC cells. Furthermore, there was a significant difference in expression of ISG-15 and MX1 genes after stimulation with poly: IC for 6 and 12 hours between cells lacking TRAF6 gene and normal EPC cells. The low expression of MX1 and ISG-15 genes in ΔTRAF6-EPC cells could be explained by lack of TRAF6 which have been identified as a major regulator of NF-κb activation (Dickson

et al., 2004). The knockout of TRAF6 in EPC cells caused a downregulation of type I interferon response. However, it is didn't impaired the MX1 and ISG-15 genes expression which could be explained by activation of type I interferon response through a different pathway.

In conclusion, we demonstrated that miR-146a is a proviral following infection with VHSV and it exerts this role by targeting fathead minnow TRAF6 in EPC cells. Furthermore, we clarified the upregulation of miR-146a upon infection with VHSV and investigated the mechanism behind it.

Chapter IV. miR-155 and its role on type I interferon response

Introduction

Viral hemorrhagic viremia (VHS) is a severe disease causing high mortality in fish farms, particularly in flat fish (Kim et al., 2009). The disease is worldwide spread and touches several species of fish and has substantial adverse effects on the fish production. The causative agent of VHS is a member of the *Novirhabdovirus* genus which belongs to the rhabdovirus family. VHSV is a negative sense single-stranded RNA virus with a size of 11 kb and contains six open reading frames which code for proteins (Lenoir et al., 1975). Regarding the order, the proteins are a nucleocapsid protein (N), phosphoprotein (P), matrix protein (M), glycoprotein (G), non-virion protein (NV), and RNA polymerase (L) (King et al., 2012).

Lately, a new group of small RNAs, called miRNAs (miRNAs) are getting much attention due to their crucial role in modulation of immunity and their response during viral infection (Ponomarev et al., 2013). Several miRNAs have been discovered to be involved in virus-host interactions such miR-146a which can create a favorable environment for virus replication through inhibition of TNFR-associated factor 6 (TRAF6) involved in type I interferon response (Wu et al., 2013). Also, miR-373 inhibit IFNα production by directly targeting Janus kinase 1 (JAK1) and IFN-regulating factor 9 (IRF9) which are involved in IFN signaling pathway (Mukherjee et al., 2015). On the other hand, several miRNAs can alter viral replication or block virus infection by targeting host's genes or inhibiting viral genes translation. The miR-32 downregulated viral translation by targeting genes of retrovirus primate foamy virus type 1 (Lecellier et al., 2005). Likewise, miR-23b inhibits viral replication of Enterovirus 71 through binding to the 3'UTR of viral protein 1(Wen et al., 2013).

As far as fish is concerned, miRNAs studies are still scarce and there are few types of research that target miRNAs and their function in fish immunity (Abdellaoui et al., 2016; Zhang et al., 2016; Abdellaoui et al., 2017). Among the well-studied miRNAs in mammals in relation with immunity, there is miR-155 that plays a crucial role during differentiation of $CD4^+$ T cells (O'Connell et al., 2010), and control $CD8^+$ T cells during viral or bacterial infections (Lind et al., 2013). It has a critical role in the production of antibodies and differentiation of B cells (Rodriguez et al., 2007; Vigorito et al., 2007).

Furthermore, the miR-155 has an antiviral role by inhibiting suppressor of cytokine signaling 1(SOCS1) during vesicular stomatitis virus infection (Wang et al., 2010). Also, the miR-155 has been used as immunostimulant against influenza A virus by incorporating its primary miRNA into the genome of influenza A virus (Izzard et al., 2017).

In our previous studies (Abdellaoui et al., 2016; Abdellaoui et al., 2017), we observed an upregulation of miR-155 expression during VHVS infection in olive flounder and EPC cells. Based on this observation, we studied the function of miR-155 and its possible role as antiviral during VHSV infection.

Materials and methods

1. Cells culture

Epithelioma papulosum cyprini (EPC) cells were grown in Leibovitz's L-15 medium (Sigma Aldrich) supplemented with 10 % of fetal bovine serum (Gibco) and 1 % of penicillin/streptomycin (Gibco).

2. MiRNA expression and plasmid construction

2.1. Prediction of miRNA precursor

The fathead minnow miR-155 is 100% similar to zebrafish miR-155 (Abdellaoui et al., 2017). The precursor of miR-155 was retrieved by blasting mature miR-155 against fathead minnow genome deposited in NCBI database. The retrieved sequence was analyzed using mFold with default parameters to predict secondary structure. Furthermore, the predicted hairpin structure was submitted to iMiRNA-SSF which classifies pre-miRNA hairpin sequences as real or pseudo-pre-miRNA.

2.2. Cloning and construction of plasmid expressing miR-155

Overexpression of miR-155 was done through cloning the precursor sequence plus flanking regions (around 200nt) into pGEM-T easy using specific primers pri-mir-155-500-NheI-F and pri-mir-155-500-NotI-R flanked with restriction sites. Then, the mir-155 was subcloned into pcDNA 3.1(+) downstream of CMV promoter by using double digestion with NotI and NheI enzymes to generate pc-mir-155. The construct was confirmed by sequencing. In the same way, the zebrafish pri-mir-155 was cloned into pc-DNA 3.1(+) vector using same restriction enzymes, and the generated vector was designated as pc-dre-mir-155.

2.3. Construction of plasmid expressing miR-155 based on flanking regions of zebrafish mir-30e

Flanking regions of mir-155 were replaced with flanking regions of mir-30e from zebrafish. First, genomic DNA of EPC cells was extracted using Exgene cell SV (Geneall) following manufacturer's instructions. The precursor of miR-155 was amplified using specific primers (mir-30e-1-mir-155-C-F and mir-155-mir-30e-2-C-R). Then PCR product was gel purified using Expin Gel SV kit (Geneall, Korea) following manufacturer's instructions. The flanking regions of mir-30e from zebrafish were amplified in the same way. First, the 5'flanking region was amplified using specific pair of primers (mir-30e-1-C-F and mir-30e-1-mir-155-C-R) and the 3'flanking region was amplified using primers (mir-155-mir-30e-2-C-F and mir-30e-2-C-R). Then PCR products were gel purified.

Overlapping PCR was done using 5'flanking region, 3'flanking region, the precursor of mir-155, and a pair of primers (mir-30e-1-C-F and mir-30e-2-C-R). The amplification included a denaturation step at 95 °C for 3 min, followed by 30 cycles of 30 s at 95 °C, 30 s at 60 °C, 30 s at 72 °C, with a final extension at 72 °C for 7 min. The pFC vector (System Bioscience, Korea) was amplified using a pair of primers (PFC-C-F and PFC-C-R) and then gel purified. Finally, pFC vector, flanking regions, and precursor mir-155 were assembled using Overlap Cloner DNA kit (Elpisbio, Korea) following manufacturer's instructions. Briefly, 100 ng of linearized vector was added to 50 ng of different inserts, then we added reaction buffer and enzyme mix and incubated at 37 °C for 30 min. Finally, the reaction was transformed using *E. coli*. The constructed vector was sequenced and designated as pFC-mir-30e-mir-155.

2.4. Transfection of EPC cells and generation of stable cells expressing miR-155

EPC cells were seeded into T-25 flasks and incubated at 28 °C in L-15 medium supplemented with 10 % of FBS and 1 % of penicillin/streptomycin. When confluency reached 80-90%, cells were transfected using Neon system following manufacturer's instructions. Briefly, cells were trypsinized, centrifuged, and counted using trypan blue. In a 35-mm culture dish, we added 2 ml of transfection medium which contains only 10 % of FBS in the L-15 medium. For transfection, we used $3x10^6$ cells and washed them with PBS

(without Ca2+ and Mg2+) by centrifugation for 5 min at 3000 rpm. The cells were resuspended using buffer R. After that; we added plasmid expressing miR-155 to the cells and electroplated the mixture with optimized pulse conditions, and then transfected cells were plated onto 35-mm dish. Cells were incubated at 28 ℃ overnight. Next day we changed the medium to culture medium and then started selection using G-418 (400 μg/ml, Sigma) antibiotic for one month.

3. In-vivo experiment

Olive flounder fingerlings weighing 8 g were randomly divided into three groups and reared in three tanks (10 fish/tank) at 20 °C. Fish were injected with PBS, empty vector (pc-DNA) or with the vector expressing mir-155 (pc-dre-mir-155) at a concentration of 10 μg/ fish/ 50μl. The injection of fish was done through the intramuscular site. Forty-hours post-injection, five fish, were randomly sampled for collection of liver, spleen, and kidney.

4. RNA extraction and real-time RT-PCR

RNA extraction was done using Hybrid-R RNA purification kit (Geneall, Korea) following constructer's instructions. Briefly, cells were lysed in 1 ml of Riboex and 200 μl of chloroform; then the mixture was incubated at RT for 2 min. The mixture was centrifuged at 13.000 rpm for 15 min at 4°C and then transferred the aqueous phase to e-tube. Using column, the aqueous phase was passed through after mixing with RB1 and then washed using SW1 and RNW. The RNA was eluted, and genomic DNA was removed using geneall Riboclear kit.

One μg was reverse transcribed using Hyperscript RT-PCR premix kit (Geneall, Korea). The mixture was incubated at 55 °C for 60 min, then further incubated at 95 °C for 5 min. The cDNA was diluted using DNase and RNase free water and stored at -20 °C until use.

qPCR was performed using Roche lightcycler 480. Briefly, two μl of cDNA was added to a mixture containing 10 ul of 2xSYBR green and one μl of specific primers (5pmol) and six μl of DNase and RNase free water. PCR conditions were as follows: initial

denaturation was done at 95 °C for 15 min, followed by 40 cycles of denaturation at 95 °C for 10 s, annealing at 60 °C for 10 s and then elongation at 72 °C for 20 s. Data analysis was done using $2^{-\Delta\Delta CT}$.

For small RNA, RNA extraction was done using miRNeasy Mini Kit (Qiagen) following constructer's instructions. Briefly, 1 ml of Qiazol and 200 µl of chloroform were added to cells pellet, followed by centrifugation at 13.000 rpm, 4 °C for 15 min. Then, 300 µl of the aqueous phase was transferred to a new tube, RNA was precipitated with 450 µl of 100% ethanol and loaded on miRNeasy purification columns. An additional step was added to remove genomic DNA by using DNase digest in the column. Purified RNA was eluted from the column with 30 µl of RNase free water.

Then MiRNAs were reverse transcribed and quantified using HB miR Multi Assay Kit TM system II (HeimBiotek, Korea). Briefly, synthesis of complementary DNA (cDNA) is done using a specific RT primer to the desired miR. After assembling the different components, RT-PCR was done in the thermal cycler with an initial step of 37 °C for 1 h followed by incubation at 95 °C for 5 min and finally held at 4 °C. The final product was stored at -20°C until use.

Two µl of cDNA was used during real-time PCR which was performed in Roche Light Cycler 480 (Roche). Amplification was done as follow: initial activation at 95 °C for 15 min, followed by 40 cycles of denaturation at 95 °C for 10 s and annealing-extension step at 60 °C for 40 s. Small nucleolar U6 was used as reference gene, and the results were analyzed using $2^{-\Delta\Delta CT}$.

Table 4- 1 Oligonucleotides used for construction of plasmids

Primers	Sequence (5'-3')
ppr-mir-155-NheI-F	GCTAGCTGGTCCATTAATATGATTTATTGTCCTTCT
ppr-mir-155-NotI-R	GCGGCCGCGAAACATTATTACTTTACCCTGTTTGTGATC
dre-mir-155-NheI-F	GCTAGCGGCATGATGGAAACTGTGCTCC
dre-mir-155-NotI-R	GCGGCCGCGTGCTAAAATAGTCTGACACTGTAAACAGGG
mir-30e-1-C-F	TAGTGAACCGTCAGATCCACAGCCATGCCATAGTTTTAGG ATAC
PFC-C-R	GGATCTGACGGTTCACTAAACCAGC
mir-30e-1-mir-155-C-F	GTACGGGCTCAGCTCGAGGTTAATGCTAATCGTG
mir-30e-1-mir-155-C-R	CTCGAGCTGAGCCCGTACTGCCAGC
mir-155-mir-30e-2-C-F	CCTGCGCTGAGCCAACTGCTGTTACTCTCG
mir-155-mir-30e-2-C-R	CAGTTGGCTCAGCGCAGGACTAATGCTAACG
mir-30e-2-C-R	ATGGCTGATTATGATCAGAGTTCATCATATGACCAGTGACT TGACT
PFC-C-F	CTGATCATAATCAGCCATACCACATTTGT

Enzyme sites are underlined.

Table 4- 2 Oligonucleotides used for real-time RT-PCR

Primers	Sequence (5'-3')
OF-b-actin-RT-Fo	GATCTGGCATCACACCTTCTAC
OF-b-actin-RT-Re	CATCTTCTCCCTGTTGGCTTTA
OF-ISG15-RT-Fo	TGCTGTATGACAACGGTCAG
OF-ISG15-RT-Re	GCTCGATCAGCAGAGACAG
OF-MX1-RT-Fo	ACCGCTGATTATTCGCTACCACCT
OF-MX1-RT-Re	AACCAATGTCCAGCTCCTCCTTCA

Results

1. Prediction of primary mir-155 in EPC cells

Mature miR-155 of zebrafish was blasted against the genome of fathead minnow, and we retrieved two hits with 100% homology to zebrafish miR-155. The predicted miR-155 was aligned with miR-155 of other fish species (Fig.25). Then, secondary structure was predicted using mFold software (Fig.26).

Figure 25. Alignment of fathead minnow miR-155 against miR-155 of other fish species. MiR-155 is highly conserved among fish.

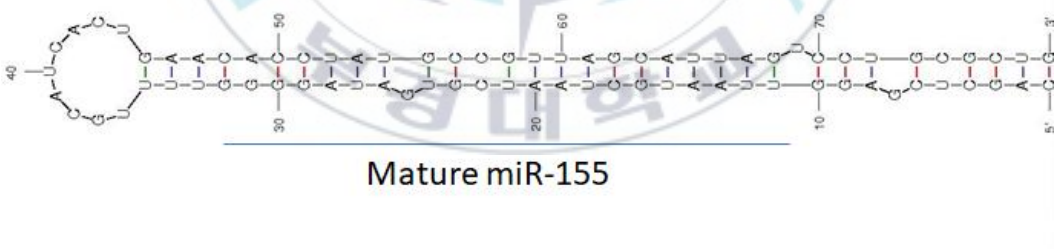

Figure 26. The secondary structure of mir-155 precursor. Prediction of the structure was made using mFold tool with default settings.

2. Generation of plasmid expressing mature miR-155 and overexpression of miR-155 in EPC cells

A plasmid expressing mature miRNA 155 (pc-pri-mir-155) was constructed. However, after transfection of the plasmid, the production of mature miR-155 was low. To overcome this issue, we cloned primary miRNA 155 from zebrafish and then transfected EPC cells with pc-dre-mir-155 (Fig.27). The vector could express miR-155 at a significant level compared to mock cells.

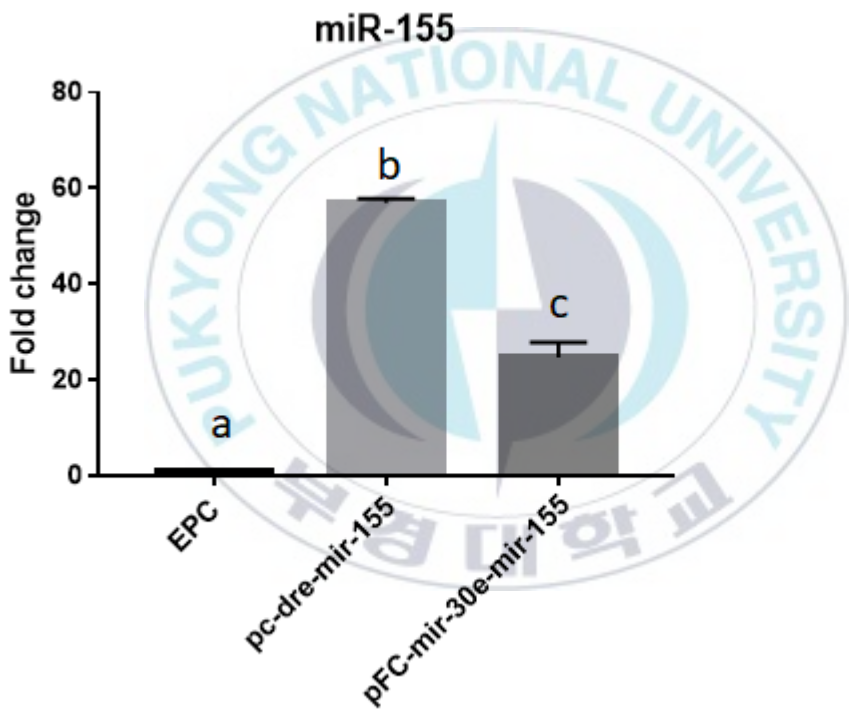

Figure 27. Quantification of miR-155 in *Epithelioma papulosum cyprini* (EPC) cells using real-time RT-PCR. Relative expression of miR-155 in EPC cells transfected with plasmid expressing miR-155 was compared to mock control cells using Ct method. Fold changes (mean ± SD based on triplicate assay) were represented in histograms. U6 gene was used as internal control. Significant differences from the control group were analyzed using Student's t-test. The letters represent a significant difference between groups at $p<0.05$.

Moreover, exchange of flanking regions of fathead minnow mir-155 with flanking regions or mir-30e from zebrafish allowed expressing of mature miR-155. However, level of expression was lower than original flanking regions (Fig.27).

3. Analysis of type I interferon response in olive flounder

Type I interferon response in olive flounder after injection with PBS, empty vector (pc-DNA), or vector expressing miR-155(pc-dre-mir-155) was analyzed using real-time RT-PCR. As results, fish injected with pc-dre-mir-155 plasmid showed a significantly higher expression of ISG15 gene compared to mock control group or group injected with empty vector (Fig. 28 A). Furthermore, expression of MX1 gene was significantly upregulated in the group injected with the vector expressing miR-155 compared to the mock group or group injected with empty vector (Fig. 28 B).

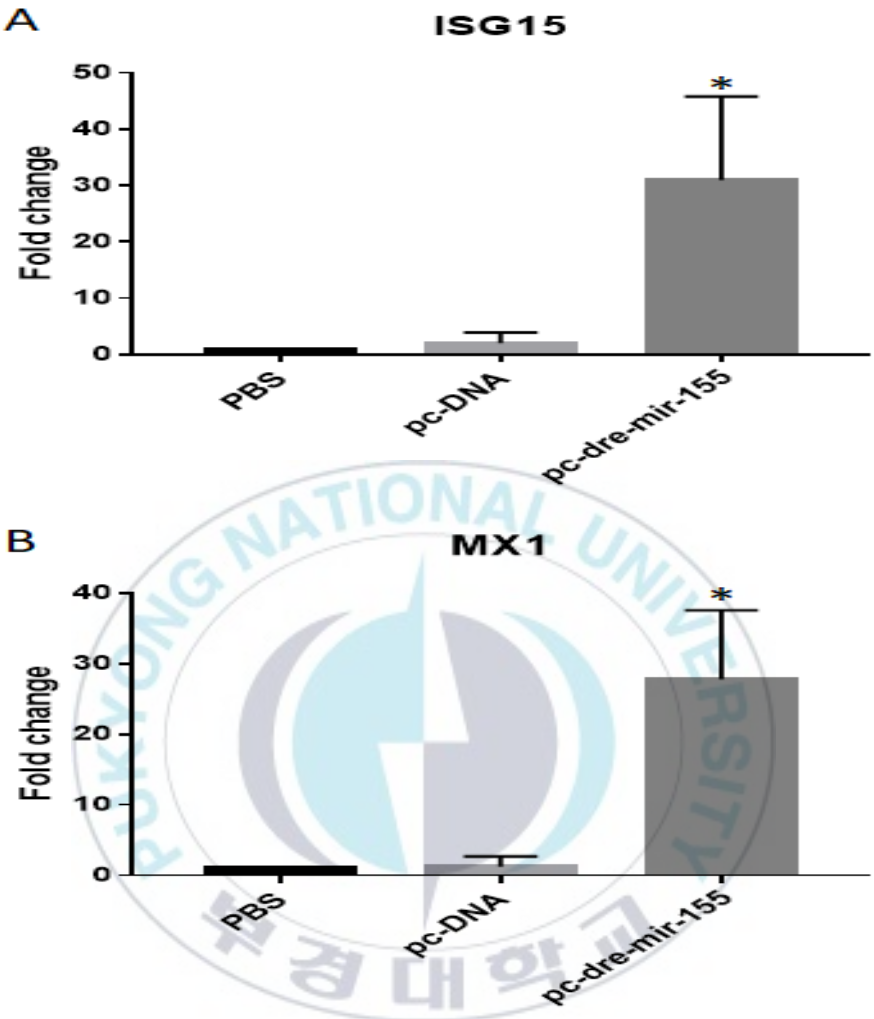

Figure 28. Quantification of ISG15 and MX1 genes in different groups using real-time RT-PCR. A. Relative expression of ISG15 was assessed in different groups. Fold change (mean ±SD) were represented in the histogram. Beta-actin gene was used as internal control. B. Relative mRNA expression of MX1 gene was determined in different groups using the comparative Ct method. Fold change (mean ±SD) were represented in the histogram. Beta-actin gene was used as internal control. The asterisk represents a significant difference at $p<0.05$.

Discussion

In our previous study, we observed upregulation of miR-155 following viral infection with VHSV in EPC cells. This finding has parallels ones in mammals such as infection with hepatitis B virus (Chakravarty et al., 2014) or following infection with Epstein-Barr virus (Cameron et al., 2008). Moreover, the miR-155 role has been extensively studied and has been well characterized in higher vertebrates compared to fish. Until now, there wasn't any study regarding miR-155 and its role in the regulation of host's immunity.

In this study, we identified miR-155 and its precursor, and we observed a high conservation of miR-155 sequence among different species of fish. These findings can suggest a conservation of miR-155 function in fish as well in mammals. The miR-155 has several roles. MiR-155 can act as oncogenic miRNA by repressing tumor protein 53-induced nuclear protein 1(TP53INP1) that lead to inhibition of apoptosis through caspase 3 activation (Gironella et al., 2007). Likewise, miR-155 has been involved in the hematopoietic process especially throughout differentiation of lymphoid and myeloid cells (Masaki et al., 2007). Furthermore, miR-155 has been highly expressed in activated B and T cells (Eis et al., 2005), as well as in activated macrophages and dendritic cells.

To investigate the role of miR-155 in boosting host's immunity, we generated a plasmid expressing mature miR-155 of fathead minnow. However, we observed low expression of miR-155 after transfection in EPC cells. This result might be explained by that is the length of flanking region of miR-155 was not adequate to produce mature miR-155. To overcome this issue, we cloned primary miRNA-155 from zebrafish and confirmed its overexpression in EPC cells.

To boost immunity of olive flounder, we injected fingerlings with a plasmid expressing miR-155. The results showed that group injected with the vector expressing miR-155 under CMV promoter induced a significantly higher level of ISG15 and MX1 mRNA compared to groups injected with either PBS or empty vector. These results suggest that miR-155 could activate type I interferon response which possibly allows protection against pathogens. As stated before, miRNAs exert their role through targeting mRNA of different genes, and miR-155 is no exception. The miR-155 has been validated to have

several target genes and among which there is suppressor of cytokine signaling 1(SOCS1). MiR-155 act as antiviral miRNA by targeting SOCS1 which enhance Type I interferon response following infection with vesicular stomatitis virus (Wang et al., 2010). Furthermore, miR-155 has been used as adjuvant against influenza virus by incorporating primary mir-155 into the genome of the virus (Izzard et al., 2017).

In the present study, we developed a system to express miRNAs using flanking regions of primary miR-30e. The swap of precursor mir-30e with precursor mir-155 led to overexpression of mature miR-155 in EPC cells. Several systems have been used to overexpress artificial miRNAs to efficiently silence a virus or target gene (Chung et al., 2006; Hu et al., 2009). This result suggests that possible to overexpress artificial miRNA and possibly could be used as a system for RNA interference.

In conclusion, we generated a vector that can produce mature miR-155 and we induced type I interferon response in olive flounder based on vector expressing miR-155. Furthermore, we could produce mature miR-155 of fathead minnow by substituting precursor mir-30e from zebrafish with precursor mir-155. To assess the efficiency of RNA interference, induced by the developed system, further analysis is needed.

Chapter V. Hypoxia-responsive miRNA-210 and study of its promoter

Introduction

Organisms living in aquatic environments are often faced with hypoxia that is caused by various environmental factors. Hypoxia can be disastrous especially for sessile organisms that are not able to move to other regions. The fish in aquaculture farms also can become a victim of hypoxia because of the restricted movement of culture facilities. Recently, the frequent occurrences of hypoxic water masses have been a threat to the fish cultured in coastal areas. Fish alter their physiological responses to cope with the hypoxia, and many factors related to oxygen sensing and transport, erythropoiesis, and angiogenesis are involved in the hypoxia adaptation

MiRNAs (miRNAs) are small noncoding RNAs (19-23 nucleotides in length) and regulate the expression of genes through binding to the corresponding sequences of mRNAs. The miRNAs are initially transcribed as long precursors, pri-miRNAs, which are processed by Drosha to generate approximately 70 nucleotide stem-loops (pre-miRNAs) that are transported to the cytoplasm where Dicer cleaves these pre-miRNAs into functional mature miRNAs (Hutvagner et al., 2002; Bartel, 2004). As one kind of miRNA can target several different mRNAs simultaneously, the expression of approximately 60% of genes in mammals is regulated by miRNAs. MiRNAs in the cytoplasm can be secreted into body fluids, which called circulating miRNAs, through being packaged in small membranous vesicles (exosomes, shedding vesicles, and apoptotic bodies) or through being associated with RNA-binding proteins or lipoprotein complexes, which protect the degradation of those extracellular miRNAs by ubiquitous ribonucleases (RNases) in circulation (Valadi et al., 2007; Gibbings et al., 2009). In mammals, the availability of circulating miRNAs as the early biomarkers for specific disease states has already been demonstrated (Mitchell et al., 2008; Zhang et al., 2010). Specifically, as the hypoxia is closely associated with cancers in human, studies on the hypoxia-responsive miRNAs in tissue and blood have been extensively conducted(Bandara et al., 2014). However, in fish, as far as we know, there is only one paper that investigated the circulating miRNAs, in which zebrafish (*Danio rerio*) exposed to 20-40 mM acetaminophen-dissolved water showed hepatotoxicity-mediated histological changes and a high expression of miR-122 in serum (Vliegenthart et al., 2014).

Although the effect of hypoxia on the expression of miRNAs in various tissues of marine medaka (*Oryzias melastigma*) was reported (Lau et al., 2014; Tse et al., 2015; Tse et al., 2016), there is no report on the hypoxia-mediated changes in the circulating miRNAs in fish. In this study, we selected four miRNAs (miR-210, miR-21, miR-26b, and miR-146a). They are representative of hypoxia-responsive circulating miRNAs in mammals (Hua et al., 2006; Kulshreshtha et al., 2007; Chan et al., 2009), and we investigated the changes of the selected circulating miRNAs in the serum of olive flounder (*Paralichthys olivaceus*), the dominant marine cultured fish in Korea, in response to hypoxia. The expression of hypoxia-related genes, hypoxia-inducible factor 1α (HIF1α) and the heat shock protein 90α (HSP90α), was also analyzed.

Furthermore, we analyzed miR-210 promoter activity in naïve EPC cells, ΔHIF-EPC cells, and ΔP53-EPC cells using luciferase assay.

Materials and methods

1. Fish and experimental design

Thirty olive flounder weighing approximately 100 g were obtained from a local fish farm and were maintained in 500 l tank with aeration. The fish were acclimated at 18 ± 1 °C under a 12 h: 12 h light: dark cycle for one week before starting the experiment. The level of dissolved oxygen (DO) was monitored using DO meter iSTEK Multi 90i (iSTEK, KOREA) throughout the experiment. Hypoxia was induced by bubbling nitrogen gas into the tank. At first, the DO was lowered and maintained at 3 mg/l for 6 hours, then, by further bubbling nitrogen gas, the DO in the tank was maintained 2 mg/l for another 6 hours. Just before lowering DO, five fish in the tank were randomly sampled and used as the control group (0 h). At each 3, 6, and 12 h post-exposure to hypoxia, five fish were randomly sampled. The collected blood from the caudal vein was stored at 4°C for 12 h, then, serum was isolated by centrifugation. The liver, brain, and muscle tissue were isolated from each fish and stored at -80°C.

2. Extraction of RNA from serum and quantitative real-time polymerase chain reaction (Q-PCR)

Total RNA was isolated from 100 µl of serum using miRNeasy serum Mini kit (Qiagen) in accordance with the manufacturer's protocol. Briefly, 500 µl of Qiazol and 100 µl of chloroform were added to 100 µl of serum, followed by centrifugation for 15 min at 12,000 g at 4°C. Next, 300 µl of the RNA-containing aqueous phase was transferred into a new tube, and RNA was precipitated with 450 µl of 100% ethanol and loaded on miRNeasy purification columns. Purified RNA was eluted from the column matrix with 14 µl of RNase free water. To adjust for variations of miRNA extraction efficiency among samples, five µl of synthetic Caenorhabditis elegans miR-39 (Syn-cel-miR-39, Qiagen) was spiked into each sample as the external reference after the addition of the denaturing solution and went through the entire RNA isolation process. To aid in improving the RNA yield, total RNA from bacteriophage MS2 (Roche) was added to each sample as a carrier.

Each total RNA (2 μl) was converted to complementary DNA (cDNA) using a miScript II RT Kit (Qiagen). Q-PCR was performed with a miScript SYBR Green PCR Kit (Qiagen) according to the manufacturer's protocol. The primers specific for each miRNA are listed in Table 1, and the Syn-cel-miR-39 was used for normalization. Cycling conditions were 95°C for 15 min followed by 45 cycles of 94°C for 15 s and 55°C for 30 s using Roche light cycler 480.

3. Extraction of RNA from tissues and Q-PCR

Total RNA was extracted from each tissue (liver, brain, and muscle) using TRIzol (Invitrogen) according to the manufacturer's instruction, and 1 μg of DNaseI (Promega)-treated total RNA was incubated with 0.5 μl of random primer (0.5 μg/ml, Promega) at 80°C for 5 min and further incubated at 42°C for 60 min in reaction mixture containing 2 μl of each 10 mM dNTP mix (TaKaRa), 0.5 μl of M-MLV reverse transcriptase (Promega) and 0.25 μl of RNase inhibitor (Promega) in a final reaction volume of 10 μl. The PCR primer pairs used for amplification of the hypoxia-related genes (HIF1α and HSP90α) and the ß-actin gene, as an internal control, are described in Table 1. The PCR reactions in a volume of 20 μl were run using 2× SYBR Green Premix (Enzynomics) with five μl of cDNA and 5 pM of each primer. Thermal cycling condition was one cycle of 15 min at 95°C (pre-incubation), followed by 40 cycles of 10 s at 95°C, 10 s at 60°C, and 20 s at 72°C.

4. Promoter analysis of miR-210 in EPC cells

4.1. Bioinformatics analysis of miR-210 promoter

Based on our previous study, fathead minnow miR-210 mature sequence is 100 % identical to zebrafish miR-210. The precursor of miR-210 was predicted by blasting zebrafish precursor against fathead minnow genome and extracted around 73 nt from the genome with high similarity to zebrafish precursor. Then, fathead minnow mir-210 precursor was analyzed using mFold software with default parameters to predict secondary structure.

One thousand base pair immediately upstream of the mir-210 precursor was retrieved and submitted to analysis using MatInspector (Cartharius et al., 2005) for promoter analysis.

4.2. Plasmid construct

Mir-210 promoter was cloned using specific primers. First, genomic DNA was extracted from EPC using Exgene cell SV (Geneall, Korea) following manufacturer's instructions. Specific primer pr-210-AfeI-F and pr-210-AgeI-R were used to amplify the promoter and then PCR products were cloned into pGEM-vector (Promega). After confirmation of sequence, the promoter was ligated into the AfeI and AgeI sites of pNFκB-MetLuc2-Reporter vector replacing NF-κb binding site and minimal promoter, and the constructed vector was designated as pr-210-luc.

4.3. In vitro luciferase expression

Naïve EPC cells, EPC-knockout HIF1α cells (ΔHIF1α-EPC), and EPC-knockout p53 cells (Δp53-EPC) were transiently transfected with pr-210-luc or pr-HRE-luc vector using the Neon system. Twenty-four hours later, cells were treated with cobalt chloride at a final concentration of 200 μM and incubated at 28 °C. Then, luciferase expression was analyzed using Ready-To-Glow Secreted Luciferase Assay kit (Clontech) in VICTOR Multilabel Plate Reader machine (PerkinElmer).

Table 5- 1 Oligonucleotides used for construction of plasmid

Primers	Sequence (5'-3')
p-210-AfeI-F	AGCGCTCGGGTGGAGCTCTTTTTTTCAAAAACAC
p-210-AgeI-R	ACCGGTTTTCAGAAATCAGAAGCCACAGGAACC

Enzyme sites are underlined.

Table 5- 2 Oligonucleotides used for real-time RT-PCR

Primers	Sequence (5'-3')
pol-miR-210-5p-F	AGCCACTGACTAACGCACATTG
pol-miR-210-3p-F	CTGTGCGTGTGACAGCGGCT
pol-miR-21-5p-F	GCTAGCTTATCAGACTGGTGTTGG
pol-miR-21-3p-F	CGACAACAGTCTGAAGGCTGTC
pol-miR-26b-F	CGCTTCAAGTAATCCAGGATAGGTT
pol-miR-146a-F	CGCTGAGAACTGAATTCCATAGATGG
cel-miR-39-F	GCAGAGCTGATTTCGTCTTG
Universal-R	Qiagen universal reverse primer
HIF1α-RT-F	GACACAGCGTGTTTGACTTTACA
HIF1α-RT-R	TGTGTTTGACTCCTTGGTCTT
HSP90α-RT-F	GGACGAAGACAAGCCAGAAA
HSP90α-RT-R	AGCTCCTCCTGGTCGATATAC
HSP90β-RT-F	CATTGTCAGTCTGGAGGGTTAG
HSP90β-RT-R	GGACTCAGGCAAAGGAATCA
Beta-actin-RT-F	GATCTGGCATCACACCTTCTAC
Beta-actin-RT-R	CATCTTCTCCCTGTTGGCTTTA

Results

1. Levels of circulatory miRNAs

Olive flounder maintained at 3 mg/l of DO for 1, 3, and 6 hours did not show any significant increase of the selected circulatory miRNAs. However, after lowering DO to 2 mg/l for another 6 hours, all the selected circulatory miRNAs, except miR-21-3p, were significantly increased when compared to those of the control fish (Fig. 29). Especially, miR-210-5p and miR-210-3p were the most increased (4-5 folds) miRNAs in the serum.

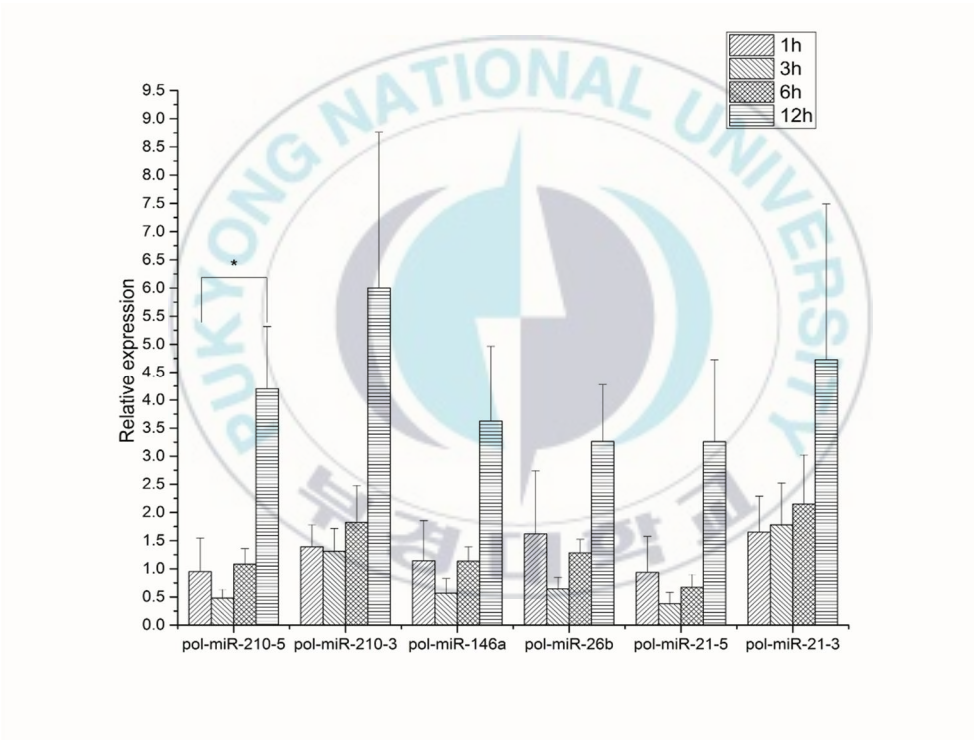

Figure 29. Expression of serum miRNAs induced by hypoxia. The quantification of miRNAs was done using q-PCR analysis. The data are presented as means±SEM; *$p<0.05$.

2. Expression of hypoxia-related genes

Although hypoxia significantly increased the expression of HIF1α in the liver, the increased amplitude was not high (Fig. 30). On the other hand, the expression of HSP90α

in the liver and muscle was significantly increased by hypoxia, more than 13 and eight times, respectively, when compared to the expression values in control fish (Fig. 30).

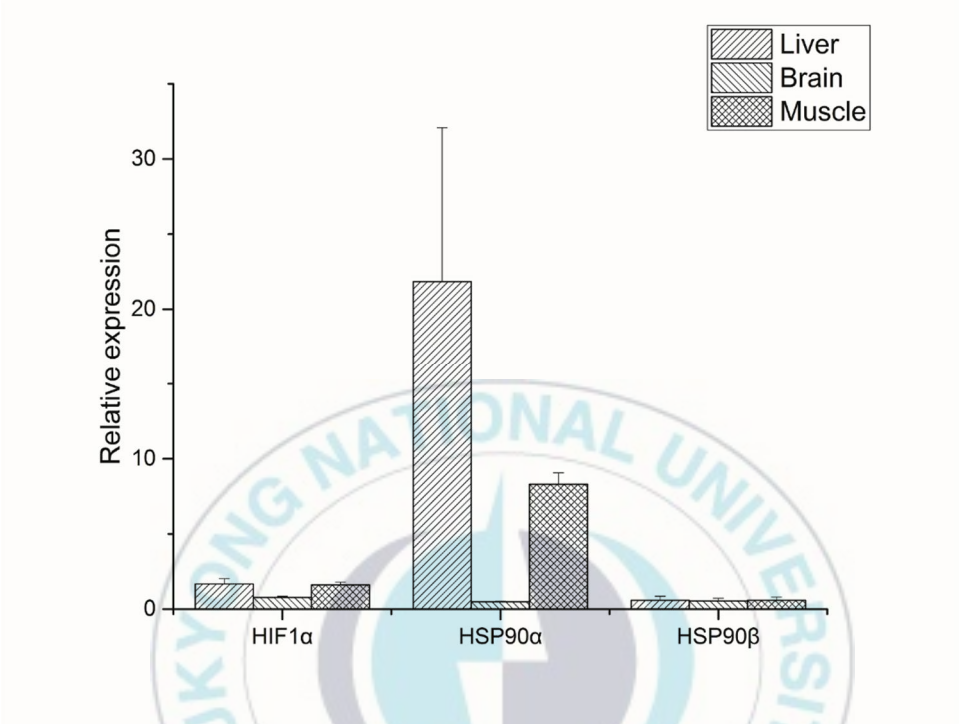

Figure 30. Relative expression of hypoxia-induced genes in different organs. The quantification of gene expression was done using real-time PCR.

3. MiR-210 promoter is under hypoxia control:

3.1. Bioinformatic characterization of miR-210

To investigate promoter of miR-210, 1 kb upstream of precursor mir-210 was retrieved and analyzed using MatInspector. By searching promoter for hypoxia response element (HRE) based on consensus sequence (A/G)CGTG, we could identify two potential HRE sites and one potential binding site for tumor protein 53 (Fig .31).

Figure 31.Structure of miR-210 promoter. TATA box is underlined, the TP53 binding site is delimited by a black box, and hypoxia response element was delimited by a blue box.

3.2. Functional analysis of miR-210 promoter

To validate potential hypoxia response element and binding site of TP53, we constructed a vector expressing luciferase gene under control of the miR-210 promoter. Furthermore, we substituted NF-κb binding site in pNFκB-MetLuc2-Reporter (Clontech) with several hypoxia response elements, and it was designated as p-HRE-Metluc.

Constructed vectors were transfected into naïve EPC cells, HIF1α-knock-out EPC cells (ΔHIF1α-EPC), and TP53-knockout EPC cells (ΔP53-EPC). Then we treated them with cobalt chloride (CoCl2) at a final concentration of 200 μM. We observed a significant

increase of luciferase activity in EPC cells and ΔP53-EPC cells transfected with p-210-Metluc at 24, and 48 hours post-transfection compared to control group naïve EPC cells (Fig.32). On the other hand, ΔHIF-EPC cells did not show any significant increase of luciferase activity compared to control EPC cells. The positive control vector p-HRE-Metluc showed a similar pattern. However, luciferase activity increase was higher than the observed one in EPC cells transfected with p-210-Metluc (Fig.32).

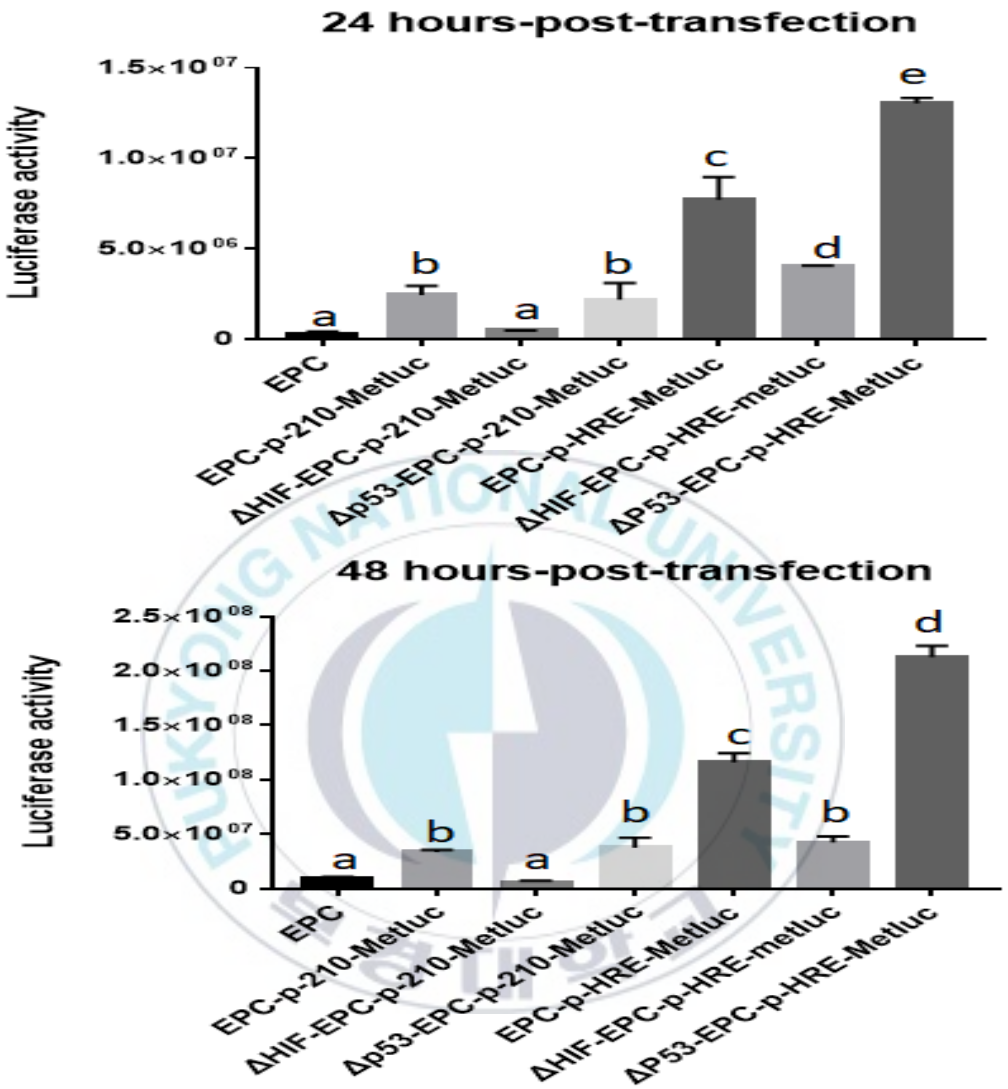

Figure 32. Analysis of miR-210 promoter activity in naïve EPC cells, ΔHIF1α-EPC cells, and ΔP53-EPC cells. Construct p-HRE-Metluc serve as a positive control. Data is shown as mean ±SD, and letters over bar indicate significant difference at $P<0.05$.

Discussion

The significant role of miRNAs in the regulation of pathophysiologic processes has been well demonstrated in mammals. Although the role of circulating miRNAs is not fully understood, recent reports showed that circulating miRNAs also participate in biological phenomena through intercellular signaling (Katakowski et al., 2010; Kharaziha et al., 2012). Hypoxia leads to the shift of cellular metabolism from mitochondrial oxidative phosphorylation to glycolysis (Granchi et al., 2014), and miRNAs are involved in the adaptation of organisms to hypoxia by the up- or down-regulation of hypoxia-related genes (Kulshreshtha et al., 2007; Ivan et al., 2008).

MiRNA-210 is the representative of hypoxia-regulated miRNA (HRM) and is up-regulated by hypoxia-inducible factor (HIF) that binds to HIF-response elements in the promoter region of miR-210 (Chan et al., 2010). One of the regulatory roles of miR-210 is the repression of mitochondrial metabolism by down-regulating several steps for electron transport chain complexes-mediated ATP production (Chan et al., 2009). In human, the important increase of the circulating miR-210 level was reported in patients with pancreatic cancer, aortic stenosis, or low maximal oxygen uptake (Ho et al., 2010; Bye et al., 2013; Røsjø et al., 2014). In this study, similar to the reports from human, miR-210-5p and miR-210-3p were the most highly increased miRNAs in the serum of olive flounder in response to hypoxia, suggesting that circulating miR-210 levels in the serum can be used as a prognostic biomarker for fish suffered hypoxia. In this study, although the fold increases were lower than miR-210, other selected miRNAs, miR-21, miR-26 and miR-146 that are known to be induced by hypoxia in human were also significantly increased in the serum by the exposure of fish to hypoxia. These results suggest that the specific miRNAs participated in the regulatory mechanisms against hypoxia might be similar for both fish and human.

The hypoxia-inducible factor 1α (HIF-1α) has been noticed as the key regulator for cellular hypoxia adaptation (Semenza, 2009). Under normoxic conditions, several proline residues of HIF-1α are hydroxylated by proline hydroxylases, which mediates binding of HIF-1α to von Hippel-Lindau tumor suppressor protein (vHL) that ubiquitinates

HIF-1α to be degraded in the proteasome (Ohh et al., 2000). However, under hypoxic conditions, hydroxylation of HIF-1α is inhibited, which leads to stabilization of HIF-1α. HIF-1α accumulated in the cytoplasm translocates to the nucleus and dimerizes with HIF-1β that is constitutively expressed irrespective of oxygen tension, then, binds to hypoxia response elements and regulates transcription of HIF-dependent genes (Kallio et al., 1997; Poellinger et al., 2004). In general, the regulation HIF-1α is dependent on the protein level rather than mRNA level, which was demonstrated in mammals and fish (Soitamo et al., 2001; Stroka et al., 2001). Similarly, in this study, although the transcriptional expression of HIF-1α in response to hypoxia was significantly increased in the liver, the increased amplitude was not high. The regulatory role of HIF-1α over multiple miRNAs including miR-210 has been reported in mammals (Huang et al., 2009). Thus, to know whether the significant increase of serum miR-210-5p and miR-210-3p in this study was controlled through HIF-1α, further studies on the regulatory interaction between HIF-1α and hypoxia-responsive miRNAs in fish are needed. A chaperone protein HSP90 plays a vital role in the regulation of the activity of transcription factors including HIF-1 under hypoxia (Minet et al., 1999). Furthermore, the association between HSP90 and Argonaute 2 (AGO2) can be induced by hypoxia, which is essential for the incorporation of miRNAs into the RNA-induced silencing complex (RISC) (Iwasaki et al., 2010). In this study, the significant up-regulation of HSP90α in the liver and muscle by hypoxia suggests that a significant amount of HSP90 is required for the hypoxia adaptation of olive flounder as in other mammals.

In this study, we identified miR-210 promoter using bioinformatics tool, and we predicted two possible hypoxia binding sites and one possible binding site for tumor protein 53. By dissecting the effect of hypoxia on promoter activity, the present results have shown a decrease in luciferase activity under hypoxic condition in the absence of HIF1α protein. However, there wasn't any significant difference between naïve EPC cells and ΔP53-EPC cells which could indicate that the predicted site for binding with P53 is not functional. The positive control vector p-HRE-Metluc showed a higher luciferase activity compared to the promoter of miR-210. These results can be explained by the low number of hypoxia response elements in miR-210 promoter compared to positive control vector. These results have confirmed the regulation of miR-210 under control of HIF1α.

Furthermore, miR-210 tightly regulated by hypoxia and under control of HIF1α (Huang et al., 2009).

Summary

The primary aim of this study is the investigation of miRNA expression following viral infection with VHSV and assessment of mechanism behind the expression of some miRNAs.

In chapter I, we infected fingerlings of olive flounder with VHSV and collected their head kidney at different point in time (0, 6, 12, 24, 48, 72 hours-post-infection). Then, we generated six libraries of small RNA using Next-generation sequencing technology. Thru infection with VHSV infection, we observed a dynamic change in miRNAs expression.

These changes can be explained by the interaction between virus and host's miRNAs. Furthermore, miRNAs have been designed as regulators of host's processes, and they exert their function by acting on post-transcriptional level. Based on bioinformatics analysis and the use of target prediction tools, we could predict targets of several miRNAs, and we could classify them depending on their interaction with the immune system.

In chapter II, to determine the effects of viral infection on miRNA profile in-vitro and to confirm the results obtained in previous study, we infected *Epithelioma papulosum cyprini* (EPC) cells with a high concentration of wild-type VHSV (MOI=1) and we investigated patterns of miRNAs at different points of time (0, 3, 12, 24, 48 hours-post-infection). Then, five libraries of small RNA sequencing were generated using Next-generation sequencing technology. The libraries were aligned against the genome of zebrafish and proteins of zebrafish to remove any possible coding sequence. Then, clean reads were aligned against zebrafish miRNAs.

The viral infection has altered the miRNAs expression dynamically and we also observed same altered miRNAs upon infection with VHSV in olive flounder. Furthermore, target prediction of miRNAs has provided us with useful information concerning possible function of miRNA. These results suggest that VHSV infection exerts action not only on the protein level of the host but alter the normal function of several small RNA as well.

In chapter III, to take advantage of previous studies, we focused on analyzing miR-146a and investigating its role following viral infection with VHSV. To study miR-146, we constructed a plasmid harboring primary mir-146a and confirmed overexpression of mature miR-146a in *Epithelioma papulosum cyprini* (EPC) cells. Then, we constructed a system that will inhibit miR-146a expression by sequestering molecules of miR-146a. Based on reporter assay, we observed a decrease of luciferase activity upon infection of EPC cells carrying sponge miRNA against miR-146a with VHSV. Furthermore, miR-146a facilitated viral replication in EPC cells harboring vector expressing miR-146a. On the other hand, sponge miRNA inhibited viral replication of VHSV. These results suggest that miR-146a has a decisive role in viral replication and can play a proviral role. To confirm our hypothesis, we used target prediction tool and found that miR-146a target the TNF receptor-associated factor 6(TRAF6). To validate the interaction between TRAF6 and miR-146a, we generated a vector expressing 3'UTR of TRAF6 linked to Metridia luciferase gene under control of CMV promoter. Also, to investigate the direct interaction between miR-146a and TRAF6, we mutated binding site in 3'UTR of TRAF6. As in infection with VHSV, we observed a decrease of luciferase activity in EPC cells transfected with 3'UTR of TRAF6 in a concentration-dependent manner. Interestingly, cells transfected with mutated 3'UTR of TRAF6 did not show any decrease of luciferase activity compared to the mock group. These results suggest that miR-146a plays a proviral role by inhibiting expression of TRAF6 which allows enhancing the replication of VHSV.

To understand the mechanism that allows miR-146a to enhance viral replication, we knock-out TRAF6 gene in EPC cells. Then, we stimulated naïve EPC cells and ΔTRAF6-EPC cells. We observed a decrease in the expression of ISG15 and MX1 genes which are involved in Type I interferon response. These findings indicate that miR-146a create a favorable environment for viral replication by inhibiting the action of TRAF6 which is involved into type I interferon response.

In chapter IV, our previous studies have indicated an upregulation of miR-155 following infection of olive flounder or EPC cells with VHSV. First, we tried to express

mature miR-155 based on fathead minnow primary mir-155. However, we could not detect any significant overexpression after transfection of EPC cells. To overcome this, we cloned primary miRNA mir-155 from zebrafish, and we confirmed overexpression in EPC cells.

Then, we injected fingerlings of olive flounder with the plasmid expressing miR-155 to investigate the role of miR-155 in stimulating immunity. We observed a significant increase of ISG15 and MX1 genes expression in the group injected with the vector expressing miR-155 compared to control group (PBS) or group injected with empty vector (pcDNA 3.1(+)). These results suggest a possible antiviral role of miR-155 by enhancing type I interferon response.

Furthermore, we exchanged precursor mir-30e with precursor mir-155 and overexpressed fathead minnow miR-155 in EPC cells. This system can be used to produce artificial silencing molecules against virus or a target gene.

In chapter V, to study miR-210 expression following hypoxia, we applied a low level of oxygen on olive flounder and extracted serum. We detected a significant upregulation of miR-210-3p compared to other miRNAs. These results indicate that miR-210 is tightly regulated by hypoxia and is possibly under control by HIF1α.

To test our hypothesis, we cloned upstream region of precursor mir-210 and transfected into naïve EPC cells, ΔHIF1α-EPC cells, and ΔP53-EPC cells. Based on reporter assay, we observed a significant increase of luciferase activity in naïve EPC cells and ΔP53-EPC cells compared to ΔHIF1α-EPC cells. These results suggest that miR-210 is under the tight control of HIF1α.

Profiling of miRNAs in olive flounder (*Paralichthys olivaceus*) and Epithelioma papulosum cyprini cells following viral hemorrhagic septicemia virus infection, and functional characterization of miR-146a, miR-155 and miR-210

Najib Abdellaoui

Department of Aquatic Life Medicine, The Graduate School

Pukyong National University

Abstract

MicroRNAs (miRNAs) are a class of small non-coding RNAs, 19-25 nucleotides. They play a regulatory role in gene expression at post-transcription level by inhibiting translation through binding to the 3'untranslated region (3'UTR) of messenger RNA (mRNA) in a specific manner. Until now, over thousands of miRNAs were discovered in different species and each of them can regulate hundreds of genes. Based on their tremendous impact on different biological and pathological processes, there is a growing interest in studying miRNAs and their action mechanisms in mammals. Therefore, gaining more understanding of the functions and action modes of miRNAs in fish would be helpful for the development of control measures against diseases.

Viral hemorrhagic septicemia virus (VHSV) is the causative agent of viral hemorrhagic septicemia (VHS) disease causing a substantial loss in aquaculture farms. This study aims exploring the effect of VHSV infection on miRNAs profile in olive flounder (*Paralichthys olivaceus*) and in *Epithelioma papulosum cyprini* (EPC) cells. In the experiment of olive flounder, fingerlings were infected with VHSV, and cellular miRNAs expression was analyzed at 0 (control), 6, 12, 24, 48 and 72 h post-infection (h.p.i.) by the high-throughput sequencing. A total of 372

mature miRNAs were identified, and, among which, 63 miRNAs were differentially expressed during VHSV infection. The differentially expressed miRNAs number was significantly increased from 24 h.p.i compared to the number at 6 and 12 h.p.i., suggesting that the alteration of miRNAs expression by VHSV infection may be related to the progression of VHSV disease. The target prediction analysis, the GO enrichment analysis, and the KEGG pathway analysis of the predicted target genes showed that various biological pathways could be affected by VHSV infection through the down-regulation or up-regulation of host miRNAs. In the experiment of EPC cells, a total of 355 conserved miRNAs and three novel miRNAs were identified, and among them, 103 miRNAs were differentially expressed. The number of differentially expressed miRNAs highly increased at 24 hours-post inoculation compared to 3 h.p.i and 12 h.p.i., suggesting that EPC cells might not actively respond to VHSV infection at an early infection period, which can allow viruses to transcribe and translate their genes enough to produce viral particles that can infect another cell. Among the differentially expressed miRNAs, two miRNAs (miR-735 and miR-738) that were reported only in fish species were highly upregulated. Based on the target prediction, they could regulate several immune pathways. Furthermore, the present results showed the upregulation of representative immune regulating miRNAs such as miR-146a, miR-155, and miR-99. The present dynamical changing patterns of differentially expressed miRNAs in response to the progression of VHSV infection suggest that miRNA profile that was analyzed at a one-time point cannot provide enough information for the interpretation of the disease mechanism. These results provide necessary information on the miRNAs related to VHSV infection in olive flounder and EPC cells. Considering the broad effects of miRNAs on various biological pathways, data in this study can be used to interpret the mechanism of VHSV pathogenesis, which, vice versa, can be used to develop control measures against VHSV.

Among the miRNAs responding to VHSV infection in olive flounder and EPC cells, we chose two miRNAs, miR-146a and miR-155, that were most highly increased by VHSV infection in both olive flounder and EPC cells. In mammals, miR-146a is known for its role in the regulation of NF-κb activation by targeting several genes involved in the pathway such as tumor necrosis factor receptor-associated factor 6 (TRAF6). We explored the effect of overexpressing miR-146a via the use of vector harboring the primary transcript of miR-146a or through transfection of miR-146a mimics on TRAF6 expression and VHSV replication. We also characterized the function of miR-155 based on bioinformatics analysis and molecular techniques. Finally, we demonstrated that hypoxia in olive flounder could induce an upregulation of circulating miR-210, and luciferase activity under control of miR-210 promoter under hypoxic condition in naïve and HIF-1α knock-out EPC cells was analyzed.

Acknowledgment

I reserve my first and foremost gratitude to my advisor, Prof. Ki Hong Kim, for his support and guidance along my study in his laboratory in Pukyong National University (PKNU). He has always encouraged me to be novel and creative in my thinking and reasoning. His knowledge, wisdom, vision, and endless effort in pursuit of excellence have profoundly influenced me with lifetime benefits. I am grateful to Professor Kim for putting me in the right path to become a professional researcher. In fact, I could not imagine having a better advisor and mentor during my research.

Besides my advisor, I would like to thank the members of the research committee: Professor Hyun Do Jeong, Professor Do Hyung Kim, Professor Tae Jin Choi, and Professor Se Ryun Kwon. Their questions and comments have motivated me to widen my research from various perspectives.

I thank my fellow lab mates for the stimulating discussions, I must admit that this work could not be appropriately conducted without the support, and the help of the members of the molecular biology laboratory. My interaction with my lab mates opened my eyes to the reality of being a professional researcher. In particular I am grateful to two members of our laboratory. My dear lab mates Min Sun Kim and Seung Hyuk Choi have taught me a lot and never stopped guiding and encouraging me. My sincere thanks also go to the rest of my colleagues in the laboratory of molecular biology: Jun soung Kwak, Chizuha Wakabayashi, Jeong In Yang, Myeong Kwang Choe, Min Jun Sin, and Hyeon Ju Lim.

A special thanks to my parents Mohamed Abdellaoui and Elbatoul Aissaoui for their unconditional love and support during my whole journey of study. My sister Nabila has always been supportive, and helpful while writing my thesis. Furthermore, my little sister Soukaina was also very supportive throughout her ideas and words.

Last but not least, I would like to thank my friend Kamal Ait Hiji for his support and wisdom. All the fondest memories I hold dear during my stay in Korea are with my friends during the Korean language course. Paulos, Bangun, and Xurshid. Thank you all for all the great time that we had spent together, and I am proud to call each one of you my brother.

References

Abdellaoui, N., M. S. Kim and K. H. Kim (2017). Viral hemorrhagic septicemia virus (VHSV) infection-mediated sequential changes in miRNAs profile of *Epithelioma papulosum cyprini* (EPC) cells. Fish & Shellfish Immunology 61: 93-99.

Abdellaoui, N., M. S. Kim, S. H. Choi, Y. J. Kang and K. H. Kim (2016). Changes in miRNAs expression profile of olive flounder (*Paralichthys olivaceus*) in response to viral hemorrhagic septicemia virus (VHSV) infection. Fish & Shellfish Immunology 51: 384-391.

Ahmad, A., K. R. Ginnebaugh, S. Sethi, W. Chen, R. Ali, S. Mittal and F. H. Sarkar (2015). miR-20b is up-regulated in brain metastases from primary breast cancers. Oncotarget 6(14): 12188-12195.

Andrews, S. (2010). FastQC:A quality control tool for high throughput sequence data.

Androulidaki, A., D. Iliopoulos, A. Arranz, C. Doxaki, S. Schworer, V. Zacharioudaki, A. N. Margioris, P. N. Tsichlis and C. Tsatsanis (2009). The Kinase Akt1 Controls Macrophage Response to Lipopolysaccharide by Regulating MiRNAs. Immunity 31(2): 220-231.

Ashraf, U., B. Zhu, J. Ye, S. Wan, Y. Nie, Z. Chen, M. Cui, C. Wang, X. Duan, H. Zhang, H. Chen and S. Cao (2016). MiRNA-19b-3p Modulates Japanese Encephalitis Virus-Mediated Inflammation via Targeting RNF11. Journal of Virology 90(9): 4780-4795.

Bae, H. J., K. H. Jung, J. W. Eun, Q. Shen, H. S. Kim, S. J. Park, W. C. Shin, H. D. Yang, W. S. Park, J. Y. Lee and S. W. Nam (2015). MiRNA-221 governs tumor suppressor HDAC6 to potentiate malignant progression of liver cancer. Journal of Hepatology 63(2): 408-419.

Bandara, V., M. Z. Michael and J. M. Gleadle (2014). Hypoxia represses miRNA biogenesis proteins in breast cancer cells. BMC Cancer 14(1): 533.

Bartel, D. P. (2004). MiRNAs: Genomics, Biogenesis, Mechanism, and Function. Cell 116(2): 281-297.

Bartel, D. P. (2009). MiRNAs: Target Recognition and Regulatory Functions. Cell 136(2): 215-233.

Behm-Ansmant, I., J. Rehwinkel, T. Doerks, A. Stark, P. Bork and E. Izaurralde (2006). mRNA degradation by miRNAs and GW182 requires both CCR4:NOT deadenylase and DCP1:DCP2 decapping complexes. Genes & Development 20(14): 1885-1898.

Bela-ong, D. B., B. D. Schyth, J. Zou, C. J. Secombes and N. Lorenzen (2015). Involvement of two miRNAs in the early immune response to DNA vaccination against a fish rhabdovirus. Vaccine 33(28): 3215-3222.

Betel, D., A. Koppal, P. Agius, C. Sander and C. Leslie (2010). Comprehensive modeling of miRNA targets predicts functional non-conserved and non-canonical sites. Genome Biology 11(8): R90.

Biacchesi, S., E. Mérour, D. Chevret, A. Lamoureux, J. Bernard and M. Brémont (2017). NV Proteins of Fish *Novirhabdovirus* Recruit Cellular PPM1Bb Protein Phosphatase and Antagonize RIG-I-Mediated IFN Induction. 7: 44025.

Bohnsack, M. T., K. Czaplinski and D. Gorlich (2004). Exportin 5 is a RanGTP-dependent dsRNA-binding protein that mediates nuclear export of pre-miRNAs. RNA 10(2): 185-191.

Bolstad, B. M. I., R. A.; Astrand, M.; Speed, T. P. (2003). A comparison of normalization methods for high density oligonucleotide array data based on variance and bias. Bioinformatics 19(2): 185-193.

Borchert, G. M., W. Lanier and B. L. Davidson (2006). RNA polymerase III transcribes human miRNAs. Nat Struct Mol Biol 13(12): 1097-1101.

Budhu, A., H.-L. Jia, M. Forgues, C.-G. Liu, D. Goldstein, A. Lam, K. A. Zanetti, Q.-H. Ye, L.-X. Qin, C. M. Croce, Z.-Y. Tang and X. W. Wang (2008). Identification of metastasis-related miRNAs in hepatocellular carcinoma. Hepatology 47(3): 897-907.

Bye, A., H. Røsjø, S. T. Aspenes, G. Condorelli, T. Omland and U. Wisløff (2013). Circulating MiRNAs and Aerobic Fitness ? The HUNT-Study. PLoS ONE 8(2): e57496.

Cai, X., C. H. Hagedorn and B. R. Cullen (2004). Human miRNAs are processed from capped, polyadenylated transcripts that can also function as mRNAs. RNA 10(12): 1957-1966.

Cai, Y., L. Zhu, Y. Zhou, X. Liu, X. Liu, X. Li, Q. Lang, X. Qiao and Z. Xu (2015). Identification and Analysis of Differentially-Expressed miRNAs in Japanese Encephalitis Virus-Infected PK-15 Cells with Deep Sequencing. International Journal of Molecular Sciences 16(1): 2204.

Cameron, J. E., C. Fewell, Q. Yin, J. McBride, X. Wang, Z. Lin and E. K. Flemington (2008). Epstein–Barr virus growth/latency III program alters cellular miRNA expression. Virology 382(2): 257-266.

Cameron, J. E., Q. Yin, C. Fewell, M. Lacey, J. McBride, X. Wang, Z. Lin, B. C. Schaefer and E. K. Flemington (2008). Epstein-Barr Virus Latent Membrane Protein 1 Induces Cellular MiRNA miR-146a, a Modulator of Lymphocyte Signaling Pathways. Journal of Virology 82(4): 1946-1958.

Carrington, J. C. and V. Ambros (2003). Role of miRNAs in plant and animal development. Science 301.

Cartharius, K., K. Frech, K. Grote, B. Klocke, M. Haltmeier, A. Klingenhoff, M. Frisch, M. Bayerlein and T. Werner (2005). MatInspector and beyond: promoter analysis based on transcription factor binding sites. Bioinformatics 21(13): 2933-2942.

Cascio, S., A. D'Andrea, R. Ferla, E. Surmacz, E. Gulotta, V. Amodeo, V. Bazan, N. Gebbia and A. Russo (2010). miR-20b modulates VEGF expression by targeting HIF-1α and STAT3 in MCF-7 breast cancer cells. Journal of Cellular Physiology 224(1): 242-249.

Chakravarty, R., N. Sarkar, R. Panigrahi, A. Pal, A. Biswas, S. P. Singh, S. Kar, M. Bandopadhyay, D. Das, D. Saha, S. Chakrabarti and A. Banerjee (2014). TLR7 Modulates the Expression of mir-155 during Hepatitis B Virus Infection. Journal of Clinical and Experimental Hepatology 4(Supplement 2): S20.

Chan, S. Y. and J. Loscalzo (2010). MiRNA-210: A unique and pleiotropic hypoxamir. Cell Cycle 9(6): 1072-1083.

Chan, S. Y., Y.-Y. Zhang, C. Hemann, C. E. Mahoney, J. L. Zweier and J. Loscalzo (2009). MiRNA-210 Controls Mitochondrial Metabolism during Hypoxia by Repressing the Iron-Sulfur Cluster Assembly Proteins ISCU1/2. Cell Metabolism 10(4): 273-284.

Chase, G., T. Deng, E. Fodor, B. W. Leung, D. Mayer, M. Schwemmle and G. Brownlee (2008). Hsp90 inhibitors reduce influenza virus replication in cell culture. Virology 377(2): 431-439.

Chaudhuri, A. A., A. Y.-L. So, N. Sinha, W. S. J. Gibson, K. D. Taganov, R. M. O'Connell and D. Baltimore (2011). MiRNA-125b Potentiates Macrophage Activation. The Journal of Immunology 187(10): 5062-5068.

Chen, J., X. Wang and B. Liu (2016). iMiRNA-SSF: Improving the Identification of MiRNA Precursors by Combining Negative Sets with Different Distributions. 6: 19062.

Chen, P., Q. Xi, Q. Wang and P. Wei (2014). Downregulation of miRNA-100 correlates with tumor progression and poor prognosis in colorectal cancer. Medical Oncology 31(10): 235.

Chu, Q. and T. Xu (2016). miR-192 targeting IL-1RI regulates the immune response in miiuy croaker after pathogen infection in vitro and in vivo. Fish & Shellfish Immunology 54: 537-543.

Chu, Q., Y. Sun, J. Cui and T. Xu (2017). Inducible miRNA-214 contributes to the suppression of NF-κB-mediated inflammatory response via targeting myd88 gene in fish. Journal of Biological Chemistry 292(13): 5282-5290.

Chun-zhi, Z., H. Lei, Z. An-ling, F. Yan-chao, Y. Xiao, W. Guang-xiu, J. Zhi-fan, P. Pei-yu, Z. Qing-yu and K. Chun-sheng (2010). MiRNA-221 and miRNA-222 regulate gastric carcinoma cell proliferation and radioresistance by targeting PTEN. BMC Cancer 10(1): 367.

Chung, K.-H., C. C. Hart, S. Al-Bassam, A. Avery, J. Taylor, P. D. Patel, A. B. Vojtek and D. L. Turner (2006). Polycistronic RNA polymerase II expression

vectors for RNA interference based on BIC/miR-155. Nucleic Acids Research 34(7): e53-e53.

Cichocki, F., M. Felices, V. McCullar, S. R. Presnell, A. Al-Attar, C. T. Lutz and J. S. Miller (2011). Cutting Edge: MiRNA-181 Promotes Human NK Cell Development by Regulating Notch Signaling. The Journal of Immunology 187(12): 6171-6175.

Cimmino, A., G. A. Calin, M. Fabbri, M. V. Iorio, M. Ferracin, M. Shimizu, S. E. Wojcik, R. I. Aqeilan, S. Zupo, M. Dono, L. Rassenti, H. Alder, S. Volinia, C.-g. Liu, T. J. Kipps, M. Negrini and C. M. Croce (2005). miR-15 and miR-16 induce apoptosis by targeting BCL2. Proceedings of the National Academy of Sciences of the United States of America 102(39): 13944-13949.

Conesa, A., S. Götz, J. M. García-Gómez, J. Terol, M. Talón and M. Robles (2005). Blast2GO: a universal tool for annotation, visualization and analysis in functional genomics research. Bioinformatics 21(18): 3674-3676.

Connor, J. H., M. O. McKenzie, G. D. Parks and D. S. Lyles (2007). Antiviral activity and RNA polymerase degradation following Hsp90 inhibition in a range of negative strand viruses. Virology 362(1): 109-119.

Curtis, A. M., C. T. Fagundes, G. Yang, E. M. Palsson-McDermott, P. Wochal, A. F. McGettrick, N. H. Foley, J. O. Early, L. Chen, H. Zhang, C. Xue, S. S. Geiger, K. Hokamp, M. P. Reilly, A. N. Coogan, E. Vigorito, G. A. FitzGerald and L. A. J. O'Neill (2015). Circadian control of innate immunity in macrophages by miR-155 targeting Bmal1. Proceedings of the National Academy of Sciences 112(23): 7231-7236.

Dickson, K. M., A. L. Bhakar and P. A. Barker (2004). TRAF6-dependent NF-kB transcriptional activity during mouse development. Developmental Dynamics 231(1): 122-127.

Ding, S.-W. and O. Voinnet (2007). Antiviral Immunity Directed by Small RNAs. Cell 130(3): 413-426.

Djuranovic, S., A. Nahvi and R. Green (2011). A Parsimonious Model for Gene Regulation by miRNAs. Science 331(6017): 550-553.

Eis, P. S., W. Tam, L. Sun, A. Chadburn, Z. Li, M. F. Gomez, E. Lund and J. E. Dahlberg (2005). Accumulation of miR-155 and BIC RNA in human B cell lymphomas. Proceedings of the National Academy of Sciences of the United States of America 102(10): 3627-3632.

Enright, A. J., B. John, U. Gaul, T. Tuschl, C. Sander and D. S. Marks (2003). MiRNA targets in Drosophila. Genome Biology 5(1): R1.

Everett, H. and G. McFadden (1999). Apoptosis: an innate immune response to virus infection. Trends Microbiol 7.

Feldman, E. R., M. Kara, C. B. Coleman, K. R. Grau, L. M. Oko, B. J. Krueger, R. Renne, L. F. van Dyk and S. A. Tibbetts (2014). Virus-Encoded MiRNAs Facilitate Gammaherpesvirus Latency and Pathogenesis In Vivo. mBio 5(3).

Felli, N., L. Fontana, E. Pelosi, R. Botta, D. Bonci, F. Facchiano, F. Liuzzi, V. Lulli, O. Morsilli, S. Santoro, M. Valtieri, G. A. Calin, C.-G. Liu, A. Sorrentino, C. M. Croce and C. Peschle (2005). MiRNAs 221 and 222 inhibit normal erythropoiesis and erythroleukemic cell growth via kit receptor down-modulation. Proceedings of the National Academy of Sciences of the United States of America 102(50): 18081-18086.

Friedländer, M. R., S. D. Mackowiak, N. Li, W. Chen and N. Rajewsky (2012). miRDeep2 accurately identifies known and hundreds of novel miRNA genes in seven animal clades. Nucleic Acids Research 40(1): 37-52.

Friedman, R. C., K. K.-H. Farh, C. B. Burge and D. P. Bartel (2009). Most mammalian mRNAs are conserved targets of miRNAs. Genome Research 19(1): 92-105.

Gao, F.-B. (2010). Context-dependent functions of specific miRNAs in neuronal development. Neural Development 5(1): 25.

Gibbings, D. J., C. Ciaudo, M. Erhardt and O. Voinnet (2009). Multivesicular bodies associate with components of miRNA effector complexes and modulate miRNA activity. Nat Cell Biol 11(9): 1143-1149.

Gironella, M., M. Seux, M.-J. Xie, C. Cano, R. Tomasini, J. Gommeaux, S. Garcia, J. Nowak, M. L. Yeung, K.-T. Jeang, A. Chaix, L. Fazli, Y. Motoo, Q.

Wang, P. Rocchi, A. Russo, M. Gleave, J.-C. Dagorn, J. L. Iovanna, A. Carrier, M.-J. Pébusque and N. J. Dusetti (2007). Tumor protein 53-induced nuclear protein 1 expression is repressed by miR-155, and its restoration inhibits pancreatic tumor development. Proceedings of the National Academy of Sciences 104(41): 16170-16175.

Gomez-Casado, E., A. Estepa and J. M. Coll (2011). A comparative review on European-farmed finfish RNA viruses and their vaccines. Vaccine 29(15): 2657-2671.

Granchi, C., D. Fancelli and F. Minutolo (2014). An update on therapeutic opportunities offered by cancer glycolytic metabolism. Bioorganic & Medicinal Chemistry Letters 24(21): 4915-4925.

Griffiths-Jones, S., R. J. Grocock, S. van Dongen, A. Bateman and A. J. Enright (2006). miRBase: miRNA sequences, targets and gene nomenclature. Nucleic Acids Res 34.

Guimbellot, J. S., S. W. Erickson, T. Mehta, H. Wen, G. P. Page, E. J. Sorscher and J. S. Hong (2009). Correlation of miRNA levels during hypoxia with predicted target mRNAs through genome-wide microarray analysis. BMC Medical Genomics 2(1): 1-17.

Guo, X. K., Q. Zhang, L. Gao, N. Li, X. X. Chen and W. H. Feng (2013). Increasing expression of miRNA 181 inhibits porcine reproductive and respiratory syndrome virus replication and has implications for controlling virus infection. J Virol 87.

Guo, Y. E., T. Oei and J. A. Steitz (2015). Herpesvirus saimiri MiRNAs Preferentially Target Host Cell Cycle Regulators. Journal of Virology 89(21): 10901-10911.

Ha, M. and V. N. Kim (2014). Regulation of miRNA biogenesis. Nat Rev Mol Cell Biol 15(8): 509-524.

Hafner, M., M. Landthaler, L. Burger, M. Khorshid, J. Hausser, P. Berninger, A. Rothballer, M. Ascano, A.-C. Jungkamp, M. Munschauer, A. Ulrich, G. S. Wardle, S. Dewell, M. Zavolan and T. Tuschl (2010). Transcriptome-wide

Identification of RNA-Binding Protein and MiRNA Target Sites by PAR-CLIP. Cell 141(1): 129-141.

Hammond, S. M., S. Boettcher, A. A. Caudy, R. Kobayashi and G. J. Hannon (2001). Argonaute2, a Link Between Genetic and Biochemical Analyses of RNAi. Science 293(5532): 1146-1150.

Hausser, J., A. P. Syed, B. Bilen and M. Zavolan (2013). Analysis of CDS-located miRNA target sites suggests that they can effectively inhibit translation. Genome Research 23(4): 604-615.

Hennessy, E. J., F. J. Sheedy, D. Santamaria, M. Barbacid and L. A. J. O'Neill (2011). Toll-like Receptor-4 (TLR4) Down-regulates MiRNA-107, Increasing Macrophage Adhesion via Cyclin-dependent Kinase 6. Journal of Biological Chemistry 286(29): 25531-25539.

Ho, A. S., X. Huang, H. Cao, C. Christman-Skieller, K. Bennewith, Q.-T. Le and A. C. Koong (2010). Circulating miR-210 as a novel hypoxia marker in pancreatic cancer. Translational Oncology 3(2): 109-113.

Hou, J., P. Wang, L. Lin, X. Liu, F. Ma, H. An, Z. Wang and X. Cao (2009). MiRNA-146a Feedback Inhibits RIG-I-Dependent Type I IFN Production in Macrophages by Targeting TRAF6, IRAK1, and IRAK2. The Journal of Immunology 183(3): 2150-2158.

Hu, T., Q. Fu, P. Chen, L. Ma, O. Sin and D. Guo (2009). Construction of an Artificial MiRNA Expression Vector for Simultaneous Inhibition of Multiple Genes in Mammalian Cells. International Journal of Molecular Sciences 10(5): 2158.

Hua, Z., Q. Lv, W. Ye, C.-K. A. Wong, G. Cai, D. Gu, Y. Ji, C. Zhao, J. Wang, B. B. Yang and Y. Zhang (2006). MiRNA-Directed Regulation of VEGF and Other Angiogenic Factors under Hypoxia. PLOS ONE 1(1): e116.

Huang, X., Q.-T. Le and A. J. Giaccia (2010). MiR-210 – micromanager of the hypoxia pathway. Trends in Molecular Medicine 16(5): 230-237.

Huang, X., L. Ding, K. L. Bennewith, R. T. Tong, S. M. Welford, K. K. Ang, M. Story, Q.-T. Le and A. J. Giaccia (2009). Hypoxia-Inducible mir-210 Regulates

Normoxic Gene Expression Involved in Tumor Initiation. Molecular Cell 35(6): 856-867.

Huang, Y., W. Wang and Q. Ren (2016). Two host miRNAs influence WSSV replication via STAT gene regulation. 6: 23643.

Hutvagner, G. and P. D. Zamore (2002). A miRNA in a multiple-turnover RNAi enzyme complex. Science 297.

Ivan, M., A. L. Harris, F. Martelli and R. Kulshreshtha (2008). Hypoxia response and miRNAs: no longer two separate worlds. Journal of Cellular and Molecular Medicine 12(5a): 1426-1431.

Iwasaki, S., M. Kobayashi, M. Yoda, Y. Sakaguchi, S. Katsuma, T. Suzuki and Y. Tomari (2010). Hsc70/Hsp90 Chaperone Machinery Mediates ATP-Dependent RISC Loading of Small RNA Duplexes. Molecular Cell 39(2): 292-299.

Izzard, L., D. Dlugolenski, Y. Xia, M. McMahon, D. Middleton, R. A. Tripp and J. Stambas (2017). Enhanced immunogenicity following miR-155 incorporation into the influenza A virus genome. Virus Research 235: 115-120.

Johnson, C. D., A. Esquela-Kerscher, G. Stefani, M. Byrom, K. Kelnar, D. Ovcharenko, M. Wilson, X. Wang, J. Shelton, J. Shingara, L. Chin, D. Brown and F. J. Slack (2007). The let-7 MiRNA Represses Cell Proliferation Pathways in Human Cells. Cancer Research 67(16): 7713-7722.

Jopling, C. L., S. Schuetz and P. Sarnow (2008). Position-dependent function for a tandem miRNA miR-122-binding site located in the hepatitis C virus RNA genome. Cell Host Microbe 4.

Jopling, C. L., M. Yi, A. M. Lancaster, S. M. Lemon and P. Sarnow (2005). Modulation of Hepatitis C Virus RNA Abundance by a Liver-Specific MiRNA. Science 309(5740): 1577-1581.

Jung, Y. J., J.-W. Kim, S. J. Park, B. Y. Min, E. S. Jang, N. Y. Kim, S.-H. Jeong, C. M. Shin, S. H. Lee, Y. S. Park, J.-H. Hwang, N. Kim and D. H. Lee (2013). c-Myc-mediated overexpression of miR-17-92 suppresses replication of hepatitis B virus in human hepatoma cells. Journal of Medical Virology 85(6): 969-978.

Kallio, P. J., I. Pongratz, K. Gradin, J. McGuire and L. Poellinger (1997). Activation of hypoxia-inducible factor 1α: Posttranscriptional regulation and conformational change by recruitment of the Arnt transcription factor. Proceedings of the National Academy of Sciences 94(11): 5667-5672.

Katakowski, M., B. Buller, X. Wang, T. Rogers and M. Chopp (2010). Functional miRNA is transferred between glioma cells. Cancer research 70(21): 8259-8263.

Kent, W. J., C. W. Sugnet, T. S. Furey, K. M. Roskin, T. H. Pringle, A. M. Zahler, Haussler and David (2002). The Human Genome Browser at UCSC. Genome Research 12(6): 996-1006.

Kertesz, M., N. Iovino, U. Unnerstall, U. Gaul and E. Segal (2007). The role of site accessibility in miRNA target recognition. Nat Genet 39(10): 1278-1284.

Kharaziha, P., S. Ceder, Q. Li and T. Panaretakis (2012). Tumor cell-derived exosomes: A message in a bottle. Biochimica et Biophysica Acta (BBA) - Reviews on Cancer 1826(1): 103-111.

Kim, M. S., D. S. Kim and K. H. Kim (2011). Generation and characterization of NV gene-knockout recombinant viral hemorrhagic septicemia virus (VHSV) genotype IVa. Diseases of Aquatic Organisms 97(1): 25-35.

Kim, S., S. Lee, J. Shin, Y. Kim, I. Evnouchidou, D. Kim, Y.-K. Kim, Y.-E. Kim, J.-H. Ahn, S. R. Riddell, E. Stratikos, V. N. Kim and K. Ahn (2011). Human cytomegalovirus miRNA miR-US4-1 inhibits CD8+ T cell responses by targeting the aminopeptidase ERAP1. Nat Immunol 12(10): 984-991.

Kim, W.-S., S.-R. Kim, D. Kim, J.-O. Kim, M.-A. Park, S.-I. Kitamura, H.-Y. Kim, D.-H. Kim, H.-J. Han, S.-J. Jung and M.-J. Oh (2009). An outbreak of VHSV (viral hemorrhagic septicemia virus) infection in farmed olive flounder *Paralichthys olivaceus* in Korea. Aquaculture 296(1): 165-168.

King, A. M. Q., E. Lefkowitz, M. J. Adams and E. B. Carstens (2012). Rhabdoviridae. Virus Taxonomy. San Diego, Elsevier**:** 686-713.

Kornobis, E., L. Cabellos, F. Aguilar, C. Frías-López, J. Rozas, J. Marco and R. Zardoya (2015). TRUFA: A User-Friendly Web Server for de novo RNA-seq

Analysis Using Cluster Computing. Evolutionary Bioinformatics 11(Supplementary Material 23873): 97-104.

Kozomara, A. and S. Griffiths-Jones (2014). miRBase: annotating high confidence miRNAs using deep sequencing data. Nucleic Acids Research 42(D1): D68-D73.

Kulshreshtha, R., M. Ferracin, S. E. Wojcik, R. Garzon, H. Alder, F. J. Agosto-Perez, R. Davuluri, C.-G. Liu, C. M. Croce, M. Negrini, G. A. Calin and M. Ivan (2007). A MiRNA Signature of Hypoxia. Molecular and Cellular Biology 27(5): 1859-1867.

Lagos-Quintana, M., R. Rauhut, W. Lendeckel and T. Tuschl (2001). Identification of Novel Genes Coding for Small Expressed RNAs. Science 294(5543): 853-858.

Lagos, D., G. Pollara, S. Henderson, F. Gratrix, M. Fabani, R. S. B. Milne, F. Gotch and C. Boshoff (2010). miR-132 regulates antiviral innate immunity through suppression of the p300 transcriptional co-activator. Nat Cell Biol 12(5): 513-519.

Lau, K., K. P. Lai, J. Y. J. Bao, N. Zhang, A. Tse, A. Tong, J. W. Li, S. Lok, R. Y. C. Kong, W. Y. Lui, A. Wong and R. S. S. Wu (2014). Identification and Expression Profiling of MiRNAs in the Brain, Liver and Gonads of Marine Medaka (*Oryzias melastigma*) and in Response to Hypoxia. PLOS ONE 9(10): e110698.

Lecellier, C.-H., P. Dunoyer, K. Arar, J. Lehmann-Che, S. Eyquem, C. Himber, A. Saïb and O. Voinnet (2005). A Cellular MiRNA Mediates Antiviral Defense in Human Cells. Science 308(5721): 557-560.

Lee, R. C., R. L. Feinbaum and V. Ambros (1993). The C. elegans heterochronic gene lin-4 encodes small RNAs with antisense complementarity to lin-14. Cell 75(5): 843-854.

Lee, Y., M. Kim, J. Han, K.-H. Yeom, S. Lee, S. H. Baek and V. N. Kim (2004). MiRNA genes are transcribed by RNA polymerase II. The EMBO Journal 23(20): 4051-4060.

Lee, Y., C. Ahn, J. Han, H. Choi, J. Kim, J. Yim, J. Lee, P. Provost, O. Radmark, S. Kim and V. N. Kim (2003). The nuclear RNase III Drosha initiates miRNA processing. Nature 425(6956): 415-419.

Lei, Z., B. Li, Z. Yang, H. Fang, G.-M. Zhang, Z.-H. Feng and B. Huang (2009). Regulation of HIF-1α and VEGF by miR-20b Tunes Tumor Cells to Adapt to the Alteration of Oxygen Concentration. PLOS ONE 4(10): e7629.

Lenoir, G. and P. de Kinkelin (1975). Fish rhabdoviruses: comparative study of protein structure. Journal of Virology 16(2): 259-262.

Lewis, B. P., I. h. Shih, M. W. Jones-Rhoades, D. P. Bartel and C. B. Burge (2003). Prediction of Mammalian MiRNA Targets. Cell 115(7): 787-798.

Li, A., W. Song, J. Qian, Y. Li, J. He, Q. Zhang, W. Li, A. Zhai, W. Kao, Y. Hu, H. Li, J. Wu, H. Ling, Z. Zhong and F. Zhang (2013). MiR-122 modulates type I interferon expression through blocking suppressor of cytokine signaling 1. The International Journal of Biochemistry & Cell Biology 45(4): 858-865.

Li, C., H. He, M. Zhu, S. Zhao and X. Li (2013). Molecular characterisation of porcine miR-155 and its regulatory roles in the TLR3/TLR4 pathways. Developmental & Comparative Immunology 39(1): 110-116.

Li, D., X. Liu, L. Lin, J. Hou, N. Li, C. Wang, P. Wang, Q. Zhang, P. Zhang, W. Zhou, Z. Wang, G. Ding, S.-M. Zhuang, L. Zheng, W. Tao and X. Cao (2011). MiRNA-99a Inhibits Hepatocellular Carcinoma Growth and Correlates with Prognosis of Patients with Hepatocellular Carcinoma. Journal of Biological Chemistry 286(42): 36677-36685.

Li, G., Y. Zhao, L. Wen, Z. Liu, F. Yan and C. Gao (2014). Identification and Characterization of MiRNAs in the Spleen of Common Carp Immune Organ. Journal of Cellular Biochemistry 115(10): 1768-1778.

Li, S., J. Ren, N. Xu, J. Zhang, Q. Geng, C. Cao, C. Lee, J. Song, J. Li and H. Chen (2014). MiRNA-19b functions as potential anti-thrombotic protector in patients with unstable angina by targeting tissue factor. Journal of Molecular and Cellular Cardiology 75: 49-57.

Lim, L. P., M. E. Glasner, S. Yekta, C. B. Burge and D. P. Bartel (2003). Vertebrate MiRNA Genes. Science 299(5612): 1540-1540.

Lima, R. T., S. Busacca, G. M. Almeida, G. Gaudino, D. A. Fennell and M. H. Vasconcelos (2011). MiRNA regulation of core apoptosis pathways in cancer. European Journal of Cancer 47(2): 163-174.

Lin, Y., W. Deng, J. Pang, T. Kemper and M. Lu (2015). P0562 : MiRNA-99 family modulates hepatitis B virus replication by targeting the phosphoinositide 3-KINASE/Akt/mTOR signaling pathway. Journal of Hepatology 62(Supplement 2): S526.

Lind, E. F., A. R. Elford and P. S. Ohashi (2013). Micro-RNA 155 Is Required for Optimal CD8+ T Cell Responses to Acute Viral and Intracellular Bacterial Challenges. The Journal of Immunology 190(3): 1210-1216.

Lingel, A., B. Simon, E. Izaurralde and M. Sattler (2003). Structure and nucleic-acid binding of the Drosophila Argonaute 2 PAZ domain. Nature 426(6965): 465-469.

Liu, Z., B. Xiao, B. Tang, B. Li, N. Li, E. Zhu, G. Guo, J. Gu, Y. Zhuang, X. Liu, H. Ding, X. Zhao, H. Guo, X. Mao and Q. Zou (2010). Up-regulated miRNA-146a negatively modulate Helicobacter pylori-induced inflammatory response in human gastric epithelial cells. Microbes and Infection 12(11): 854-863.

Lu, J., S. Guo, B. L. Ebert, H. Zhang, X. Peng, J. Bosco, J. Pretz, R. Schlanger, J. Y. Wang, R. H. Mak, D. M. Dombkowski, F. I. Preffer, D. T. Scadden and T. R. Golub (2008). MiRNA-Mediated Control of Cell Fate in Megakaryocyte-Erythrocyte Progenitors. Developmental Cell 14(6): 843-853.

MacRae, I. J., K. Zhou, F. Li, A. Repic, A. N. Brooks, W. Z. Cande, P. D. Adams and J. A. Doudna (2006). Structural Basis for Double-Stranded RNA Processing by Dicer. Science 311(5758): 195-198.

Marianne, R.-H., K. V. Tuija, R.-P. Eija, S. Sanna, S. Helle Frank, J. O. Niels and T. Hannele (2006). Viral haemorrhagic septicaemia (VHS) outbreaks in Finnish rainbow trout farms. Diseases of Aquatic Organisms 72(3): 201-211.

Masaki, S., R. Ohtsuka, Y. Abe, K. Muta and T. Umemura (2007). Expression patterns of miRNAs 155 and 451 during normal human erythropoiesis. Biochemical and Biophysical Research Communications 364(3): 509-514.

Masoudi-Nejad, A., K. Tonomura, S. Kawashima, Y. Moriya, M. Suzuki, M. Itoh, M. Kanehisa, T. Endo and S. Goto (2006). EGassembler: online bioinformatics service for large-scale processing, clustering and assembling ESTs and genomic DNA fragments. Nucleic Acids Research 34(suppl_2): W459-W462.

Meyers, T. R. and J. R. Winton (1995). Viral hemorrhagic septicemia virus in North America. Annual Review of Fish Diseases 5: 3-24.

Min, X. J., G. Butler, R. Storms and A. Tsang (2005). OrfPredictor: predicting protein-coding regions in EST-derived sequences. Nucleic Acids Research 33(suppl_2): W677-W680.

Minet, E., D. Mottet, G. Michel, I. Roland, M. Raes, J. Remacle and C. Michiels (1999). Hypoxia-induced activation of HIF-1: role of HIF-1α-Hsp90 interaction. FEBS Letters 460(2): 251-256.

Miranda, K. C., T. Huynh, Y. Tay, Y.-S. Ang, W.-L. Tam, A. M. Thomson, B. Lim and I. Rigoutsos (2006). A Pattern-Based Method for the Identification of MiRNA Binding Sites and Their Corresponding Heteroduplexes. Cell 126(6): 1203-1217.

Mitchell, P. S., R. K. Parkin, E. M. Kroh, B. R. Fritz, S. K. Wyman, E. L. Pogosova-Agadjanyan, A. Peterson, J. Noteboom, K. C. O'Briant, A. Allen, D. W. Lin, N. Urban, C. W. Drescher, B. S. Knudsen, D. L. Stirewalt, R. Gentleman, R. L. Vessella, P. S. Nelson, D. B. Martin and M. Tewari (2008). Circulating miRNAs as stable blood-based markers for cancer detection. Proceedings of the National Academy of Sciences 105(30): 10513-10518.

Montague, T. G., J. M. Cruz, J. A. Gagnon, G. M. Church and E. Valen (2014). CHOPCHOP: a CRISPR/Cas9 and TALEN web tool for genome editing. Nucleic Acids Research 42(W1): W401-W407.

Morais, D. R., S. T. Reis, N. Viana, C. B. Piantino, C. Massoco, C. Moura, N. Dip, I. A. Silva, M. Srougi and K. R. Leite (2014). The involvement of miR-100 in bladder urothelial carcinogenesis changing the expression levels of mRNA and

proteins of genes related to cell proliferation, survival, apoptosis and chromosomal stability. Cancer Cell International 14(1): 119.

Moriya, Y., M. Itoh, S. Okuda, A. C. Yoshizawa and M. Kanehisa (2007). KAAS: an automatic genome annotation and pathway reconstruction server. Nucleic Acids Research 35(suppl_2): W182-W185.

Mukherjee, A., A. M. Di Bisceglie and R. B. Ray (2015). Hepatitis C Virus-Mediated Enhancement of MiRNA miR-373 Impairs the JAK/STAT Signaling Pathway. Journal of Virology 89(6): 3356-3365.

Nawrocki, E. P., S. W. Burge, A. Bateman, J. Daub, R. Y. Eberhardt, S. R. Eddy, E. W. Floden, P. P. Gardner, T. A. Jones, J. Tate and R. D. Finn (2015). Rfam 12.0: updates to the RNA families database. Nucleic Acids Research 43(D1): D130-D137.

Ni, S., Y. Yan, H. Cui, Y. Yu, Y. Huang and Q. Qin (2017). Fish miR-146a promotes Singapore grouper iridovirus infection by regulating cell apoptosis and NF-κB activation. Journal of General Virology 98(6): 1489-1499.

O'Carroll, D. and A. Schaefer (2013). General Principals of miRNA Biogenesis and Regulation in the Brain. Neuropsychopharmacology 38(1): 39-54.

O'Connell, R. M., D. Kahn, W. S. J. Gibson, J. L. Round, R. L. Scholz, A. A. Chaudhuri, M. E. Kahn, D. S. Rao and D. Baltimore (2010). MiRNA-155 Promotes Autoimmune Inflammation by Enhancing Inflammatory T Cell Development. Immunity 33(4): 607-619.

Ohh, M., C. W. Park, M. Ivan, M. A. Hoffman, T.-Y. Kim, L. E. Huang, N. Pavletich, V. Chau and W. G. Kaelin (2000). Ubiquitination of hypoxia-inducible factor requires direct binding to the β-domain of the von Hippel–Lindau protein. Nature Cell Biology 2: 423.

Okamura, K., A. Ishizuka, H. Siomi and M. C. Siomi (2004). Distinct roles for Argonaute proteins in small RNA-directed RNA cleavage pathways. Genes & Development 18(14): 1655-1666.

Ordas, A., Z. Kanwal, V. Lindenberg, J. Rougeot, M. Mink, H. P. Spaink and A. H. Meijer (2013). MiRNA-146 function in the innate immune transcriptome

response of zebrafish embryos to Salmonella typhimurium infection. BMC Genomics 14(1): 696.

Pan, D., O. Flores, Jennifer L. Umbach, Jean M. Pesola, P. Bentley, Pamela C. Rosato, David A. Leib, Bryan R. Cullen and Donald M. Coen (2014). A Neuron-Specific Host MiRNA Targets Herpes Simplex Virus-1 ICP0 Expression and Promotes Latency. Cell Host & Microbe 15(4): 446-456.

Pareek, S., S. Roy, B. Kumari, P. Jain, A. Banerjee and S. Vrati (2014). miR-155 induction in microglial cells suppresses Japanese encephalitis virus replication and negatively modulates innate immune responses. Journal of Neuroinflammation 11(1): 97.

Park, J.-E., I. Heo, Y. Tian, D. K. Simanshu, H. Chang, D. Jee, D. J. Patel and V. N. Kim (2011). Dicer recognizes the 5' end of RNA for efficient and accurate processing. Nature 475(7355): 201-205.

Park, M. H., S. S. Bae, K.-Y. Choi and D. S. Min (2015). Phospholipase D2 promotes degradation of hypoxia-inducible factor-1α independent of lipase activity. Experimental & Molecular Medicine 47(11): e196.

Pasquinelli, A. E. (2012). MiRNAs and their targets: recognition, regulation and an emerging reciprocal relationship. Nat Rev Genet 13(4): 271-282.

Pasquinelli, A. E., B. J. Reinhart, F. Slack, M. Q. Martindale, M. I. Kuroda, B. Maller, D. C. Hayward, E. E. Ball, B. Degnan, P. Muller, J. Spring, A. Srinivasan, M. Fishman, J. Finnerty, J. Corbo, M. Levine, P. Leahy, E. Davidson and G. Ruvkun (2000). Conservation of the sequence and temporal expression of let-7 heterochronic regulatory RNA. Nature 408(6808): 86-89.

Patrick, D. M., C. C. Zhang, Y. Tao, H. Yao, X. Qi, R. J. Schwartz, L. Jun-Shen Huang and E. N. Olson (2010). Defective erythroid differentiation in miR-451 mutant mice mediated by 14-3-3ζ. Genes & Development 24(15): 1614-1619.

Pedersen, I. M., G. Cheng, S. Wieland, S. Volinia, C. M. Croce, F. V. Chisari and M. David (2007). Interferon modulation of cellular miRNAs as an antiviral mechanism. Nature 449.

Perry, M. M., S. A. Moschos, A. E. Williams, N. J. Shepherd, H. M. Larner-Svensson and M. A. Lindsay (2008). Rapid Changes in MiRNA-146a Expression Negatively Regulate the IL-1β-Induced Inflammatory Response in Human Lung Alveolar Epithelial Cells. The Journal of Immunology 180(8): 5689-5698.

Poellinger, L. and R. S. Johnson (2004). HIF-1 and hypoxic response: the plot thickens. Current Opinion in Genetics & Development 14(1): 81-85.

Ponomarev, E. D., T. Veremeyko and H. L. Weiner (2013). MiRNAs are universal regulators of differentiation, activation, and polarization of microglia and macrophages in normal and diseased CNS. Glia 61(1): 91-103.

Potenza, N., U. Papa, N. Mosca, F. Zerbini, V. Nobile and A. Russo (2011). Human miRNA hsa-miR-125a-5p interferes with expression of hepatitis B virus surface antigen. Nucleic Acids Research 39(12): 5157-5163.

Punj, V., H. Matta, S. Schamus, A. Tamewitz, B. Anyang and P. M. Chaudhary (2010). Kaposi's sarcoma-associated herpesvirus-encoded viral FLICE inhibitory protein (vFLIP) K13 suppresses CXCR4 expression by upregulating miR-146a. Oncogene 29(12): 1835-1844.

Rajaram, M. V. S., B. Ni, J. D. Morris, M. N. Brooks, T. K. Carlson, B. Bakthavachalu, D. R. Schoenberg, J. B. Torrelles and L. S. Schlesinger (2011). *Mycobacterium tuberculosis* lipomannan blocks TNF biosynthesis by regulating macrophage MAPK-activated protein kinase 2 (MK2) and miRNA miR-125b. Proceedings of the National Academy of Sciences 108(42): 17408-17413.

Riaz, A., I. Dry, C. S. Levy, J. Hopkins, F. Grey, D. J. Shaw and R. G. Dalziel (2014). Ovine herpesvirus-2 encoded miRNAs target virus genes involved in virus latency. The Journal of general virology 95(Pt 2): 472-480.

Richards, J. G. (2011). Physiological, behavioral and biochemical adaptations of intertidal fishes to hypoxia. The Journal of Experimental Biology 214(2): 191-199.

Rodriguez, A., E. Vigorito, S. Clare, M. V. Warren, P. Couttet, D. R. Soond, S. van Dongen, R. J. Grocock, P. P. Das and E. A. Miska (2007). Requirement of bic/miRNA-155 for normal immune function. Science 316.

Rodriguez, A., E. Vigorito, S. Clare, M. V. Warren, P. Couttet, D. R. Soond, S. van Dongen, R. J. Grocock, P. P. Das, E. A. Miska, D. Vetrie, K. Okkenhaug, A. J. Enright, G. Dougan, M. Turner and A. Bradley (2007). Requirement of bic/miRNA-155 for Normal Immune Function. Science 316(5824): 608-611.

Rommer, A., K. Steinleitner, H. Hackl, C. Schneckenleithner, M. Engelmann, M. Scheideler, I. Vlatkovic, R. Kralovics, S. Cerny-Reiterer, P. Valent, H. Sill and R. Wieser (2013). Overexpression of primary miRNA 221/222 in acute myeloid leukemia. BMC Cancer 13(1): 364.

Røsjø, H., M. B. Dahl, A. Bye, J. Andreassen, M. Jørgensen, U. Wisløff, G. Christensen, T. Edvardsen and T. Omland (2014). Prognostic Value of Circulating MiRNA-210 Levels in Patients with Moderate to Severe Aortic Stenosis. PLoS ONE 9(3): e91812.

Rueda, A., G. Barturen, R. Lebrón, C. Gómez-Martín, Á. Alganza, J. L. Oliver and M. Hackenberg (2015). sRNAtoolbox: an integrated collection of small RNA research tools. Nucleic Acids Research 43(W1): W467-W473.

Schnall-Levin, M., Y. Zhao, N. Perrimon and B. Berger (2010). Conserved miRNA targeting in Drosophila is as widespread in coding regions as in 3′UTRs. Proceedings of the National Academy of Sciences 107(36): 15751-15756.

Schulte, L. N., A. J. Westermann and J. Vogel (2013). Differential activation and functional specialization of miR-146 and miR-155 in innate immune sensing. Nucleic Acids Research 41(1): 542-553.

Schulte, L. N., A. Eulalio, H. J. Mollenkopf, R. Reinhardt and J. Vogel (2011). Analysis of the host miRNA response to salmonella uncovers the control of major cytokines by the let-7 family. EMBO J 30.

Schyth, B. D., D. B. Bela-ong, S. A. H. Jalali, L. B. J. Kristensen, K. Einer-Jensen, F. S. Pedersen and N. Lorenzen (2015). Two Virus-Induced MiRNAs Known Only from Teleost Fishes Are Orthologues of MiRNAs Involved in Cell Cycle Control in Humans. PLOS ONE 10(7): e0132434.

Semenza, G. L. (2009). Regulation of Oxygen Homeostasis by Hypoxia-Inducible Factor 1. Physiology 24(2): 97-106.

Shen, W.-F., Y.-L. Hu, L. Uttarwar, E. Passegue and C. Largman (2008). MiRNA-126 Regulates HOXA9 by Binding to the Homeobox. Molecular and Cellular Biology 28(14): 4609-4619.

Shi, J., Z. Duan, J. Sun, M. Wu, B. Wang, J. Zhang, H. Wang, N. Hu and Y. Hu (2014). Identification and validation of a novel miRNA-like molecule derived from a cytoplasmic RNA virus antigenome by bioinformatics and experimental approaches. Virology Journal 11(1): 121.

Skall, H. F., N. J. Olesen and S. Mellergaard (2005). Viral haemorrhagic septicaemia virus in marine fish and its implications for fish farming – a review. Journal of Fish Diseases 28(9): 509-529.

Soitamo, A. J., C. M. I. Råbergh, M. Gassmann, L. Sistonen and M. Nikinmaa (2001). Characterization of a Hypoxia-inducible Factor (HIF-1α) from Rainbow Trout: accumulation of protein occurs at normal venous oxygen tension. Journal of Biological Chemistry 276(23): 19699-19705.

Stroka, D. M., T. Burkhardt, I. Desbaillets, R. H. Wenger, D. A. H. Neil, C. Bauer, M. Gassmann and D. Candinas (2001). HIF-1 is expressed in normoxic tissue and displays an organ-specific regulation under systemic hypoxia. The FASEB Journal 15(13): 2445-2453.

Tadashi, I., N. Toyohiko, K. Tatsuya, N. Taizou and M. Teruo (2001). An outbreak of VHSV (viral hemorrhagic septicemia virus) infection in farmed Japanese flounder *Paralichthys olivaceus* in Japan. Diseases of Aquatic Organisms 47(2): 87-99.

Taganov, K. D., M. P. Boldin, K. J. Chang and D. Baltimore (2006). NF-kappaB-dependent induction of miRNA miR-146, an inhibitor targeted to signaling proteins of innate immune responses. Proc Natl Acad Sci U S A 103.

TAN, S.-L. and P. J. PARKER (2003). Emerging and diverse roles of protein kinase C in immune cell signalling. Biochemical Journal 376(3): 545-552.

Tang, Y., X. Luo, H. Cui, X. Ni, M. Yuan, Y. Guo, X. Huang, H. Zhou, N. de Vries, P. P. Tak, S. Chen and N. Shen (2009). MiRNA-146a contributes to abnormal activation of the type I interferon pathway in human lupus by targeting the key signaling proteins. Arthritis & Rheumatism 60(4): 1065-1075.

Tay, Y., J. Zhang, A. M. Thomson, B. Lim and I. Rigoutsos (2008). MiRNAs to Nanog, Oct4 and Sox2 coding regions modulate embryonic stem cell differentiation. Nature 455(7216): 1124-1128.

Thai, T.-H., D. P. Calado, S. Casola, K. M. Ansel, C. Xiao, Y. Xue, A. Murphy, D. Frendewey, D. Valenzuela, J. L. Kutok, M. Schmidt-Supprian, N. Rajewsky, G. Yancopoulos, A. Rao and K. Rajewsky (2007). Regulation of the Germinal Center Response by MiRNA-155. Science 316(5824): 604-608.

Triboulet, R., B. Mari, Y.-L. Lin, C. Chable-Bessia, Y. Bennasser, K. Lebrigand, B. Cardinaud, T. Maurin, P. Barbry, V. Baillat, J. Reynes, P. Corbeau, K.-T. Jeang and M. Benkirane (2007). Suppression of MiRNA-Silencing Pathway by HIV-1 During Virus Replication. Science 315(5818): 1579-1582.

Trobaugh, D. W., C. L. Gardner, C. Sun, A. D. Haddow, E. Wang, E. Chapnik, A. Mildner, S. C. Weaver, K. D. Ryman and W. B. Klimstra (2014). RNA viruses can hijack vertebrate miRNAs to suppress innate immunity. Nature 506(7487): 245-248.

Tse, A. C.-K., J.-W. Li, T.-F. Chan, R. S.-S. Wu and K.-P. Lai (2015). Hypoxia induces miR-210, leading to anti-apoptosis in ovarian follicular cells of marine medaka *Oryzias melastigma*. Aquatic Toxicology 165(Supplement C): 189-196.

Tse, A. C.-K., J.-W. Li, S. Y. Wang, T.-F. Chan, K. P. Lai and R. S.-S. Wu (2016). Hypoxia alters testicular functions of marine medaka through miRNAs regulation. Aquatic Toxicology 180(Supplement C): 266-273.

Valadi, H., K. Ekstrom, A. Bossios, M. Sjostrand, J. J. Lee and J. O. Lotvall (2007). Exosome-mediated transfer of mRNAs and miRNAs is a novel mechanism of genetic exchange between cells. Nat Cell Biol 9(6): 654-659.

Valencia-Sanchez, M. A., J. Liu, G. J. Hannon and R. Parker (2006). Control of translation and mRNA degradation by miRNAs and siRNAs. Genes & Development 20(5): 515-524.

Varnholt, H., U. Drebber, F. Schulze, I. Wedemeyer, P. Schirmacher, H.-P. Dienes and M. Odenthal (2008). MiRNA gene expression profile of hepatitis C virus–associated hepatocellular carcinoma. Hepatology 47(4): 1223-1232.

Vigorito, E., K. L. Perks, C. Abreu-Goodger, S. Bunting, Z. Xiang, S. Kohlhaas, P. P. Das, E. A. Miska, A. Rodriguez, A. Bradley, K. G. C. Smith, C. Rada, A. J. Enright, K.-M. Toellner, I. C. M. MacLennan and M. Turner (2007). miRNA-155 Regulates the Generation of Immunoglobulin Class-Switched Plasma Cells. Immunity 27(6): 847-859.

Vliegenthart, A. D. B., P. S. Lewis, C. S. Tucker, J. Del Pozo, S. Rider, D. J. Antoine, V. Dubost, M. Westphal, P. Moulin, M. A. Bailey, J. G. Moggs, C. E. Goldring, B. K. Park and J. W. Dear (2014). Retro-orbital blood acquisition facilitates circulating miRNA measurement in zebrafish with paracetamol hepatotoxicity. Zebrafish 11(3): 219-226.

Wakiyama, M., K. Takimoto, O. Ohara and S. Yokoyama (2007). Let-7 miRNA-mediated mRNA deadenylation and translational repression in a mammalian cell-free system. Genes & Development 21(15): 1857-1862.

Wang a, X., S. Zhou a, X. Ding, G. Zhu and J. Guo (2010). Effect of triazophos, fipronil and their mixture on miRNA expression in adult zebrafish. Journal of Environmental Science and Health, Part B 45(7): 648-657.

Wang, B., Z. Gan, S. Cai, Z. Wang, D. Yu, Z. Lin, Y. Lu, Z. Wu and J. Jian (2016). Comprehensive identification and profiling of Nile tilapia (*Oreochromis niloticus*) miRNAs response to *Streptococcus agalactiae* infection through high-throughput sequencing. Fish & Shellfish Immunology 54: 93-106.

Wang, P., J. Hou, L. Lin, C. Wang, X. Liu, D. Li, F. Ma, Z. Wang and X. Cao (2010). Inducible miRNA-155 Feedback Promotes Type I IFN Signaling in Antiviral Innate Immunity by Targeting Suppressor of Cytokine Signaling 1. The Journal of Immunology 185(10): 6226-6233.

Wang, S., L. Qiu, X. Yan, W. Jin, Y. Wang, L. Chen, E. Wu, X. Ye, G. F. Gao, F. Wang, Y. Chen, Z. Duan and S. Meng (2012). Loss of miRNA 122 expression in patients with hepatitis B enhances hepatitis B virus replication through cyclin G1-modulated P53 activity. Hepatology 55(3): 730-741.

Wang, S., X. Zhang, Y. Ju, B. Zhao, X. Yan, J. Hu, L. Shi, L. Yang, Z. Ma, L. Chen, Y. Liu, Z. Duan, X. Chen and S. Meng (2013). MiRNA-146a Feedback Suppresses T Cell Immune Function by Targeting Stat1 in Patients with Chronic Hepatitis B. The Journal of Immunology 191(1): 293-301.

Wang, Y., S. Juranek, H. Li, G. Sheng, T. Tuschl and D. J. Patel (2008). Structure of an argonaute silencing complex with a seed-containing guide DNA and target RNA duplex. Nature 456(7224): 921-926.

Wang, Y., L. Jiang, X. Ji, B. Yang, Y. Zhang and X.-D. Fu (2013). Hepatitis B Viral RNA Directly Mediates Down-regulation of the Tumor Suppressor MiRNA miR-15a/miR-16-1 in Hepatocytes. Journal of Biological Chemistry 288(25): 18484-18493.

Wang, Y., V. Brahmakshatriya, B. Lupiani, S. M. Reddy, B. Soibam, A. L. Benham, P. Gunaratne, H.-c. Liu, N. Trakooljul, N. Ing, R. Okimoto and H. Zhou (2012). Integrated analysis of miRNA expression and mRNA transcriptome in lungs of avian influenza virus infected broilers. BMC Genomics 13(1): 278.

Wen, B., H. Dai, Y. Yang, Y. Zhuang and R. Sheng (2013). MiRNA-23b Inhibits Enterovirus 71 Replication through Downregulation of EV71 VPl Protein. Intervirology 56(3): 195-200.

Willimott, S. and S. D. Wagner (2012). miR-125b and miR-155 Contribute to BCL2 Repression and Proliferation in Response to CD40 Ligand (CD154) in Human Leukemic B-cells. Journal of Biological Chemistry 287(4): 2608-2617.

Winter, J., S. Jung, S. Keller, R. I. Gregory and S. Diederichs (2009). Many roads to maturity: miRNA biogenesis pathways and their regulation. Nat Cell Biol 11(3): 228-234.

Wu, S., L. Liu, A. Zohaib, L. Lin, J. Yuan, M. Wang and X. Liu (2015). MiRNA profile analysis of Epithelioma papulosum cyprini cell line before and after SVCV infection. Developmental & Comparative Immunology 48(1): 124-128.

Wu, S., L. He, Y. Li, T. Wang, L. Feng, L. Jiang, P. Zhang and X. Huang (2013). miR-146a facilitates replication of dengue virus by dampening interferon induction by targeting TRAF6. J Infect 67.

Yang, L., G. Yang and X. Zhang (2014). The miR-100-mediated pathway regulates apoptosis against virus infection in shrimp. Fish & Shellfish Immunology 40(1): 146-153.

Yang, S., H. Zhang, L. Guo, Y. Zhao and F. Chen (2014). Reconstructing the coding and non-coding RNA regulatory networks of miRNAs and mRNAs in breast cancer. Gene 548(1): 6-13.

Zhang, B.-c., J. Zhang and L. Sun (2014). In-depth profiling and analysis of host and viral miRNAs in Japanese flounder (*Paralichthys olivaceus*) infected with megalocytivirus reveal involvement of miRNAs in host-virus interaction in teleost fish. BMC Genomics 15(1): 878.

Zhang, B.-c., Z.-j. Zhou and L. Sun (2016). pol-miR-731, a teleost miRNA upregulated by megalocytivirus, negatively regulates virus-induced type I interferon response, apoptosis, and cell cycle arrest. Scientific Reports 6: 28354.

Zhang, C., C. Wang, X. Chen, C. Yang, K. Li, J. Wang, J. Dai, Z. Hu, X. Zhou, L. Chen, Y. Zhang, Y. Li, H. Qiu, J. Xing, Z. Liang, B. Ren, C. Yang, K. Zen and C.-Y. Zhang (2010). Expression Profile of MiRNAs in Serum: A Fingerprint for Esophageal Squamous Cell Carcinoma. Clinical Chemistry 56(12): 1871-1879.

Zhang, M., X. Wang, W. Li and Y. Cui (2015). miR-107 and miR-25 simultaneously target LATS2 and regulate proliferation and invasion of gastric adenocarcinoma (GAC) cells. Biochemical and Biophysical Research Communications 460(3): 806-812.

Zhang, Y., D. Zheng, Y. Xiong, C. Xue, G. Chen, B. Yan and Q. Ye (2014). miR-202 suppresses cell proliferation in human hepatocellular carcinoma by downregulating LRP6 post-transcriptionally. FEBS Letters 588(10): 1913-1920.

Zhang, Z., L. Zhang, Z.-Y. Yin, X.-L. Fan, B. Hu, L.-Q. Wang and D. Zhang (2014). miR-107 regulates cisplatin chemosensitivity of A549 non small cell lung cancer cell line by targeting cyclin dependent kinase 8. International Journal of Clinical and Experimental Pathology 7(10): 7236-7241.

Zuker, M. (2003). Mfold web server for nucleic acid folding and hybridization prediction. Nucleic Acids Research 31(13): 3406-3415.

Supplements

Chapter I. Changes in miRNAs expression profile of olive flounder (*Paralichthys olivaceus*) in response to viral hemorrhagic septicemia virus (VHSV)

Supplement 1. MiRNAs of olive flounder and their homologs in zebrafish and other vertebrates and candidate of novel miRNAs

miRNA name	Sequence	Homologue in other species	miRNA name	Sequence	Homologue in other species
pol-let-7a	TGAGGTAGTAGGTTGTATAGTT	dre-let-7a	**pol-miR-223**	TGTCAGTTTGTCAAATACCCC	dre-miR-223
pol-let-7b	TGAGGTAGTAGGTTGTGTGGTT	dre-let-7b	**pol-miR-22a-3p**	AAGCTGCCAGCTGAAGAACTGT	dre-miR-22a-3p
pol-let-7c-3p	CTGTACAACCTTCTAGCTTTCC	dre-let-7c-3p	**pol-miR-22a-5p**	AGTTCTTCACTGGCAAGCTTTA	dre-miR-22a-5p
pol-let-7c-5p	TGAGGTAGTAGGTTGTATGGTT	dre-let-7c-5p	**pol-miR-22b-3p**	AAGCTGCCAGTTGAAGAGCTGT	dre-miR-22b-3p
pol-let-7d-3p	CTGTACAACCTTCTAGCTTTCC	dre-let-7d-3p	**pol-miR-22b-5p**	CGTTCTTCACTGGCTAGCTTTA	dre-miR-22b-5p
pol-let-7d-5p	TGAGGTAGTTGGTTGTATGGTT	dre-let-7d-5p	**pol-miR-23a-3-5p**	GGATTCCTGGCAGAGTGATTT	dre-miR-23a-3-5p
pol-let-7e	TGAGGTAGTAGATTGAATAGTT	dre-let-7e	**pol-miR-23a-3p**	ATCACATTGCCAGGGATTTCCA	dre-miR-23a-3p
pol-let-7f	TGAGGTAGTAGATTGTATAGTT	dre-let-7f	**pol-miR-23a-5p**	GAATTCCTGGCAGAGTGATTT	dre-miR-23a-5p
pol-let-7g	TGAGGTAGTAGTTTGTATAGTT	dre-let-7g	**pol-miR-23b**	ATCACATTGCCAGGGATTACCA	dre-miR-23b
pol-let-7h	TGAGGTAGTAAGTTGTGTTGTT	dre-let-7h	**pol-miR-24**	TGGCTCAGTTCAGCAGGAACAG	dre-miR-24
pol-let-7i	TGAGGTAGTAGTTTGTGCTGTT	dre-let-7i	**pol-miR-25-3p**	CATTGCACTTGTCTCGGTCTGA	dre-miR-25-3p
pol-let-7j	TGAGGTAGTTGTTTGTACAGTT	dre-let-7j	**pol-miR-25-5p**	AGGCGGAGACTTGGGCAGCTGCC	dre-miR-25-5p
pol-miR-1	TGGAATGTAAAGAAGTATGTAT	dre-miR-1	**pol-miR-26a-2-3p**	CCTATTCATGATTACTTGCACT	dre-miR-26a-2-3p
pol-miR-100-2-3p	CAAGCTCGTGTCTATAGGTATG	dre-miR-100-2-3p	**pol-miR-26a-3p**	CCTATTCGGGATGACTTGGTTC	dre-miR-26a-3p
pol-miR-100-3p	CAAGCTTGTATCTATAGGTATC	dre-miR-100-3p	**pol-miR-26a-5p**	TTCAAGTAATCCAGGATAGGCT	dre-miR-26a-5p
pol-miR-100-5p	AACCCGTAGATCCGAACTTGTG	dre-miR-100-5p	**pol-miR-26b**	TTCAAGTAATCCAGGATAGGTT	dre-miR-26b
pol-miR-101a	TACAGTACTGTGATAACTGAAG	dre-miR-101a	**pol-miR-27a-3p**	TTCACAGTGGCTAAGTTCCGCT	dre-miR-27a-3p
pol-miR-101b	TACAGTACTATGATAACTGAAG	dre-miR-101b	**pol-miR-27a-5p**	AGGACTTAGCTCACTCTGTGAACA	dre-miR-27a-5p
pol-miR-103	AGCAGCATTGTACAGGGCTATGA	dre-miR-103	**pol-miR-27b-3p**	TTCACAGTGGCTAAGTTCTGCA	dre-miR-27b-3p
pol-miR-107a-3p	AGCAGCATTGTACAGGGCTATCA	dre-miR-107a-3p	**pol-miR-27b-5p**	AGAGCTTAGCTGATTGGTGAACA	dre-miR-27b-5p
pol-miR-107a-5p	AGCTTCTTTACAGTGTTGTCTTG	dre-miR-107a-5p	**pol-miR-27c-3p**	TTCACAGTGGTTAAGTTCTGC	dre-miR-27c-3p
pol-miR-107b	AGCAGCATTGTACAGGGCTTT	dre-miR-107b	**pol-miR-27c-5p**	CTTAACCCACTTGTGAACAATG	dre-miR-27c-5p
pol-miR-10a-3p	CAAATTCGTGTCTTGGGGAATA	dre-miR-10a-3p	**pol-miR-27d**	TTCACAGTGGCTAAGTTCTTCA	dre-miR-27d
pol-miR-10a-5p	TACCCTGTAGATCCGAATTTGT	dre-miR-10a-5p	**pol-miR-27e**	TTCACAGTGGCTAAGTTCAGTG	dre-miR-27e
pol-miR-10b-2-3p	CAAATACGTCTCTACAGGAAT	dre-miR-10b-2-3p	**pol-miR-29a**	TAGCACCATTTGAAATCGGTTA	dre-miR-29a
pol-miR-10b-3p	ACAGATTCGATTCTAGGGGAGT	dre-miR-10b-3p	**pol-miR-29b**	TAGCACCATTTGAAATCAGTGT	dre-miR-29b
pol-miR-10b-5p	TACCCTGTAGAACCGAATTTGTG	dre-miR-10b-5p	**pol-miR-301a**	CAGTGCAATAGTATTGTCAAAG	dre-miR-301a
pol-miR-10c-3p	AAATTCGTATCTAGGGGAGTA	dre-miR-10c-3p	**pol-miR-301b-3p**	CAGTGCAATAGTATTGTCATTG	dre-miR-301b-3p
pol-miR-10c-5p	TACCCTGTAGATCCGGATTTGT	dre-miR-10c-5p	**pol-miR-301b-5p**	GCTTTGACGATGTTGCACTAC	dre-miR-301b-5p

pol-miR-10d-3p	CAGATTCGGTTTTAGGGGAGTA	dre-miR-10d-3p	**pol-miR-301c-3p**	CAGTGCAATAGTATTGTCATAG	dre-miR-301c-3p
pol-miR-10d-5p	TACCCTGTAGAACCGAATGTGTG	dre-miR-10d-5p	**pol-miR-301c-5p**	GCTCTGACGATGTTGCACTAC	dre-miR-301c-5p
pol-miR-122	TGGAGTGTGACAATGGTGTTTG	dre-miR-122	**pol-miR-30a-3p**	CTTTCAGTCTGATGTTTGCTGC	dre-miR-30a-3p
pol-miR-124-3p	TAAGGCACGCGGTGAATGCCAA	dre-miR-124-3p	**pol-miR-30a-5p**	TGTAAACATTCCCGACTGGAAG	dre-miR-30a-5p
pol-miR-124-4-5p	TGTGTTCACAGTGGACCTTGAT	dre-miR-124-4-5p	**pol-miR-30b**	TGTAAACATCCTACACTCAGCT	dre-miR-30b
pol-miR-124-5p	CGTGTTCACAGCGGACCTTGAT	dre-miR-124-5p	**pol-miR-30c-3p**	CCGGGAGTGGGATGTTTGCGCT	dre-miR-30c-3p
pol-miR-124-6-5p	CGTGTTCACGGCGGACCTTGAT	dre-miR-124-6-5p	**pol-miR-30c-5p**	TGTAAACATCCTACACTCTCAG	dre-miR-30c-5p
pol-miR-125a	TCCCTGAGACCCTTAACCTGTG	dre-miR-125a	**pol-miR-30d**	TGTAAACATCCCCGACTGGAAG	dre-miR-30d
pol-miR-125b-1-3p	ACGGGTTAGGTTCTTGGGAGCT	dre-miR-125b-1-3p	**pol-miR-30e-3p**	CTTTCAGTCGGATGTTTGCAGC	dre-miR-30e-3p
pol-miR-125b-2-3p	CGGGTTGGGTTCTCGGGAGCT	dre-miR-125b-2-3p	**pol-miR-30e-5p**	TGTAAACATCCTTGACTGGAAG	dre-miR-30e-5p
pol-miR-125b-3-3p	ACAGGTTAAGCTCTTGGGACCT	dre-miR-125b-3-3p	**pol-miR-31**	GGCAAGATGTTGGCATAGCTG	dre-miR-31
pol-miR-125b-5p	TCCCTGAGACCCTAACTTGTGA	dre-miR-125b-5p	**pol-miR-338**	TCCAGCATCAGTGATTTTGTTG	dre-miR-338
pol-miR-125c-3p	ACGGGTCAGGAGCTTGGGAGAC	dre-miR-125c-3p	**pol-miR-34a**	TGGCAGTGTCTTAGCTGGTTGT	dre-miR-34a
pol-miR-125c-5p	TCCCTGAGACCCTAACTCGTGA	dre-miR-125c-5p	**pol-miR-34b**	TAGGCAGTGTTGTTAGCTGATTG	dre-miR-34b
pol-miR-126a-3p	TCGTACCGTGAGTAATAATGC	dre-miR-126a-3p	**pol-miR-34c-3p**	AATCACTAACCTCACTACCAGG	dre-miR-34c-3p
pol-miR-126a-5p	CATTATTACTTTTGGTACGCG	dre-miR-126a-5p	**pol-miR-34c-5p**	AGGCAGTGCAGTTAGTTGATTAC	dre-miR-34c-5p
pol-miR-126b-3p	TCGTACCGTGAGTAATAGTGCA	dre-miR-126b-3p	**pol-miR-363-3p**	AATTGCACGGTATCCATCTGTA	dre-miR-363-3p
pol-miR-126b-5p	CATTATTACTTTTGGTACGCG	dre-miR-126b-5p	**pol-miR-363-5p**	CGGGTGGATGACTCTGCAATTTT	dre-miR-363-5p
pol-miR-128-3p	TCACAGTGAACCGGTCTCTTTT	dre-miR-128-3p	**pol-miR-365**	TAATGCCCCTAAAAATCCTTAT	dre-miR-365
pol-miR-128-5p	CGGGGCCGTGGCACTGTATGAGA	dre-miR-128-5p	**pol-miR-375**	TTTGTTCGTTCGGCTCGCGTTA	dre-miR-375
pol-miR-129-1-3p	GAAGCCCTTACCCCAAAAAGT	dre-miR-129-1-3p	**pol-miR-3906**	AAAAGCATTTTGAATGCAGATTT	dre-miR-3906
pol-miR-129-3p	AAGCCCTTACCCCAAAAAGCAT	dre-miR-129-3p	**pol-miR-429a**	TAATACTGTCTGGTAATGCCGT	dre-miR-429a
pol-miR-129-5p	CTTTTTGCGGTCTGGGCTTGCT	dre-miR-129-5p	**pol-miR-429b**	TAATACTGCCTGGTAATGCCAT	dre-miR-429b
pol-miR-1306	CCACCTCCCCTGCAAACGTCCA	dre-miR-1306	**pol-miR-430a-11-5p**	ACCCTCACAAAAGCACTGACT	dre-miR-430a-11-5p
pol-miR-130a	CAGTGCAATGTTAAAAGGGCAT	dre-miR-130a	**pol-miR-430a-12-5p**	ACCCTCACAAAAGCACTGACT	dre-miR-430a-12-5p
pol-miR-130b	CAGTGCAATAATGAAAGGGCAT	dre-miR-130b	**pol-miR-430a-13-5p**	ACCCTCACAAAAGCACTGACT	dre-miR-430a-13-5p
pol-miR-130c-3p	CAGTGCAATATTAAAAGGGCAT	dre-miR-130c-3p	**pol-miR-430a-14-5p**	ACCCTCACAAAAGCACTGACT	dre-miR-430a-14-5p
pol-miR-130c-5p	GCCCTTTTTCTGTTGTACTACT	dre-miR-130c-5p	**pol-miR-430a-15-5p**	ACCCTCACAAAAGCACTGACT	dre-miR-430a-15-5p
pol-miR-132-3p	TAACAGTCTACAGCCATGGTCG	dre-miR-132-3p	**pol-miR-430a-16-5p**	ACCCTCACAAAAGCACTGACT	dre-miR-430a-16-5p
pol-miR-132-5p	ACCGTGGCATTAGATTGTTACT	dre-miR-132-5p	**pol-miR-430a-17-5p**	ACCCTCACAAAAGCACTGACT	dre-miR-430a-17-5p
pol-miR-133a-2-5p	AGCTGGTAAAATGGAACCAAA	dre-miR-133a-2-5p	**pol-miR-430a-3p**	TAAGTGCTATTTGTTGGGGTAG	dre-miR-430a-3p
pol-miR-133a-3p	TTTGGTCCCCTTCAACCAGCTG	dre-miR-133a-3p	**pol-miR-430a-4-5p**	ACCCTCACAAAAGCACTGACT	dre-miR-430a-4-5p
pol-miR-133a-5p	AGCTGGTAAAATGGAACCAAAT	dre-miR-133a-5p	**pol-miR-430a-5p**	ACCCTCACAAAGGCACTGACT	dre-miR-430a-5p
pol-miR-133b-3p	TTTGGTCCCCTTCAACCAGCTA	dre-miR-133b-3p	**pol-miR-430b-3p**	AAAGTGCTATCAAGTTGGGGTAG	dre-miR-430b-3p
pol-miR-133b-5p	GCTGGTCAAATGGAACCAAGTC	dre-miR-133b-5p	**pol-miR-430b-5p**	CAACTCTAACTTTAGCATCTTTC	dre-miR-430b-5p
pol-miR-133c-3p	TTTGGTCCCTTTCAACCAGCTA	dre-miR-133c-3p	**pol-miR-430c-3p**	TAAGTGCTTCTCTTTGGGGTAG	dre-miR-430c-3p
pol-miR-133c-5p	GCTGGTAAAACGGAACCAAGTC	dre-miR-133c-5p	**pol-miR-430c-5p**	CACTTCAAACAGGAGCATTGA	dre-miR-430c-5p
pol-miR-135a	TATGGCTTTTTATTCCTATGTGA	dre-miR-135a	**pol-miR-430i-3p**	TAAGTGCTATTTGTTGGCGTAG	dre-miR-430i-3p

pol-miR-135b-3p	ATATAGGGATGGAAGCCATGCA	dre-miR-135b-3p	**pol-miR-430i-5p**	ACCCTCACAAAAGCACTGACT	dre-miR-430i-5p
pol-miR-135b-5p	TATGGCTTTTTATTCCTATCTG	dre-miR-135b-5p	**pol-miR-451**	AAACCGTTACCATTACTGAGTT	dre-miR-451
pol-miR-135c	TATGGCTTTCTATTCCTATGTG	dre-miR-135c	**pol-miR-454a**	TAGTGCAATATTGCTAATAGGG	dre-miR-454a
pol-miR-137-3p	TTATTGCTTAAGAATACGCGTA	dre-miR-137-3p	**pol-miR-454b**	TAGTGCAATATTGCTTATAGGG	dre-miR-454b
pol-miR-137-5p	ACGGGTATTCTTGGGTGGATAATA	dre-miR-137-5p	**pol-miR-455-2-5p**	GTATGTGCCCTTGGACTACATT	dre-miR-455-2-5p
pol-miR-138-3p	GCTATTTCACAACACCAGGGT	dre-miR-138-3p	**pol-miR-455-3p**	ATGCAGTCCATGGGCATATACAC	dre-miR-455-3p
pol-miR-138-5p	AGCTGGTGTTGTGAATCAGGCC	dre-miR-138-5p	**pol-miR-455-5p**	TATGTGCCCTTGGACTACATCG	dre-miR-455-5p
pol-miR-1388-3p	ATCTCAGGTTCGTCAGCCCATG	dre-miR-1388-3p	**pol-miR-456**	CAGGCTGGTTAGATGGTTGTCA	dre-miR-456
pol-miR-1388-5p	AGGACTGTCCAACCTGAGAATG	dre-miR-1388-5p	**pol-miR-457a**	AAGCAGCACATCAATATTGGCA	dre-miR-457a
pol-miR-139-3p	TGGGGAGGCAGCGCTGTTGGAAT	dre-miR-139-3p	**pol-miR-457b-3p**	TCCAGTATTGCTGTTCTGCTGT	dre-miR-457b-3p
pol-miR-139-5p	TCTACAGTGCATGTGTCT	dre-miR-139-5p	**pol-miR-457b-5p**	AAGCAGCACATAAATACTGGAG	dre-miR-457b-5p
pol-miR-140-3p	TACCACAGGGTAGAACCACGGAC	dre-miR-140-3p	**pol-miR-458-3p**	ATAGCTCTTTGAATGGTACTGC	dre-miR-458-3p
pol-miR-140-5p	CAGTGGTTTTACCCTATGGTAG	dre-miR-140-5p	**pol-miR-458-5p**	AGCGCCATTTACAGAGCTATAA	dre-miR-458-5p
pol-miR-141-3p	TAACACTGTCTGGTAACGATGC	dre-miR-141-3p	**pol-miR-459-3p**	CAGGGAATCTCTGTTACTGGGG	dre-miR-459-3p
pol-miR-141-5p	CATCTTACCTGACAGTGCTTGG	dre-miR-141-5p	**pol-miR-459-5p**	TCAGTAACAAGGATTCATCCTG	dre-miR-459-5p
pol-miR-142a-3p	TGTAGTGTTTCCTACTTTATGGA	dre-miR-142a-3p	**pol-miR-460-3p**	CACAGCGCATACAATGTGGATG	dre-miR-460-3p
pol-miR-142a-5p	CATAAAGTAGAAAGCACTACT	dre-miR-142a-5p	**pol-miR-460-5p**	CCTGCATTGTACACACTGTGCG	dre-miR-460-5p
pol-miR-142b-5p	CATAAAGTAGACAGCACTACTA	dre-miR-142b-5p	**pol-miR-461**	TCAGGAATGGGCTAAATGCCAA	dre-miR-461
pol-miR-143	TGAGATGAAGCACTGTAGCTC	dre-miR-143	**pol-miR-462**	TAACGGAACCCATAATGCAGCT	dre-miR-462
pol-miR-144-3p	TACAGTATAGATGATGTACT	dre-miR-144-3p	**pol-miR-489**	AGTGACATCATATGTACGGCTGC	dre-miR-489
pol-miR-144-5p	GGATATCATCGTATACTGTAAGT	dre-miR-144-5p	**pol-miR-499-3p**	AACATCACTTTAAGTCTGTGCT	dre-miR-499-3p
pol-miR-145-3p	GGATTCCTGGAAATACTGTTCT	dre-miR-145-3p	**pol-miR-499-5p**	TTAAGACTTGCAGTGATGTTTA	dre-miR-499-5p
pol-miR-145-5p	GTCCAGTTTTCCCAGGAATCCC	dre-miR-145-5p	**pol-miR-7145**	ACAATGGAAGCCAATGGTTACC	dre-miR-7145
pol-miR-146a	TGAGAACTGAATTCCATAGATGG	dre-miR-146a	**pol-miR-7146-3p**	TGAAGGTCAATGGTTACCAGTT	dre-miR-7146-3p
pol-miR-146b	TGAGAACTGAATTCCAAGGGTG	dre-miR-146b	**pol-miR-7146-5p**	GTAACCATTGACCTCCATAGT	dre-miR-7146-5p
pol-miR-148	TCAGTGCATTACAGAACTTTGT	dre-miR-148	**pol-miR-7147**	TGTACCATGCTGGTAGCCAGT	dre-miR-7147
pol-miR-150	TCTCCCAATCCTTGTACCAGTG	dre-miR-150	**pol-miR-7148-3p**	TATAAGCCAGTATTTCCGAT	dre-miR-7148-3p
pol-miR-152	TCAGTGCATGACAGAACTTTGG	dre-miR-152	**pol-miR-7148-5p**	ATGGAAATACTCGCTGATACTG	dre-miR-7148-5p
pol-miR-153a-3p	TTGCATAGTCACAAAAGTGATC	dre-miR-153a-3p	**pol-miR-7149-3p**	TTCCAAGTGTTATGAGTCAAAGT	dre-miR-7149-3p
pol-miR-153a-5p	GTCATTTTTGTGATGTTGCAGCT	dre-miR-153a-5p	**pol-miR-7149-5p**	TGTGAATCCTACACTGGAAGG	dre-miR-7149-5p
pol-miR-153b-3p	TTGCATAGTCACAAAAATGAGC	dre-miR-153b-3p	**pol-miR-722**	TTTTTTGCAGAAACGTTTCAGATT	dre-miR-722
pol-miR-153b-5p	GTCATTTTTGTGGTTTGCAGCT	dre-miR-153b-5p	**pol-miR-723-3p**	AAGACATCAATTAAATCTGTGCT	dre-miR-723-3p
pol-miR-153c-3p	TTGCATAGTCACAAAAATGATC	dre-miR-153c-3p	**pol-miR-723-5p**	GACAGTTTTAAATGATGTTACTTT	dre-miR-723-5p
pol-miR-153c-5p	GTCATTTTTGTGATTTGCAGCT	dre-miR-153c-5p	**pol-miR-724**	TTAAAGGGAATTTGCGACTGTT	dre-miR-724
pol-miR-155	TTAATGCTAATCGTGATAGGGG	dre-miR-155	**pol-miR-725-3p**	TTCAGTCATTGTTTCTAGTAGT	dre-miR-725-3p
pol-miR-15a-3p	CAGGCCGTACTGTGCTGCGGCA	dre-miR-15a-3p	**pol-miR-725-5p**	TGCTAGGAATGGTGGCTGAGAT	dre-miR-725-5p
pol-miR-15a-5p	TAGCAGCACAGAATGGTTTGTG	dre-miR-15a-5p	**pol-miR-726**	TTCACTACTAGCAGAACTCGG	dre-miR-726
pol-miR-15b-3p	CGAATCATGATGTGCTGTCACT	dre-miR-15b-3p	**pol-miR-727-3p**	GTTGAGGCGAGTTGAAGACTTA	dre-miR-727-3p

pol-miR-15b-5p	TAGCAGCACATCATGGTTTGTA	dre-miR-15b-5p	**pol-miR-727-5p**	TCAGTCTTCAATTCCTCCCAGC	dre-miR-727-5p
pol-miR-15c	AAGCAGCGCGTCATGGTTTTC	dre-miR-15c	**pol-miR-728**	ATACTAAGTACACTACGTTTTC	dre-miR-728
pol-miR-16a	TAGCAGCACGTAAATATTGGTG	dre-miR-16a	**pol-miR-729**	CATGGGTATGATACGACCTGGGTT	dre-miR-729
pol-miR-16b	TAGCAGCACGTAAATATTGGAG	dre-miR-16b	**pol-miR-730**	TCCTCATTGTGCATGCTGTGTGT	dre-miR-730
pol-miR-16c-3p	TCCAATATTGCTCGTGCTGCTGA	dre-miR-16c-3p	**pol-miR-731**	AATGACACGTTTTCTCCCGGATCG	dre-miR-731
pol-miR-16c-5p	TAGCAGCATGTAAATATTGGAG	dre-miR-16c-5p	**pol-miR-732**	CTCAAAGCAGAGAACTCTCGGT	dre-miR-732
pol-miR-1788-3p	CAGGCAGCTAAAGCAAGTCTG	dre-miR-1788-3p	**pol-miR-733**	TGCGTTGGTTTAGCTCAGTGGTT	dre-miR-733
pol-miR-1788-5p	GGCTTGTTTTAAGTTGCCTGCG	dre-miR-1788-5p	**pol-miR-734**	GTAAATGCTGCAGAATCGTACCG	dre-miR-734
pol-miR-17a-2-3p	ACTGCAGTGGAGGCACTTCAAGC	dre-miR-17a-2-3p	**pol-miR-735-3p**	CTCTCCCACCGCTAAACTTGAC	dre-miR-735-3p
pol-miR-17a-3p	ACTGCAGTGGAGGCACTTCTAG	dre-miR-17a-3p	**pol-miR-735-5p**	GGCTGGTCCGAAGGCGGT	dre-miR-735-5p
pol-miR-17a-5p	CAAAGTGCTTACAGTGCAGGTA	dre-miR-17a-5p	**pol-miR-736**	GTAAGACGAACAAAAAGTTTT	dre-miR-736
pol-miR-181a-2-3p	ACCATCGACCGTTGACTGTACC	dre-miR-181a-2-3p	**pol-miR-737-3p**	AATCAAAACCTAAAGAAAATA	dre-miR-737-3p
pol-miR-181a-3p	ACCATCGACCGTTGATTGTACC	dre-miR-181a-3p	**pol-miR-737-5p**	GTTTTTTTAGGTTTTGATTTT	dre-miR-737-5p
pol-miR-181a-5p	AACATTCAACGCTGTCGGTGAGT	dre-miR-181a-5p	**pol-miR-738**	GCTACGGCCCGCGTCGGGACCTC	dre-miR-738
pol-miR-181b-3p	CTCACTGATCAATGAATGCAAA	dre-miR-181b-3p	**pol-miR-740**	ATAAAAAGTGGTATGGTACAGT	dre-miR-740
pol-miR-181b-5p	AACATTCATTGCTGTCGGTGGG	dre-miR-181b-5p	**pol-miR-7a**	TGGAAGACTAGTGATTTTGTTGT	dre-miR-7a
pol-miR-181c-3p	CTCGCCGGACAATGAATGAGAA	dre-miR-181c-3p	**pol-miR-7b**	TGGAAGACTTGTGATTTTGTT	dre-miR-7b
pol-miR-181c-5p	CACATTCATTGCTGTCGGTGGG	dre-miR-181c-5p	**pol-miR-92a-2-5p**	AGGTTGGGATCGGCCGCAATGCT	dre-miR-92a-2-5p
pol-miR-182-3p	TGGTTCTAGACTTGCCAACTA	dre-miR-182-3p	**pol-miR-92a-3p**	TATTGCACTTGTCCCGGCCTGT	dre-miR-92a-3p
pol-miR-182-5p	TTTGGCAATGGTAGAACTCACA	dre-miR-182-5p	**pol-miR-92a-5p**	AGGTTGGGATTGGTAGCAATGCT	dre-miR-92a-5p
pol-miR-183-3p	TGAATTACCAAAGGGCCATAA	dre-miR-183-3p	**pol-miR-92b-3p**	TATTGCACTCGTCCCGGCCTCC	dre-miR-92b-3p
pol-miR-183-5p	TATGGCACTGGTAGAATTCACTG	dre-miR-183-5p	**pol-miR-92b-5p**	AGGTGTGGGATGTTGTGCAGTGTT	dre-miR-92b-5p
pol-miR-184	TGGACGGAGAACTGATAAGGGC	dre-miR-184	**pol-miR-93**	AAAAGTGCTGTTTGTGCAGGTA	dre-miR-93
pol-miR-187	TCGTGTCTTGTGTTGCAGCC	dre-miR-187	**pol-miR-9-3p**	TAAAGCTAGATAACCGAAAGT	dre-miR-9-3p
pol-miR-18a	TAAGGTGCATCTAGTGCAGATA	dre-miR-18a	**pol-miR-9-4-3p**	TAAAGCTAGAGAACCGAATGTA	dre-miR-9-4-3p
pol-miR-18b-3p	CTGCCCTAAGTGCCCCTTCTGG	dre-miR-18b-3p	**pol-miR-9-5p**	TCTTTGGTTATCTAGCTGTATGA	dre-miR-9-5p
pol-miR-18b-5p	TAAGGTGCATTTAGTGCAGATA	dre-miR-18b-5p	**pol-miR-96-3p**	CAATTATGTGTAGTGCCAATAT	dre-miR-96-3p
pol-miR-18c	TAAGGTGCATCTTGTGTAGTTA	dre-miR-18c	**pol-miR-96-5p**	TTTGGCACTAGCACATTTTTGCT	dre-miR-96-5p
pol-miR-190a	TGATATGTTTGATATATTAGGT	dre-miR-190a	**pol-miR-9-7-3p**	TAAAGCTAGAGAACCGAAAGTA	dre-miR-9-7-3p
pol-miR-190b	TGATATGTTTGATATTCGGTTG	dre-miR-190b	**pol-miR-99**	AACCCGTAGATCCGATCTTGTG	dre-miR-99
pol-miR-192	ATGACCTATGAATTGACAGCC	dre-miR-192	**pol-miR-21-3p**	CAGCCTACAGACTGTTGTCGCC	gga-miR-21-3p
pol-miR-193a-3p	AACTGGCCTACAAAGTCCCAGT	dre-miR-193a-3p	**pol-miR-456**	CTGGCTGGTTAGATGGTTGA	dre-miR-456
pol-miR-193a-5p	TGGGTCTTTGCGGGCAAGGTGA	dre-miR-193a-5p	**pol-miR-142-3p**	TCCATAAAGTAGGAAACACTA	bta-miR-142-3p
pol-miR-193b-3p	AACTGGCCCGCAAAGTCCCGCT	dre-miR-193b-3p	**pol-miR-142-5p**	CATAAAGTAGGAAACACTAC	gga-miR-142-5p
pol-miR-193b-5p	CGGGACTTTGGGGGCGAGATG	dre-miR-193b-5p	**pol-miR-100-3p**	ATACCTATAGATACAAGCTTGT	hsa-miR-100-3p
pol-miR-194a	TGTAACAGCAACTCCATGTGG	dre-miR-194a	**pol-miR-132b**	ACCATGGCTGTAGACTGTTACC	ccr-miR-132b
pol-miR-194b	TGTAACAGCCGCTCCATGTGGA	dre-miR-194b	**pol-miR-143**	TGAGAGGAAGTACTGTAGCT	efu-miR-143
pol-miR-196a-3p	CTGCAACGTGAAACTGTCTTAA	dre-miR-196a-3p	**pol-miR-203b-5p**	AAGTGGTCCTAAACATTTCACA	hsa-miR-203b-5p

pol-miR-196a-5p	TAGGTAGTTTCATGTTGTTGGG	dre-miR-196a-5p	**pol-miR-124c-3p**	TCAAGGTCCACTGTGAACACGT	gga-miR-124c-3p
pol-miR-196b	TAGGTAGTTTCAAGTTGTTGGG	dre-miR-196b	**pol-miR-24**	TGGCTCAGTTCAGCAGGAAC	cfa-miR-24
pol-miR-196c	TAGGTAGTTTGATGTTGTTGGG	dre-miR-196c	**pol-miR-124c-3p**	TCAAGGTCCGCTGTGAACACGA	gga-miR-124c-3p
pol-miR-196d	TAGGTAGTTTTATGTTGTTGGG	dre-miR-196d	**pol-miR-214-5p**	CACAGCAAGTGTAGACAGGCAG	hsa-miR-214-5p
pol-miR-199-3-3p	ACAGTAGTCCGCACATTGGTT	dre-miR-199-3-3p	**pol-miR-181a**	TACAATCAACGGTCGATGGTTT	efu-miR-181a
pol-miR-199-3p	TACAGTAGTCTGCACATTGGTT	dre-miR-199-3p	**pol-miR-205-3p**	ACTTCACACCACTGAAATCTG	dre-miR-205-3p
pol-miR-199-5p	CCCAGTGTTCAGACTACCTGTTC	dre-miR-199-5p	**pol-miR-29c**	TAGCACCATTTGAAATCGGTC	efu-miR-29c
pol-miR-19a-3p	TGTGCAAATCTATGCAAAACTGA	dre-miR-19a-3p	**pol-miR-4286**	ACCCCACTCCTGGTACCA	hsa-miR-4286
pol-miR-19a-5p	CTAGTTTTGCATAGTTGCACTA	dre-miR-19a-5p	**pol-miR-9-3p**	TTTCGGTTATCTAGCTTTATGA	mml-miR-9-3p
pol-miR-19b-3p	TGTGCAAATCCATGCAAAACTGA	dre-miR-19b-3p	**pol-miR-574**	TGTGTGTGTGTGTGTGTGTGTG	bta-miR-574
pol-miR-19b-5p	AGTTTTGCTGGTTTGCATTCAG	dre-miR-19b-5p	**pol-miR-100-3p**	TACCTATAGACACGAGCTTGT	hsa-miR-100-3p
pol-miR-19c-3p	TGTGCAAATCCATGCAAAACTCG	dre-miR-19c-3p	**pol-miR-100-3p**	ATACCTATAGACACGAGCTTGT	hsa-miR-100-3p
pol-miR-19c-5p	AGTTTTGCAGGATTGCATCCGG	dre-miR-19c-5p	**pol-miR-222b-5p**	TGCTCAGTGGTCAGTGTAGGTC	gga-miR-222b-5p
pol-miR-19d-3p	TGTGCAAACCCATGCAAAACTGA	dre-miR-19d-3p	**pol-miR-222-3p**	AGCTACATCCGGCTACTGGGTCTC	cgr-miR-222-3p
pol-miR-19d-5p	AGCTTTGCGGGGTGGGCAGTCAGC	dre-miR-19d-5p	**chr1_1136**	TGCAGACATCCTTGACTGG	
pol-miR-200a-3p	TAACACTGTCTGGTAACGATGT	dre-miR-200a-3p	**chr11_2213**	TCGAAACCGGGCGGAAACAAC	
pol-miR-200a-5p	CATCTTACCGGACAGTGCTGGA	dre-miR-200a-5p	**chr15_4278**	CCAACACCAGTCTGATAAGCT	
pol-miR-200b-3p	TAATACTGCCTGGTAATGATGA	dre-miR-200b-3p	**chr16_4157**	CCTGATTCACAACACCAGCTGT	
pol-miR-200b-5p	CATCTTACGAGGCAGCATTGGA	dre-miR-200b-5p	**chr16_4797**	TTACCACTGAATTCCATAGA	
pol-miR-200c-3p	TAATACTGCCTGGTAATGATGC	dre-miR-200c-3p	**chr17_5120**	ATCCTGTTCGTGACGCCA	
pol-miR-200c-5p	CATCTTACAAGGCAGTTTTGGA	dre-miR-200c-5p	**chr17_5367**	TTACAATTAAAGGATATTTCTT	
pol-miR-202-3p	AGAGGCATAGGGCATGGGAAAA	dre-miR-202-3p	**chr17_5605**	AGTACTTGGATGGGAGACC	
pol-miR-202-5p	TTCCTATGCATATACCTCTTTG	dre-miR-202-5p	**chr19_5662**	TGTTATAGTAGTTTGTGCTGT	
pol-miR-203a-3p	GTGAAATGTTTAGGACCACTTG	dre-miR-203a-3p	**chr19_6353**	ATCCGGCTCGAAGGACCA	
pol-miR-203a-5p	AGTGGTTCTTAACAGTTCAACAGT	dre-miR-203a-5p	**chr2_5758**	TGAGATGAAGCCCTGTGGCT	
pol-miR-203b-3p	GTGAAATGTTCAGGACCACTTG	dre-miR-203b-3p	**chr2_6729**	AGCACTGCCAGCTGAAGATCT	
pol-miR-203b-5p	AGTGGTTCTCAACAGTTCAACA	dre-miR-203b-5p	**chr2_6979**	AGGAATGAGCAGTATCTG	
pol-miR-204-2-3p	GCTGGGACAGCAAAGGGAGGT	dre-miR-204-2-3p	**chr20_7545**	TAAGTTAGTAGATTGACTAGT	
pol-miR-204-3p	GGCTGGGAAGTCAAAGGGACGC	dre-miR-204-3p	**chr20_8521**	GTTGGAAAGGCTGGGGGC	
pol-miR-204-5p	TTCCCTTTGTCATCCTATGCCT	dre-miR-204-5p	**chr22_6758**	CGTTATGAAGCACTGTAGCT	
pol-miR-205-3p	GATTTCAGTGGTGTGAAGTGTA	dre-miR-205-3p	**chr22_8318**	GTTATGAAGCACTGTAGCT	
pol-miR-205-5p	TCCTTCATTCCACCGGAGTCTG	dre-miR-205-5p	**chr23_7333**	GGTGAGCTGGTTTAAGGC	
pol-miR-206-3p	TGGAATGTAAGGAAGTGTGTGG	dre-miR-206-3p	**chr23_9130**	TGCGCTGAAGCGCTGTAG	
pol-miR-206-5p	ACATGCTTCCTTATATGCCCATA	dre-miR-206-5p	**chr24_9471**	TGTCCTCTGATTGGCTCGGACA	
pol-miR-20a-3p	ACTGCAGTGTGAGCACTTGAAG	dre-miR-20a-3p	**chr25_9133**	CAACGGCTGTTTTCTTTTTGC	
pol-miR-20a-5p	TAAAGTGCTTATAGTGCAGGTAG	dre-miR-20a-5p	**chr3_10421**	AACAGGTAGTCTGAACACTGGGC	
pol-miR-20b-3p	ACTGCAATGTCTGCACTTCAAGT	dre-miR-20b-3p	**chr3_8437**	AGGGGTATGATTCTCGCT	
pol-miR-20b-5p	CAAAGTGCTCACAGTGCAGGTAG	dre-miR-20b-5p	**chr4_10212**	CCCGGATAGCTCAGTCGGTAGA	

pol-miR-21	TAGCTTATCAGACTGGTGTTGGC	dre-miR-21	**chr4_11366**	GTGAGGTCCTCGGATCGGCCCCG
pol-miR-210-3p	CTGTGCGTGTGACAGCGGCTAA	dre-miR-210-3p	**chr4_11444**	TCGGTAGAGCATGAGACT
pol-miR-210-5p	AGCCACTGACTAACGCACATTG	dre-miR-210-5p	**chr4_11809**	TGGGAATACCAGGTGCTGTAAGCTT
pol-miR-212	TAACAGTCTACAGTCATGGCT	dre-miR-212	**chr4_11912**	TAGGGGTATGATTCTCGCT
pol-miR-214	ACAGCAGGCACAGACAGGCAG	dre-miR-214	**chr4_12507**	GCTTACGGCCATACCACC
pol-miR-216a	TAATCTCAGCTGGCAACTGTGA	dre-miR-216a	**chr5_11379**	CACCGGTACCATGATAACTGAA
pol-miR-216b	TAATCTCTGCAGGCAACTGTGA	dre-miR-216b	**chr5_12400**	TGATTTCCAATAATTGAGACAG
pol-miR-217	TACTGCATCAGGAACTGATTGG	dre-miR-217	**chr5_12752**	TAGTGCTTTCTACTTTATGGAT
pol-miR-2184	AACAGTAAGAGTTTATGTGCT	dre-miR-2184	**chr5_13070**	ATCATGGACAAAAAGTCC
pol-miR-2185-3p	GCCGCGATCAGCTGCACCAGC	dre-miR-2185-3p	**chr6_13181**	CACTACCTCATCTGAGCTTG
pol-miR-2185-5p	CGGTGCAGGACTCCGCGGCTC	dre-miR-2185-5p	**chr6_13287**	AAGCTGTGATGATGATGAC
pol-miR-2186	AAGTGGCCTCTAAAAGTCTA	dre-miR-2186	**chr7_13285**	TGTCACCACAGTGATGTCATTG
pol-miR-2187-3p	TTACAGGCTATGCTAATCTATG	dre-miR-2187-3p	**chr7_14065**	TGATGTAGTTGTTTGTAAAGTT
pol-miR-2187-5p	TTAATTAGTATAGCCTGTTTTA	dre-miR-2187-5p	**chr8_14672**	TTCCTGCTGAACTGAGCCAGT
pol-miR-2188-3p	CTGTGTGAGGTTAGACCTATC	dre-miR-2188-3p	**chr9_12541**	ACCCAGTAGCCAGATGTAGCTG
pol-miR-2188-5p	AAGGTCCAACCTCACATGTCC	dre-miR-2188-5p	**chr9_15229**	TCTACACTGACTACTGAGCATC
pol-miR-2189	TGATTGTTTGTATCAGCTGTGT	dre-miR-2189	**Zv9_NA251_602**	TCAGTAGAGCATGAGACC
pol-miR-218a	TTGTGCTTGATCTAACCATGTG	dre-miR-218a	**Zv9_NA889_569**	TGGCGGTCCGCCGCGAGGC
pol-miR-218b	TTGTGCTTGATCTAACCATGCA	dre-miR-218b	**Zv9_scaffold3472_92**	CAGTCGGTAGAGCATCAGAC
pol-miR-2191	TCACACCTACAATCCCTGGCA	dre-miR-2191	**Zv9_scaffold3487_134**	GACTTGGTCTAAGCTCCTCAGT
pol-miR-2192	AAAGTGAAAGGTGACTGAGAC	dre-miR-2192	**Zv9_scaffold3503_234**	CGCCGTGATCGTATAGTGGTTA
pol-miR-2193	TATGTGTGTATCAATTGTGTGAAA	dre-miR-2193	**Zv9_scaffold3503_287**	GGCTAGCTCAGTCGGTAGAG
pol-miR-219-3p	GGAGTTGTGGATGGACATCACGC	dre-miR-219-3p	**Zv9_scaffold3530_374**	TAGTGGTTAGTACTCTGCGTT
pol-miR-2194	GTAATGCTTCGACTGATTGGTG	dre-miR-2194		
pol-miR-2195	AGATTGGGGTGAGTTAGGGTG	dre-miR-2195		
pol-miR-219-5p	TGATTGTCCAAACGCAATTCTT	dre-miR-219-5p		
pol-miR-2196	CCTCTCTGTGCTGCCATTTGGGAC	dre-miR-2196		
pol-miR-2197	ATGATTCGACTCATATGGTG	dre-miR-2197		
pol-miR-2198	AGCTCGTGTCCCAAGGCGCCT	dre-miR-2198		
pol-miR-221-3p	AGCTACATTGTCTGCTGGGTTTC	dre-miR-221-3p		
pol-miR-221-5p	ACCTGGCATACAATGTAGATTTCTGT	dre-miR-221-5p		
pol-miR-222a-3p	AGCTACATCTGGCTACTGGGTCTC	dre-miR-222a-3p		
pol-miR-222a-5p	TGCTCAGTAGTCAGTGTAGATCC	dre-miR-222a-5p		
pol-miR-222b	AGCTACATCTGAATACTGGGTCA	dre-miR-222b		

Supplement 2. Fold change of differentially expressed miRNAs at different points of time

Mature miRNA	6 h.p.i	12 h.p.i	24 h.p.i	48 h.p.i	72 h.p.i
pol-miR-100-5p	-1.26043	1.070933	-1.1071	**-1.72222**	**-3.657112**
pol-miR-107b	-1.25338	**-1.8441**	**-2.60541**	**-1.73669**	**-1.693607**
pol-miR-122	-1.03563	-1.03563	**-1.6624**	**-1.5391**	**-1.516988**
pol-miR-133a-2-5p	1.41393	1.121138	1.015902	**1.931566**	**-1.60411**
pol-miR-133a-3p	-1.05905	1.063703	**1.631308**	**1.764555**	-1.248068
pol-miR-133a-5p	1.41393	1.121138	1.015902	**1.931566**	**-1.60411**
pol-miR-133b-3p	-1.44323	-1.48334	**1.570348**	**1.517838**	-1.172331
pol-miR-135a	-1.03131	-1.01901	1.163487	-1.1073	**1.685217**
pol-miR-135b-3p	**1.647525**	1.0988	1.072486	1.334492	-1.079654
pol-miR-135b-5p	1.358603	1.076245	**1.518928**	1.172451	1.025654
pol-miR-135c	1.210184	-1.12453	1.366912	1.210184	**1.527618**
pol-miR-137-3p	**1.822955**	1.458735	1.49176	**1.643203**	**2.496225**
pol-miR-1388-5p	1	-1.21697	-1.38329	**-1.51934**	-1.481814
pol-miR-145-3p	-1.27429	-1.08751	-1.27429	-1.27429	**-1.638145**
pol-miR-145-5p	1	1.261116	**1.61778**	1.392954	1.098457
pol-miR-146a	1.25274	-1.13326	**1.868443**	**3.634803**	**4.138208**
pol-miR-150	-1.22547	-1.10065	-1.22547	**-1.53028**	1.268553
pol-miR-153b-3p	1.269013	1.372919	1.389744	**1.691087**	**1.579086**
pol-miR-155	1.262355	1.089391	**14.36252**	**29.85027**	**36.104946**
pol-miR-15b-5p	-1.06058	-1.16688	**-1.59133**	-1.4908	**-1.591325**
pol-miR-16c-3p	-1.22084	-1.35848	-1.26171	**-1.79134**	-1.415768
pol-miR-1788-3p	1.083491	**2.315048**	**-1.64625**	1.047648	**-2.575175**
pol-miR-1788-5p	1.049878	**2.069042**	1.072582	1.009064	-1.078638
pol-miR-181a-2-3p	1.211545	-1.42221	**-1.79609**	**-1.79609**	**-1.866617**
pol-miR-181a-5p	-1.23521	-1.35515	-1.23521	-1.35515	**-1.513339**
pol-miR-181c-5p	1.018733	-1.12951	-1.08482	-1.36691	**-1.613983**
pol-miR-182-5p	-1.10454	1.161402	-1.49812	**-1.93705**	-1.321856
pol-miR-183-5p	-1.42893	1.129508	-1.25653	**-1.63344**	-1.210184
pol-miR-184	1.046975	1.009456	-1.06722	**-1.54363**	-1.313831
pol-miR-18c	1	-1.25443	-1.27833	-1.27833	**-1.768611**
pol-miR-190a	1.264177	1.401816	**1.694885**	1.452972	**1.648531**
pol-miR-193a-5p	1.089795	**1.501344**	-1.11308	-1.0816	-1.097228
pol-miR-196a-5p	**1.875671**	1.46813	1.220988	**1.875671**	1.153166
pol-miR-196c	**1.502126**	1.472964	1.177279	1.306971	1.182165
pol-miR-19a-3p	1.139214	1.17658	**1.862958**	1.308293	1.47293
pol-miR-19b-3p	1.44675	1.210461	**2.26534**	**1.656743**	**1.656743**

pol-miR-19c-3p	1.106667	1.173748	**1.846299**	1.351227	1.351227
pol-miR-19d-3p	1.215012	1.133343	**1.581091**	1.262281	1.498116
pol-miR-202-5p	**2.961607**	**4.129605**	**1.891383**	**1.552929**	**5.004339**
pol-miR-205-5p	1.337751	-1.19695	**1.979514**	1	1.137546
pol-miR-206-3p	-1.23548	1	**1.593633**	**1.538804**	-1.293302
pol-miR-20b-5p	-1.36956	**-1.5344**	**-1.5344**	**-1.8168**	**-2.230742**
pol-miR-210-3p	1.034468	-1.01475	**-1.77954**	1.034468	-1.014751
pol-miR-214	-1.34808	-1.07685	**-1.52762**	-1.39229	-1.348075
pol-miR-217	1.157973	1.094543	1.325138	**1.713881**	1.157973
pol-miR-2188-5p	**-1.61392**	1.359337	-1.09103	-1.39737	-1.214252
pol-miR-221-5p	1.461717	**1.619784**	**3.193286**	**1.963239**	**1.854018**
pol-miR-223	-1.34069	-1.18903	**-1.6098**	-1.24592	-1.466726
pol-miR-27b-5p	-1.04549	1	**-1.56193**	-1.25148	**-1.544344**
pol-miR-375	1.145808	1.027308	**-1.91794**	**-2.24797**	-1.043634
pol-miR-430a-3p	-1.3716	-1.34958	1.432965	**1.838762**	1.247611
pol-miR-430c-3p	**1.739151**	1.475782	**1.739151**	**2.575175**	1.326561
pol-miR-458-3p	1.212357	1	**-1.82153**	-1.45644	**-1.576095**
pol-miR-458-5p	-1.08205	-1.41495	**-1.65362**	-1.17147	1.256538
pol-miR-459-5p	1.068875	**-2.05562**	**-3.12714**	-1.04351	**-1.926506**
pol-miR-462	1.149207	1.149207	1.366375	**1.555612**	**2.01058**
pol-miR-489	1.235309	-1.02304	**-1.70885**	**-1.64761**	1
pol-miR-722	**1.741804**	1.204696	1.303368	**1.709775**	1.112319
pol-miR-730	-1.31576	-1.38665	-1.31576	**-1.70451**	-1.27094
pol-miR-731	1.114028	-1.01662	**2.334522**	**2.1099**	**2.1099**
pol-miR-737-5p	1.120342	1.09026	**1.648531**	1.195751	**1.946848**
pol-miR-9-4-3p	-1.33734	1.037018	-1.10351	-1.3041	**-1.847745**
pol-miR-99	-1.1695	1.249005	1.089951	-1.1695	**-2.513811**

Supplement 3. Predicted target genes of differentially expressed miRNAs based on miRanda and RNA22 tools and the function of different genes.

MiRNA	Target gene	MiRNA	Target gene
pol-miR-100-5p	transcription factor C/EBPalpha mRNA, complete cds.	pol-miR-193a-5p	cathepsin K mRNA, complete cds.
pol-miR-100-5p	myD88 mRNA for myeloid differentiaton factor 88, complete cds.	pol-miR-193a-5p	progranulin type II (pGRN) mRNA, complete cds, alternatively spliced.
pol-miR-107b	apoA-I mRNA for apolipoprotein A-I, complete cds.	pol-miR-193a-5p	progranulin type I (pGRN) mRNA, complete cds, alternatively spliced.
pol-miR-107b	B7-H1/DC mRNA, complete cds.	pol-miR-193a-5p	serotransferrin precursor (SroTP) mRNA, complete cds.
pol-miR-107b	ITGAL mRNA, complete cds.	pol-miR-193a-5p	DnaJ-like subfamily B member 11 (Hsp40B11) mRNA, complete cds.
pol-miR-107b	CD83 transcript 2 mRNA, complete cds, alternatively spliced.	pol-miR-193a-5p	putative fast skeletal muscle troponin mRNA, partial cds.
pol-miR-107b	nascent polypeptide-associated complex alpha mRNA, complete cds.	pol-miR-193a-5p	signal transducer and activator of transcription 1 mRNA, complete cds.
pol-miR-107b	transcription factor SOX-1b (Sox1b) mRNA, complete cds.	pol-miR-193a-5p	mRNA for CC chemokine-like molecule, complete cds.
pol-miR-107b	melanin-concentrating hormone receptor 2 mRNA, complete cds.	pol-miR-193a-5p	mRNA for Hoxd-4, complete cds.
pol-miR-107b	complement C1q-like protein 3 (C1ql3) mRNA, complete cds.	pol-miR-193a-5p	heat shock protein 90 beta (Hsp90beta) mRNA, complete cds.
pol-miR-107b	paired box protein 3b isoform Pax3b-1 (Pax3a) mRNA, complete cds.	pol-miR-193a-5p	heat shock protein 90 alpha (Hsp90alpha) mRNA, complete cds.
pol-miR-107b	vasa-like protein mRNA, complete cds.	pol-miR-193a-5p	glucose-regulated protein 78 (Grp78) mRNA, complete cds.
pol-miR-107b	HSL1 mRNA for hormone-sensitive lipase1, complete cds.	pol-miR-193a-5p	JFC/EBPb mRNA for CCAAT/Enhancer binding protein beta, complete cds.
pol-miR-107b	phospholipase C delta 1B Lf mRNA, complete cds.	pol-miR-193a-5p	calreticulin mRNA, complete cds.
pol-miR-107b	vasa mRNA, complete cds.	pol-miR-193a-5p	MHC class IIb antigen mRNA, complete cds.
pol-miR-107b	growth hormone-releasing hormone (GHRH) mRNA, complete cds.	pol-miR-193a-5p	mRNA for CD3 epsilon, complete cds.
pol-miR-107b	LGP2 mRNA, complete cds.	pol-miR-193a-5p	CPB mRNA for carboxypeptidase B, partial cds.
pol-miR-107b	syntenin mRNA, complete cds.	pol-miR-193a-5p	ctrlr mRNA for calcitonin receptor-like receptor, complete cds.
pol-miR-107b	phospholipase D (PLD) mRNA, complete cds.	pol-miR-193a-5p	cgrpr mRNA for calcitonin gene-related peptide receptor, complete cds.
pol-miR-107b	interferon regulatory factor 3 variant 2 (IRF3) mRNA, complete cds.	pol-miR-193a-5p	empty spiracles homeobox 2 (Emx2) mRNA, complete cds.
pol-miR-107b	interferon regulatory factor 3 variant 1 (IRF3) mRNA, complete cds.	pol-miR-193a-5p	lipoprotein lipase (LPL) mRNA, complete cds.
pol-miR-107b	macrophage stimulating-1 protein mRNA, complete cds.	pol-miR-193a-5p	TANK binding kinase 1 splice variant 3 (TBK1) mRNA, complete cds, alternatively spliced.
pol-miR-107b	cathepsin D mRNA, complete cds.	pol-miR-193a-5p	CD4-1 mRNA for T-cell surface glycoprotein CD4-1, complete cds.
pol-miR-107b	serotransferrin precursor (SroTP) mRNA, complete cds.	pol-miR-193a-5p	CD8 beta mRNA for T-cell surface glycoprotein CD8 beta chain, complete cds.
pol-miR-107b	DnaJ-like subfamily B member 11 (Hsp40B11) mRNA, complete cds.	pol-miR-193a-5p	toll-like receptor 5 soluble form mRNA, complete cds.

pol-miR-107b	calmodulin mRNA, complete cds.
pol-miR-107b	signal transducer and activator of transcription 1 mRNA, complete cds.
pol-miR-107b	mRNA for elastase 4 precursor, partial cds.
pol-miR-107b	inhibitor kappa B alpha mRNA, complete cds.
pol-miR-107b	heat shock protein 90 alpha (Hsp90alpha) mRNA, complete cds.
pol-miR-107b	glucose-regulated protein 78 (Grp78) mRNA, complete cds.
pol-miR-107b	JFC/EBPb mRNA for CCAAT/Enhancer binding protein beta, complete cds.
pol-miR-107b	TCR beta mRNA for T cell receptor beta chain, complete cds.
pol-miR-107b	mRNA for interferon regulatory factor, complete cds.
pol-miR-107b	mRNA for transferrin, complete cds.
pol-miR-107b	mRNA for serine protease I-2, complete cds.
pol-miR-107b	mRNA for serine protease I-1, complete cds.
pol-miR-107b	TNFR-1 mRNA for tumor necrosis factor receptor-1, complete cds.
pol-miR-107b	IL-8 receptor mRNA for interleukin-8 receptor, complete cds.
pol-miR-107b	heat shock protein 60 kDa (hsp60) mRNA, complete cds.
pol-miR-107b	myD88 mRNA for myeloid differentiaton factor 88, complete cds.
pol-miR-107b	CPB mRNA for carboxypeptidase B, partial cds.
pol-miR-107b	cgrpr mRNA for calcitonin gene-related peptide receptor, complete cds.
pol-miR-107b	mRNA for complement component C9, complete cds.
pol-miR-107b	empty spiracles homeobox 2 (Emx2) mRNA, complete cds.
pol-miR-107b	melanin-concentrating hormone receptor 2 (MCHR2) mRNA, complete cds.
pol-miR-107b	Wap65-1 mRNA, complete cds.
pol-miR-107b	TANK binding kinase 1 splice variant 3 (TBK1) mRNA, complete cds, alternatively spliced.
pol-miR-107b	phospholipase C delta 1 B short form (PLC) mRNA, complete cds.
pol-miR-107b	serine protease I-1 mRNA, complete cds.
pol-miR-107b	galectin mRNA, complete cds.
pol-miR-107b	testis enhanced gene transcript-like protein mRNA, complete cds.
pol-miR-193a-5p	doublesex and mab-3 related transcription factor 1 (DMRT1) mRNA, complete cds.
pol-miR-193a-5p	mitogen-activated protein kinase mRNA, complete cds.
pol-miR-193a-5p	heat shock protein 90 beta mRNA, complete cds.
pol-miR-193a-5p	ornithine decarboxylase antizyme small isoform ORF1 and ornithine decarboxylase antizyme small isoform mRNA, complete cds.
pol-miR-193a-5p	TFIIA P12 subunit mRNA, complete cds.
pol-miR-193a-5p	prolactin precursor, mRNA, complete cds.
pol-miR-193a-5p	calmodulin mRNA, partial cds.
pol-miR-193a-5p	proopiomelanocortin-III (POMC-III) mRNA, complete cds.
pol-miR-193a-5p	phospholipase D1B mRNA, complete cds.
pol-miR-193a-5p	phospholipase D2 mRNA, complete cds.
pol-miR-193a-5p	mRNA for Hoxb-5, partial cds.
pol-miR-193a-5p	M17h mRNA for M17 homologue, complete cds.
pol-miR-193a-5p	COL1A2 mRNA for type 1 collagen alpha 2, complete cds.
pol-miR-193a-5p	COL1A1 mRNA for type 1 collagen alpha 1, complete cds.
pol-miR-193a-5p	mRNA for granzyme I-2, complete cds.
pol-miR-193a-5p	mRNA for glucocorticoid receptor, complete cds.
pol-miR-196a-5p	transcription factor T-bet (TBX21) mRNA, complete cds.
pol-miR-196a-5p	GPR43 mRNA, complete cds.
pol-miR-196a-5p	phospholipase C gamma 2 (PLC-gamma2) mRNA, complete cds.
pol-miR-196a-5p	mRNA for microtubule aggregate protein homolog isotype-1, complete cds.
pol-miR-196a-5p	ornithine decarboxylase mRNA, complete cds.
pol-miR-196a-5p	macrophage stimulating-1 protein mRNA, complete cds.
pol-miR-196a-5p	DnaJ-like subfamily B member 11 (Hsp40B11) mRNA, complete cds.
pol-miR-196a-5p	preprovasoactive intestinal peptide mRNA, complete cds.
pol-miR-196a-5p	dio1 mRNA for iodothyronine deiodinase type I, complete cds.
pol-miR-196a-5p	heat shock protein 60 kDa (hsp60) mRNA, complete cds.
pol-miR-196a-5p	PYY mRNA for peptide YY, complete cds.

pol-miR-107b	transferrin mRNA, complete cds.	**pol-miR-196a-5p**	lipoprotein lipase (LPL) mRNA, complete cds.
pol-miR-107b	prolactin precursor, mRNA, complete cds.	**pol-miR-196a-5p**	EF1a mRNA for elongation factor 1 alpha, complete cds.
pol-miR-107b	insulin-like growth factor I mRNA, complete cds.	**pol-miR-196a-5p**	Wap65-2 mRNA, complete cds.
pol-miR-107b	phospholipase D1B mRNA, complete cds.	**pol-miR-196a-5p**	phospholipase C beta 4 mRNA, complete cds.
pol-miR-107b	phospholipase D2 mRNA, complete cds.	**pol-miR-196a-5p**	ornithine decarboxylase antizyme large isoform ORF1 and ornithine decarboxylase antizyme large isoform mRNA, complete cds.
pol-miR-107b	phospholipase C delta 3A mRNA, complete cds.	**pol-miR-196a-5p**	phospholipase C delta 3A mRNA, complete cds.
pol-miR-107b	protein arginine methyltransferase 1 (PRMT1) mRNA, complete cds.	**pol-miR-196a-5p**	spaw mRNA for southpaw, complete cds.
pol-miR-107b	COL1A2 mRNA for type 1 collagen alpha 2, complete cds.	**pol-miR-196a-5p**	COL1A1 mRNA for type 1 collagen alpha 1, complete cds.
pol-miR-107b	G-CSF mRNA for Granulocyte Colony-Stimulating Factor, complete cds.	**pol-miR-196a-5p**	MMP9 mRNA for gelatinase, complete cds.
pol-miR-107b	mRNA for granzyme I-2, complete cds.	**pol-miR-196c**	GPR43 mRNA, complete cds.
pol-miR-107b	MMP2 mRNA for gelatinase, complete cds.	**pol-miR-196c**	phospholipase C gamma 2 (PLC-gamma2) mRNA, complete cds.
pol-miR-107b	mRNA for glucocorticoid receptor, complete cds.	**pol-miR-196c**	17-alpha-hydroxylase mRNA, complete cds.
pol-miR-122	SOD2 mRNA for Mn-superoxide dismutase, complete cds.	**pol-miR-196c**	macrophage stimulating-1 protein mRNA, complete cds.
pol-miR-122	fNKCC mRNA for Na-K-Cl cotransporter, complete cds.	**pol-miR-196c**	DnaJ-like subfamily B member 11 (Hsp40B11) mRNA, complete cds.
pol-miR-122	mitfa mRNA for microphthalmia-associated transcription factor a, complete cds.	**pol-miR-196c**	calmodulin mRNA, complete cds.
pol-miR-122	gch2 mRNA for GTcyclohydrolase 2, complete cds.	**pol-miR-196c**	creatine kinase 1 mRNA, complete cds.
pol-miR-122	mRNA for CD40, complete cds.	**pol-miR-196c**	TCR beta mRNA for T cell receptor beta chain, complete cds.
pol-miR-122	ITGAM mRNA, complete cds.	**pol-miR-196c**	mRNA for serine protease I-2, complete cds.
pol-miR-122	DEAD box helicase 3-2 (DDX3-2) mRNA, complete cds.	**pol-miR-196c**	betaine homocysteine S-methyltansferase (BHMT) mRNA, complete cds.
pol-miR-122	melanin-concentrating hormone receptor 1 mRNA, complete cds.	**pol-miR-196c**	PYY mRNA for peptide YY, complete cds.
pol-miR-122	deleted in azoospermia-like protein 2 (DAZL) mRNA, DAZL-2 allele, complete cds.	**pol-miR-196c**	empty spiracles homeobox 2 (Emx2) mRNA, complete cds.
pol-miR-122	deleted in azoospermia-like protein 1 (DAZL) mRNA, DAZL-1 allele, complete cds.	**pol-miR-196c**	Wap65-2 mRNA, complete cds.
pol-miR-122	complement C1q-like protein 3 (C1ql3) mRNA, complete cds.	**pol-miR-196c**	phospholipase C beta 4 mRNA, complete cds.
pol-miR-122	ras-2 mRNA, complete cds.	**pol-miR-196c**	stanniocalcin-1 (STC1) mRNA, complete cds.
pol-miR-122	YGHL1 mRNA, complete cds.	**pol-miR-196c**	insulin-like growth factor I mRNA, complete cds.
pol-miR-122	mRNA for preprosomatostatin I, complete cds.	**pol-miR-196c**	phospholipase D1B mRNA, complete cds.
pol-miR-122	transcription factor PU.1 mRNA, complete cds, alternatively spliced.	**pol-miR-196c**	phospholipase D2 mRNA, complete cds.

pol-miR-122	LGP2 mRNA, complete cds.
pol-miR-122	syntenin mRNA, complete cds.
pol-miR-122	cathepsin B mRNA, complete cds.
pol-miR-122	ornithine decarboxylase mRNA, complete cds.
pol-miR-122	gonadotropin I beta subunit mRNA, complete cds.
pol-miR-122	macrophage stimulating-1 protein mRNA, complete cds.
pol-miR-122	serotransferrin precursor (SroTP) mRNA, complete cds.
pol-miR-122	beta-2-microglobulin precursor, mRNA, complete cds.
pol-miR-122	DnaJ-like subfamily B member 11 (Hsp40B11) mRNA, complete cds.
pol-miR-122	mRNA for trypsinogen 2, partial cds.
pol-miR-122	mRNA for trypsinogen 1, complete cds.
pol-miR-122	heat shock protein 90 beta (Hsp90beta) mRNA, complete cds.
pol-miR-122	JFC/EBPe mRNA for CCAAT/Enhancer binding protein epsilon, complete cds.
pol-miR-122	mRNA for interferon regulatory factor, complete cds.
pol-miR-122	mRNA for transferrin, complete cds.
pol-miR-122	MHC class IIb antigen mRNA, complete cds.
pol-miR-122	betaine homocysteine S-methyltansferase (BHMT) mRNA, complete cds.
pol-miR-122	mRNA for CD3 epsilon, complete cds.
pol-miR-122	CCR9 mRNA for C-C chemokine receptor 9, complete cds.
pol-miR-122	CCR3 mRNA for C-C chemokine receptor-3, complete cds.
pol-miR-122	TNFR-1 mRNA for tumor necrosis factor receptor-1, complete cds.
pol-miR-122	myD88 mRNA for myeloid differentiaton factor 88, complete cds.
pol-miR-122	pigment epithelium-derived factor mRNA, complete cds.
pol-miR-122	CPA2 mRNA for carboxypeptidase A2, complete cds.
pol-miR-122	fIGF-IR-2 mRNA for type 1 insulin-like growth factor receptor, complete cds.
pol-miR-122	fIR-2 mRNA for insulin receptor, complete cds.
pol-miR-122	fIR-1 mRNA for insulin receptor, complete cds.
pol-miR-196c	phospholipase C delta 3B mRNA, complete cds.
pol-miR-196c	phospholipase C delta 3A mRNA, complete cds.
pol-miR-196c	spaw mRNA for southpaw, complete cds.
pol-miR-196c	COL1A1 mRNA for type 1 collagen alpha 1, complete cds.
pol-miR-196c	G-CSF mRNA for Granulocyte Colony-Stimulating Factor, complete cds.
pol-miR-196c	TIMP-2 mRNA for tissue inhibitor of metalloproteinase-2, complete cds.
pol-miR-196c	MMP9 mRNA for gelatinase, complete cds.
pol-miR-196c	mRNA for glucocorticoid receptor, complete cds.
pol-miR-19a-3p	TLR14 mRNA for toll like receptor 14, complete cds.
pol-miR-19a-3p	DEAD box helicase 3-1 (DDX3-1) mRNA, complete cds.
pol-miR-19a-3p	isolate Po-P1 PR domain containing 1 (PRDM1) mRNA, complete cds.
pol-miR-19a-3p	macrophage stimulating-1 protein mRNA, complete cds.
pol-miR-19a-3p	TNFR-1 mRNA for tumor necrosis factor receptor-1, complete cds.
pol-miR-19a-3p	DnaJ-like subfamily B member 6 (Hsp40B6) mRNA, complete cds.
pol-miR-19a-3p	transmembrane 4 L6 family member 4 mRNA, complete cds.
pol-miR-19b-3p	apoA-I mRNA for apolipoprotein A-I, complete cds
pol-miR-19b-3p	DEAD box helicase 3-1 (DDX3-1) mRNA, complete cds.
pol-miR-19b-3p	isolate Po-P1 PR domain containing 1 (PRDM1) mRNA, complete cds.
pol-miR-19b-3p	interleukin-10 precursor, mRNA, complete cds.
pol-miR-19b-3p	ornithine decarboxylase mRNA, complete cds.
pol-miR-19b-3p	macrophage stimulating-1 protein mRNA, complete cds.
pol-miR-19b-3p	serotransferrin precursor (SroTP) mRNA, complete cds.
pol-miR-19b-3p	TNFR-1 mRNA for tumor necrosis factor receptor-1, complete cds.
pol-miR-19b-3p	DnaJ-like subfamily B member 6 (Hsp40B6) mRNA, complete cds.
pol-miR-19b-3p	cgrpr mRNA for calcitonin gene-related peptide receptor, complete cds.
pol-miR-19b-3p	protein arginine methyltransferase 1 (PRMT1) mRNA, complete cds.
pol-miR-19c-3p	TLR14 mRNA for toll like receptor 14, complete cds.

pol-miR-122	ERb mRNA for estrogen receptor beta, complete cds.
pol-miR-122	ERa mRNA for estrogen receptor alpha, complete cds.
pol-miR-122	mRNA for gonadotropin (GTH-I) beta subunit, complete cds.
pol-miR-122	mRNA for complement component C9, complete cds.
pol-miR-122	empty spiracles homeobox 2 (Emx2) mRNA, complete cds.
pol-miR-122	melanin-concentrating hormone receptor 1 (MCHR1) mRNA, complete cds.
pol-miR-122	phospholipase C beta 4 mRNA, complete cds.
pol-miR-122	doublesex and mab-3 related transcription factor 1 (DMRT1) mRNA, complete cds.
pol-miR-122	decorin mRNA, complete cds.
pol-miR-122	stanniocalcin-1 (STC1) mRNA, complete cds.
pol-miR-122	heat shock protein 90 beta mRNA, complete cds.
pol-miR-122	ornithine decarboxylase antizyme large isoform ORF1 and ornithine decarboxylase antizyme large isoform mRNA, complete cds.
pol-miR-122	ornithine decarboxylase antizyme small isoform ORF1 and ornithine decarboxylase antizyme small isoform mRNA, complete cds.
pol-miR-122	beta-2 microglobulin mRNA, complete cds.
pol-miR-122	transferrin mRNA, complete cds.
pol-miR-122	syntaxin-binding protein 3 isoform 1-like protein mRNA, partial cds.
pol-miR-122	phospholipase D2 mRNA, complete cds.
pol-miR-122	thymosin beta mRNA, complete cds.
pol-miR-122	phospholipase C delta 4 mRNA, complete cds.
pol-miR-122	phospholipase C delta 3A mRNA, complete cds.
pol-miR-122	G-CSF mRNA for Granulocyte Colony-Stimulating Factor, complete cds.
pol-miR-122	mRNA for granzyme I-2, complete cds.
pol-miR-122	MMP2 mRNA for gelatinase, complete cds.
pol-miR-122	pitx2 mRNA, complete cds.
pol-miR-133a-2-5p	DEAD box helicase 3-1 (DDX3-1) mRNA, complete cds.
pol-miR-133a-2-5p	insulin-like growth factor binding protein-4 (IGFBP-4) mRNA, complete cds.
pol-miR-133a-2-5p	insulin-like growth factor binding protein 4 mRNA, complete cds.
pol-miR-19c-3p	apoA-I mRNA for apolipoprotein A-I, complete cds.
pol-miR-19c-3p	DEAD box helicase 3-1 (DDX3-1) mRNA, complete cds.
pol-miR-19c-3p	interleukin-10 precursor, mRNA, complete cds.
pol-miR-19c-3p	ornithine decarboxylase mRNA, complete cds.
pol-miR-19c-3p	serotransferrin precursor (SroTP) mRNA, complete cds.
pol-miR-19c-3p	JFC/EBPb mRNA for CCAAT/Enhancer binding protein beta, complete cds.
pol-miR-19c-3p	TNFR-1 mRNA for tumor necrosis factor receptor-1, complete cds.
pol-miR-19c-3p	cgrpr mRNA for calcitonin gene-related peptide receptor, complete cds.
pol-miR-19c-3p	mRNA for complement component C9, complete cds.
pol-miR-19c-3p	phospholipase D2 mRNA, complete cds.
pol-miR-19c-3p	interleukin-10 precursor, mRNA, complete cds.
pol-miR-19d-3p	macrophage stimulating-1 protein mRNA, complete cds.
pol-miR-19d-3p	progranulin type II (pGRN) mRNA, complete cds, alternatively spliced.
pol-miR-19d-3p	progranulin type I (pGRN) mRNA, complete cds, alternatively spliced.
pol-miR-19d-3p	serotransferrin precursor (SroTP) mRNA, complete cds.
pol-miR-19d-3p	mRNA for serine protease I-2, complete cds.
pol-miR-19d-3p	DnaJ-like subfamily B member 6 (Hsp40B6) mRNA, complete cds.
pol-miR-19d-3p	cgrpr mRNA for calcitonin gene-related peptide receptor, complete cds.
pol-miR-19d-3p	TFIIA P12 subunit mRNA, complete cds.
pol-miR-19d-3p	protein arginine methyltransferase 1 (PRMT1) mRNA, complete cds.
pol-miR-19d-3p	paired box protein 3b isoform Pax3b-1 (Pax3a) mRNA, complete cds.
pol-miR-202-5p	insulin-like growth factor binding protein 3 mRNA, complete cds.
pol-miR-202-5p	nucleotide-binding oligomerization domain 1 protein (NOD1) mRNA, complete cds.
pol-miR-202-5p	mRNA for trypsinogen 3, complete cds.
pol-miR-202-5p	heat shock protein 90 beta (Hsp90beta) mRNA, complete cds.
pol-miR-202-5p	ornithine decarboxylase antizyme large isoform ORF1 and ornithine decarboxylase antizyme large isoform mRNA, complete cds.
pol-miR-202-5p	ornithine decarboxylase antizyme small isoform ORF1 and ornithine decarboxylase antizyme small isoform mRNA, complete cds.

pol-miR-133a-2-5p	parvalbumin mRNA sequence, partial.	**pol-miR-202-5p**	MMP9 mRNA for gelatinase, complete cds.
pol-miR-133a-2-5p	cathepsin F mRNA, complete cds.	**pol-miR-205-5p**	TLR14 mRNA for toll like receptor 14, complete cds.
pol-miR-133a-2-5p	serotransferrin precursor (SroTP) mRNA, complete cds.	**pol-miR-205-5p**	myostatin (MSTN) mRNA, complete cds.
pol-miR-133a-2-5p	PYY mRNA for peptide YY, complete cds.	**pol-miR-205-5p**	CD18 transcript 2 mRNA, complete cds, alternatively spliced.
pol-miR-133a-2-5p	VDRa mRNA for vitamin D receptor a, complete cds.	**pol-miR-205-5p**	CD18 transcript 1 mRNA, complete cds, alternatively spliced.
pol-miR-133a-2-5p	testis enhanced gene transcript-like protein mRNA, complete cds.	**pol-miR-205-5p**	deleted in azoospermia-like protein 2 (DAZL) mRNA, DAZL-2 allele, complete cds.
pol-miR-133a-2-5p	G-CSF mRNA for Granulocyte Colony-Stimulating Factor, complete cds.	**pol-miR-205-5p**	deleted in azoospermia-like protein 1 (DAZL) mRNA, DAZL-1 allele, complete cds.
pol-miR-133a-3p	TLR14 mRNA for toll like receptor 14, complete cds.	**pol-miR-205-5p**	complement C1q-like protein 3 (C1ql3) mRNA, complete cds.
pol-miR-133a-3p	transcription factor T-bet (TBX21) mRNA, complete cds.	**pol-miR-205-5p**	paired box protein 3b isoform Pax3b-1 (Pax3a) mRNA, complete cds.
pol-miR-133a-3p	mRNA for interleukin-8 like CXC chemokine 2, complete cds.	**pol-miR-205-5p**	phospholipase C-beta 1 (PLC-beta1) mRNA, complete cds.
pol-miR-133a-3p	phospholipase C-beta 1 (PLC-beta1) mRNA, complete cds.	**pol-miR-205-5p**	interferon regulatory factor 2 (IRF2) mRNA, complete cds.
pol-miR-133a-3p	transcription factor C/EBPalpha mRNA, complete cds.	**pol-miR-205-5p**	cathepsin K mRNA, complete cds.
pol-miR-133a-3p	proteasome activator subunit 2 mRNA, complete cds.	**pol-miR-205-5p**	putative fast skeletal muscle troponin mRNA, partial cds.
pol-miR-133a-3p	macrophage stimulating-1 protein mRNA, complete cds.	**pol-miR-205-5p**	eIF5A mRNA, complete cds.
pol-miR-133a-3p	serotransferrin precursor (SroTP) mRNA, complete cds.	**pol-miR-205-5p**	mRNA for trypsinogen 3, complete cds.
pol-miR-133a-3p	protein tyrosine phosphatase alpha mRNA, complete cds.	**pol-miR-205-5p**	mRNA for Hoxd-4, complete cds.
pol-miR-133a-3p	mRNA for trypsinogen 3, complete cds.	**pol-miR-205-5p**	IL-8 receptor mRNA for interleukin-8 receptor, complete cds.
pol-miR-133a-3p	hypothetical protein mRNA, complete cds.	**pol-miR-205-5p**	myD88 mRNA for myeloid differentiaton factor 88, complete cds.
pol-miR-133a-3p	heat shock protein 90 beta (Hsp90beta) mRNA, complete cds.	**pol-miR-205-5p**	VDRa mRNA for vitamin D receptor a, complete cds.
pol-miR-133a-3p	mRNA for CXC chemokine, complete cds.	**pol-miR-205-5p**	mRNA for complement component C3, complete cds.
pol-miR-133a-3p	VDRb mRNA for vitamin D receptor b, complete cds.	**pol-miR-205-5p**	empty spiracles homeobox 2 (Emx2) mRNA, complete cds.
pol-miR-133a-3p	TANK binding kinase 1 splice variant 3 (TBK1) mRNA, complete cds, alternatively spliced.	**pol-miR-205-5p**	Wap65-1 mRNA, complete cds.
pol-miR-133a-3p	TANK binding kinase 1 splice variant 2 (TBK1) mRNA, complete cds, alternatively spliced.	**pol-miR-205-5p**	phospholipase C beta 4 mRNA, complete cds.
pol-miR-133a-3p	TANK binding kinase 1 splice variant 1 (TBK1) mRNA, complete cds, alternatively spliced.	**pol-miR-205-5p**	phosphoinositide 3-kinase gamma mRNA, complete cds.
pol-miR-133a-3p	interleukine-8 (IL-8) mRNA, complete cds.	**pol-miR-205-5p**	stanniocalcin-1 (STC1) mRNA, complete cds.
pol-miR-133a-3p	heat shock protein 90 beta mRNA, complete cds.	**pol-miR-205-5p**	ornithine decarboxylase antizyme large isoform ORF1 and ornithine decarboxylase antizyme large isoform mRNA, complete cds.
pol-miR-133a-3p	ornithine decarboxylase antizyme small isoform ORF1 and ornithine decarboxylase antizyme small isoform mRNA, complete cds.	**pol-miR-205-5p**	ornithine decarboxylase antizyme small isoform ORF1 and ornithine decarboxylase antizyme small isoform mRNA, complete cds.

pol-miR-133a-3p	galectin mRNA, complete cds.
pol-miR-133a-3p	testis enhanced gene transcript-like protein mRNA, complete cds.
pol-miR-133a-3p	insulin-like growth factor I mRNA, complete cds.
pol-miR-133a-5p	DEAD box helicase 3-1 (DDX3-1) mRNA, complete cds.
pol-miR-133a-5p	insulin-like growth factor binding protein-4 (IGFBP-4) mRNA, complete cds.
pol-miR-133a-5p	insulin-like growth factor binding protein 4 mRNA, complete cds.
pol-miR-133a-5p	parvalbumin mRNA sequence, partial.
pol-miR-133a-5p	cathepsin F mRNA, complete cds.
pol-miR-133a-5p	serotransferrin precursor (SroTP) mRNA, complete cds.
pol-miR-133a-5p	PYY mRNA for peptide YY, complete cds.
pol-miR-133a-5p	VDRa mRNA for vitamin D receptor a, complete cds.
pol-miR-133a-5p	testis enhanced gene transcript-like protein mRNA, complete cds.
pol-miR-133a-5p	G-CSF mRNA for Granulocyte Colony-Stimulating Factor, complete cds.
pol-miR-133b-3p	TLR14 mRNA for toll like receptor 14, complete cds.
pol-miR-133b-3p	phospholipase C-beta 1 (PLC-beta1) mRNA, complete cds.
pol-miR-133b-3p	proteasome activator subunit 2 mRNA, complete cds.
pol-miR-133b-3p	macrophage stimulating-1 protein mRNA, complete cds.
pol-miR-133b-3p	protein tyrosine phosphatase alpha mRNA, complete cds.
pol-miR-133b-3p	mRNA for trypsinogen 3, complete cds.
pol-miR-133b-3p	hypothetical protein mRNA, complete cds.
pol-miR-133b-3p	heat shock protein 90 beta (Hsp90beta) mRNA, complete cds.
pol-miR-133b-3p	mRNA for CXC chemokine, complete cds.
pol-miR-133b-3p	VDRb mRNA for vitamin D receptor b, complete cds.
pol-miR-133b-3p	TANK binding kinase 1 splice variant 3 (TBK1) mRNA, complete cds, alternatively spliced.
pol-miR-133b-3p	interleukine-8 (IL-8) mRNA, complete cds.
pol-miR-133b-3p	heat shock protein 90 beta mRNA, complete cds.
pol-miR-133b-3p	ornithine decarboxylase antizyme small isoform ORF1 and ornithine decarboxylase antizyme small isoform mRNA, complete cds.
pol-miR-205-5p	testis enhanced gene transcript-like protein mRNA, complete cds.
pol-miR-205-5p	prolactin precursor, mRNA, complete cds.
pol-miR-205-5p	chymotrypsin B mRNA, partial cds.
pol-miR-205-5p	phospholipase C delta 3B mRNA, complete cds.
pol-miR-205-5p	mRNA for Hoxb-5, partial cds.
pol-miR-205-5p	GDF8 type 2 mRNA, complete cds.
pol-miR-205-5p	GDF8 type 1 mRNA, complete cds.
pol-miR-206-3p	SOD2 mRNA for Mn-superoxide dismutase, complete cds.
pol-miR-206-3p	TLR14 mRNA for toll like receptor 14, complete cds.
pol-miR-206-3p	interferon regulatory factor 8 (IRF8) mRNA, complete cds.
pol-miR-206-3p	myostatin (MSTN) mRNA, complete cds.
pol-miR-206-3p	mRNA for CD40, complete cds.
pol-miR-206-3p	endoribonuclease dicer-like protein (dcl) mRNA, complete cds.
pol-miR-206-3p	DEAD box helicase 3-2 (DDX3-2) mRNA, complete cds.
pol-miR-206-3p	complement C1q-like protein 3 (C1ql3) mRNA, complete cds.
pol-miR-206-3p	paired box protein 3b isoform Pax3b-1 (Pax3a) mRNA, complete cds.
pol-miR-206-3p	interferon regulatory factor 9 (IRF9) mRNA, complete cds.
pol-miR-206-3p	akirin mRNA, complete cds.
pol-miR-206-3p	ras-2 mRNA, complete cds.
pol-miR-206-3p	phospholipase C gamma 2 (PLC-gamma2) mRNA, complete cds.
pol-miR-206-3p	scinderin-like protein mRNA, complete cds.
pol-miR-206-3p	interferon regulatory factor 2 (IRF2) mRNA, complete cds.
pol-miR-206-3p	beta-actin mRNA, complete cds.
pol-miR-206-3p	cathepsin F mRNA, complete cds.
pol-miR-206-3p	serotransferrin precursor (SroTP) mRNA, complete cds.
pol-miR-206-3p	DnaJ-like subfamily B member 11 (Hsp40B11) mRNA, complete cds.
pol-miR-206-3p	ppsb mRNA for pancreatic protein with two somatomedin B domains, complete cds.

pol-miR-133b-3p	galectin mRNA, complete cds.
pol-miR-133b-3p	testis enhanced gene transcript-like protein mRNA, complete cds.
pol-miR-133b-3p	insulin-like growth factor I mRNA, complete cds.
pol-miR-135a	transcription factor SOX-1a (Sox1a) mRNA, complete cds.
pol-miR-135a	DEAD box helicase 3-1 (DDX3-1) mRNA, complete cds.
pol-miR-135a	isolate Po-P1 PR domain containing 1 (PRDM1) mRNA, complete cds.
pol-miR-135a	nuclear receptor DAX1 mRNA, complete cds.
pol-miR-135a	toll-like receptor 21 mRNA, complete cds.
pol-miR-135a	peptidoglycan recognition protein (PGRP) mRNA, complete cds.
pol-miR-135a	scinderin-like protein mRNA, complete cds.
pol-miR-135a	elastase-like serine protease (ELSrP) mRNA, complete cds.
pol-miR-135a	serotransferrin precursor (SroTP) mRNA, complete cds.
pol-miR-135a	TNFR-1 mRNA for tumor necrosis factor receptor-1, complete cds.
pol-miR-135a	heat shock protein 60 kDa (hsp60) mRNA, complete cds.
pol-miR-135a	mRNA for granzyme III-2, complete cds.
pol-miR-135a	mRNA for granzyme III-1, complete cds.
pol-miR-135a	charon mRNA for DAN related protein, complete cds.
pol-miR-135b-3p	TLR14 mRNA for toll like receptor 14, complete cds.
pol-miR-135b-3p	gch2 mRNA for GTcyclohydrolase 2, complete cds.
pol-miR-135b-3p	transcription factor T-bet (TBX21) mRNA, complete cds.
pol-miR-135b-3p	endoribonuclease dicer-like protein (dcl) mRNA, complete cds.
pol-miR-135b-3p	DEAD box helicase 3-2 (DDX3-2) mRNA, complete cds.
pol-miR-135b-3p	isolate Po-P1 PR domain containing 1 (PRDM1) mRNA, complete cds.
pol-miR-135b-3p	akirin mRNA, complete cds.
pol-miR-135b-3p	interferon-induced transmembrane protein 1 (IFITM1) mRNA, complete cds.
pol-miR-135b-3p	phospholipase C-beta 1 (PLC-beta1) mRNA, complete cds.
pol-miR-135b-3p	YGHL1 mRNA, complete cds.
pol-miR-206-3p	signal transducer and activator of transcription 1 mRNA, complete cds.
pol-miR-206-3p	dio3 mRNA for iodothyronine deiodinase type III, complete cds.
pol-miR-206-3p	mRNA for serine protease I-2, complete cds.
pol-miR-206-3p	mRNA for serine protease I-1, complete cds.
pol-miR-206-3p	betaine homocysteine S-methyltansferase (BHMT) mRNA, complete cds.
pol-miR-206-3p	natural resistance-associated macrophage protein mRNA, complete cds.
pol-miR-206-3p	fIR-1 mRNA for insulin receptor, complete cds.
pol-miR-206-3p	NPY mRNA for neuropeptide Y, complete cds.
pol-miR-206-3p	phospholipase C beta 4 mRNA, complete cds.
pol-miR-206-3p	ornithine decarboxylase antizyme large isoform ORF1 and ornithine decarboxylase antizyme large isoform mRNA, complete cds.
pol-miR-206-3p	testis enhanced gene transcript-like protein mRNA, complete cds.
pol-miR-206-3p	insulin-like growth factor I mRNA, complete cds.
pol-miR-206-3p	phospholipase D2 mRNA, complete cds.
pol-miR-206-3p	GDF8 type 2 mRNA, complete cds.
pol-miR-206-3p	GDF8 type 1 mRNA, complete cds.
pol-miR-206-3p	lefty mRNA for lefty/antivin, complete cds.
pol-miR-206-3p	COL1A2 mRNA for type 1 collagen alpha 2, complete cds.
pol-miR-206-3p	G-CSF mRNA for Granulocyte Colony-Stimulating Factor, complete cds.
pol-miR-206-3p	mRNA for granzyme III-2, complete cds.
pol-miR-206-3p	mRNA for granzyme I-2, complete cds.
pol-miR-206-3p	mRNA for granzyme I-1, complete cds.
pol-miR-206-3p	mRNA for glucocorticoid receptor, complete cds.
pol-miR-206-3p	myostatin (MSTN) mRNA, complete cds.
pol-miR-20b-5p	cathepsin Z cysteine protease mRNA, complete cds.
pol-miR-20b-5p	mRNA for CD40, complete cds.
pol-miR-20b-5p	GPR43 mRNA, complete cds.
pol-miR-20b-5p	transcription factor SOX-1b (Sox1b) mRNA, complete cds.

pol-miR-135b-3p	cathepsin L mRNA, complete cds.
pol-miR-135b-3p	fibrinogen beta chain precursor, mRNA, complete cds.
pol-miR-135b-3p	progranulin type II (pGRN) mRNA, complete cds, alternatively spliced.
pol-miR-135b-3p	progranulin type I (pGRN) mRNA, complete cds, alternatively spliced.
pol-miR-135b-3p	calmodulin mRNA, complete cds.
pol-miR-135b-3p	heat shock protein 90 beta (Hsp90beta) mRNA, complete cds.
pol-miR-135b-3p	natural resistance-associated macrophage protein mRNA, complete cds.
pol-miR-135b-3p	myD88 mRNA for myeloid differentiaton factor 88, complete cds.
pol-miR-135b-3p	TLR9 mRNA for Toll-like receptor 9, complete cds.
pol-miR-135b-3p	natural killer enhancing factor (NKEF) mRNA, complete cds.
pol-miR-135b-3p	MIS mRNA for Mullerian inihibiting substance, complete cds.
pol-miR-135b-3p	CPB mRNA for carboxypeptidase B, partial cds.
pol-miR-135b-3p	VDRb mRNA for vitamin D receptor b, complete cds.
pol-miR-135b-3p	il8-2 mRNA for interleukin 8 isoform 2, complete cds.
pol-miR-135b-3p	doublesex and mab-3 related transcription factor 1 (DMRT1) mRNA, complete cds.
pol-miR-135b-3p	heat shock protein 90 beta mRNA, complete cds.
pol-miR-135b-3p	testis enhanced gene transcript-like protein mRNA, complete cds.
pol-miR-135b-3p	chymotrypsin B mRNA, partial cds.
pol-miR-135b-3p	phospholipase D2 mRNA, complete cds.
pol-miR-135b-3p	mRNA for tumor necrosis factor, complete cds.
pol-miR-135b-3p	MMP2 mRNA for gelatinase, complete cds.
pol-miR-135b-5p	transcription factor SOX-1a (Sox1a) mRNA, complete cds.
pol-miR-135b-5p	DEAD box helicase 3-1 (DDX3-1) mRNA, complete cds.
pol-miR-135b-5p	nuclear receptor DAX1 mRNA, complete cds.
pol-miR-135b-5p	toll-like receptor 21 mRNA, complete cds.
pol-miR-135b-5p	peptidoglycan recognition protein (PGRP) mRNA, complete cds.
pol-miR-135b-5p	scinderin-like protein mRNA, complete cds.
pol-miR-20b-5p	complement C1q-like protein 3 (C1ql3) mRNA, complete cds.
pol-miR-20b-5p	paired box protein 3b isoform Pax3b-1 (Pax3a) mRNA, complete cds.
pol-miR-20b-5p	NOD-like receptor C (NLRC) mRNA, complete cds.
pol-miR-20b-5p	cathepsin L mRNA, complete cds.
pol-miR-20b-5p	LGP2 mRNA, complete cds.
pol-miR-20b-5p	syntenin mRNA, complete cds.
pol-miR-20b-5p	macrophage stimulating-1 protein mRNA, complete cds.
pol-miR-20b-5p	cathepsin K mRNA, complete cds.
pol-miR-20b-5p	dio3 mRNA for iodothyronine deiodinase type III, complete cds.
pol-miR-20b-5p	TCR beta mRNA for T cell receptor beta chain, complete cds.
pol-miR-20b-5p	mRNA for serine protease I-2, complete cds.
pol-miR-20b-5p	mRNA for serine protease I-1, complete cds.
pol-miR-20b-5p	mRNA for perforin, complete cds.
pol-miR-20b-5p	mRNA for IL-1b, complete cds.
pol-miR-20b-5p	serine protease I-1 mRNA, complete cds.
pol-miR-20b-5p	ornithine decarboxylase antizyme small isoform ORF1 and ornithine decarboxylase antizyme small isoform mRNA, complete cds.
pol-miR-20b-5p	galectin mRNA, complete cds.
pol-miR-20b-5p	insulin-like growth factor I mRNA, complete cds.
pol-miR-20b-5p	IL-11b mRNA for interleukin 11 type b, complete cds.
pol-miR-20b-5p	phospholipase D1B mRNA, complete cds.
pol-miR-20b-5p	mRNA for granzyme III-2, complete cds.
pol-miR-20b-5p	mRNA for granzyme III-1, complete cds.
pol-miR-20b-5p	mRNA for granzyme I-2, complete cds.
pol-miR-20b-5p	mRNA for granzyme I-1, complete cds.
pol-miR-20b-5p	mRNA for granzyme II, complete cds.
pol-miR-20b-5p	14kDa-apo mRNA for 14 kDa-apolipoprotein, complete cds.
pol-miR-210-3p	PoLCE mRNA for hatching enzyme, complete cds.
pol-miR-210-3p	

pol-miR-135b-5p	serotransferrin precursor (SroTP) mRNA, complete cds.
pol-miR-135b-5p	mRNA for Hoxd-4, complete cds.
pol-miR-135b-5p	heat shock protein 60 kDa (hsp60) mRNA, complete cds.
pol-miR-135b-5p	mRNA for granzyme III-2, complete cds.
pol-miR-135b-5p	mRNA for granzyme III-1, complete cds.
pol-miR-135b-5p	charon mRNA for DAN related protein, complete cds.
pol-miR-135c	DEAD box helicase 3-1 (DDX3-1) mRNA, complete cds.
pol-miR-135c	isolate Po-P1 PR domain containing 1 (PRDM1) mRNA, complete cds.
pol-miR-135c	toll-like receptor 21 mRNA, complete cds.
pol-miR-135c	peptidoglycan recognition protein (PGRP) mRNA, complete cds.
pol-miR-135c	scinderin-like protein mRNA, complete cds.
pol-miR-135c	macrophage stimulating-1 protein mRNA, complete cds.
pol-miR-135c	serotransferrin precursor (SroTP) mRNA, complete cds.
pol-miR-135c	TNFR-1 mRNA for tumor necrosis factor receptor-1, complete cds.
pol-miR-135c	doublesex and mab-3 related transcription factor 1 (DMRT1) mRNA, complete cds.
pol-miR-135c	insulin-like growth factor I mRNA, complete cds.
pol-miR-137-3p	GPR43 mRNA, complete cds.
pol-miR-137-3p	JFC/EBPb mRNA for CCAAT/Enhancer binding protein beta, complete cds.
pol-miR-137-3p	calreticulin mRNA, complete cds.
pol-miR-137-3p	TNFR-1 mRNA for tumor necrosis factor receptor-1, complete cds.
pol-miR-1388-5p	complement C1q-like protein 3 (C1ql3) mRNA, complete cds.
pol-miR-1388-5p	lipopolysaccharide-induced tumor necrosis factor-alpha factor mRNA, complete cds.
pol-miR-1388-5p	interferon regulatory factor 2 (IRF2) mRNA, complete cds.
pol-miR-1388-5p	lipopolysaccharide-binding protein/bactericidal permeability-increasing protein mRNA, complete cds.
pol-miR-1388-5p	macrophage stimulating-1 protein mRNA, complete cds.
pol-miR-1388-5p	serotransferrin precursor (SroTP) mRNA, complete cds.
pol-miR-1388-5p	JFC/EBPb mRNA for CCAAT/Enhancer binding protein beta, complete cds.
pol-miR-210-3p	cathepsin Z cysteine protease mRNA, complete cds.
pol-miR-210-3p	endoribonuclease dicer-like protein (dcl) mRNA, complete cds.
pol-miR-210-3p	ITGAM mRNA, complete cds.
pol-miR-210-3p	DEAD box helicase 3-1 (DDX3-1) mRNA, complete cds.
pol-miR-210-3p	melanin-concentrating hormone receptor 2 mRNA, complete cds.
pol-miR-210-3p	melanin-concentrating hormone receptor 1 mRNA, complete cds.
pol-miR-210-3p	membrane progestin receptor-like mRNA, complete cds.
pol-miR-210-3p	interferon regulatory factor 9 (IRF9) mRNA, complete cds.
pol-miR-210-3p	ras-2 mRNA, complete cds.
pol-miR-210-3p	HSL1 mRNA for hormone-sensitive lipase1, complete cds.
pol-miR-210-3p	fibrinogen-related protein 1 (FREP1) mRNA, complete cds.
pol-miR-210-3p	phospholipase C-beta 1 (PLC-beta1) mRNA, complete cds.
pol-miR-210-3p	nucleotide-binding oligomerization domain 1 protein (NOD1) mRNA, complete cds.
pol-miR-210-3p	NOD-like receptor C (NLRC) mRNA, complete cds.
pol-miR-210-3p	LGP2 mRNA, complete cds.
pol-miR-210-3p	cathepsin F mRNA, complete cds.
pol-miR-210-3p	interleukin-1 receptor type II mRNA, complete cds.
pol-miR-210-3p	cathepsin B mRNA, complete cds.
pol-miR-210-3p	phospholipase D (PLD) mRNA, complete cds.
pol-miR-210-3p	interferon regulatory factor 3 variant 2 (IRF3) mRNA, complete cds.
pol-miR-210-3p	interferon regulatory factor 3 variant 1 (IRF3) mRNA, complete cds.
pol-miR-210-3p	splicing factor arginine/serine-rich 3 mRNA, complete cds.
pol-miR-210-3p	macrophage stimulating-1 protein mRNA, complete cds.
pol-miR-210-3p	serotransferrin precursor (SroTP) mRNA, complete cds.
pol-miR-210-3p	heat shock protein 10 kDa (hsp10) mRNA, complete cds.
pol-miR-210-3p	DnaJ-like subfamily B member 11 (Hsp40B11) mRNA, complete cds.
pol-miR-210-3p	GDF15 mRNA for growth differentiation factor 15, complete cds.

pol-miR-1388-5p	mRNA for Mx, complete cds.
pol-miR-1388-5p	phosphoinositide 3-kinase gamma mRNA, complete cds.
pol-miR-1388-5p	phospholipase D2 mRNA, complete cds.
pol-miR-1388-5p	GAPDH mRNA for glyceraldehyde-3-phosphate dehydrogenase, complete cds.
pol-miR-1388-5p	G-CSF mRNA for Granulocyte Colony-Stimulating Factor, complete cds.
pol-miR-1388-5p	mRNA for granzyme I-2, complete cds.
pol-miR-145-3p	TLR14 mRNA for toll like receptor 14, complete cds.
pol-miR-145-3p	fNKCC mRNA for Na-K-Cl cotransporter, complete cds.
pol-miR-145-3p	paired box protein 3b isoform Pax3b-1 (Pax3a) mRNA, complete cds.
pol-miR-145-3p	interferon regulatory factor 9 (IRF9) mRNA, complete cds.
pol-miR-145-3p	ras-2 mRNA, complete cds.
pol-miR-145-3p	YGHL1 mRNA, complete cds.
pol-miR-145-3p	cathepsin K mRNA, complete cds.
pol-miR-145-3p	retinoid X receptor beta mRNA, complete cds.
pol-miR-145-3p	mRNA for CD3 epsilon, complete cds.
pol-miR-145-3p	fIR-1 mRNA for insulin receptor, complete cds.
pol-miR-145-3p	TANK binding kinase 1 splice variant 3 (TBK1) mRNA, complete cds, alternatively spliced.
pol-miR-145-3p	decorin mRNA, complete cds.
pol-miR-145-3p	stanniocalcin 2 mRNA, complete cds.
pol-miR-145-3p	phospholipase D1B mRNA, complete cds.
pol-miR-145-3p	mRNA for tumor necrosis factor, complete cds.
pol-miR-145-5p	gch2 mRNA for GTcyclohydrolase 2, complete cds.
pol-miR-145-5p	ITGAL mRNA, complete cds.
pol-miR-145-5p	insulin-like growth factor binding protein-4 (IGFBP-4) mRNA, complete cds.
pol-miR-145-5p	insulin-like growth factor binding protein 4 mRNA, complete cds.
pol-miR-145-5p	insulin-like growth factor binding protein 3 mRNA, complete cds.
pol-miR-145-5p	HSL1 mRNA for hormone-sensitive lipase1, complete cds.
pol-miR-210-3p	dio3 mRNA for iodothyronine deiodinase type III, complete cds.
pol-miR-210-3p	dio1 mRNA for iodothyronine deiodinase type I, complete cds.
pol-miR-210-3p	hypothetical protein mRNA, complete cds.
pol-miR-210-3p	inhibitor kappa B alpha mRNA, complete cds.
pol-miR-210-3p	mRNA for serine protease I-2, complete cds.
pol-miR-210-3p	mRNA for serine protease I-1, complete cds.
pol-miR-210-3p	CCR3 mRNA for C-C chemokine receptor-3, complete cds.
pol-miR-210-3p	DnaJ-like subfamily B member 6 (Hsp40B6) mRNA, complete cds.
pol-miR-210-3p	ERa mRNA for estrogen receptor alpha, complete cds.
pol-miR-210-3p	mRNA for complement component C9, complete cds.
pol-miR-210-3p	empty spiracles homeobox 2 (Emx2) mRNA, complete cds.
pol-miR-210-3p	melanin-concentrating hormone receptor 2 (MCHR2) mRNA, complete cds.
pol-miR-210-3p	melanin-concentrating hormone receptor 1 (MCHR1) mRNA, complete cds.
pol-miR-210-3p	Wap65-1 mRNA, complete cds.
pol-miR-210-3p	B cell accessory protein (CD79b) mRNA, complete cds.
pol-miR-210-3p	phospholipase C beta 4 mRNA, complete cds.
pol-miR-210-3p	insulin-like growth factor I mRNA, complete cds.
pol-miR-210-3p	proopiomelanocortin-III (POMC-III) mRNA, complete cds.
pol-miR-210-3p	phospholipase D1B mRNA, complete cds.
pol-miR-210-3p	phospholipase D2 mRNA, complete cds.
pol-miR-210-3p	mRNA for Hoxb-5, partial cds.
pol-miR-210-3p	mRNA for tumor necrosis factor, complete cds.
pol-miR-210-3p	protein arginine methyltransferase 1 (PRMT1) mRNA, complete cds.
pol-miR-210-3p	sqt mRNA for squint, complete cds.
pol-miR-210-3p	G-CSF mRNA for Granulocyte Colony-Stimulating Factor, complete cds.
pol-miR-210-3p	TIMP-2 mRNA for tissue inhibitor of metalloproteinase-2, complete cds.
pol-miR-210-3p	mRNA for CD40, complete cds.
pol-miR-214	

pol-miR-145-5p	phospholipase C delta 1B Lf mRNA, complete cds.
pol-miR-145-5p	interferon regulatory factor 5 (IRF5) mRNA, complete cds.
pol-miR-145-5p	mitochondrial antiviral signaling protein IPS-1 mRNA, complete cds; nuclear gene for mitochondrial product.
pol-miR-145-5p	ornithine decarboxylase mRNA, complete cds.
pol-miR-145-5p	macrophage stimulating-1 protein mRNA, complete cds.
pol-miR-145-5p	serotransferrin precursor (SroTP) mRNA, complete cds.
pol-miR-145-5p	beta-2-microglobulin precursor, mRNA, complete cds.
pol-miR-145-5p	protein tyrosine phosphatase alpha mRNA, complete cds.
pol-miR-145-5p	dio3 mRNA for iodothyronine deiodinase type III, complete cds.
pol-miR-145-5p	glucose-regulated protein 78 (Grp78) mRNA, complete cds.
pol-miR-145-5p	mRNA for interferon regulatory factor, complete cds.
pol-miR-145-5p	calreticulin mRNA, complete cds.
pol-miR-145-5p	VDRb mRNA for vitamin D receptor b, complete cds.
pol-miR-145-5p	ctrlr mRNA for calcitonin receptor-like receptor, complete cds.
pol-miR-145-5p	lipoprotein lipase (LPL) mRNA, complete cds.
pol-miR-145-5p	CD4-1 mRNA for T-cell surface glycoprotein CD4-1, complete cds.
pol-miR-145-5p	phospholipase C delta 1 B short form (PLC) mRNA, complete cds.
pol-miR-145-5p	doublesex and mab-3 related transcription factor 1 (DMRT1) mRNA, complete cds.
pol-miR-145-5p	ornithine decarboxylase antizyme large isoform ORF1 and ornithine decarboxylase antizyme large isoform mRNA, complete cds.
pol-miR-145-5p	beta-2 microglobulin mRNA, complete cds.
pol-miR-145-5p	proopiomelanocortin-III (POMC-III) mRNA, complete cds.
pol-miR-145-5p	phospholipase C delta 3A mRNA, complete cds.
pol-miR-145-5p	protein arginine methyltransferase 1 (PRMT1) mRNA, complete cds.
pol-miR-145-5p	COL1A2 mRNA for type 1 collagen alpha 2, complete cds.
pol-miR-145-5p	MMP2 mRNA for gelatinase, complete cds.
pol-miR-146a	fads2-like desaturase mRNA, complete cds.
pol-miR-146a	phospholipase C-beta 1 (PLC-beta1) mRNA, complete cds.
pol-miR-214	ITGAL mRNA, complete cds.
pol-miR-214	CD83 transcript 2 mRNA, complete cds, alternatively spliced.
pol-miR-214	paired box protein 7b (Pax7b) mRNA, complete cds.
pol-miR-214	DEAD box helicase 3-1 (DDX3-1) mRNA, complete cds.
pol-miR-214	paired box protein 3b isoform Pax3b-1 (Pax3a) mRNA, complete cds.
pol-miR-214	interferon regulatory factor 9 (IRF9) mRNA, complete cds.
pol-miR-214	vasa-like protein mRNA, complete cds.
pol-miR-214	HSL1 mRNA for hormone-sensitive lipase1, complete cds.
pol-miR-214	phospholipase C-beta 1 (PLC-beta1) mRNA, complete cds.
pol-miR-214	vasa mRNA, complete cds.
pol-miR-214	peroxisome proliferator-activated receptors alpha mRNA, complete cds.
pol-miR-214	beclin-1 mRNA, complete cds.
pol-miR-214	cathepsin L mRNA, complete cds.
pol-miR-214	interferon regulatory factor 2 (IRF2) mRNA, complete cds.
pol-miR-214	cathepsin F mRNA, complete cds.
pol-miR-214	interferon regulatory factor 3 variant 2 (IRF3) mRNA, complete cds.
pol-miR-214	interferon regulatory factor 3 variant 1 (IRF3) mRNA, complete cds.
pol-miR-214	serotransferrin precursor (SroTP) mRNA, complete cds.
pol-miR-214	calmodulin mRNA, complete cds.
pol-miR-214	hypothetical protein mRNA, complete cds.
pol-miR-214	inhibitor kappa B alpha mRNA, complete cds.
pol-miR-214	glucose-regulated protein 78 (Grp78) mRNA, complete cds.
pol-miR-214	TCR beta mRNA for T cell receptor beta chain, complete cds.
pol-miR-214	mRNA for interferon regulatory factor, complete cds.
pol-miR-214	MHC class IIb antigen mRNA, complete cds.
pol-miR-214	mRNA for serine protease I-2, complete cds.
pol-miR-214	mRNA for serine protease I-1, complete cds.

pol-miR-146a	cathepsin F mRNA, complete cds.
pol-miR-146a	cathepsin K mRNA, complete cds.
pol-miR-146a	dio2 mRNA for iodothyronine deiodinase type II, complete cds.
pol-miR-146a	dio1 mRNA for iodothyronine deiodinase type I, complete cds.
pol-miR-146a	ctrlr mRNA for calcitonin receptor-like receptor, complete cds.
pol-miR-146a	doublesex and mab-3 related transcription factor 1 (DMRT1) mRNA, complete cds.
pol-miR-146a	ornithine decarboxylase antizyme large isoform ORF1 and ornithine decarboxylase antizyme large isoform mRNA, complete cds.
pol-miR-146a	testis enhanced gene transcript-like protein mRNA, complete cds.
pol-miR-146a	phospholipase D1B mRNA, complete cds.
pol-miR-150	TLR14 mRNA for toll-like receptor 14, complete cds.
pol-miR-150	lipopolysaccharide-binding protein/bactericidal permeability-increasing protein mRNA, complete cds.
pol-miR-150	mRNA for trypsinogen 3, complete cds.
pol-miR-150	inhibitor kappa B alpha mRNA, complete cds.
pol-miR-150	VDRb mRNA for vitamin D receptor b, complete cds.
pol-miR-150	phospholipase C beta 4 mRNA, complete cds.
pol-miR-150	phospholipase D2 mRNA, complete cds.
pol-miR-153b-3p	14kDa-apo mRNA for 14 kDa-apolipoprotein, complete cds.
pol-miR-153b-3p	TLR3 mRNA for Toll-like receptor 3, complete cds.
pol-miR-153b-3p	glucose-regulated protein 78 (Grp78) mRNA, complete cds.
pol-miR-153b-3p	PY mRNA for peptide Y, complete cds.
pol-miR-153b-3p	B cell accessory protein (CD79b) mRNA, complete cds.
pol-miR-153b-3p	phospholipase D1B mRNA, complete cds.
pol-miR-155	deleted in azoospermia-like protein 2 (DAZL) mRNA, DAZL-2 allele, complete cds.
pol-miR-155	deleted in azoospermia-like protein 1 (DAZL) mRNA, DAZL-1 allele, complete cds.
pol-miR-155	NOD-like receptor C (NLRC) mRNA, complete cds.
pol-miR-155	heat shock protein 90 beta (Hsp90beta) mRNA, complete cds.
pol-miR-155	mRNA for complement component C9, complete cds.
pol-miR-214	IL-8 receptor mRNA for interleukin-8 receptor, complete cds.
pol-miR-214	DnaJ-like subfamily B member 6 (Hsp40B6) mRNA, complete cds.
pol-miR-214	myD88 mRNA for myeloid differentiation factor 88, complete cds.
pol-miR-214	CPB mRNA for carboxypeptidase B, partial cds.
pol-miR-214	CPA1 mRNA for carboxypeptidase A1, partial cds.
pol-miR-214	fIGF-IR-2 mRNA for type 1 insulin-like growth factor receptor, complete cds.
pol-miR-214	empty spiracles homeobox 2 (Emx2) mRNA, complete cds.
pol-miR-214	TANK-binding kinase 1 splice variant 3 (TBK1) mRNA, complete cds, alternatively spliced.
pol-miR-214	TANK binding kinase 1 splice variant 2 (TBK1) mRNA, complete cds, alternatively spliced.
pol-miR-214	serine protease I-1 mRNA, complete cds.
pol-miR-214	insulin-like growth factor I mRNA, complete cds.
pol-miR-214	glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds.
pol-miR-214	phospholipase D1B mRNA, complete cds.
pol-miR-214	phospholipase D2 mRNA, complete cds.
pol-miR-214	transmembrane 4 L6 family member 4 mRNA, complete cds.
pol-miR-214	G-CSF mRNA for Granulocyte Colony-Stimulating Factor, complete cds.
pol-miR-214	mRNA for granzyme I-2, complete cds.
pol-miR-214	mRNA for glucocorticoid receptor, complete cds.
pol-miR-217	mRNA for CD40, complete cds.
pol-miR-217	ITGAL mRNA, complete cds.
pol-miR-217	membrane progestin receptor-like mRNA, complete cds.
pol-miR-217	cathepsin F mRNA, complete cds.
pol-miR-217	syntenin mRNA, complete cds.
pol-miR-217	splicing factor arginine/serine-rich 3 mRNA, complete cds.
pol-miR-217	macrophage stimulating-1 protein mRNA, complete cds.
pol-miR-217	calreticulin mRNA, complete cds.
pol-miR-217	TNFR-1 mRNA for tumor necrosis factor receptor-1, complete cds.

pol-miR-155	heat shock protein 90 beta mRNA, complete cds.
pol-miR-15b-5p	CD18 transcript 2 mRNA, complete cds, alternatively spliced.
pol-miR-15b-5p	CD18 transcript 1 mRNA, complete cds, alternatively spliced.
pol-miR-15b-5p	ras-2 mRNA, complete cds.
pol-miR-15b-5p	phospholipase C delta 1B Lf mRNA, complete cds.
pol-miR-15b-5p	mRNA for microtubule aggregate protein homolog isotype-1, complete cds.
pol-miR-15b-5p	LGP2 mRNA, complete cds.
pol-miR-15b-5p	phospholipase D (PLD) mRNA, complete cds.
pol-miR-15b-5p	dsRNA-dependent protein kinase (PKR) mRNA, complete cds.
pol-miR-15b-5p	beta-defensin I-5 mRNA, complete cds.
pol-miR-15b-5p	beta-defensin I-3 mRNA, complete cds.
pol-miR-15b-5p	beta-defensin I-2 mRNA, complete cds.
pol-miR-15b-5p	beta-defensin I-1 mRNA, complete cds.
pol-miR-15b-5p	serotransferrin precursor (SroTP) mRNA, complete cds.
pol-miR-15b-5p	signal transducer and activator of transcription 1 mRNA, complete cds.
pol-miR-15b-5p	dio3 mRNA for iodothyronine deiodinase type III, complete cds.
pol-miR-15b-5p	mRNA for elastase 4 precursor, partial cds.
pol-miR-15b-5p	hypothetical protein mRNA, complete cds.
pol-miR-15b-5p	glucose-regulated protein 78 (Grp78) mRNA, complete cds.
pol-miR-15b-5p	TCR alpha mRNA for T cell receptor alpha chain, complete cds.
pol-miR-15b-5p	mRNA for transferrin, complete cds.
pol-miR-15b-5p	CCR9 mRNA for C-C chemokine receptor 9, complete cds.
pol-miR-15b-5p	natural killer enhancing factor (NKEF) mRNA, complete cds.
pol-miR-15b-5p	fIGF-IR-2 mRNA for type 1 insulin-like growth factor receptor, complete cds.
pol-miR-15b-5p	CD8 beta mRNA for T-cell surface glycoprotein CD8 beta chain, complete cds.
pol-miR-15b-5p	phospholipase C delta 1 B short form (PLC) mRNA, complete cds.
pol-miR-15b-5p	doublesex and mab-3 related transcription factor 1 (DMRT1) mRNA, complete cds.
pol-miR-217	NPY mRNA for neuropeptide Y, complete cds.
pol-miR-217	prolactin precursor, mRNA, complete cds.
pol-miR-217	MMP2 mRNA for gelatinase, complete cds.
pol-miR-2188-5p	CD4-2 mRNA for T-cell surface glycoprotein CD4-2, complete cds.
pol-miR-2188-5p	FASL mRNA for Fas ligand, complete cds.
pol-miR-2188-5p	PAC1 receptor mRNA, complete cds.
pol-miR-2188-5p	beclin-1 mRNA, complete cds.
pol-miR-2188-5p	glucose-regulated protein 78 (Grp78) mRNA, complete cds.
pol-miR-2188-5p	VDRa mRNA for vitamin D receptor a, complete cds.
pol-miR-2188-5p	POMC-II precursor protein mRNA, complete cds.
pol-miR-2188-5p	p53 tumor supressor protein (p53) mRNA, complete cds.
pol-miR-221-5p	serum response factor protein mRNA, complete cds.
pol-miR-221-5p	CD18 transcript 2 mRNA, complete cds, alternatively spliced.
pol-miR-221-5p	CD18 transcript 1 mRNA, complete cds, alternatively spliced.
pol-miR-221-5p	paired box protein 3b isoform Pax3b-1 (Pax3a) mRNA, complete cds.
pol-miR-221-5p	nuclear receptor DAX1 mRNA, complete cds.
pol-miR-221-5p	phospholipase C delta 1A mRNA, complete cds.
pol-miR-221-5p	mRNA for microtubule aggregate protein homolog isotype-1, complete cds.
pol-miR-221-5p	interferon regulatory factor 2 (IRF2) mRNA, complete cds.
pol-miR-221-5p	elastase-like serine protease (ELSrP) mRNA, complete cds.
pol-miR-221-5p	voltage-dependent anion channel (VDAC) mRNA, complete cds.
pol-miR-221-5p	natural resistance-associated macrophage protein mRNA, complete cds.
pol-miR-221-5p	cgrpr mRNA for calcitonin gene-related peptide receptor, complete cds.
pol-miR-221-5p	il8-2 mRNA for interleukin 8 isoform 2, complete cds.
pol-miR-221-5p	AMPD1 mRNA, complete cds.
pol-miR-221-5p	insulin-like growth factor I mRNA, complete cds.
pol-miR-221-5p	phospholipase D1B mRNA, complete cds.

pol-miR-15b-5p	POMC-II precursor protein mRNA, complete cds.
pol-miR-15b-5p	testis enhanced gene transcript-like protein mRNA, complete cds.
pol-miR-15b-5p	transferrin mRNA, complete cds.
pol-miR-15b-5p	insulin-like growth factor I mRNA, complete cds.
pol-miR-15b-5p	proopiomelanocortin-III (POMC-III) mRNA, complete cds.
pol-miR-15b-5p	phospholipase D1B mRNA, complete cds.
pol-miR-15b-5p	phospholipase D2 mRNA, complete cds.
pol-miR-15b-5p	transmembrane 4 L6 family member 4 mRNA, complete cds.
pol-miR-15b-5p	mRNA for granzyme I-2, complete cds.
pol-miR-15b-5p	MMP9 mRNA for gelatinase, complete cds.
pol-miR-16c-3p	mRNA for CD40, complete cds.
pol-miR-16c-3p	DEAD box helicase 3-2 (DDX3-2) mRNA, complete cds.
pol-miR-16c-3p	melanoma differentiation-associated protein 5 (mda5) mRNA, complete cds.
pol-miR-16c-3p	C-type lectin domain family 4 member E mRNA, complete cds.
pol-miR-16c-3p	putative fast skeletal muscle troponin mRNA, partial cds.
pol-miR-16c-3p	dio3 mRNA for iodothyronine deiodinase type III, complete cds.
pol-miR-16c-3p	mRNA for trypsinogen 3, complete cds.
pol-miR-16c-3p	ERb mRNA for estrogen receptor beta, complete cds.
pol-miR-1788-3p	p65 NF-κb subunit mRNA, complete cds.
pol-miR-1788-3p	mRNA for CD40, complete cds.
pol-miR-1788-3p	GPR43 mRNA, complete cds.
pol-miR-1788-3p	ITGAL mRNA, complete cds.
pol-miR-1788-3p	transcription factor SOX-1b (Sox1b) mRNA, complete cds.
pol-miR-1788-3p	deleted in azoospermia-like protein 2 (DAZL) mRNA, DAZL-2 allele, complete cds.
pol-miR-1788-3p	deleted in azoospermia-like protein 1 (DAZL) mRNA, DAZL-1 allele, complete cds.
pol-miR-1788-3p	phospholipase C delta 1B Lf mRNA, complete cds.
pol-miR-1788-3p	scinderin-like protein mRNA, complete cds.
pol-miR-221-5p	GAPDH mRNA for glyceraldehyde-3-phosphate dehydrogenase, complete cds.
pol-miR-221-5p	mRNA for granzyme I-2, complete cds.
pol-miR-223	serum response factor protein mRNA, complete cds.
pol-miR-223	ITGAL mRNA, complete cds.
pol-miR-223	isolate Po-P1 PR domain containing 1 (PRDM1) mRNA, complete cds.
pol-miR-223	pannexin 1 mRNA, complete cds.
pol-miR-223	GDF15 mRNA for growth differentiation factor 15, complete cds.
pol-miR-223	Wap65-2 mRNA, complete cds.
pol-miR-223	TANK binding kinase 1 splice variant 3 (TBK1) mRNA, complete cds, alternatively spliced.
pol-miR-223	mc-5r mRNA for melanocortin-5 receptor, complete cds.
pol-miR-223	GAPDH mRNA for glyceraldehyde-3-phosphate dehydrogenase, complete cds.
pol-miR-223	G-CSF mRNA for Granulocyte Colony-Stimulating Factor, complete cds.
pol-miR-27b-5p	alkaline phosphatase (alp) mRNA, complete cds.
pol-miR-27b-5p	myostatin (MSTN) mRNA, complete cds.
pol-miR-27b-5p	DEAD box helicase 3-1 (DDX3-1) mRNA, complete cds.
pol-miR-27b-5p	melanin-concentrating hormone receptor 1 mRNA, complete cds.
pol-miR-27b-5p	deleted in azoospermia-like protein 2 (DAZL) mRNA, DAZL-2 allele, complete cds.
pol-miR-27b-5p	deleted in azoospermia-like protein 1 (DAZL) mRNA, DAZL-1 allele, complete cds.
pol-miR-27b-5p	transcription factor SOX-2 (Sox2) mRNA, complete cds.
pol-miR-27b-5p	ras-2 mRNA, complete cds.
pol-miR-27b-5p	peptidoglycan recognition protein (PGRP) mRNA, complete cds.
pol-miR-27b-5p	scinderin-like protein mRNA, complete cds.
pol-miR-27b-5p	phospholipase C-beta 1 (PLC-beta1) mRNA, complete cds.
pol-miR-27b-5p	YGHL1 mRNA, complete cds.
pol-miR-27b-5p	parvalbumin mRNA sequence, partial.
pol-miR-27b-5p	beclin-1 mRNA, complete cds.
pol-miR-27b-5p	elastase-like serine protease (ELSrP) mRNA, complete cds.

pol-miR-1788-3p	cathepsin B mRNA, complete cds.
pol-miR-1788-3p	voltage-dependent anion channel (VDAC) mRNA, complete cds.
pol-miR-1788-3p	proteasome activator subunit 2 mRNA, complete cds.
pol-miR-1788-3p	macrophage stimulating-1 protein mRNA, complete cds.
pol-miR-1788-3p	DnaJ-like subfamily B member 11 (Hsp40B11) mRNA, complete cds.
pol-miR-1788-3p	DnaJ-like subfamily A member 4 (Hsp40A4) mRNA, complete cds.
pol-miR-1788-3p	TCR alpha mRNA for T cell receptor alpha chain, complete cds.
pol-miR-1788-3p	calreticulin mRNA, complete cds.
pol-miR-1788-3p	asparaginyl endopeptidase (AEP) mRNA, AEP-Legumain allele, complete cds.
pol-miR-1788-3p	TNFR-1 mRNA for tumor necrosis factor receptor-1, complete cds.
pol-miR-1788-3p	myD88 mRNA for myeloid differentiaton factor 88, complete cds.
pol-miR-1788-3p	ERa mRNA for estrogen receptor alpha, complete cds.
pol-miR-1788-3p	phospholipase C delta 1 B short form (PLC) mRNA, complete cds.
pol-miR-1788-3p	pemRNA for pepsinogen, complete cds.
pol-miR-1788-3p	doublesex and mab-3 related transcription factor 1 (DMRT1) mRNA, complete cds.
pol-miR-1788-3p	ornithine decarboxylase antizyme large isoform ORF1 and ornithine decarboxylase antizyme large isoform mRNA, complete cds.
pol-miR-1788-3p	insulin-like growth factor I mRNA, complete cds.
pol-miR-1788-3p	phospholipase D1B mRNA, complete cds.
pol-miR-1788-3p	phospholipase D2 mRNA, complete cds.
pol-miR-1788-3p	trypsinogen 2 precursor (TRP2) mRNA, complete cds.
pol-miR-1788-3p	G-CSF mRNA for Granulocyte Colony-Stimulating Factor, complete cds.
pol-miR-1788-5p	SOD2 mRNA for Mn-superoxide dismutase, complete cds.
pol-miR-1788-5p	TLR14 mRNA for toll like receptor 14, complete cds.
pol-miR-1788-5p	CTL mRNA for C-type lectin, complete cds.
pol-miR-1788-5p	GPR43 mRNA, complete cds.
pol-miR-1788-5p	Nanos3 (nanos3) mRNA, complete cds.
pol-miR-1788-5p	interleukin-10 precursor, mRNA, complete cds.
pol-miR-27b-5p	POMC-I precursor protein mRNA, complete cds.
pol-miR-27b-5p	preprovasoactive intestinal peptide mRNA, complete cds.
pol-miR-27b-5p	JFCXCL13-like mRNA for CXC chemokine, complete cds.
pol-miR-27b-5p	mRNA for CD3 epsilon, complete cds.
pol-miR-27b-5p	CCR9 mRNA for C-C chemokine receptor 9, complete cds.
pol-miR-27b-5p	heat shock protein 60 kDa (hsp60) mRNA, complete cds.
pol-miR-27b-5p	myD88 mRNA for myeloid differentiaton factor 88, complete cds.
pol-miR-27b-5p	melanin-concentrating hormone receptor 1 (MCHR1) mRNA, complete cds.
pol-miR-27b-5p	CD8 beta mRNA for T-cell surface glycoprotein CD8 beta chain, complete cds.
pol-miR-27b-5p	AMPD1 mRNA, complete cds.
pol-miR-27b-5p	ornithine decarboxylase antizyme large isoform ORF1 and ornithine decarboxylase antizyme large isoform mRNA, complete cds.
pol-miR-27b-5p	ornithine decarboxylase antizyme small isoform ORF1 and ornithine decarboxylase antizyme small isoform mRNA, complete cds.
pol-miR-27b-5p	melanin-concentrating hormone-like protein mRNA, complete cds.
pol-miR-27b-5p	testis enhanced gene transcript-like protein mRNA, complete cds.
pol-miR-27b-5p	phospholipase D1B mRNA, complete cds.
pol-miR-27b-5p	phospholipase D2 mRNA, complete cds.
pol-miR-27b-5p	GDF8 type 2 mRNA, complete cds.
pol-miR-27b-5p	GDF8 type 1 mRNA, complete cds.
pol-miR-27b-5p	mRNA for granzyme III-2, complete cds.
pol-miR-27b-5p	pitx2 mRNA, complete cds.
pol-miR-375	CD4-2 mRNA for T-cell surface glycoprotein CD4-2, complete cds.
pol-miR-375	TLR14 mRNA for toll like receptor 14, complete cds.
pol-miR-375	hdac4 (hdac4) mRNA, complete cds.
pol-miR-375	interferon regulatory factor 7 (IRF7) mRNA, complete cds.
pol-miR-375	fushi tarazu factor 1 mRNA, complete cds.
pol-miR-375	DEAD box helicase 3-2 (DDX3-2) mRNA, complete cds.
pol-miR-375	isolate Po-P14 PR domain containing 14 (PRDM14) mRNA, complete cds.

pol-miR-1788-5p	paired box protein 3b isoform Pax3b-1 (Pax3a) mRNA, complete cds.
pol-miR-1788-5p	interferon regulatory factor 9 (IRF9) mRNA, complete cds.
pol-miR-1788-5p	phospholipase C delta 1A mRNA, complete cds.
pol-miR-1788-5p	peptidoglycan recognition protein (PGRP) mRNA, complete cds.
pol-miR-1788-5p	scinderin-like protein mRNA, complete cds.
pol-miR-1788-5p	phospholipase C-beta 1 (PLC-beta1) mRNA, complete cds.
pol-miR-1788-5p	17-alpha-hydroxylase mRNA, complete cds.
pol-miR-1788-5p	interleukin-1 receptor type II mRNA, complete cds.
pol-miR-1788-5p	syntenin mRNA, complete cds.
pol-miR-1788-5p	serotransferrin precursor (SroTP) mRNA, complete cds.
pol-miR-1788-5p	JFC/EBPb mRNA for CCAAT/Enhancer binding protein beta, complete cds.
pol-miR-1788-5p	calreticulin mRNA, complete cds.
pol-miR-1788-5p	mRNA for serine protease I-2, complete cds.
pol-miR-1788-5p	CCR3 mRNA for C-C chemokine receptor-3, complete cds.
pol-miR-1788-5p	mRNA for CXC chemokine, complete cds.
pol-miR-1788-5p	VDRb mRNA for vitamin D receptor b, complete cds.
pol-miR-1788-5p	il8-2 mRNA for interleukin 8 isoform 2, complete cds.
pol-miR-1788-5p	interleukine-8 (IL-8) mRNA, complete cds.
pol-miR-1788-5p	ornithine decarboxylase antizyme small isoform ORF1 and ornithine decarboxylase antizyme small isoform mRNA, complete cds.
pol-miR-1788-5p	testis enhanced gene transcript-like protein mRNA, complete cds.
pol-miR-1788-5p	stanniocalcin 2 mRNA, complete cds.
pol-miR-1788-5p	IL-11b mRNA for interleukin 11 type b, complete cds.
pol-miR-1788-5p	proopiomelanocortin-III (POMC-III) mRNA, complete cds.
pol-miR-1788-5p	phospholipase D2 mRNA, complete cds.
pol-miR-1788-5p	thymosin beta mRNA, complete cds.
pol-miR-1788-5p	M17h mRNA for M17 homologue, complete cds.
pol-miR-1788-5p	mRNA for granzyme III-2, complete cds.
pol-miR-375	purinergic receptor P2X ligand-gated ion channel 7a mRNA, complete cds.
pol-miR-375	vasa-like protein mRNA, complete cds.
pol-miR-375	phospholipase C delta 1B Lf mRNA, complete cds.
pol-miR-375	toll-like receptor 1 mRNA, complete cds.
pol-miR-375	vasa mRNA, complete cds.
pol-miR-375	interferon regulatory factor 2 (IRF2) mRNA, complete cds.
pol-miR-375	beta-actin mRNA, complete cds.
pol-miR-375	syntenin mRNA, complete cds.
pol-miR-375	phospholipase D (PLD) mRNA, complete cds.
pol-miR-375	macrophage stimulating-1 protein mRNA, complete cds.
pol-miR-375	putative fast skeletal muscle troponin mRNA, partial cds.
pol-miR-375	preprovasoactive intestinal peptide mRNA, complete cds.
pol-miR-375	liver-expressed antimicrobial peptide 2 mRNA, complete cds.
pol-miR-375	Par o 1 mRNA for parvalbumin, complete cds.
pol-miR-375	inhibitor kappa B alpha mRNA, complete cds.
pol-miR-375	glucose-regulated protein 78 (Grp78) mRNA, complete cds.
pol-miR-375	JFC/EBPe mRNA for CCAAT/Enhancer binding protein epsilon, complete cds.
pol-miR-375	heat shock protein 60 kDa (hsp60) mRNA, complete cds.
pol-miR-375	VDRb mRNA for vitamin D receptor b, complete cds.
pol-miR-375	ctrlr mRNA for calcitonin receptor-like receptor, complete cds.
pol-miR-375	il8-2 mRNA for interleukin 8 isoform 2, complete cds.
pol-miR-375	lipoprotein lipase (LPL) mRNA, complete cds.
pol-miR-375	TANK binding kinase 1 splice variant 3 (TBK1) mRNA, complete cds, alternatively spliced.
pol-miR-375	TANK binding kinase 1 splice variant 2 (TBK1) mRNA, complete cds, alternatively spliced.
pol-miR-375	TANK binding kinase 1 splice variant 1 (TBK1) mRNA, complete cds, alternatively spliced.
pol-miR-375	B cell accessory protein (CD79b) mRNA, complete cds.
pol-miR-375	phospholipase C delta 1 B short form (PLC) mRNA, complete cds.

pol-miR-1788-5p	mRNA for granzyme III-1, complete cds.
pol-miR-1788-5p	mRNA for granzyme I-2, complete cds.
pol-miR-1788-5p	mRNA for granzyme I-1, complete cds.
pol-miR-1788-5p	mRNA for granzyme II, complete cds.
pol-miR-1788-5p	MMP2 mRNA for gelatinase, complete cds.
pol-miR-181a-2-3p	transcription factor PU.1 mRNA, complete cds, alternatively spliced.
pol-miR-181a-2-3p	melanocortin 4 receptor (MC4R) mRNA, complete cds.
pol-miR-181a-2-3p	progranulin type II (pGRN) mRNA, complete cds, alternatively spliced.
pol-miR-181a-2-3p	progranulin type I (pGRN) mRNA, complete cds, alternatively spliced.
pol-miR-181a-2-3p	DnaJ-like subfamily B member 11 (Hsp40B11) mRNA, complete cds.
pol-miR-181a-2-3p	mRNA for trypsinogen 3, complete cds.
pol-miR-181a-2-3p	VDRa mRNA for vitamin D receptor a, complete cds.
pol-miR-181a-2-3p	cgrpr mRNA for calcitonin gene-related peptide receptor, complete cds.
pol-miR-181a-2-3p	IL-11b mRNA for interleukin 11 type b, complete cds.
pol-miR-181a-2-3p	phospholipase D1B mRNA, complete cds.
pol-miR-181a-2-3p	MMP2 mRNA for gelatinase, complete cds.
pol-miR-181a-5p	TLR14 mRNA for toll like receptor 14, complete cds.
pol-miR-181a-5p	mRNA for CD40, complete cds.
pol-miR-181a-5p	transcription factor T-bet (TBX21) mRNA, complete cds.
pol-miR-181a-5p	ITGAL mRNA, complete cds.
pol-miR-181a-5p	DEAD box helicase 3-1 (DDX3-1) mRNA, complete cds.
pol-miR-181a-5p	interferon regulatory factor 9 (IRF9) mRNA, complete cds.
pol-miR-181a-5p	lipopolysaccharide-induced tumor necrosis factor-alpha factor mRNA, complete cds.
pol-miR-181a-5p	HSL1 mRNA for hormone-sensitive lipase1, complete cds.
pol-miR-181a-5p	TLR3 mRNA for Toll-like receptor 3, complete cds.
pol-miR-181a-5p	YGHL1 mRNA, complete cds.
pol-miR-181a-5p	LGP2 mRNA, complete cds.
pol-miR-375	doublesex and mab-3 related transcription factor 1 (DMRT1) mRNA, complete cds.
pol-miR-375	ornithine decarboxylase antizyme large isoform ORF1 and ornithine decarboxylase antizyme large isoform mRNA, complete cds.
pol-miR-375	POMC-II precursor protein mRNA, complete cds.
pol-miR-375	prolactin precursor, mRNA, complete cds.
pol-miR-375	insulin-like growth factor I mRNA, complete cds.
pol-miR-375	IL-11b mRNA for interleukin 11 type b, complete cds.
pol-miR-375	phospholipase D1B mRNA, complete cds.
pol-miR-375	phospholipase D2 mRNA, complete cds.
pol-miR-375	sqt mRNA for squint, complete cds.
pol-miR-375	spaw mRNA for southpaw, complete cds.
pol-miR-375	COL1A2 mRNA for type 1 collagen alpha 2, complete cds.
pol-miR-375	mRNA for granzyme I-2, complete cds.
pol-miR-375	pitx2 mRNA, complete cds.
pol-miR-375	myostatin (MSTN) mRNA, complete cds.
pol-miR-430a-3p	GPR43 mRNA, complete cds.
pol-miR-430a-3p	DEAD box helicase 3-2 (DDX3-2) mRNA, complete cds.
pol-miR-430a-3p	akirin mRNA, complete cds.
pol-miR-430a-3p	YGHL1 mRNA, complete cds.
pol-miR-430a-3p	transcription factor C/EBPalpha mRNA, complete cds.
pol-miR-430a-3p	LGP2 mRNA, complete cds.
pol-miR-430a-3p	beta-actin mRNA, complete cds.
pol-miR-430a-3p	syntenin mRNA, complete cds.
pol-miR-430a-3p	phospholipase D (PLD) mRNA, complete cds.
pol-miR-430a-3p	lipopolysaccharide-binding protein/bactericidal permeability-increasing protein mRNA, complete cds.
pol-miR-430a-3p	DnaJ-like subfamily B member 11 (Hsp40B11) mRNA, complete cds.
pol-miR-430a-3p	preprovasoactive intestinal peptide mRNA, complete cds.
pol-miR-430a-3p	ppsb mRNA for pancreatic protein with two somatomedin B domains, complete cds.

pol-miR-181a-5p	lipopolysaccharide-binding protein/bactericidal permeability-increasing protein mRNA, complete cds.
pol-miR-181a-5p	hypothetical protein mRNA, complete cds.
pol-miR-181a-5p	inhibitor kappa B alpha mRNA, complete cds.
pol-miR-181a-5p	TCR alpha mRNA for T cell receptor alpha chain, complete cds.
pol-miR-181a-5p	DnaJ-like subfamily B member 6 (Hsp40B6) mRNA, complete cds.
pol-miR-181a-5p	VDRa mRNA for vitamin D receptor a, complete cds.
pol-miR-181a-5p	VDRb mRNA for vitamin D receptor b, complete cds.
pol-miR-181a-5p	TFIIA P12 subunit mRNA, complete cds.
pol-miR-181a-5p	testis enhanced gene transcript-like protein mRNA, complete cds.
pol-miR-181a-5p	proopiomelanocortin-III (POMC-III) mRNA, complete cds.
pol-miR-181a-5p	transmembrane 4 L6 family member 4 mRNA, complete cds.
pol-miR-181c-5p	TLR14 mRNA for toll like receptor 14, complete cds.
pol-miR-181c-5p	hdac4 (hdac4) mRNA, complete cds.
pol-miR-181c-5p	fNKCC mRNA for Na-K-Cl cotransporter, complete cds.
pol-miR-181c-5p	alkaline phosphatase (alp) mRNA, complete cds.
pol-miR-181c-5p	PoLCE mRNA for hatching enzyme, complete cds.
pol-miR-181c-5p	transcription factor T-bet (TBX21) mRNA, complete cds.
pol-miR-181c-5p	B7-H1/DC mRNA, complete cds.
pol-miR-181c-5p	ITGAL mRNA, complete cds.
pol-miR-181c-5p	transcription factor SOX-1b (Sox1b) mRNA, complete cds.
pol-miR-181c-5p	isolate Po-P1 PR domain containing 1 (PRDM1) mRNA, complete cds.
pol-miR-181c-5p	lipopolysaccharide-induced tumor necrosis factor-alpha factor mRNA, complete cds.
pol-miR-181c-5p	HSL1 mRNA for hormone-sensitive lipase1, complete cds.
pol-miR-181c-5p	TLR3 mRNA for Toll-like receptor 3, complete cds.
pol-miR-181c-5p	transcription factor PU.1 mRNA, complete cds, alternatively spliced.
pol-miR-181c-5p	LGP2 mRNA, complete cds.
pol-miR-181c-5p	interferon regulatory factor 3 variant 1 (IRF3) mRNA, complete cds.
pol-miR-430a-3p	TNFR-1 mRNA for tumor necrosis factor receptor-1, complete cds.
pol-miR-430a-3p	ornithine decarboxylase antizyme small isoform ORF1 and ornithine decarboxylase antizyme small isoform mRNA, complete cds.
pol-miR-430a-3p	mRNA for Hoxb-5, partial cds.
pol-miR-430a-3p	M17h mRNA for M17 homologue, complete cds.
pol-miR-430a-3p	lefty mRNA for lefty/antivin, complete cds.
pol-miR-430a-3p	COL1A2 mRNA for type 1 collagen alpha 2, complete cds.
pol-miR-430c-3p	myostatin (MSTN) mRNA, complete cds.
pol-miR-430c-3p	DEAD box helicase 3-2 (DDX3-2) mRNA, complete cds.
pol-miR-430c-3p	beta-actin mRNA, complete cds.
pol-miR-430c-3p	phospholipase D (PLD) mRNA, complete cds.
pol-miR-430c-3p	lipopolysaccharide-binding protein/bactericidal permeability-increasing protein mRNA, complete cds.
pol-miR-430c-3p	DnaJ-like subfamily B member 11 (Hsp40B11) mRNA, complete cds.
pol-miR-430c-3p	GDF15 mRNA for growth differentiation factor 15, complete cds.
pol-miR-430c-3p	preprovasoactive intestinal peptide mRNA, complete cds.
pol-miR-430c-3p	ppsb mRNA for pancreatic protein with two somatomedin B domains, complete cds.
pol-miR-430c-3p	inhibitor kappa B alpha mRNA, complete cds.
pol-miR-430c-3p	glucose-regulated protein 78 (Grp78) mRNA, complete cds.
pol-miR-430c-3p	mRNA for serine protease I-2, complete cds.
pol-miR-430c-3p	heat shock protein 60 kDa (hsp60) mRNA, complete cds.
pol-miR-430c-3p	fIR-1 mRNA for insulin receptor, complete cds.
pol-miR-430c-3p	ornithine decarboxylase antizyme small isoform ORF1 and ornithine decarboxylase antizyme small isoform mRNA, complete cds.
pol-miR-430c-3p	M17h mRNA for M17 homologue, complete cds.
pol-miR-430c-3p	lefty mRNA for lefty/antivin, complete cds.
pol-miR-430c-3p	COL1A2 mRNA for type 1 collagen alpha 2, complete cds.
pol-miR-430c-3p	mRNA for granzyme III-2, complete cds.
pol-miR-430c-3p	mRNA for granzyme III-1, complete cds.
pol-miR-430c-3p	mRNA for granzyme I-2, complete cds.

pol-miR-181c-5p	voltage-dependent anion channel (VDAC) mRNA, complete cds.
pol-miR-181c-5p	serotransferrin precursor (SroTP) mRNA, complete cds.
pol-miR-181c-5p	hypothetical protein mRNA, complete cds.
pol-miR-181c-5p	inhibitor kappa B alpha mRNA, complete cds.
pol-miR-181c-5p	cd3-1 mRNA for CD3 epsilon, complete cds.
pol-miR-181c-5p	betaine homocysteine S-methyltansferase (BHMT) mRNA, complete cds.
pol-miR-181c-5p	CCR3 mRNA for C-C chemokine receptor-3, complete cds.
pol-miR-181c-5p	TNFR-1 mRNA for tumor necrosis factor receptor-1, complete cds.
pol-miR-181c-5p	mRNA for IL-1b, complete cds.
pol-miR-181c-5p	natural killer enhancing factor (NKEF) mRNA, complete cds.
pol-miR-181c-5p	fIGF-IR-2 mRNA for type 1 insulin-like growth factor receptor, complete cds.
pol-miR-181c-5p	VDRa mRNA for vitamin D receptor a, complete cds.
pol-miR-181c-5p	empty spiracles homeobox 2 (Emx2) mRNA, complete cds.
pol-miR-181c-5p	TFIIA P12 subunit mRNA, complete cds.
pol-miR-181c-5p	phospholipase D2 mRNA, complete cds.
pol-miR-181c-5p	phospholipase C delta 3A mRNA, complete cds.
pol-miR-181c-5p	transmembrane 4 L6 family member 4 mRNA, complete cds.
pol-miR-181c-5p	cd3-2 mRNA for CD3 epsilon, complete cds.
pol-miR-182-5p	alkaline phosphatase (alp) mRNA, complete cds.
pol-miR-182-5p	transcription factor T-bet (TBX21) mRNA, complete cds.
pol-miR-182-5p	ITGAM mRNA, complete cds.
pol-miR-182-5p	ITGAL mRNA, complete cds.
pol-miR-182-5p	cathepsin B mRNA, complete cds.
pol-miR-182-5p	ornithine decarboxylase mRNA, complete cds.
pol-miR-182-5p	lipopolysaccharide-binding protein/bactericidal permeability-increasing protein mRNA, complete cds.
pol-miR-182-5p	heat shock protein 70 (HSP70) mRNA, complete cds.
pol-miR-182-5p	macrophage stimulating-1 protein mRNA, complete cds.
pol-miR-430c-3p	mRNA for granzyme I-1, complete cds.
pol-miR-430c-3p	mRNA for granzyme II, complete cds.
pol-miR-458-3p	fChi1 mRNA for chitinase1, complete cds.
pol-miR-458-3p	SOD2 mRNA for Mn-superoxide dismutase, complete cds.
pol-miR-458-3p	transcription factor SOX-1b (Sox1b) mRNA, complete cds.
pol-miR-458-3p	deleted in azoospermia-like protein 2 (DAZL) mRNA, DAZL-2 allele, complete cds.
pol-miR-458-3p	deleted in azoospermia-like protein 1 (DAZL) mRNA, DAZL-1 allele, complete cds.
pol-miR-458-3p	phospholipase C delta 1B Lf mRNA, complete cds.
pol-miR-458-3p	phospholipase C-beta 1 (PLC-beta1) mRNA, complete cds.
pol-miR-458-3p	interferon regulatory factor 3 variant 1 (IRF3) mRNA, complete cds.
pol-miR-458-3p	lipopolysaccharide-binding protein/bactericidal permeability-increasing protein mRNA, complete cds.
pol-miR-458-3p	serotransferrin precursor (SroTP) mRNA, complete cds.
pol-miR-458-3p	JFC/EBPe mRNA for CCAAT/Enhancer binding protein epsilon, complete cds.
pol-miR-458-3p	TNFR-2 mRNA for tumor necrosis factor receptor-2, complete cds.
pol-miR-458-3p	ctrlr mRNA for calcitonin receptor-like receptor, complete cds.
pol-miR-458-3p	cgrpr mRNA for calcitonin gene-related peptide receptor, complete cds.
pol-miR-458-3p	il8-2 mRNA for interleukin 8 isoform 2, complete cds.
pol-miR-458-3p	TANK binding kinase 1 splice variant 3 (TBK1) mRNA, complete cds, alternatively spliced.
pol-miR-458-3p	phospholipase C delta 1 B short form (PLC) mRNA, complete cds.
pol-miR-458-3p	prolactin precursor, mRNA, complete cds.
pol-miR-458-3p	phospholipase D1B mRNA, complete cds.
pol-miR-458-5p	transcription factor SOX-3 (Sox3) mRNA, complete cds.
pol-miR-458-5p	DEAD box helicase 3-1 (DDX3-1) mRNA, complete cds.
pol-miR-458-5p	melanin-concentrating hormone receptor 2 mRNA, complete cds.
pol-miR-458-5p	mRNA for microtubule aggregate protein homolog isotype-1, complete cds.
pol-miR-458-5p	LGP2 mRNA, complete cds.
pol-miR-458-5p	phospholipase D (PLD) mRNA, complete cds.

pol-miR-182-5p	inducible heat shock protein 70 (Hsp70) mRNA, complete cds.
pol-miR-182-5p	mRNA for trypsinogen 3, complete cds.
pol-miR-182-5p	Par o 1 mRNA for parvalbumin, complete cds.
pol-miR-182-5p	heat shock cognate 71 (Hsc71) mRNA, complete cds.
pol-miR-182-5p	CPA1 mRNA for carboxypeptidase A1, partial cds.
pol-miR-182-5p	il8-2 mRNA for interleukin 8 isoform 2, complete cds.
pol-miR-182-5p	phospholipase D1B mRNA, complete cds.
pol-miR-182-5p	phospholipase C delta 4 mRNA, complete cds.
pol-miR-182-5p	mRNA for hsc71, complete cds.
pol-miR-183-5p	TLR5M mRNA for toll-like receptor 5 membrane form, complete cds.
pol-miR-183-5p	transcription factor SOX-3 (Sox3) mRNA, complete cds.
pol-miR-183-5p	isolate Po-P14 PR domain containing 14 (PRDM14) mRNA, complete cds.
pol-miR-183-5p	akirin mRNA, complete cds.
pol-miR-183-5p	phospholipase C gamma 2 (PLC-gamma2) mRNA, complete cds.
pol-miR-183-5p	splicing factor arginine/serine-rich 3 mRNA, complete cds.
pol-miR-183-5p	mRNA for Hoxd-4, complete cds.
pol-miR-183-5p	mRNA for serine protease I-2, complete cds.
pol-miR-183-5p	mRNA for serine protease I-1, complete cds.
pol-miR-183-5p	betaine homocysteine S-methyltansferase (BHMT) mRNA, complete cds.
pol-miR-183-5p	TNFR-1 mRNA for tumor necrosis factor receptor-1, complete cds.
pol-miR-183-5p	toll-like receptor 5 membrane form mRNA, complete cds.
pol-miR-183-5p	serine protease I-1 mRNA, complete cds.
pol-miR-183-5p	TFIIA P12 subunit mRNA, complete cds.
pol-miR-183-5p	testis enhanced gene transcript-like protein mRNA, complete cds.
pol-miR-183-5p	MMP2 mRNA for gelatinase, complete cds.
pol-miR-184	apoA-I mRNA for apolipoprotein A-I, complete cds.
pol-miR-184	transcription factor SOX-3 (Sox3) mRNA, complete cds.
pol-miR-458-5p	serotransferrin precursor (SroTP) mRNA, complete cds.
pol-miR-458-5p	preprovasoactive intestinal peptide mRNA, complete cds.
pol-miR-458-5p	mRNA for trypsinogen 3, complete cds.
pol-miR-458-5p	melanin-concentrating hormone receptor 2 (MCHR2) mRNA, complete cds.
pol-miR-458-5p	insulin-like growth factor I mRNA, complete cds.
pol-miR-458-5p	phospholipase D2 mRNA, complete cds.
pol-miR-458-5p	fNKCC mRNA for Na-K-Cl cotransporter, complete cds.
pol-miR-459-5p	myostatin (MSTN) mRNA, complete cds.
pol-miR-459-5p	gch2 mRNA for GTcyclohydrolase 2, complete cds.
pol-miR-459-5p	transcription factor T-bet (TBX21) mRNA, complete cds.
pol-miR-459-5p	ITGAL mRNA, complete cds.
pol-miR-459-5p	CD83 transcript 2 mRNA, complete cds, alternatively spliced.
pol-miR-459-5p	isolate Po-P1 PR domain containing 1 (PRDM1) mRNA, complete cds.
pol-miR-459-5p	interferon regulatory factor 9 (IRF9) mRNA, complete cds.
pol-miR-459-5p	mRNA for arginine vasotocin precursor, complete cds.
pol-miR-459-5p	phospholipase C-beta 1 (PLC-beta1) mRNA, complete cds.
pol-miR-459-5p	YGHL1 mRNA, complete cds.
pol-miR-459-5p	parvalbumin mRNA sequence, partial.
pol-miR-459-5p	beclin-1 mRNA, complete cds.
pol-miR-459-5p	lipopolysaccharide-binding protein/bactericidal permeability-increasing protein mRNA, complete cds.
pol-miR-459-5p	DnaJ-like subfamily B member 11 (Hsp40B11) mRNA, complete cds.
pol-miR-459-5p	chaperonin containing TCP1 subunit 6A (Cctz) mRNA, partial cds.
pol-miR-459-5p	JFC/EBPb mRNA for CCAAT/Enhancer binding protein beta, complete cds.
pol-miR-459-5p	il8-2 mRNA for interleukin 8 isoform 2, complete cds.
pol-miR-459-5p	ornithine decarboxylase antizyme large isoform ORF1 and ornithine decarboxylase antizyme large isoform mRNA, complete cds.
pol-miR-459-5p	ornithine decarboxylase antizyme small isoform ORF1 and ornithine decarboxylase antizyme small isoform mRNA, complete cds.
pol-miR-459-5p	TFIIA P12 subunit mRNA, complete cds.

pol-miR-184	CD18 transcript 2 mRNA, complete cds, alternatively spliced.	**pol-miR-459-5p**	testis enhanced gene transcript-like protein mRNA, complete cds.
pol-miR-184	CD18 transcript 1 mRNA, complete cds, alternatively spliced.	**pol-miR-459-5p**	prolactin precursor, mRNA, complete cds.
pol-miR-184	transcription factor SOX-1a (Sox1a) mRNA, complete cds.	**pol-miR-459-5p**	insulin-like growth factor I mRNA, complete cds.
pol-miR-184	DEAD box helicase 3-2 (DDX3-2) mRNA, complete cds.	**pol-miR-459-5p**	GDF8 type 2 mRNA, complete cds.
pol-miR-184	DEAD box helicase 3-1 (DDX3-1) mRNA, complete cds.	**pol-miR-459-5p**	GDF8 type 1 mRNA, complete cds.
pol-miR-184	Nanos3 (nanos3) mRNA, complete cds.	**pol-miR-459-5p**	mRNA for tumor necrosis factor, complete cds.
pol-miR-184	isolate Po-P1 PR domain containing 1 (PRDM1) mRNA, complete cds.	**pol-miR-459-5p**	mRNA for granzyme III-2, complete cds.
pol-miR-184	paired box protein 3b isoform Pax3b-1 (Pax3a) mRNA, complete cds.	**pol-miR-459-5p**	mRNA for granzyme I-2, complete cds.
pol-miR-184	tropomyosin alpha-1 mRNA, complete cds.	**pol-miR-459-5p**	mRNA for granzyme I-1, complete cds.
pol-miR-184	phospholipase C-beta 1 (PLC-beta1) mRNA, complete cds.	**pol-miR-462**	GPR43 mRNA, complete cds.
pol-miR-184	mRNA for preprosomatostatin I, complete cds.	**pol-miR-462**	cathepsin F mRNA, complete cds.
pol-miR-184	transcription factor C/EBPalpha mRNA, complete cds.	**pol-miR-462**	DnaJ-like subfamily B member 6 (Hsp40B6) mRNA, complete cds.
pol-miR-184	growth hormone-releasing hormone (GHRH) mRNA, complete cds.	**pol-miR-462**	testis enhanced gene transcript-like protein mRNA, complete cds.
pol-miR-184	beta-actin mRNA, complete cds.	**pol-miR-489**	p65 NF-κb subunit mRNA, complete cds.
pol-miR-184	macrophage stimulating-1 protein mRNA, complete cds.	**pol-miR-489**	mRNA for CD40, complete cds.
pol-miR-184	serotransferrin precursor (SroTP) mRNA, complete cds.	**pol-miR-489**	akirin mRNA, complete cds.
pol-miR-184	DnaJ-like subfamily B member 11 (Hsp40B11) mRNA, complete cds.	**pol-miR-489**	HSL1 mRNA for hormone-sensitive lipase1, complete cds.
pol-miR-184	calmodulin mRNA, complete cds.	**pol-miR-489**	scinderin-like protein mRNA, complete cds.
pol-miR-184	preprovasoactive intestinal peptide mRNA, complete cds.	**pol-miR-489**	YGHL1 mRNA, complete cds.
pol-miR-184	mRNA for elastase 1 precursor, complete cds.	**pol-miR-489**	LGP2 mRNA, complete cds.
pol-miR-184	creatine kinase 1 mRNA, complete cds.	**pol-miR-489**	cathepsin F mRNA, complete cds.
pol-miR-184	MHC class IIb antigen mRNA, complete cds.	**pol-miR-489**	splicing factor arginine/serine-rich 3 mRNA, complete cds.
pol-miR-184	asparaginyl endopeptidase (AEP) mRNA, AEP-Legumain allele, complete cds.	**pol-miR-489**	heat shock protein 70 (HSP70) mRNA, complete cds.
pol-miR-184	IL-8 receptor mRNA for interleukin-8 receptor, complete cds.	**pol-miR-489**	serotransferrin precursor (SroTP) mRNA, complete cds.
pol-miR-184	natural killer enhancing factor (NKEF) mRNA, complete cds.	**pol-miR-489**	inducible heat shock protein 70 (Hsp70) mRNA, complete cds.
pol-miR-184	fIR-1 mRNA for insulin receptor, complete cds.	**pol-miR-489**	heat shock cognate 71 (Hsc71) mRNA, complete cds.
pol-miR-184	empty spiracles homeobox 2 (Emx2) mRNA, complete cds.	**pol-miR-489**	TNFR-1 mRNA for tumor necrosis factor receptor-1, complete cds.

pol-miR-184	TANK-binding kinase 1 splice variant 3 (TBK1) mRNA, complete cds, alternatively spliced.
pol-miR-184	B cell accessory protein (CD79b) mRNA, complete cds.
pol-miR-184	CD8 beta mRNA for T-cell surface glycoprotein CD8 beta chain, complete cds.
pol-miR-184	phospholipase C beta 4 mRNA, complete cds.
pol-miR-184	doublesex and mab-3 related transcription factor 1 (DMRT1) mRNA, complete cds.
pol-miR-184	ornithine decarboxylase antizyme large isoform ORF1 and ornithine decarboxylase antizyme large isoform mRNA, complete cds.
pol-miR-184	beta-2 microglobulin mRNA, complete cds.
pol-miR-184	insulin-like growth factor I mRNA, complete cds.
pol-miR-184	phospholipase D2 mRNA, complete cds.
pol-miR-184	lefty mRNA for lefty/antivin, complete cds.
pol-miR-184	G-CSF mRNA for Granulocyte Colony-Stimulating Factor, complete cds.
pol-miR-184	chicken-type gonadotropin-releasing hormone 2 precursor, mRNA, complete cds.
pol-miR-184	mRNA for granzyme III-2, complete cds.
pol-miR-184	mRNA for granzyme I-2, complete cds.
pol-miR-184	mRNA for granzyme I-1, complete cds.
pol-miR-18c	GPR43 mRNA, complete cds.
pol-miR-18c	fushi tarazu factor 1 mRNA, complete cds.
pol-miR-18c	interferon regulatory factor 9 (IRF9) mRNA, complete cds.
pol-miR-18c	transcription factor SOX-2 (Sox2) mRNA, complete cds.
pol-miR-18c	cathepsin L mRNA, complete cds.
pol-miR-18c	syntenin mRNA, complete cds.
pol-miR-18c	progranulin type II (pGRN) mRNA, complete cds, alternatively spliced.
pol-miR-18c	progranulin type I (pGRN) mRNA, complete cds, alternatively spliced.
pol-miR-18c	VDRa mRNA for vitamin D receptor a, complete cds.
pol-miR-18c	lipoprotein lipase (LPL) mRNA, complete cds.
pol-miR-18c	phospholipase D2 mRNA, complete cds.
pol-miR-18c	COL1A2 mRNA for type 1 collagen alpha 2, complete cds.
pol-miR-489	natural resistance-associated macrophage protein mRNA, complete cds.
pol-miR-489	myD88 mRNA for myeloid differentiaton factor 88, complete cds.
pol-miR-489	VDRa mRNA for vitamin D receptor a, complete cds.
pol-miR-489	VDRb mRNA for vitamin D receptor b, complete cds.
pol-miR-489	mRNA for complement component C9, complete cds.
pol-miR-489	empty spiracles homeobox 2 (Emx2) mRNA, complete cds.
pol-miR-489	phospholipase D2 mRNA, complete cds.
pol-miR-489	mRNA for tumor necrosis factor, complete cds.
pol-miR-489	mRNA for hsc71, complete cds.
pol-miR-722	GPR43 mRNA, complete cds.
pol-miR-722	nuclear receptor DAX1 mRNA, complete cds.
pol-miR-722	phospholipase C delta 1B Lf mRNA, complete cds.
pol-miR-722	ERb mRNA for estrogen receptor beta, complete cds.
pol-miR-722	phospholipase C delta 1 B short form (PLC) mRNA, complete cds.
pol-miR-722	phospholipase D2 mRNA, complete cds.
pol-miR-730	transcription factor T-bet (TBX21) mRNA, complete cds.
pol-miR-730	endoribonuclease dicer-like protein (dcl) mRNA, complete cds.
pol-miR-730	CD83 transcript 2 mRNA, complete cds, alternatively spliced.
pol-miR-730	transcription factor SOX-1b (Sox1b) mRNA, complete cds.
pol-miR-730	DEAD box helicase 3-2 (DDX3-2) mRNA, complete cds.
pol-miR-730	DEAD box helicase 3-1 (DDX3-1) mRNA, complete cds.
pol-miR-730	interferon regulatory factor 9 (IRF9) mRNA, complete cds.
pol-miR-730	nuclear receptor DAX1 mRNA, complete cds.
pol-miR-730	PRP/PACAprecursor, mRNA, complete cds.
pol-miR-730	phospholipase C-beta 1 (PLC-beta1) mRNA, complete cds.
pol-miR-730	YGHL1 mRNA, complete cds.
pol-miR-730	LGP2 mRNA, complete cds.

pol-miR-190a	peroxisome proliferator-activated receptors alpha mRNA, complete cds.
pol-miR-190a	LGP2 mRNA, complete cds.
pol-miR-193a-5p	TLR14 mRNA for toll like receptor 14, complete cds.
pol-miR-193a-5p	TLR5S mRNA for toll-like receptor 5 soluble form, complete cds.
pol-miR-193a-5p	TPA
pol-miR-193a-5p	hdac4 (hdac4) mRNA, complete cds.
pol-miR-193a-5p	interferon regulatory factor 8 (IRF8) mRNA, complete cds.
pol-miR-193a-5p	alkaline phosphatase (alp) mRNA, complete cds.
pol-miR-193a-5p	mRNA for CD40, complete cds.
pol-miR-193a-5p	T-cell receptor complex zeta chain (CD3z) mRNA, complete cds.
pol-miR-193a-5p	transcription factor T-bet (TBX21) mRNA, complete cds.
pol-miR-193a-5p	endoribonuclease dicer-like protein (dcl) mRNA, complete cds.
pol-miR-193a-5p	CD18 transcript 2 mRNA, complete cds, alternatively spliced.
pol-miR-193a-5p	CD18 transcript 1 mRNA, complete cds, alternatively spliced.
pol-miR-193a-5p	ITGAL mRNA, complete cds.
pol-miR-193a-5p	fushi tarazu factor 1 mRNA, complete cds.
pol-miR-193a-5p	transcription factor SOX-1a (Sox1a) mRNA, complete cds.
pol-miR-193a-5p	Nanos3 (nanos3) mRNA, complete cds.
pol-miR-193a-5p	deleted in azoospermia-like protein 2 (DAZL) mRNA, DAZL-2 allele, complete cds.
pol-miR-193a-5p	deleted in azoospermia-like protein 1 (DAZL) mRNA, DAZL-1 allele, complete cds.
pol-miR-193a-5p	insulin-like growth factor binding protein-4 (IGFBP-4) mRNA, complete cds.
pol-miR-193a-5p	insulin-like growth factor binding protein 5 mRNA, complete cds.
pol-miR-193a-5p	insulin-like growth factor binding protein 4 mRNA, complete cds.
pol-miR-193a-5p	vasa-like protein mRNA, complete cds.
pol-miR-193a-5p	lipopolysaccharide-induced tumor necrosis factor-alpha factor mRNA, complete cds.
pol-miR-193a-5p	nuclear receptor DAX1 mRNA, complete cds.
pol-miR-193a-5p	peptidoglycan recognition protein (PGRP) mRNA, complete cds.
pol-miR-730	low molecular weight polypeptide LMP7 mRNA, complete cds.
pol-miR-730	cathepsin F mRNA, complete cds.
pol-miR-730	syntenin mRNA, complete cds.
pol-miR-730	dsRNA-dependent protein kinase (PKR) mRNA, complete cds.
pol-miR-730	POMC-I precursor protein mRNA, complete cds.
pol-miR-730	cathepsin K mRNA, complete cds.
pol-miR-730	serotransferrin precursor (SroTP) mRNA, complete cds.
pol-miR-730	ppsb mRNA for pancreatic protein with two somatomedin B domains, complete cds.
pol-miR-730	mRNA for trypsinogen 3, complete cds.
pol-miR-730	PYY mRNA for peptide YY, complete cds.
pol-miR-730	ctrlr mRNA for calcitonin receptor-like receptor, complete cds.
pol-miR-730	empty spiracles homeobox 2 (Emx2) mRNA, complete cds.
pol-miR-730	Wap65-1 mRNA, complete cds.
pol-miR-730	TANK binding kinase 1 splice variant 3 (TBK1) mRNA, complete cds, alternatively spliced.
pol-miR-730	mitogen-activated protein kinase mRNA, complete cds.
pol-miR-730	stanniocalcin-1 (STC1) mRNA, complete cds.
pol-miR-730	galectin mRNA, complete cds.
pol-miR-730	insulin-like growth factor I mRNA, complete cds.
pol-miR-730	syntaxin-binding protein 3 isoform 1-like protein mRNA, partial cds.
pol-miR-730	phospholipase D2 mRNA, complete cds.
pol-miR-730	CD4-2 mRNA for T-cell surface glycoprotein CD4-2, complete cds.
pol-miR-731	transcription factor SOX-1a (Sox1a) mRNA, complete cds.
pol-miR-731	macrophage stimulating-1 protein mRNA, complete cds.
pol-miR-731	p53 tumor supressor protein (p53) mRNA, complete cds.
pol-miR-731	mRNA for interleukin-8 like CXC chemokine 3, complete cds.
pol-miR-737-5p	mRNA for interleukin-8 like CXC chemokine 2, complete cds.
pol-miR-737-5p	mRNA for interleukin-8 like CXC chemokine 1, complete cds.
pol-miR-737-5p	

pol-miR-193a-5p	phospholipase C-beta 1 (PLC-beta1) mRNA, complete cds.	**pol-miR-737-5p**	NOD-like receptor C (NLRC) mRNA, complete cds.
pol-miR-193a-5p	histone H1-like protein mRNA, complete cds.	**pol-miR-737-5p**	DnaJ-like subfamily A member 4 (Hsp40A4) mRNA, complete cds.
pol-miR-193a-5p	YGHL1 mRNA, complete cds.	**pol-miR-737-5p**	mRNA for CD3 epsilon, complete cds.
pol-miR-193a-5p	nucleotide-binding oligomerization domain 1 protein (NOD1) mRNA, complete cds.	**pol-miR-737-5p**	mRNA for CXC chemokine, complete cds.
pol-miR-193a-5p	vasa mRNA, complete cds.	**pol-miR-737-5p**	insulin-like growth factor I mRNA, complete cds.
pol-miR-193a-5p	mRNA for preprosomatostatin I, complete cds.	**pol-miR-9-4-3p**	phospholipase C delta 1B Lf mRNA, complete cds.
pol-miR-193a-5p	transcription factor C/EBPalpha mRNA, complete cds.	**pol-miR-9-4-3p**	LGP2 mRNA, complete cds.
pol-miR-193a-5p	interferon regulatory factor 2 (IRF2) mRNA, complete cds.	**pol-miR-9-4-3p**	inhibitor kappa B alpha mRNA, complete cds.
pol-miR-193a-5p	melanocortin 4 receptor (MC4R) mRNA, complete cds.	**pol-miR-9-4-3p**	phospholipase C delta 1 B short form (PLC) mRNA, complete cds.
pol-miR-193a-5p	fibrinogen beta chain precursor, mRNA, complete cds.	**pol-miR-9-4-3p**	ornithine decarboxylase antizyme large isoform ORF1 and ornithine decarboxylase antizyme large isoform mRNA, complete cds.
pol-miR-193a-5p	beta-actin mRNA, complete cds.	**pol-miR-9-4-3p**	cell division cycle 48 mRNA, complete cds.
pol-miR-193a-5p	interferon regulatory factor 3 variant 2 (IRF3) mRNA, complete cds.	**pol-miR-99**	insulin-like growth factor binding protein 3 mRNA, complete cds.
pol-miR-193a-5p	interferon regulatory factor 3 variant 1 (IRF3) mRNA, complete cds.	**pol-miR-99**	transcription factor C/EBPalpha mRNA, complete cds.
pol-miR-193a-5p	ornithine decarboxylase mRNA, complete cds.	**pol-miR-99**	mRNA for trypsinogen 3, complete cds.
pol-miR-193a-5p	lipopolysaccharide-binding protein/bactericidal permeability-increasing protein mRNA, complete cds.	**pol-miR-99**	myD88 mRNA for myeloid differentiaton factor 88, complete cds.
pol-miR-193a-5p	macrophage stimulating-1 protein mRNA, complete cds.	**pol-miR-99**	empty spiracles homeobox 2 (Emx2) mRNA, complete cds.

Supplement 4. Gene ontology of predicted target genes of differentially expressed miRNAs of olive flounder and their number in each GO.

GO	number of target genes	GO	number of target genes
regulation of transcription, DNA-templated	32	protein tetramerization	1
proteolysis	30	positive regulation of protein phosphorylation	1
G-protein coupled receptor signaling pathway	16	regulation of nitric-oxide synthase activity	1
immune response	15	protein export from nucleus	1
inflammatory response	9	convergent extension involved in axis elongation	1
lipid catabolic process	9	positive regulation of translational termination	1
steroid hormone mediated signaling pathway	9	protein N-linked glycosylation via asparagine	1
oxidation-reduction process	9	positive regulation of translational elongation	1
defense response to bacterium	9	ossification	1
intracellular signal transduction	9	RNA processing	1
chemokine-mediated signaling pathway	8	prechordal plate formation	1
defense response to virus	7	negative regulation of neuron apoptotic process	1
regulation of cell proliferation	7	acute-phase response	1
regulation of apoptotic process	7	inner ear morphogenesis	1
protein folding	7	phosphatidylinositol metabolic process	1
neutrophil activation	7	heart jogging	1
MyD88-dependent toll-like receptor signaling pathway	6	regulation of high voltage-gated calcium channel activity	1
neuropeptide signaling pathway	6	cation transmembrane transport	1
response to lipopolysaccharide	6	regulation of protein kinase activity	1
regulation of cell growth	5	phospholipid catabolic process	1
positive regulation of inflammatory response	5	RNA secondary structure unwinding	1
MyD88-independent toll-like receptor signaling pathway	5	negative regulation of transcription, DNA-templated	1
regulation of cytokine secretion	5	face morphogenesis	1
metabolic process	5	notochord formation	1
toll-like receptor 3 signaling pathway	5	central nervous system projection neuron axonogenesis	1
positive regulation of leukocyte chemotaxis	5	lipid transport	1
neutrophil chemotaxis	5	methionine biosynthetic process	1
positive regulation of chemokine production	5	sequestering of actin monomers	1
response to exogenous dsRNA	5	cytolysis	1
signal transduction	5	MAPK cascade	1
brain development	4	response to salt stress	1
regulation of MAPK cascade	4	response to antibiotic	1
positive regulation of pathway-restricted SMAD protein phosphorylation	4	T-helper 1 type immune response	1
cell surface receptor signaling pathway	4	regulation of store-operated calcium channel activity	1

SMAD protein signal transduction	4	regulation of phosphatidylinositol 3-kinase activity	1
determination of left/right asymmetry in diencephalon	4	positive regulation of muscle cell differentiation	1
chordate embryonic development	4	cellular response to heat	1
negative regulation of endopeptidase activity	4	homophilic cell adhesion via plasma membrane adhesion molecules	1
transport	4	small GTPase mediated signal transduction	1
protein phosphorylation	4	thyroid hormone metabolic process	1
glucose metabolic process	4	intracellular receptor signaling pathway	1
growth	4	positive regulation of cell proliferation	1
toll-like receptor 5 signaling pathway	4	mesoderm development	1
transmembrane receptor protein tyrosine kinase signaling pathway	3	fibril organization	1
negative regulation of apoptotic process	3	adenylate cyclase-inhibiting dopamine receptor signaling pathway	1
hormone biosynthetic process	3	response to stress	1
response to estrogen	3	blood coagulation, fibrin clot formation	1
digestion	3	immune response involved in response to exogenous dsRNA	1
determination of left/right asymmetry in lateral mesoderm	3	carbohydrate metabolic process	1
insulin receptor signaling pathway	3	transcription initiation from RNA polymerase II promoter	1
iron ion homeostasis	3	IMP salvage	1
platelet activation	3	positive regulation of protein import into nucleus, translocation	1
ion transport	3	positive regulation of cyclic nucleotide metabolic process	1
regulation of transcription from RNA polymerase II promoter	3	regulation of appetite	1
chemotaxis	3	feeding behavior	1
translational initiation	3	endothelial cell differentiation	1
angiogenesis	3	convergent extension involved in gastrulation	1
response to bacterium	3	glucocorticoid receptor signaling pathway	1
heart looping	3	regulation of macrophage differentiation	1
protein autophosphorylation	3	embryonic pectoral fin morphogenesis	1
synaptic transmission	3	regulation of interferon-gamma-mediated signaling pathway	1
cell chemotaxis	3	camera-type eye development	1
positive regulation of protein serine/threonine kinase activity	3	negative regulation of pancreatic A cell differentiation	1
innate immune response	3	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	1
fin regeneration	3	response to calcium ion	1
cell development	3	removal of superoxide radicals	1
regulation of phagocytosis	2	determination of digestive tract left/right asymmetry	1
neurotrophin TRK receptor signaling pathway	2	negative regulation of cell proliferation	1
positive regulation of transcription from RNA polymerase II promoter	2	purinergic nucleotide receptor signaling pathway	1
retinal ganglion cell axon guidance	2	regulation of ossification	1
positive regulation of cyclic-nucleotide phosphodiesterase activity	2	telencephalon development	1
integrin-mediated signaling pathway	2	regulation of heart contraction	1

detection of calcium ion	2	response to ATP	1
Ras protein signal transduction	2	acrosome reaction	1
cytokine-mediated signaling pathway	2	retinoic acid receptor signaling pathway	1
axon guidance	2	regulation of type I interferon-mediated signaling pathway	1
antigen processing and presentation of peptide antigen via MHC class I	2	cellular response to organic cyclic compound	1
RNA phosphodiester bond hydrolysis, endonucleolytic	2	transmembrane transport	1
regulation of cell communication by electrical coupling involved in cardiac conduction	2	muscle cell fate determination	1
positive regulation of phosphoprotein phosphatase activity	2	determination of pancreatic left/right asymmetry	1
activation of phospholipase C activity	2	regulation of neutrophil differentiation	1
regulation of rhodopsin mediated signaling pathway	2	translation	1
embryonic viscerocranium morphogenesis	2	regulation of anion transmembrane transport	1
response to mechanical stimulus	2	pharyngeal system development	1
stimulatory C-type lectin receptor signaling pathway	2	cation transport	1
Fc-epsilon receptor signaling pathway	2	regulation of vascular permeability	1
regulation of cell migration	2	calcium ion transmembrane import into mitochondrion	1
cell-cell signaling	2	vasculogenesis	1
regulation of insulin-like growth factor receptor signaling pathway	2	regulation of calcium ion transport	1
response to yeast	2	cartilage development involved in endochondral bone morphogenesis	1
platelet degranulation	2	lymph vessel development	1
anterior/posterior pattern specification	2	axon regeneration	1
activation of MAPKK activity	2	regulation of DNA methylation	1
polyamine metabolic process	2	inner ear development	1
mesoderm formation	2	myofibril assembly	1
protein refolding	2	virion attachment to host cell	1
receptor-mediated endocytosis	2	translational frameshifting	1
vitamin D receptor signaling pathway	2	gonad development	1
positive regulation of apoptotic process	2	chloride transmembrane transport	1
glycolytic process	2	chondroitin sulfate proteoglycan metabolic process	1
regulation of BMP signaling pathway involved in heart jogging	2	positive regulation of JAK-STAT cascade	1
lipid metabolic process	2	regulation of gene expression	1
sex determination	2	collagen catabolic process	1
chromatin modification	2	defense response to Gram-negative bacterium	1
primitive hemopoiesis	2	positive regulation of nitric-oxide synthase activity	1
response to heat	2	response to activity	1
multicellular organismal development	2	vesicle docking involved in exocytosis	1
regulation of catalytic activity	2	Spemann organizer formation	1
fibroblast growth factor receptor signaling pathway	2	embryonic eye morphogenesis	1
negative regulation of peptidyl-threonine phosphorylation	2	developmental pigmentation	1

inositol phosphate metabolic process	2	complement activation, alternative pathway	1
phosphatidic acid biosynthetic process	2	hypothalamus development	1
embryonic heart tube left/right pattern formation	2	regulation of cell cycle	1
neuron development	2	regulation of osteoclast differentiation	1
cell adhesion	2	toll-like receptor 6 signaling pathway	1
glycogen catabolic process	2	closure of optic fissure	1
protein transport	2	phosphatidylinositol phosphorylation	1
inositol lipid-mediated signaling	2	negative regulation of transcription from RNA polymerase II promoter	1
cell cycle	2	placenta development	1
positive regulation of protein autophosphorylation	2	cell proliferation	1
positive regulation of sequence-specific DNA binding transcription factor activity	2	pancreatic epsilon cell differentiation	1
apoptotic process	2	pathogen-associated molecular pattern dependent induction by symbiont of host innate immune response	1
dorsal/ventral pattern formation	2	steroid biosynthetic process	1
vascular endothelial growth factor receptor signaling pathway	2	positive regulation of cell size	1
toll-like receptor signaling pathway	2	blood vessel development	1
peptidyl-tyrosine phosphorylation	2	tissue regeneration	1
regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion	2	negative regulation of type B pancreatic cell development	1
positive regulation of ryanodine-sensitive calcium-release channel activity	2	nucleoside transmembrane transport	1
definitive hemopoiesis	2	mRNA stabilization	1
response to unfolded protein	2	cell fate determination	1
negative regulation of ryanodine-sensitive calcium-release channel activity	2	cellular calcium ion homeostasis	1
nervous system development	2	cartilage development	1
epidermal growth factor receptor signaling pathway	2	eye photoreceptor cell development	1
membrane organization	2	positive regulation of interleukin-6 biosynthetic process	1
mesendoderm development	2	peptidoglycan catabolic process	1
retina development in camera-type eye	2	embryonic axis specification	1
regulation of cytokinesis	2	response to corticosterone	1
nitric oxide metabolic process	2	translesion synthesis	1
negative regulation of catalytic activity	2	tetrahydrobiopterin biosynthetic process	1
positive regulation of peptidyl-threonine phosphorylation	2	endoderm formation	1
substantia nigra development	2	positive regulation of nitric oxide biosynthetic process	1
regulation of heart rate	2	regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process	1
cell-matrix adhesion	2	cellular response to cold	1
fin morphogenesis	2	glucocorticoid mediated signaling pathway	1
polyamine biosynthetic process	1	regulation of immune response	1
positive regulation of granuloma formation	1	embryonic neurocranium morphogenesis	1
pectoral fin development	1	antibacterial humoral response	1
cell growth	1	neural crest cell development	1

negative regulation of activin receptor signaling pathway	1	fever generation	1
chitin catabolic process	1	determination of heart left/right asymmetry	1
single-organism process	1	ER-associated ubiquitin-dependent protein catabolic process	1
positive regulation of protein binding	1	chromosome segregation	1
specification of organ axis polarity	1	methylation	1
S-methylmethionine cycle	1	mRNA export from nucleus	1
positive regulation of neuron differentiation	1	habenula development	1
complement activation, classical pathway	1	peptidyl-tyrosine dephosphorylation	1
translational elongation	1	response to amphetamine	1
protein dephosphorylation	1	protein polymerization	1
response to cold	1	response to biotic stimulus	1
phosphorylation	1	positive regulation of cell division	1
embryonic heart tube development	1	melanocyte differentiation	1
cholesterol metabolic process	1	protein methylation	1
autophagy	1	embryonic skeletal system morphogenesis	1
double-strand break repair	1	nucleosome assembly	1
leukocyte migration	1	positive regulation of I-kappaB kinase/NF-kappaB signaling	1
cell division	1	intracellular estrogen receptor signaling pathway	1
eye development	1	detection of diacyl bacterial lipopeptide	1
tetrahydrofolate biosynthetic process	1	proteasome-mediated ubiquitin-dependent protein catabolic process	1
negative regulation of proteasomal ubiquitin-dependent protein catabolic process	1	positive regulation of striated muscle cell differentiation	1
response to hormone	1	muscle organ development	1
activation of adenylate cyclase activity	1	lipoprotein metabolic process	1
hematopoietic stem cell migration	1	G2/M transition of mitotic cell cycle	1
proteasomal ubiquitin-independent protein catabolic process	1	mast cell migration	1
floor plate formation	1	multicellular organismal process	1
prolactin secretion	1	anterior/posterior axis specification	1
positive regulation of NF-kappaB transcription factor activity	1		
developmental growth	1		
cellular response to interleukin-4	1		

Supplement 5. KEGG pathways of predicted target genes of differentially expressed miRNAs and their abundance

KEGG pathway	number of target genes	KEGG pathway	number of target genes
Ras signaling pathway	11	p53 signaling pathway	3
Neuroactive ligand-receptor interaction	11	Gap junction	3
Cytokine-cytokine receptor interaction	11	Arginine and proline metabolism	2
Rap1 signaling pathway	10	Folate biosynthesis	2
cAMP signaling pathway	10	Proteasome	2
PI3K-Akt signaling pathway	10	MAPK signaling pathway - fly	2
NF-kappa B signaling pathway	9	Peroxisome	2
TNF signaling pathway	9	Tight junction	2
HIF-1 signaling pathway	9	Carbon metabolism	1
FoxO signaling pathway	9	Fatty acid metabolism	1
Phospholipase D signaling pathway	9	Biosynthesis of amino acids	1
Sphingolipid signaling pathway	9	Glycolysis / Gluconeogenesis	1
MAPK signaling pathway	8	Amino sugar and nucleotide sugar metabolism	1
Regulation of actin cytoskeleton	8	Carbon fixation in photosynthetic organisms	1
Apoptosis	8	Steroid hormone biosynthesis	1
Protein processing in endoplasmic reticulum	7	Glycerolipid metabolism	1
TGF-beta signaling pathway	7	Glycerophospholipid metabolism	1
cGMP - PKG signaling pathway	7	Ether lipid metabolism	1
Signaling pathways regulating pluripotency of stem cells	7	alpha-Linolenic acid metabolism	1
Calcium signaling pathway	6	Biosynthesis of unsaturated fatty acids	1
Lysosome	6	Purine metabolism	1
Focal adhesion	6	Glycine, serine and threonine metabolism	1
Jak-STAT signaling pathway	5	Cysteine and methionine metabolism	1
Phosphatidylinositol signaling system	5	Glutathione metabolism	1
Phagosome	5	Aminobenzoate degradation	1
ErbB signaling pathway	4	Basal transcription factors	1
Wnt signaling pathway	4	Spliceosome	1
Hippo signaling pathway	4	RNA transport	1
VEGF signaling pathway	4	Protein export	1
AMPK signaling pathway	4	RNA degradation	1
mTOR signaling pathway	4	Two-component system	1
Oocyte meiosis	4	Hippo signaling pathway -fly	1
Adherens junction	4	ECM-receptor interaction	1
Inositol phosphate metabolism	3	Regulation of autophagy	1
Endocytosis	3	Cell cycle	1

Chapter II. Viral hemorrhagic septicemia virus (VHSV) infection-mediated sequential changes in miRNAs profile of *Epithelioma papulosum cyprini* (EPC) cells.

Supplement 1. MiRNAs of olive flounder expressed during VHSV infection. Sequences that different from recorded vertebrate miRNAs were considered as candidates of novel miRNAs

miRNA name	sequence	homolog in other species	miRNA name	sequence	homolog in other species
let-7a	TGAGGTAGTAGGTTGTATAGTT	dre-let-7a	**miR-20b-3p**	ACTGCAATGTCTGCACTTCAAGT	dre-miR-20b-3p
let-7b	TGAGGTAGTAGGTTGTGTGGTT	dre-let-7b	**miR-20b-5p**	CAAAGTGCTCACAGTGCAGGTAG	dre-miR-20b-5p
let-7c-3p	CTGTACAACCTTCTAGCTTTCC	dre-let-7c-3p	**miR-21**	TAGCTTATCAGACTGGTGTTGGC	dre-miR-21
let-7c-5p	TGAGGTAGTAGGTTGTATGGTT	dre-let-7c-5p	**miR-210-3p**	CTGTGCGTGTGACAGCGGCTAA	dre-miR-210-3p
let-7d-3p	CTGTACAACCTTCTAGCTTTCC	dre-let-7d-3p	**miR-210-5p**	AGCCACTGACTAACGCACATTG	dre-miR-210-5p
let-7d-5p	TGAGGTAGTTGGTTGTATGGTT	dre-let-7d-5p	**miR-212**	TAACAGTCTACAGTCATGGCT	dre-miR-212
let-7e	TGAGGTAGTAGATTGAATAGTT	dre-let-7e	**miR-214**	ACAGCAGGCACAGACAGGCAG	dre-miR-214
let-7f	TGAGGTAGTAGATTGTATAGTT	dre-let-7f	**miR-216a**	TAATCTCAGCTGGCAACTGTGA	dre-miR-216a
let-7g	TGAGGTAGTAGTTTGTATAGTT	dre-let-7g	**miR-216b**	TAATCTCTGCAGGCAACTGTGA	dre-miR-216b
let-7h	TGAGGTAGTAAGTTGTGTTGTT	dre-let-7h	**miR-217**	TACTGCATCAGGAACTGATTGG	dre-miR-217
let-7i	TGAGGTAGTAGTTTGTGCTGTT	dre-let-7i	**miR-2184**	AACAGTAAGAGTTTATGTGCT	dre-miR-2184
let-7j	TGAGGTAGTTGTTTGTACAGTT	dre-let-7j	**miR-2185-3p**	GCCGCGATCAGCTGCACCAGC	dre-miR-2185-3p
miR-1	TGGAATGTAAAGAAGTATGTAT	dre-miR-1	**miR-2185-5p**	CGGTGCAGGACTCCGCGGCTC	dre-miR-2185-5p
miR-100-2-3p	CAAGCTCGTGTCTATAGGTATG	dre-miR-100-2-3p	**miR-2186**	AAGTGGCCTCTAAAAGTCTA	dre-miR-2186
miR-100-3p	CAAGCTTGTATCTATAGGTATC	dre-miR-100-3p	**miR-2187-3p**	TTACAGGCTATGCTAATCTATG	dre-miR-2187-3p
miR-100-5p	AACCCGTAGATCCGAACTTGTG	dre-miR-100-5p	**miR-2187-5p**	TTAATTAGTATAGCCTGTTTTA	dre-miR-2187-5p
miR-101a	TACAGTACTGTGATAACTGAAG	dre-miR-101a	**miR-2188-3p**	CTGTGTGAGGTTAGACCTATC	dre-miR-2188-3p
miR-101b	TACAGTACTATGATAACTGAAG	dre-miR-101b	**miR-2188-5p**	AAGGTCCAACCTCACATGTCC	dre-miR-2188-5p
miR-103	AGCAGCATTGTACAGGGCTATGA	dre-miR-103	**miR-2189**	TGATTGTTTGTATCAGCTGTGT	dre-miR-2189
miR-107a-3p	AGCAGCATTGTACAGGGCTATCA	dre-miR-107a-3p	**miR-218a**	TTGTGCTTGATCTAACCATGTG	dre-miR-218a
miR-107a-5p	AGCTTCTTTACAGTGTTGTCTTG	dre-miR-107a-5p	**miR-218b**	TTGTGCTTGATCTAACCATGCA	dre-miR-218b
miR-107b	AGCAGCATTGTACAGGGCTTT	dre-miR-107b	**miR-2191**	TCACACCTACAATCCCTGGCA	dre-miR-2191
miR-10a-3p	CAAATTCGTGTCTTGGGGAATA	dre-miR-10a-3p	**miR-2192**	AAAGTGAAAGGTGACTGAGAC	dre-miR-2192
miR-10a-5p	TACCCTGTAGATCCGAATTTGT	dre-miR-10a-5p	**miR-2193**	TATGTGTGTATCAATTGTGTGAAA	dre-miR-2193
miR-10b-2-3p	CAAATACGTCTCTACAGGAAT	dre-miR-10b-2-3p	**miR-219-3p**	GGAGTTGTGGATGGACATCACGC	dre-miR-219-3p
miR-10b-3p	ACAGATTCGATTCTAGGGGAGT	dre-miR-10b-3p	**miR-2194**	GTAATGCTTCGACTGATTGGTG	dre-miR-2194
miR-10b-5p	TACCCTGTAGAACCGAATTTGTG	dre-miR-10b-5p	**miR-2195**	AGATTGGGGTGAGTTAGGGTG	dre-miR-2195
miR-10c-3p	AAATTCGTATCTAGGGGAGTA	dre-miR-10c-3p	**miR-219-5p**	TGATTGTCCAAACGCAATTCTT	dre-miR-219-5p
miR-10c-5p	TACCCTGTAGATCCGGATTTGT	dre-miR-10c-5p	**miR-2196**	CCTCTCTGTGCTGCCATTTGGGAC	dre-miR-2196
miR-10d-3p	CAGATTCGGTTTTAGGGGAGTA	dre-miR-10d-3p	**miR-2197**	ATGATTCGACTCATATGGTG	dre-miR-2197
miR-10d-5p	TACCCTGTAGAACCGAATGTGTG	dre-miR-10d-5p	**miR-2198**	AGCTCGTGTCCCAAGGCGCCT	dre-miR-2198

miR-122	TGGAGTGTGACAATGGTGTTTG	dre-miR-122	**miR-221-3p**	AGCTACATTGTCTGCTGGGTTTC	dre-miR-221-3p
miR-124-3p	TAAGGCACGCGGTGAATGCCAA	dre-miR-124-3p	**miR-221-5p**	ACCTGGCATACAATGTAGATTTCTGT	dre-miR-221-5p
miR-124-4-5p	TGTGTTCACAGTGGACCTTGAT	dre-miR-124-4-5p	**miR-222a-3p**	AGCTACATCTGGCTACTGGGTCTC	dre-miR-222a-3p
miR-124-5p	CGTGTTCACAGCGGACCTTGAT	dre-miR-124-5p	**miR-222a-5p**	TGCTCAGTAGTCAGTGTAGATCC	dre-miR-222a-5p
miR-124-6-5p	CGTGTTCACGGCGGACCTTGAT	dre-miR-124-6-5p	**miR-222b**	AGCTACATCTGAATACTGGGTCA	dre-miR-222b
miR-125a	TCCCTGAGACCCTTAACCTGTG	dre-miR-125a	**miR-223**	TGTCAGTTTGTCAAATACCCC	dre-miR-223
miR-125b-1-3p	ACGGGTTAGGTTCTTGGGAGCT	dre-miR-125b-1-3p	**miR-22a-3p**	AAGCTGCCAGCTGAAGAACTGT	dre-miR-22a-3p
miR-125b-2-3p	CGGGTTGGGTTCTCGGGAGCT	dre-miR-125b-2-3p	**miR-22a-5p**	AGTTCTTCACTGGCAAGCTTTA	dre-miR-22a-5p
miR-125b-3-3p	ACAGGTTAAGCTCTTGGGACCT	dre-miR-125b-3-3p	**miR-22b-3p**	AAGCTGCCAGTTGAAGAGCTGT	dre-miR-22b-3p
miR-125b-5p	TCCCTGAGACCCTAACTTGTGA	dre-miR-125b-5p	**miR-22b-5p**	CGTTCTTCACTGGCTAGCTTTA	dre-miR-22b-5p
miR-125c-3p	ACGGGTCAGGAGCTTGGGAGAC	dre-miR-125c-3p	**miR-23a-3-5p**	GGATTCCTGGCAGAGTGATTT	dre-miR-23a-3-5p
miR-125c-5p	TCCCTGAGACCCTAACTCGTGA	dre-miR-125c-5p	**miR-23a-3p**	ATCACATTGCCAGGGATTTCCA	dre-miR-23a-3p
miR-126a-3p	TCGTACCGTGAGTAATAATGC	dre-miR-126a-3p	**miR-23a-5p**	GAATTCCTGGCAGAGTGATTT	dre-miR-23a-5p
miR-126a-5p	CATTATTACTTTTGGTACGCG	dre-miR-126a-5p	**miR-23b**	ATCACATTGCCAGGGATTACCA	dre-miR-23b
miR-126b-3p	TCGTACCGTGAGTAATAGTGCA	dre-miR-126b-3p	**miR-24**	TGGCTCAGTTCAGCAGGAACAG	dre-miR-24
miR-126b-5p	CATTATTACTTTTGGTACGCG	dre-miR-126b-5p	**miR-25-3p**	CATTGCACTTGTCTCGGTCTGA	dre-miR-25-3p
miR-128-3p	TCACAGTGAACCGGTCTCTTTT	dre-miR-128-3p	**miR-25-5p**	AGGCGGAGACTTGGGCAGCTGCC	dre-miR-25-5p
miR-128-5p	CGGGGCCGTGGCACTGTATGAGA	dre-miR-128-5p	**miR-26a-2-3p**	CCTATTCATGATTACTTGCACT	dre-miR-26a-2-3p
miR-129-1-3p	GAAGCCCTTACCCCAAAAAGT	dre-miR-129-1-3p	**miR-26a-3p**	CCTATTCGGGATGACTTGGTTC	dre-miR-26a-3p
miR-129-3p	AAGCCCTTACCCCAAAAAGCAT	dre-miR-129-3p	**miR-26a-5p**	TTCAAGTAATCCAGGATAGGCT	dre-miR-26a-5p
miR-129-5p	CTTTTTGCGGTCTGGGCTTGCT	dre-miR-129-5p	**miR-26b**	TTCAAGTAATCCAGGATAGGTT	dre-miR-26b
miR-1306	CCACCTCCCCTGCAAACGTCCA	dre-miR-1306	**miR-27a-3p**	TTCACAGTGGCTAAGTTCCGCT	dre-miR-27a-3p
miR-130a	CAGTGCAATGTTAAAAGGGCAT	dre-miR-130a	**miR-27a-5p**	AGGACTTAGCTCACTCTGTGAACA	dre-miR-27a-5p
miR-130b	CAGTGCAATAATGAAAGGGCAT	dre-miR-130b	**miR-27b-3p**	TTCACAGTGGCTAAGTTCTGCA	dre-miR-27b-3p
miR-130c-3p	CAGTGCAATATTAAAAGGGCAT	dre-miR-130c-3p	**miR-27b-5p**	AGAGCTTAGCTGATTGGTGAACA	dre-miR-27b-5p
miR-130c-5p	GCCCTTTTTCTGTTGTACTACT	dre-miR-130c-5p	**miR-27c-3p**	TTCACAGTGGTTAAGTTCTGC	dre-miR-27c-3p
miR-132-3p	TAACAGTCTACAGCCATGGTCG	dre-miR-132-3p	**miR-27c-5p**	CTTAACCCACTTGTGAACAATG	dre-miR-27c-5p
miR-132-5p	ACCGTGGCATTAGATTGTTACT	dre-miR-132-5p	**miR-27d**	TTCACAGTGGCTAAGTTCTTCA	dre-miR-27d
miR-133a-2-5p	AGCTGGTAAAATGGAACCAAA	dre-miR-133a-2-5p	**miR-27e**	TTCACAGTGGCTAAGTTCAGTG	dre-miR-27e
miR-133a-3p	TTTGGTCCCCTTCAACCAGCTG	dre-miR-133a-3p	**miR-29a**	TAGCACCATTTGAAATCGGTTA	dre-miR-29a
miR-133a-5p	AGCTGGTAAAATGGAACCAAAT	dre-miR-133a-5p	**miR-29b**	TAGCACCATTTGAAATCAGTGT	dre-miR-29b
miR-133b-3p	TTTGGTCCCCTTCAACCAGCTA	dre-miR-133b-3p	**miR-301a**	CAGTGCAATAGTATTGTCAAAG	dre-miR-301a
miR-133b-5p	GCTGGTCAAATGGAACCAAGTC	dre-miR-133b-5p	**miR-301b-3p**	CAGTGCAATAGTATTGTCATTG	dre-miR-301b-3p
miR-133c-3p	TTTGGTCCCTTTCAACCAGCTA	dre-miR-133c-3p	**miR-301b-5p**	GCTTTGACGATGTTGCACTAC	dre-miR-301b-5p
miR-133c-5p	GCTGGTAAAACGGAACCAAGTC	dre-miR-133c-5p	**miR-301c-3p**	CAGTGCAATAGTATTGTCATAG	dre-miR-301c-3p
miR-135a	TATGGCTTTTTATTCCTATGTGA	dre-miR-135a	**miR-301c-5p**	GCTCTGACGATGTTGCACTAC	dre-miR-301c-5p
miR-135b-3p	ATATAGGGATGGAAGCCATGCA	dre-miR-135b-3p	**miR-30a-3p**	CTTTCAGTCTGATGTTTGCTGC	dre-miR-30a-3p
miR-135b-5p	TATGGCTTTTTATTCCTATCTG	dre-miR-135b-5p	**miR-30a-5p**	TGTAAACATTCCCGACTGGAAG	dre-miR-30a-5p

miR-135c	TATGGCTTTCTATTCCTATGTG	dre-miR-135c	**miR-30b**	TGTAAACATCCTACACTCAGCT	dre-miR-30b
miR-137-3p	TTATTGCTTAAGAATACGCGTA	dre-miR-137-3p	**miR-30c-3p**	CCGGGAGTGGGATGTTTGCGCT	dre-miR-30c-3p
miR-137-5p	ACGGGTATTCTTGGGTGGATAATA	dre-miR-137-5p	**miR-30c-5p**	TGTAAACATCCTACACTCTCAG	dre-miR-30c-5p
miR-138-3p	GCTATTTCACAACACCAGGGT	dre-miR-138-3p	**miR-30d**	TGTAAACATCCCCGACTGGAAG	dre-miR-30d
miR-138-5p	AGCTGGTGTTGTGAATCAGGCC	dre-miR-138-5p	**miR-30e-3p**	CTTTCAGTCGGATGTTTGCAGC	dre-miR-30e-3p
miR-1388-3p	ATCTCAGGTTCGTCAGCCCATG	dre-miR-1388-3p	**miR-30e-5p**	TGTAAACATCCTTGACTGGAAG	dre-miR-30e-5p
miR-1388-5p	AGGACTGTCCAACCTGAGAATG	dre-miR-1388-5p	**miR-31**	GGCAAGATGTTGGCATAGCTG	dre-miR-31
miR-139-3p	TGGGGAGGCAGCGCTGTTGGAAT	dre-miR-139-3p	**miR-338**	TCCAGCATCAGTGATTTTGTTG	dre-miR-338
miR-139-5p	TCTACAGTGCATGTGTCT	dre-miR-139-5p	**miR-34a**	TGGCAGTGTCTTAGCTGGTTGT	dre-miR-34a
miR-140-3p	TACCACAGGGTAGAACCACGGAC	dre-miR-140-3p	**miR-34b**	TAGGCAGTGTTGTTAGCTGATTG	dre-miR-34b
miR-140-5p	CAGTGGTTTTACCCTATGGTAG	dre-miR-140-5p	**miR-34c-3p**	AATCACTAACCTCACTACCAGG	dre-miR-34c-3p
miR-141-3p	TAACACTGTCTGGTAACGATGC	dre-miR-141-3p	**miR-34c-5p**	AGGCAGTGCAGTTAGTTGATTAC	dre-miR-34c-5p
miR-141-5p	CATCTTACCTGACAGTGCTTGG	dre-miR-141-5p	**miR-363-3p**	AATTGCACGGTATCCATCTGTA	dre-miR-363-3p
miR-142a-3p	TGTAGTGTTTCCTACTTTATGGA	dre-miR-142a-3p	**miR-363-5p**	CGGGTGGATGACTCTGCAATTTT	dre-miR-363-5p
miR-142a-5p	CATAAAGTAGAAAGCACTACT	dre-miR-142a-5p	**miR-365**	TAATGCCCCTAAAAATCCTTAT	dre-miR-365
miR-142b-5p	CATAAAGTAGACAGCACTACTA	dre-miR-142b-5p	**miR-375**	TTTGTTCGTTCGGCTCGCGTTA	dre-miR-375
miR-143	TGAGATGAAGCACTGTAGCTC	dre-miR-143	**miR-3906**	AAAAGCATTTTGAATGCAGATTT	dre-miR-3906
miR-144-3p	TACAGTATAGATGATGTACT	dre-miR-144-3p	**miR-429a**	TAATACTGTCTGGTAATGCCGT	dre-miR-429a
miR-144-5p	GGATATCATCGTATACTGTAAGT	dre-miR-144-5p	**miR-429b**	TAATACTGCCTGGTAATGCCAT	dre-miR-429b
miR-145-3p	GGATTCCTGGAAATACTGTTCT	dre-miR-145-3p	**miR-430a-11-5p**	ACCCTCACAAAAGCACTGACT	dre-miR-430a-11-5p
miR-145-5p	GTCCAGTTTTCCCAGGAATCCC	dre-miR-145-5p	**miR-430a-12-5p**	ACCCTCACAAAAGCACTGACT	dre-miR-430a-12-5p
miR-146a	TGAGAACTGAATTCCATAGATGG	dre-miR-146a	**miR-430a-13-5p**	ACCCTCACAAAAGCACTGACT	dre-miR-430a-13-5p
miR-146b	TGAGAACTGAATTCCAAGGGTG	dre-miR-146b	**miR-430a-14-5p**	ACCCTCACAAAAGCACTGACT	dre-miR-430a-14-5p
miR-148	TCAGTGCATTACAGAACTTTGT	dre-miR-148	**miR-430a-15-5p**	ACCCTCACAAAAGCACTGACT	dre-miR-430a-15-5p
miR-150	TCTCCCAATCCTTGTACCAGTG	dre-miR-150	**miR-430a-16-5p**	ACCCTCACAAAAGCACTGACT	dre-miR-430a-16-5p
miR-152	TCAGTGCATGACAGAACTTTGG	dre-miR-152	**miR-430a-17-5p**	ACCCTCACAAAAGCACTGACT	dre-miR-430a-17-5p
miR-153a-3p	TTGCATAGTCACAAAAGTGATC	dre-miR-153a-3p	**miR-430a-3p**	TAAGTGCTATTTGTTGGGGTAG	dre-miR-430a-3p
miR-153a-5p	GTCATTTTTGTGATGTTGCAGCT	dre-miR-153a-5p	**miR-430a-4-5p**	ACCCTCACAAAAGCACTGACT	dre-miR-430a-4-5p
miR-153b-3p	TTGCATAGTCACAAAAATGAGC	dre-miR-153b-3p	**miR-430a-5p**	ACCCTCACAAAGGCACTGACT	dre-miR-430a-5p
miR-153b-5p	GTCATTTTTGTGGTTTGCAGCT	dre-miR-153b-5p	**miR-430b-3p**	AAAGTGCTATCAAGTTGGGGTAG	dre-miR-430b-3p
miR-153c-3p	TTGCATAGTCACAAAAATGATC	dre-miR-153c-3p	**miR-430b-5p**	CAACTCTAACTTTAGCATCTTTC	dre-miR-430b-5p
miR-153c-5p	GTCATTTTTGTGATTTGCAGCT	dre-miR-153c-5p	**miR-430c-3p**	TAAGTGCTTCTCTTTGGGGTAG	dre-miR-430c-3p
miR-155	TTAATGCTAATCGTGATAGGGG	dre-miR-155	**miR-430c-5p**	CACTTCAAACAGGAGCATTGA	dre-miR-430c-5p
miR-15a-3p	CAGGCCGTACTGTGCTGCGGCA	dre-miR-15a-3p	**miR-430i-3p**	TAAGTGCTATTTGTTGGCGTAG	dre-miR-430i-3p
miR-15a-5p	TAGCAGCACAGAATGGTTTGTG	dre-miR-15a-5p	**miR-430i-5p**	ACCCTCACAAAAGCACTGACT	dre-miR-430i-5p
miR-15b-3p	CGAATCATGATGTGCTGTCACT	dre-miR-15b-3p	**miR-451**	AAACCGTTACCATTACTGAGTT	dre-miR-451
miR-15b-5p	TAGCAGCACATCATGGTTTGTA	dre-miR-15b-5p	**miR-454a**	TAGTGCAATATTGCTAATAGGG	dre-miR-454a
miR-15c	AAGCAGCGCGTCATGGTTTTC	dre-miR-15c	**miR-454b**	TAGTGCAATATTGCTTATAGGG	dre-miR-454b

miR-16a	TAGCAGCACGTAAATATTGGTG	dre-miR-16a	**miR-455-2-5p**	GTATGTGCCCTTGGACTACATT	dre-miR-455-2-5p
miR-16b	TAGCAGCACGTAAATATTGGAG	dre-miR-16b	**miR-455-3p**	ATGCAGTCCATGGGCATATACAC	dre-miR-455-3p
miR-16c-3p	TCCAATATTGCTCGTGCTGCTGA	dre-miR-16c-3p	**miR-455-5p**	TATGTGCCCTTGGACTACATCG	dre-miR-455-5p
miR-16c-5p	TAGCAGCATGTAAATATTGGAG	dre-miR-16c-5p	**miR-456**	CAGGCTGGTTAGATGGTTGTCA	dre-miR-456
miR-1788-3p	CAGGCAGCTAAAGCAAGTCTG	dre-miR-1788-3p	**miR-457a**	AAGCAGCACATCAATATTGGCA	dre-miR-457a
miR-1788-5p	GGCTTGTTTTAAGTTGCCTGCG	dre-miR-1788-5p	**miR-457b-3p**	TCCAGTATTGCTGTTCTGCTGT	dre-miR-457b-3p
miR-17a-2-3p	ACTGCAGTGGAGGCACTTCAAGC	dre-miR-17a-2-3p	**miR-457b-5p**	AAGCAGCACATAAATACTGGAG	dre-miR-457b-5p
miR-17a-3p	ACTGCAGTGGAGGCACTTCTAG	dre-miR-17a-3p	**miR-458-3p**	ATAGCTCTTTGAATGGTACTGC	dre-miR-458-3p
miR-17a-5p	CAAAGTGCTTACAGTGCAGGTA	dre-miR-17a-5p	**miR-458-5p**	AGCGCCATTTACAGAGCTATAA	dre-miR-458-5p
miR-181a-2-3p	ACCATCGACCGTTGACTGTACC	dre-miR-181a-2-3p	**miR-459-3p**	CAGGGAATCTCTGTTACTGGGG	dre-miR-459-3p
miR-181a-3p	ACCATCGACCGTTGATTGTACC	dre-miR-181a-3p	**miR-459-5p**	TCAGTAACAAGGATTCATCCTG	dre-miR-459-5p
miR-181a-5p	AACATTCAACGCTGTCGGTGAGT	dre-miR-181a-5p	**miR-460-3p**	CACAGCGCATACAATGTGGATG	dre-miR-460-3p
miR-181b-3p	CTCACTGATCAATGAATGCAAA	dre-miR-181b-3p	**miR-460-5p**	CCTGCATTGTACACACTGTGCG	dre-miR-460-5p
miR-181b-5p	AACATTCATTGCTGTCGGTGGG	dre-miR-181b-5p	**miR-461**	TCAGGAATGGGCTAAATGCCAA	dre-miR-461
miR-181c-3p	CTCGCCGGACAATGAATGAGAA	dre-miR-181c-3p	**miR-462**	TAACGGAACCCATAATGCAGCT	dre-miR-462
miR-181c-5p	CACATTCATTGCTGTCGGTGGG	dre-miR-181c-5p	**miR-489**	AGTGACATCATATGTACGGCTGC	dre-miR-489
miR-182-3p	TGGTTCTAGACTTGCCAACTA	dre-miR-182-3p	**miR-499-3p**	AACATCACTTTAAGTCTGTGCT	dre-miR-499-3p
miR-182-5p	TTTGGCAATGGTAGAACTCACA	dre-miR-182-5p	**miR-499-5p**	TTAAGACTTGCAGTGATGTTTA	dre-miR-499-5p
miR-183-3p	TGAATTACCAAAGGGCCATAA	dre-miR-183-3p	**miR-7145**	ACAATGGAAGCCAATGGTTACC	dre-miR-7145
miR-183-5p	TATGGCACTGGTAGAATTCACTG	dre-miR-183-5p	**miR-7146-3p**	TGAAGGTCAATGGTTACCAGTT	dre-miR-7146-3p
miR-184	TGGACGGAGAACTGATAAGGGC	dre-miR-184	**miR-7146-5p**	GTAACCATTGACCTCCATAGT	dre-miR-7146-5p
miR-187	TCGTGTCTTGTGTTGCAGCC	dre-miR-187	**miR-7147**	TGTACCATGCTGGTAGCCAGT	dre-miR-7147
miR-18a	TAAGGTGCATCTAGTGCAGATA	dre-miR-18a	**miR-7148-3p**	TATAAGCCAGTATTTCCGAT	dre-miR-7148-3p
miR-18b-3p	CTGCCCTAAGTGCCCCTTCTGG	dre-miR-18b-3p	**miR-7148-5p**	ATGGAAATACTCGCTGATACTG	dre-miR-7148-5p
miR-18b-5p	TAAGGTGCATTTAGTGCAGATA	dre-miR-18b-5p	**miR-7149-3p**	TTCCAAGTGTTATGAGTCAAAGT	dre-miR-7149-3p
miR-18c	TAAGGTGCATCTTGTGTAGTTA	dre-miR-18c	**miR-7149-5p**	TGTGAATCCTACACTGGAAGG	dre-miR-7149-5p
miR-190a	TGATATGTTTGATATATTAGGT	dre-miR-190a	**miR-722**	TTTTTTGCAGAAACGTTTCAGATT	dre-miR-722
miR-190b	TGATATGTTTGATATTCGGTTG	dre-miR-190b	**miR-723-3p**	AAGACATCAATTAAATCTGTGCT	dre-miR-723-3p
miR-192	ATGACCTATGAATTGACAGCC	dre-miR-192	**miR-723-5p**	GACAGTTTTAAATGATGTTACTTT	dre-miR-723-5p
miR-193a-3p	AACTGGCCTACAAAGTCCCAGT	dre-miR-193a-3p	**miR-724**	TTAAAGGGAATTTGCGACTGTT	dre-miR-724
miR-193a-5p	TGGGTCTTTGCGGGCAAGGTGA	dre-miR-193a-5p	**miR-725-3p**	TTCAGTCATTGTTTCTAGTAGT	dre-miR-725-3p
miR-193b-3p	AACTGGCCCGCAAAGTCCCGCT	dre-miR-193b-3p	**miR-725-5p**	TGCTAGGAATGGTGGCTGAGAT	dre-miR-725-5p
miR-193b-5p	CGGGACTTTGGGGGCGAGATG	dre-miR-193b-5p	**miR-726**	TTCACTACTAGCAGAACTCGG	dre-miR-726
miR-194a	TGTAACAGCAACTCCATGTGG	dre-miR-194a	**miR-727-3p**	GTTGAGGCGAGTTGAAGACTTA	dre-miR-727-3p
miR-194b	TGTAACAGCCGCTCCATGTGGA	dre-miR-194b	**miR-727-5p**	TCAGTCTTCAATTCCTCCCAGC	dre-miR-727-5p
miR-196a-3p	CTGCAACGTGAAACTGTCTTAA	dre-miR-196a-3p	**miR-728**	ATACTAAGTACACTACGTTTTC	dre-miR-728
miR-196a-5p	TAGGTAGTTTCATGTTGTTGGG	dre-miR-196a-5p	**miR-729**	CATGGGTATGATACGACCTGGGTT	dre-miR-729
miR-196b	TAGGTAGTTTCAAGTTGTTGGG	dre-miR-196b	**miR-730**	TCCTCATTGTGCATGCTGTGTGT	dre-miR-730

miR-196c	TAGGTAGTTTGATGTTGTTGGG	dre-miR-196c	**miR-731**	AATGACACGTTTTCTCCCGGATCG	dre-miR-731
miR-196d	TAGGTAGTTTTATGTTGTTGGG	dre-miR-196d	**miR-732**	CTCAAAGCAGAGAACTCTCGGT	dre-miR-732
miR-199-3-3p	ACAGTAGTCCGCACATTGGTT	dre-miR-199-3-3p	**miR-733**	TGCGTTGGTTTAGCTCAGTGGTT	dre-miR-733
miR-199-3p	TACAGTAGTCTGCACATTGGTT	dre-miR-199-3p	**miR-734**	GTAAATGCTGCAGAATCGTACCG	dre-miR-734
miR-199-5p	CCCAGTGTTCAGACTACCTGTTC	dre-miR-199-5p	**miR-735-3p**	CTCTCCCACCGCTAAACTTGAC	dre-miR-735-3p
miR-19a-3p	TGTGCAAATCTATGCAAAACTGA	dre-miR-19a-3p	**miR-735-5p**	GGCTGGTCCGAAGGCGGT	dre-miR-735-5p
miR-19a-5p	CTAGTTTTGCATAGTTGCACTA	dre-miR-19a-5p	**miR-736**	GTAAGACGAACAAAAAGTTTT	dre-miR-736
miR-19b-3p	TGTGCAAATCCATGCAAAACTGA	dre-miR-19b-3p	**miR-737-3p**	AATCAAAACCTAAAGAAAATA	dre-miR-737-3p
miR-19b-5p	AGTTTTGCTGGTTTGCATTCAG	dre-miR-19b-5p	**miR-737-5p**	GTTTTTTTAGGTTTTGATTTT	dre-miR-737-5p
miR-19c-3p	TGTGCAAATCCATGCAAAACTCG	dre-miR-19c-3p	**miR-738**	GCTACGGCCCGCGTCGGGACCTC	dre-miR-738
miR-19c-5p	AGTTTTGCAGGATTGCATCCGG	dre-miR-19c-5p	**miR-740**	ATAAAAAGTGGTATGGTACAGT	dre-miR-740
miR-19d-3p	TGTGCAAACCCATGCAAAACTGA	dre-miR-19d-3p	**miR-7a**	TGGAAGACTAGTGATTTTGTTGT	dre-miR-7a
miR-19d-5p	AGCTTTGCGGGGTGGGCAGTCAGC	dre-miR-19d-5p	**miR-7b**	TGGAAGACTTGTGATTTTGTT	dre-miR-7b
miR-200a-3p	TAACACTGTCTGGTAACGATGT	dre-miR-200a-3p	**miR-92a-2-5p**	AGGTTGGGATCGGCCGCAATGCT	dre-miR-92a-2-5p
miR-200a-5p	CATCTTACCGGACAGTGCTGGA	dre-miR-200a-5p	**miR-92a-3p**	TATTGCACTTGTCCCGGCCTGT	dre-miR-92a-3p
miR-200b-3p	TAATACTGCCTGGTAATGATGA	dre-miR-200b-3p	**miR-92a-5p**	AGGTTGGGATTGGTAGCAATGCT	dre-miR-92a-5p
miR-200b-5p	CATCTTACGAGGCAGCATTGGA	dre-miR-200b-5p	**miR-92b-3p**	TATTGCACTCGTCCCGGCCTCC	dre-miR-92b-3p
miR-200c-3p	TAATACTGCCTGGTAATGATGC	dre-miR-200c-3p	**miR-92b-5p**	AGGTGTGGGATGTTGTGCAGTGTT	dre-miR-92b-5p
miR-200c-5p	CATCTTACAAGGCAGTTTTGGA	dre-miR-200c-5p	**miR-93**	AAAAGTGCTGTTTGTGCAGGTA	dre-miR-93
miR-202-3p	AGAGGCATAGGGCATGGGAAAA	dre-miR-202-3p	**miR-9-3p**	TAAAGCTAGATAACCGAAAGT	dre-miR-9-3p
miR-202-5p	TTCCTATGCATATACCTCTTTG	dre-miR-202-5p	**miR-9-4-3p**	TAAAGCTAGAGAACCGAATGTA	dre-miR-9-4-3p
miR-203a-3p	GTGAAATGTTTAGGACCACTTG	dre-miR-203a-3p	**miR-9-5p**	TCTTTGGTTATCTAGCTGTATGA	dre-miR-9-5p
miR-203a-5p	AGTGGTTCTTAACAGTTCAACAGT	dre-miR-203a-5p	**miR-96-3p**	CAATTATGTGTAGTGCCAATAT	dre-miR-96-3p
miR-203b-3p	GTGAAATGTTCAGGACCACTTG	dre-miR-203b-3p	**miR-96-5p**	TTTGGCACTAGCACATTTTTGCT	dre-miR-96-5p
miR-203b-5p	AGTGGTTCTCAACAGTTCAACA	dre-miR-203b-5p	**miR-9-7-3p**	TAAAGCTAGAGAACCGAAAGTA	dre-miR-9-7-3p
miR-204-2-3p	GCTGGGACAGCAAAGGGAGGT	dre-miR-204-2-3p	**miR-99**	AACCCGTAGATCCGATCTTGTG	dre-miR-99
miR-204-3p	GGCTGGGAAGTCAAAGGGACGC	dre-miR-204-3p	**chr10_3661/1-23**	AGCCATGACTGTAGACTGTTACT	fru-miR-212
miR-204-5p	TTCCCTTTGTCATCCTATGCCT	dre-miR-204-5p	**chr7_30477/1-22**	CTGGGCTGGAAAAGTGATAAGG	gga-miR-184-5p
miR-205-3p	GATTTCAGTGGTGTGAAGTGTA	dre-miR-205-3p	**chr7_27496/1-22**	AGCGGCGTCAGAAGCGATGGCC	ipu-miR-7547
miR-205-5p	TCCTTCATTCCACCGGAGTCTG	dre-miR-205-5p	**chr5_24760/1-22**	TTTCGGTTATCTAGCTTTATGA	oha-miR-9-2-5p
miR-206-3p	TGGAATGTAAGGAAGTGTGTGG	dre-miR-206-3p	**chr25_20042/1-23**	AGGTAGACTGTGACTTGTTGTCA	ssa-miR-7a-4-3p
miR-206-5p	ACATGCTTCCTTATATGCCCATA	dre-miR-206-5p	**chr10_3653/1-25**	TTTGTCACTACCTCATCTGAGCTTG	
miR-20a-3p	ACTGCAGTGTGAGCACTTGAAG	dre-miR-20a-3p	**chr10_3663/1-18**	GCTTACGGCCATACCACC	
miR-20a-5p	TAAAGTGCTTATAGTGCAGGTAG	dre-miR-20a-5p	**chr6_29548/1-22**	TATGGAAGTCAATGGGAACAGT	

Supplement 2. Fold change of differentially expressed miRNAs at different points of time

Mature miRNA	3 h.p.i	12 h.p.i	24 h.p.i	48 h.p.i	Mature miRNA	3 h.p.i	12 h.p.i	24 h.p.i	48 h.p.i
let-7c-3p	1.35167	1.124782	-1.36047	-4.92018	**miR-19c-3p**	-1.14797	1	1.504995	1.225893
let-7d-3p	1.35167	1.124782	-1.36047	-4.92018	**miR-19d-3p**	-1.57849	-1.33057	1.472884	1.036826
let-7d-5p	1	-1.27603	-1.5324	-1.27603	**miR-19d-5p**	-1.40761	-1.96679	-2.83527	-5.24503
let-7e	-1.10074	-1.2072	-1.54356	-1.50686	**miR-200a-3p**	1.070732	1.031064	1.63315	2.70767
let-7f	-1.06908	-1.17402	-1.73318	-1.56646	**miR-200a-5p**	-1.12192	1.475692	1.358416	2.195043
let-7i	-1.03882	-1.4656	-1.88403	-1.4656	**miR-200b-3p**	1.044562	1.471081	1.820556	1.646917
miR-100-2-3p	-1.26764	-1.3361	-2.10027	-1.72843	**miR-200c-3p**	-1.03106	1.028619	1.892506	1.389598
miR-100-3p	1.050162	1.179864	-2.95174	-2.393	**miR-203a-5p**	1.00864	-1.03667	1.588519	1.247316
miR-100-5p	1.379178	1.379178	2.220019	1.847839	**miR-204-5p**	1.154398	-1.0519	1.422063	1.793134
miR-101a	-1.06322	-1.10992	-1.95978	-1.51686	**miR-20b-5p**	1	1.026402	1.754444	1.513497
miR-10d-5p	-1.38009	-1.33136	-2.24295	-1.20962	**miR-210-3p**	-1.05014	-1.16023	1.130443	1.541292
miR-124-3p	-1.77187	-2.61798	-1.7333	1.22387	**miR-210-5p**	-1.23675	-1.23675	-1.52527	-1.4714
miR-125b-1-3p	1.080156	-1.24008	-1.53334	-2.50875	**miR-2192**	1.26624	1.229455	1.504566	1.229455
miR-125b-2-3p	-1.2746	-2.05952	-4.52251	-5.88977	**miR-221-3p**	1.114332	1.114332	1.504098	1.504098
miR-125b-3-3p	1.043784	-1.04363	-2.8258	-5.19438	**miR-221-5p**	-1.23329	1.031072	-1.74185	-2.53998
miR-125b-5p	1	1.131224	1.797299	1.236126	**miR-222a-3p**	-1.11433	-1.08787	-1.08787	-1.6125
miR-126a-3p	1.056142	-1.01972	1.328727	2.044632	**miR-222a-5p**	1.356139	1.254857	-1.7841	-1.7841
miR-126a-5p	1.146535	1.196646	1.721548	1.765357	**miR-24**	1.205385	-1.08041	1.757967	1.591887
miR-126b-5p	1.146535	1.196646	1.721548	1.765357	**miR-25-5p**	-1.1739	-1.51546	-1.16642	-1.49247
miR-128-5p	1.13581	-1.12246	-1.19721	-1.7548	**miR-26a-2-3p**	1.246465	-1.02065	-2.14188	-2.71753
miR-129-3p	-1.14959	-1.01335	1.455349	1.670899	**miR-26a-3p**	1.31016	1.159525	1.159525	-4.49284
miR-137-5p	-1.60375	-2.40333	-1.78994	-2.0403	**miR-27a-5p**	-1.29141	1.092467	-2.95282	-1.82067
miR-1388-5p	-1.07493	1.034685	-1.81787	-1.22867	**miR-27b-5p**	1.036606	-1.11584	-1.71678	-1.62522
miR-140-5p	-1.05363	-1.05363	1.781928	1.280078	**miR-29b**	1.196081	-1.01291	1.634613	1.122425
miR-141-3p	1.147966	1.186285	1.777561	2.052601	**miR-30c-3p**	1.018013	1.024946	-1.53002	-1.01113
miR-142a-3p	1.166231	1.069373	1.18403	2.019078	**miR-30e-3p**	1.043615	1.013357	-1.37808	-1.60977
miR-144-3p	1.046281	1.03358	1.251444	1.601725	**miR-34b**	-1.18733	-1.08565	-1.35006	-1.6418
miR-145-3p	1.798518	1.683517	2.05801	1.955837	**miR-375**	-1.08095	-1.08095	1.181792	1.57826
miR-146a	1.147529	1.302306	3.426014	4.489138	**miR-429a**	1.090915	1.129909	1.571012	1.66974
miR-155	-1.17765	-1.05547	1.635521	1.505512	**miR-430a-3p**	1.009666	-1.33891	-2.31007	-1.40654
miR-16a	-1.06069	1.100424	1.951022	1.796267	**miR-430b-3p**	1.063001	1.143441	1.143441	1.926078
miR-16b	-1.06836	-1.08768	1.647191	-1.09437	**miR-430c-3p**	-1.07662	1.283164	-1.40988	1.991388
miR-16c-3p	-1.22333	-1.03846	-2.44157	-1.4684	**miR-454a**	1.053457	1.230099	1.600421	1.592742
miR-16c-5p	1.109921	1.04392	1.553306	1.109921	**miR-455-2-5p**	1.214096	1	1.523294	1.318897
miR-17a-3p	-1.01519	-1.09697	-1.55668	-2.03616	**miR-455-5p**	1.194405	1.074924	1.519209	1.167679
miR-181a-2-3p	1.217928	1.051839	-1.85595	-2.04293	**miR-457a**	1.097562	1	1.578494	1.041147

miR-181b-3p	1.030912	-1.16144	-2.68414	-4.25495	**miR-460-5p**	1.15096	1.2052	1.302807	1.583385
miR-181c-3p	-1.30848	-1.63614	-4.38269	-5.30473	**miR-462**	-1.24441	-1.07163	-1.73219	-1.24441
miR-182-5p	-1.62407	-1.10139	-2.67086	-1.43389	**miR-727-3p**	-1.30574	-1.03899	-1.5301	-1.0813
miR-183-5p	1	-1.12356	1.132213	1.706195	**miR-729**	1.053348	1.238491	1.235971	1.604154
miR-184	-1.10727	-1.10727	2.194552	2.092142	**miR-735-3p**	1.056307	-1.31751	3.015576	15.90082
miR-190b	1.139872	1.007107	1.083413	1.606771	**miR-735-5p**	1.677767	1.035306	5.402792	6.003128
miR-192	1.058245	1.291972	1.291972	1.97421	**miR-737-5p**	1.155421	1	-1.82494	-2.43848
miR-193a-3p	1.192451	1.12072	1.751	1.508632	**miR-738**	-1.1368	1.032301	2.748542	13.02029
miR-193a-5p	-1.27119	-1.16975	-1.73632	-1.70525	**miR-9-3p**	1.25412	1.798273	1.387628	1.511575
miR-193b-3p	1.063085	-1.22936	1.803527	1.755332	**miR-9-4-3p**	1.290974	1.719233	1.510119	1.585075
miR-194a	1.062843	1.303232	1.474168	1.662154	**miR-9-5p**	-1.09816	1.7748	1.517585	2.014182
miR-196a-5p	-1.66778	-1.58323	-1.73675	-2.43755	**miR-9-7-3p**	1.384701	1.651168	1.574132	1.881955
miR-19a-3p	-1.73048	-1.48965	-1.30732	-1.91898	**miR-92a-5p**	1.139463	-1.84716	-3.70158	-5.40709
miR-19a-5p	1.071854	-1.03531	-1.31173	-1.80712	**miR-92b-3p**	-1.13986	-1.08344	-1.58395	-1.75308
miR-19b-3p	-1.67344	-1.39985	1.313587	-1.57413	**miR-99**	1.788246	2.406732	2.406732	3.145706

Supplement 3. Predicted target genes of differentially expressed miRNAs based on miRanda and RNA22 tools and the function of different genes.

MiRNA	Target gene	MiRNA	Target gene
let-7c-3p	ubiquitin-conjugating enzyme E2 D3	**miR-200a-3p**	tRNA (cytosine(34)-C(5))-methyltransferase
let-7c-3p	tumor suppressor candidate 2-like	**miR-200a-3p**	serine threonine- kinase PAK 4-like
let-7c-3p	von Hippel-Lindau disease tumor suppressor	**miR-200a-3p**	band 3 anion exchange -like
let-7c-3p	serine threonine- kinase PAK 4-like	**miR-200a-3p**	rogdi homolog
let-7c-3p	MHC class I alpha chain, partial	**miR-200a-3p**	SAM and SH3 domain-containing 3-like
let-7c-3p	beta-catenin-interacting 1	**miR-200a-3p**	Red
let-7c-3p	CCAAT enhancer-binding alpha	**miR-200a-3p**	peptidyl-prolyl cis-trans isomerase FKBP1B isoform X1
let-7c-3p	prefoldin subunit 2	**miR-200a-3p**	coronin-1A-like
let-7c-3p	Golgi phospho 3-like	**miR-200a-3p**	S-phase kinase-associated 1
let-7c-3p	c-C motif chemokine 25-like	**miR-200a-3p**	cAMP-dependent kinase type I-alpha regulatory subunit
let-7c-3p	complement C1r subcomponent-like	**miR-200a-3p**	40S ribosomal S14
let-7c-3p	ras-related Rab-32	**miR-200a-3p**	DNA topoisomerase 2-binding 1-A-like
let-7c-3p	cellular tumor antigen p53	**miR-200a-3p**	multidrug resistance 1-like
let-7c-3p	14-3-3 beta alpha	**miR-200a-3p**	nck-associated 1-like
let-7c-3p	transforming isoform X1	**miR-200a-3p**	homeobox Meis1
let-7c-3p	prefoldin subunit 2	**miR-200a-3p**	receptor-type tyrosine- phosphatase C isoform X1
let-7c-3p	dynein light chain 2, cytoplasmic-like	**miR-200a-3p**	C-type lectin domain family 4 member F-like
let-7c-3p	myelin expression factor 2-like	**miR-200a-3p**	c-C chemokine receptor type 9-like
let-7c-3p	serine arginine-rich splicing factor 4	**miR-200a-5p**	transmembrane 14C
let-7c-3p	MHC class II alpha chain, partial	**miR-200a-5p**	SPARC precursor
let-7c-3p	myelin expression factor 2-like	**miR-200a-5p**	mediator of RNA polymerase II transcription subunit 12
let-7d-3p	ubiquitin-conjugating enzyme E2 D3	**miR-200b-3p**	tubulin beta chain
let-7d-3p	tumor suppressor candidate 2-like	**miR-200b-3p**	adenylate kinase 7
let-7d-3p	von Hippel-Lindau disease tumor suppressor	**miR-200b-3p**	homeobox Meis1-like
let-7d-3p	serine threonine- kinase PAK 4-like	**miR-200b-3p**	cpG-binding -like
let-7d-3p	MHC class I alpha chain, partial	**miR-200b-3p**	tRNA (cytosine(34)-C(5))-methyltransferase
let-7d-3p	beta-catenin-interacting 1	**miR-200b-3p**	SAM and SH3 domain-containing 3-like
let-7d-3p	CCAAT enhancer-binding alpha	**miR-200b-3p**	F-box only 9-like
let-7d-3p	prefoldin subunit 2	**miR-200b-3p**	transferrin receptor 1-like
let-7d-3p	Golgi phospho 3-like	**miR-200b-3p**	peptidyl-prolyl cis-trans isomerase FKBP1B isoform X1
let-7d-3p	c-C motif chemokine 25-like	**miR-200b-3p**	tafazzin
let-7d-3p	complement C1r subcomponent-like	**miR-200b-3p**	SPARC precursor
let-7d-3p	ras-related Rab-32	**miR-200b-3p**	cAMP-dependent kinase type I-alpha regulatory subunit
let-7d-3p	cellular tumor antigen p53	**miR-200b-3p**	plasminogen activator inhibitor 1-like

let-7d-3p	14-3-3 beta alpha	**miR-200b-3p**	ras-related R-Ras
let-7d-3p	transforming isoform X1	**miR-200b-3p**	actin-related 3
let-7d-3p	prefoldin subunit 2	**miR-200b-3p**	LSM14 homolog A isoform X3
let-7d-3p	dynein light chain 2, cytoplasmic-like	**miR-200b-3p**	apolipo E
let-7d-3p	myelin expression factor 2-like	**miR-200b-3p**	nck-associated 1-like
let-7d-3p	serine arginine-rich splicing factor 4	**miR-200b-3p**	transferrin receptor 1-like
let-7d-3p	MHC class II alpha chain, partial	**miR-200b-3p**	proto-oncogene tyrosine- kinase Yrk-like isoform X2
let-7d-3p	myelin expression factor 2-like	**miR-200b-3p**	LSM14 homolog A isoform 3
let-7d-5p	pituitary tumor-transforming gene 1 -interacting -like	**miR-200b-3p**	traf2 and NCK-interacting kinase-like
let-7d-5p	serine threonine- phosphatase PP1-alpha catalytic subunit-like	**miR-200b-3p**	NHS 2-like isoform X2
let-7d-5p	activin receptor type-1B isoform X2	**miR-200b-3p**	novel MHCII alpha chain
let-7d-5p	ribosomal S24	**miR-200c-3p**	tubulin beta chain
let-7d-5p	cornichon homolog	**miR-200c-3p**	adenylate kinase 7
let-7e	pituitary tumor-transforming gene 1 -interacting -like	**miR-200c-3p**	homeobox Meis1-like
let-7e	serine threonine- phosphatase PP1-alpha catalytic subunit-like	**miR-200c-3p**	cpG-binding -like
let-7e	c-C motif chemokine 25-like	**miR-200c-3p**	tRNA (cytosine(34)-C(5))-methyltransferase
let-7e	tyrosine- kinase JAK1 isoform X1	**miR-200c-3p**	SAM and SH3 domain-containing 3-like
let-7f	pituitary tumor-transforming gene 1 -interacting -like	**miR-200c-3p**	F-box only 9-like
let-7f	serine threonine- phosphatase PP1-alpha catalytic subunit-like	**miR-200c-3p**	peptidyl-prolyl cis-trans isomerase FKBP1B isoform X1
let-7f	activin receptor type-1B isoform X2	**miR-200c-3p**	tafazzin
let-7i	pituitary tumor-transforming gene 1 -interacting -like	**miR-200c-3p**	SPARC precursor
let-7i	sodium potassium-transporting ATPase subunit alpha-3-like	**miR-200c-3p**	cAMP-dependent kinase type I-alpha regulatory subunit
miR-100-2-3p	cpG-binding -like	**miR-200c-3p**	plasminogen activator inhibitor 1-like
miR-100-2-3p	proto-oncogene c-Rel-like	**miR-200c-3p**	ADP-ribosylation factor 1
miR-100-2-3p	14-3-3 beta alpha	**miR-200c-3p**	cellular tumor antigen p53
miR-100-3p	dynein light chain 2, cytoplasmic-like	**miR-200c-3p**	LSM14 homolog A isoform X3
miR-100-3p	von Hippel-Lindau disease tumor suppressor	**miR-200c-3p**	apolipo E
miR-100-3p	argonaute-3 isoform X2	**miR-200c-3p**	transferrin receptor 1-like
miR-100-3p	Golgi phospho 3-like	**miR-200c-3p**	proto-oncogene tyrosine- kinase Yrk-like isoform X2
miR-100-3p	splicing factor, arginine serine-rich 3	**miR-200c-3p**	LSM14 homolog A isoform 3
miR-100-3p	calcineurin subunit B type 1	**miR-200c-3p**	integumentary mucin -like
miR-100-5p	nudC domain-containing 1-like	**miR-200c-3p**	NHS 2-like isoform X2
miR-100-5p	kinase C alpha type	**miR-200c-3p**	novel MHCII alpha chain
miR-100-5p	complement factor B	**miR-203a-5p**	peptidoglycan recognition 6
miR-100-5p	redox-regulatory FAM213A	**miR-203a-5p**	beta-catenin-interacting 1
miR-101a	cell division cycle 5	**miR-203a-5p**	cellular tumor antigen p53
miR-101a	ATP-binding cassette sub-family C member 8-like	**miR-203a-5p**	sodium potassium-transporting ATPase subunit beta-2-like isoform X2
miR-101a	phosphoacetylglucosamine mutase-like	**miR-204-5p**	MHC class I antigen

miR-101a	caspase 8	**miR-204-5p**	adiponectin
miR-101a	Wiskott-Aldrich syndrome homolog	**miR-204-5p**	SAM and SH3 domain-containing 3-like
miR-101a	proteoglycan 4-like isoform X1	**miR-204-5p**	MHC class I alpha chain, partial
miR-101a	transcription factor	**miR-204-5p**	Golgi phospho 3-like
miR-101a	peptidyl-prolyl cis-trans isomerase-like	**miR-204-5p**	cellular tumor antigen p53
miR-101a	MHC class II antigen beta chain	**miR-204-5p**	cell division cycle-associated 7-like
miR-101a	ADP-ribosylation factor 1	**miR-204-5p**	14-3-3 beta alpha
miR-101a	cellular tumor antigen p53	**miR-204-5p**	sodium potassium-transporting ATPase subunit alpha-3-like
miR-101a	cell division cycle-associated 7-like	**miR-204-5p**	evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial-like
miR-101a	cleavage and polyadenylation specificity factor subunit 1-like	**miR-204-5p**	high mobility group B2-like
miR-101a	AP-2 complex subunit mu-A-like isoform X2	**miR-20b-5p**	stromal cell-derived factor 1-like
miR-101a	TSC22 domain family 3 isoform X2	**miR-20b-5p**	endoplasmic reticulum aminopeptidase 1-like
miR-101a	spermine oxidase isoform X1	**miR-20b-5p**	hsp90 co-chaperone Cdc37-like 1
miR-101a	dynein light chain 2, cytoplasmic-like	**miR-20b-5p**	CCAAT enhancer-binding alpha
miR-101a	serine arginine-rich splicing factor 3-like isoform X2	**miR-20b-5p**	suppressor of Ty 5 homolog (cerevisiae), isoform CRA_a
miR-101a	nck-associated 1-like	**miR-20b-5p**	Ubiquitin FUBI
miR-101a	guanine nucleotide exchange factor VAV3 isoform X1	**miR-20b-5p**	PREDICTED: uncharacterized protein C12orf29 homolog isoform X1
miR-101a	amyloid beta A4 precursor -binding family B member 1-interacting	**miR-20b-5p**	GA-binding alpha chain
miR-101a	WD repeat and FYVE domain-containing 1-like	**miR-20b-5p**	mitochondrial ubiquitin ligase activator of nfkb 1-A-like
miR-101a	c-C chemokine receptor type 9-like	**miR-20b-5p**	mediator of RNA polymerase II transcription subunit 18
miR-101a	cornichon homolog	**miR-20b-5p**	dynein light chain 2, cytoplasmic-like
miR-10d-5p	tubulin beta chain	**miR-20b-5p**	transport Sec61 subunit gamma
miR-10d-5p	High affinity immunoglobulin epsilon receptor subunit gamma precursor	**miR-20b-5p**	stromal cell-derived factor 1-like
miR-10d-5p	c-C motif chemokine 25-like	**miR-20b-5p**	calcineurin subunit B type 1
miR-10d-5p	transcription factor E3-like	**miR-20b-5p**	serine threonine- kinase B-raf
miR-124-3p	ubiquitin-conjugating enzyme E2 D3	**miR-20b-5p**	mediator of RNA polymerase II transcription subunit 18
miR-124-3p	proto-oncogene c-Rel-like	**miR-20b-5p**	calcineurin B homologous 3-like
miR-124-3p	plastin-2-like	**miR-20b-5p**	40S ribosomal S24
miR-124-3p	src substrate p85-like	**miR-20b-5p**	redox-regulatory FAM213A
miR-124-3p	NF-kappa-B essential modulator	**miR-20b-5p**	redox-regulatory FAM213A
miR-124-3p	CCAAT enhancer-binding alpha	**miR-210-3p**	SAM and SH3 domain-containing 3-like
miR-124-3p	ras-related Rab-32	**miR-210-3p**	26S protease regulatory subunit 6B
miR-124-3p	NDRG1-like isoform X1	**miR-210-3p**	SUMO-activating enzyme subunit 1
miR-124-3p	ras-related R-Ras	**miR-210-3p**	catenin beta-1
miR-124-3p	phosphatidylinositol 3-kinase catalytic subunit type 3-like	**miR-210-3p**	proto-oncogene tyrosine- kinase Yrk-like isoform X2
miR-124-3p	apolipo E	**miR-210-5p**	transcription factor
miR-124-3p	complement C2-like	**miR-210-5p**	cAMP-dependent kinase type I-alpha regulatory subunit
miR-124-3p	leptin receptor gene-related -like	**miR-2192**	tubulin beta chain

miR-125b-1-3p	basic leucine zipper transcriptional factor ATF-like 3	**miR-2192**	tafazzin
miR-125b-2-3p	cpG-binding -like	**miR-2192**	serine threonine- phosphatase PP1-alpha catalytic subunit-like
miR-125b-2-3p	sorting nexin-5-like	**miR-2192**	von Hippel-Lindau disease tumor suppressor
miR-125b-3-3p	CD209 antigen	**miR-2192**	SAM and SH3 domain-containing 3-like
miR-125b-3-3p	ragulator complex LAMTOR3	**miR-2192**	probable C-mannosyltransferase DPY19L1-like
miR-125b-3-3p	NF-kappa-B essential modulator	**miR-2192**	argonaute-3 isoform X2
miR-125b-3-3p	zinc finger 629-like isoform X1	**miR-2192**	invariant chain 14-1
miR-125b-3-3p	c-C motif chemokine 25-like	**miR-2192**	proteasome subunit beta type-9 precursor
miR-125b-3-3p	c-C motif chemokine 2-like	**miR-2192**	S-phase kinase-associated 1
miR-125b-3-3p	ADP-ribosylation factor 1	**miR-2192**	Golgi phospho 3-like
miR-125b-3-3p	Golgi phospho 3	**miR-2192**	c-C motif chemokine 25-like
miR-125b-3-3p	calcineurin subunit B type 1	**miR-2192**	MHC class I antigen
miR-125b-3-3p	ubiquitin-conjugating enzyme E2 A isoform X2	**miR-2192**	exosome complex component RRP46
miR-125b-3-3p	bromodomain-containing 3-like isoform X2	**miR-2192**	DNA-directed RNA polymerase III subunit RPC2
miR-125b-3-3p	40S ribosomal S24	**miR-2192**	redox-regulatory FAM213A isoform X3
miR-125b-3-3p	c-C chemokine receptor type 9-like	**miR-2192**	NEDD8-conjugating enzyme Ubc12
miR-125b-5p	src kinase-associated phospho 2	**miR-2192**	CREB-binding isoform X2
miR-125b-5p	Wiskott-Aldrich syndrome homolog	**miR-2192**	adenosine receptor A1-like
miR-125b-5p	cellular tumor antigen p53	**miR-2192**	ras-related Rab-8B
miR-126a-3p	activin receptor type-1B isoform X2	**miR-2192**	serine arginine-rich splicing factor 4
miR-126a-5p	translocator	**miR-2192**	redox-regulatory FAM213A
miR-126a-5p	40S ribosomal S29	**miR-2192**	small inducible cytokine
miR-126a-5p	caspase 8	**miR-221-3p**	tubulin beta chain
miR-126a-5p	Wiskott-Aldrich syndrome homolog	**miR-221-3p**	cpG-binding -like
miR-126a-5p	beta-galactosidase-1 2-like	**miR-221-3p**	ankyrin repeat and KH domain-containing 1-like
miR-126a-5p	PDZK1 interacting 1, like precursor	**miR-221-3p**	zinc finger 629-like isoform X1
miR-126a-5p	src substrate p85-like	**miR-221-3p**	Golgi phospho 3-like
miR-126a-5p	exocyst complex component 6 isoform X4	**miR-221-3p**	deoxyhypusine synthase
miR-126a-5p	Glutaredoxin-related 5	**miR-221-3p**	serine arginine-rich splicing factor 3-like isoform X2
miR-126a-5p	Golgi phospho 3-like	**miR-221-3p**	Glutamate receptor interacting 1
miR-126a-5p	plexin-D1-like	**miR-221-3p**	tyrosine- kinase FRK-like
miR-126a-5p	MHC class II antigen beta chain	**miR-221-5p**	ubiquitin-conjugating enzyme E2 A

miR-126a-5p	MHC class I antigen
miR-126a-5p	prohibitin isoform X1
miR-126a-5p	beta-galactosidase-1 2-like
miR-126a-5p	Ig kappa chain V-IV region STH
miR-126a-5p	gap junction alpha-1 -like
miR-126a-5p	death ligand 3
miR-126a-5p	serine arginine-rich splicing factor 4
miR-126a-5p	ras-related R-Ras-like
miR-126b-5p	translocator
miR-126b-5p	40S ribosomal S29
miR-126b-5p	caspase 8
miR-126b-5p	Wiskott-Aldrich syndrome homolog
miR-126b-5p	beta-galactosidase-1 2-like
miR-126b-5p	PDZK1 interacting 1, like precursor
miR-126b-5p	src substrate p85-like
miR-126b-5p	exocyst complex component 6 isoform X4
miR-126b-5p	Glutaredoxin-related 5
miR-126b-5p	Golgi phospho 3-like
miR-126b-5p	plexin-D1-like
miR-126b-5p	MHC class II antigen beta chain
miR-126b-5p	MHC class I antigen
miR-126b-5p	prohibitin isoform X1
miR-126b-5p	beta-galactosidase-1 2-like
miR-126b-5p	Ig kappa chain V-IV region STH
miR-126b-5p	gap junction alpha-1 -like
miR-126b-5p	death ligand 3
miR-126b-5p	serine arginine-rich splicing factor 4
miR-126b-5p	ras-related R-Ras-like
miR-128-5p	growth factor receptor-bound 2
miR-1388-5p	cpG-binding -like
miR-1388-5p	ADP-ribosylation factor 6
miR-1388-5p	NF-kappa-B essential modulator
miR-1388-5p	ubiquitin-40S ribosomal S27a
miR-1388-5p	nucleophosmin-like
miR-1388-5p	cysteine-rich 3
miR-1388-5p	PRELI domain-containing 1, mitochondrial-like
miR-1388-5p	Dual oxidase 1
miR-1388-5p	calmodulin
miR-221-5p	SAM and SH3 domain-containing 3-like
miR-221-5p	H ACA ribonucleo complex subunit 4-like
miR-221-5p	SUMO-activating enzyme subunit 1
miR-221-5p	multidrug resistance 1-like
miR-221-5p	calcineurin subunit B type 1
miR-221-5p	WD repeat and FYVE domain-containing 1-like
miR-221-5p	neurofibromin isoform X1
miR-222a-3p	ankyrin repeat and KH domain-containing 1-like
miR-222a-3p	kinase C alpha type
miR-222a-3p	NF-kappa-B essential modulator
miR-222a-3p	zinc finger 629-like isoform X1
miR-222a-3p	H ACA ribonucleo complex subunit 1-like
miR-222a-3p	catenin beta-1
miR-222a-3p	deoxyhypusine synthase
miR-222a-3p	Glutamate receptor interacting 1
miR-222a-3p	bromodomain-containing 3-like isoform X2
miR-222a-5p	maternal embryonic leucine zipper kinase
miR-222a-5p	tubulin beta chain
miR-222a-5p	DNA mismatch repair Mlh1-like
miR-222a-5p	actin-binding anillin
miR-222a-5p	transmembrane 203
miR-222a-5p	complement component C6
miR-222a-5p	plasminogen activator inhibitor 1-like
miR-222a-5p	suppressor of cytokine signaling 1
miR-222a-5p	splicing factor, arginine serine-rich 3
miR-222a-5p	AP-2 complex subunit mu-A-like isoform X2
miR-222a-5p	Dual oxidase 1
miR-222a-5p	proto-oncogene tyrosine- kinase Yrk-like isoform X2
miR-222a-5p	insulin-like growth factor 1 receptor 1
miR-222a-5p	mediator of RNA polymerase II transcription subunit 12
miR-222a-5p	serine threonine- kinase D1-like
miR-24	tubulin beta chain
miR-24	ubiquitin-conjugating enzyme E2 D3
miR-24	c-C motif chemokine 25-like
miR-24	rhombotin-1
miR-24	guanine nucleotide-binding subunit alpha-13
miR-24	phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1-like
miR-25-5p	src kinase-associated phospho 2

miR-1388-5p	Proteasome (prosome, macropain) 26S subunit, ATPase, 6	**miR-25-5p**	ADP-ribosylation factor 1
miR-1388-5p	tyrosine- phosphatase non-receptor type 11	**miR-25-5p**	probable ATP-dependent RNA helicase DHX36
miR-1388-5p	traf2 and NCK-interacting kinase-like	**miR-26a-2-3p**	tubulin beta chain
miR-140-5p	dynein light chain 2, cytoplasmic-like	**miR-26a-2-3p**	adenylate kinase 2, mitochondrial isoform X2
miR-140-5p	src kinase-associated phospho 2	**miR-26a-2-3p**	prohibitin isoform X1
miR-140-5p	peptidoglycan recognition 6	**miR-26a-2-3p**	Dystrobrevin binding 1a
miR-140-5p	transmembrane 14C	**miR-26a-2-3p**	UPF0369 C6orf57 homolog
miR-140-5p	serine threonine- kinase PAK 4-like	**miR-26a-2-3p**	unc-93 homolog B1-like
miR-140-5p	peptidyl-prolyl cis-trans isomerase FKBP1B isoform X1	**miR-26a-3p**	large proline-rich BAG6 isoform X2
miR-140-5p	Golgi phospho 3-like	**miR-26a-3p**	src kinase-associated phospho 1
miR-140-5p	sodium potassium-transporting ATPase subunit alpha-3-like	**miR-27a-5p**	canopy homolog 3-like
miR-140-5p	transforming isoform X1	**miR-27a-5p**	complement C1r subcomponent-like
miR-140-5p	myelin expression factor 2-like	**miR-27a-5p**	calmodulin
miR-140-5p	adenosine deaminase CECR1-A-like	**miR-27a-5p**	dynein light chain 2, cytoplasmic-like
miR-141-3p	transcription elongation factor SPT6	**miR-27a-5p**	suppressor of cytokine signaling 6
miR-141-3p	cytoplasmic NCK1 isoform X1	**miR-27b-5p**	SAM and SH3 domain-containing 3-like
miR-141-3p	stromal cell-derived factor 1-like	**miR-27b-5p**	CCAAT enhancer-binding alpha
miR-141-3p	MAP kinase-activated kinase 2	**miR-27b-5p**	S-phase kinase-associated 1
miR-141-3p	cpG-binding -like	**miR-27b-5p**	activin receptor type-1B isoform X2
miR-141-3p	tRNA (cytosine(34)-C(5))-methyltransferase	**miR-27b-5p**	serine arginine-rich splicing factor 3-like isoform X2
miR-141-3p	serine threonine- kinase PAK 4-like	**miR-27b-5p**	adenylate kinase 2, mitochondrial-like
miR-141-3p	band 3 anion exchange -like	**miR-27b-5p**	zinc finger Gfi-1b-like
miR-141-3p	rogdi homolog	**miR-29b**	proto-oncogene c-Fos-like
miR-141-3p	SAM and SH3 domain-containing 3-like	**miR-29b**	transferrin receptor 1-like
miR-141-3p	Red	**miR-29b**	DNA polymerase beta
miR-141-3p	peptidyl-prolyl cis-trans isomerase FKBP1B isoform X1	**miR-29b**	spermine oxidase isoform X1
miR-141-3p	invariant chain 14-1	**miR-29b**	transport Sec61 subunit gamma
miR-141-3p	S-phase kinase-associated 1	**miR-29b**	large proline-rich BAG6 isoform X2
miR-141-3p	cAMP-dependent kinase type I-alpha regulatory subunit	**miR-30c-3p**	actin-related 2 isoform X2
miR-141-3p	40S ribosomal S14	**miR-30c-3p**	cAMP-dependent kinase type I-alpha regulatory subunit
miR-141-3p	polycomb complex BMI-1	**miR-30e-3p**	tubulin beta chain
miR-141-3p	nck-associated 1-like	**miR-30e-3p**	ubiquitin-conjugating enzyme E2 D3
miR-141-3p	transferrin receptor 1-like	**miR-30e-3p**	complement factor B-like
miR-141-3p	homeobox Meis1	**miR-30e-3p**	telomerase reverse transcriptase
miR-141-3p	c-C chemokine receptor type 9-like	**miR-30e-3p**	beta-2 microglobulin
miR-142a-3p	ubiquitin-conjugating enzyme E2 D3	**miR-30e-3p**	transmembrane 14C

miR-142a-3p	von Hippel-Lindau disease tumor suppressor	**miR-30e-3p**	proto-oncogene c-Rel-like
miR-142a-3p	beta-galactosidase-1 2-like	**miR-30e-3p**	phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit beta isoform-like
miR-142a-3p	rogdi homolog	**miR-30e-3p**	growth factor receptor-bound 2
miR-142a-3p	proteoglycan 4-like isoform X1	**miR-30e-3p**	von Hippel-Lindau disease tumor suppressor
miR-142a-3p	plasminogen activator inhibitor 1-like	**miR-30e-3p**	ankyrin repeat and KH domain-containing 1-like
miR-142a-3p	ADP-ribosylation factor 1	**miR-30e-3p**	beta-galactosidase-1 2-like
miR-142a-3p	ADP-ribosylation factor 1	**miR-30e-3p**	ADP-ribosylation factor 6
miR-142a-3p	ubiquitin-conjugating enzyme E2Q 1	**miR-30e-3p**	interferon regulatory factor 5
miR-142a-3p	transport Sec61 subunit gamma	**miR-30e-3p**	MHC class I alpha chain, partial
miR-142a-3p	catenin beta-1	**miR-30e-3p**	phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and dual-specificity phosphatase PTEN-like isoform X1
miR-142a-3p	beta-galactosidase-1 2-like	**miR-30e-3p**	adenylate kinase 2, mitochondrial isoform X2
miR-142a-3p	14-3-3 beta alpha	**miR-30e-3p**	plasminogen activator inhibitor 1-like
miR-142a-3p	gap junction alpha-1 -like	**miR-30e-3p**	ADP-ribosylation factor 1
miR-142a-3p	sodium potassium-transporting ATPase subunit alpha-3-like	**miR-30e-3p**	eukaryotic translation initiation factor 2 subunit 1
miR-142a-3p	mitogen-activated kinase 14A-like isoform X2	**miR-30e-3p**	catenin beta-1
miR-142a-3p	ras-related R-Ras-like	**miR-30e-3p**	AP-2 complex subunit mu-A-like isoform X2
miR-144-3p	ubiquitin-conjugating enzyme E2 A	**miR-30e-3p**	Dual oxidase 1
miR-144-3p	ragulator complex LAMTOR3	**miR-30e-3p**	apolipo E
miR-144-3p	peroxiredoxin 1 variant 2	**miR-30e-3p**	Golgi phospho 3
miR-144-3p	Histone deacetylase 1	**miR-30e-3p**	calmodulin
miR-144-3p	ubiquitin-conjugating enzyme E2 variant 1	**miR-30e-3p**	proto-oncogene tyrosine- kinase Yrk-like isoform X2
miR-144-3p	DNA excision repair ERCC-1-like	**miR-30e-3p**	beta-galactosidase-1 2-like
miR-144-3p	Golgi phospho 3-like	**miR-30e-3p**	LSM14 homolog A isoform 3
miR-144-3p	DNA polymerase beta	**miR-30e-3p**	calcineurin subunit B type 1
miR-144-3p	mitochondrial ubiquitin ligase activator of nfkb 1-A-like	**miR-30e-3p**	integumentary mucin -like
miR-144-3p	tumor necrosis factor receptor superfamily member 14-like	**miR-30e-3p**	NHS 2-like isoform X2
miR-144-3p	polycomb complex BMI-1	**miR-30e-3p**	cornichon homolog
miR-144-3p	serine arginine-rich splicing factor 3-like isoform X2	**miR-30e-3p**	methionine synthase
miR-144-3p	sodium potassium-transporting ATPase subunit alpha-3-like	**miR-30e-3p**	endoplasmic reticulum aminopeptidase 1-like
miR-144-3p	hematopoietically-expressed homeobox hhex	**miR-30e-3p**	ADP-ribosylation factor 1
miR-144-3p	complement C3	**miR-30e-3p**	c-C chemokine receptor type 9-like
miR-145-3p	WD repeat and FYVE domain-containing 1-like	**miR-30e-3p**	cornichon homolog
miR-145-3p	inactive phospholipase C 2-like	**miR-34b**	stromal cell-derived factor 1-like
miR-146a	transmembrane 14C	**miR-34b**	complement component C6
miR-146a	transcription initiation factor TFIID subunit 3-like	**miR-34b**	SAM and SH3 domain-containing 3-like
miR-146a	beta-2-microglobulin precursor	**miR-34b**	cAMP-dependent kinase type I-alpha regulatory subunit
miR-146a	beta-2-microglobulin precursor	**miR-34b**	Proteasome (prosome, macropain) 26S subunit, ATPase, 6
miR-146a	MHC class I alpha chain	**miR-34b**	Ig kappa chain V-IV region STH

miR-146a	cAMP-specific 3 ,5 -cyclic phosphodiesterase 4D-like
miR-146a	probable ATP-dependent RNA helicase DDX41
miR-146a	calmodulin
miR-146a	complement C3
miR-146a	paired amphipathic helix Sin3a
miR-146a	catenin beta-1
miR-146a	MHC class I alpha chain, partial
miR-146a	c-C motif chemokine 19-like
miR-146a	WAS WASL-interacting family member 1
miR-146a	c-C motif chemokine 19-like
miR-146a	40S ribosomal S24
miR-146a	redox-regulatory FAM213A
miR-146a	MHC class I alpha chain, partial
miR-146a	redox-regulatory FAM213A
miR-155	maternal embryonic leucine zipper kinase
miR-155	Sorting nexin-10
miR-155	transmembrane 203
miR-155	beta-galactosidase-1 2-like
miR-155	ADP-ribosylation factor 6
miR-155	E3 ubiquitin- ligase TRAF7
miR-155	SNF-related serine threonine- kinase-like
miR-155	cellular tumor antigen p53
miR-155	apolipo E
miR-155	proto-oncogene tyrosine- kinase Yrk-like isoform X2
miR-155	insulin-like growth factor 1 receptor 1
miR-155	cullin-1-like, partial
miR-155	calcineurin subunit B type 1
miR-155	unc-93 homolog B1-like
miR-155	dynein light chain 2, cytoplasmic-like
miR-155	c-C chemokine receptor type 9-like
miR-16a	MAP kinase-activated kinase 2
miR-16a	growth factor receptor-bound 2
miR-16a	ETS translocation variant 5-like isoform X2
miR-16a	sumo-conjugating enzyme ubc9
miR-16a	complement C3-like
miR-16a	A Chain A, Orally Active 2-Amino Thienopyrimidine Inhibitors Of The Hsp90 Chaperone
miR-16b	growth factor receptor-bound 2
miR-16b	von Hippel-Lindau disease tumor suppressor
miR-34b	phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit gamma isoform
miR-34b	tyrosine- kinase FRK-like
miR-34b	small inducible cytokine
miR-375	ubiquitin-conjugating enzyme E2 A
miR-375	ubiquitin-conjugating enzyme e2 n
miR-375	complement component C7
miR-375	Red
miR-375	PREDICTED: uncharacterized protein C12orf29 homolog isoform X1
miR-429a	tubulin beta chain
miR-429a	adenylate kinase 7
miR-429a	homeobox Meis1-like
miR-429a	phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and dual-specificity phosphatase PTEN-like isoform X2
miR-429a	tRNA (cytosine(34)-C(5))-methyltransferase
miR-429a	band 3 anion exchange -like
miR-429a	rogdi homolog
miR-429a	SAM and SH3 domain-containing 3-like
miR-429a	F-box only 9-like
miR-429a	transferrin receptor 1-like
miR-429a	peptidyl-prolyl cis-trans isomerase FKBP1B isoform X1
miR-429a	heat shock HSP 90-beta
miR-429a	tafazzin
miR-429a	chemokine (C-X-C motif) ligand C1c precursor
miR-429a	cAMP-dependent kinase type I-alpha regulatory subunit
miR-429a	plasminogen activator inhibitor 1-like
miR-429a	ras-related R-Ras
miR-429a	ADP-ribosylation factor 1
miR-429a	cellular tumor antigen p53
miR-429a	apolipo E
miR-429a	polycomb complex BMI-1
miR-429a	nck-associated 1-like
miR-429a	phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit alpha isoform-like
miR-429a	LSM14 homolog A isoform 3
miR-429a	14-3-3 beta alpha
miR-429a	traf2 and NCK-interacting kinase-like
miR-429a	NHS 2-like isoform X2
miR-429a	novel MHCII alpha chain
miR-430a-3p	maternal embryonic leucine zipper kinase
miR-430a-3p	complement C3

miR-16b	PRELI domain-containing 1, mitochondrial-like	**miR-430a-3p**	stromal cell-derived factor 1-like
miR-16b	basic leucine zipper transcriptional factor ATF-like 3	**miR-430a-3p**	endoplasmic reticulum aminopeptidase 1-like
miR-16b	ETS translocation variant 5-like isoform X2	**miR-430a-3p**	von Hippel-Lindau disease tumor suppressor
miR-16b	sumo-conjugating enzyme ubc9	**miR-430a-3p**	CCAAT enhancer-binding alpha
miR-16b	complement C3-like	**miR-430a-3p**	interferon regulatory factor 8
miR-16c-3p	transferrin receptor 1-like	**miR-430a-3p**	actin-related 2 isoform X2
miR-16c-3p	zinc finger 629-like isoform X1	**miR-430a-3p**	ras-related Rab-32
miR-16c-3p	canopy homolog 3-like	**miR-430a-3p**	Dual oxidase 1
miR-16c-3p	DNA-directed RNA polymerase III subunit RPC6	**miR-430a-3p**	transport Sec61 subunit gamma
miR-16c-3p	exosome complex component RRP46	**miR-430a-3p**	ras-related Rab-33A-like
miR-16c-3p	importin-7	**miR-430a-3p**	ribosomal S24
miR-16c-5p	DNA-directed RNA polymerases I, II, and III subunit RPABC3	**miR-430a-3p**	calcineurin B homologous 3-like
miR-16c-5p	Sorting nexin-10	**miR-430b-3p**	maternal embryonic leucine zipper kinase
miR-16c-5p	growth factor receptor-bound 2	**miR-430b-3p**	stromal cell-derived factor 1-like
miR-16c-5p	ADP-ribosylation factor 6	**miR-430b-3p**	endoplasmic reticulum aminopeptidase 1-like
miR-16c-5p	PRELI domain-containing 1, mitochondrial-like	**miR-430b-3p**	von Hippel-Lindau disease tumor suppressor
miR-16c-5p	ETS translocation variant 5-like isoform X2	**miR-430b-3p**	F-box only 9-like
miR-16c-5p	complement C3-like	**miR-430b-3p**	CCAAT enhancer-binding alpha
miR-16c-5p	A Chain A, Orally Active 2-Amino Thienopyrimidine Inhibitors Of The Hsp90 Chaperone	**miR-430b-3p**	S-phase kinase-associated 1
miR-17a-3p	cpG-binding -like	**miR-430b-3p**	ras-related Rab-32
miR-17a-3p	MHC class II beta chain	**miR-430b-3p**	Dual oxidase 1
miR-17a-3p	ADP-ribosylation factor 6	**miR-430b-3p**	stromal cell-derived factor 1-like
miR-17a-3p	transcription factor	**miR-430b-3p**	death ligand 3
miR-17a-3p	sorting nexin-3	**miR-430b-3p**	ribosomal S24
miR-17a-3p	c-C motif chemokine 25-like	**miR-430b-3p**	calcineurin B homologous 3-like
miR-17a-3p	nucleophosmin-like	**miR-430c-3p**	maternal embryonic leucine zipper kinase
miR-17a-3p	small ubiquitin-related modifier 3	**miR-430c-3p**	cpG-binding -like
miR-17a-3p	PAX-interacting 1-like	**miR-430c-3p**	stromal cell-derived factor 1-like
miR-17a-3p	complement C3	**miR-430c-3p**	DNA-binding inhibitor ID-2
miR-17a-3p	cullin-1-like, partial	**miR-430c-3p**	endoplasmic reticulum aminopeptidase 1-like
miR-17a-3p	AP-1 complex subunit beta-1-like isoform X2	**miR-430c-3p**	cpG-binding -like
miR-17a-3p	calcineurin subunit B type 1	**miR-430c-3p**	von Hippel-Lindau disease tumor suppressor
miR-17a-3p	LIM domain-binding 1 isoform X2	**miR-430c-3p**	CCAAT enhancer-binding alpha
miR-17a-3p	angiopoietin-1 receptor isoform 3	**miR-430c-3p**	fatty acid-binding , liver
miR-17a-3p	E3 ubiquitin- ligase TRIM39	**miR-430c-3p**	ras-related Rab-32
miR-181a-2-3p	ubiquitin-conjugating enzyme E2 D3	**miR-430c-3p**	Dual oxidase 1
miR-181a-2-3p	Red	**miR-430c-3p**	dynein light chain 2, cytoplasmic-like

miR-181a-2-3p	transferrin receptor 1-like	**miR-430c-3p**	calmodulin
miR-181a-2-3p	peptidyl-prolyl cis-trans isomerase FKBP1B isoform X1	**miR-430c-3p**	proto-oncogene tyrosine- kinase Yrk-like isoform X2
miR-181a-2-3p	AP-2 complex subunit mu-A-like isoform X2	**miR-430c-3p**	stromal cell-derived factor 1-like
miR-181a-2-3p	complement C2-like	**miR-430c-3p**	calcineurin subunit B type 1
miR-181b-3p	cell division cycle 5	**miR-430c-3p**	spermine oxidase-like
miR-181b-3p	hsp90 co-chaperone Cdc37-like 1	**miR-430c-3p**	calcineurin B homologous 3-like
miR-181b-3p	proteoglycan 4-like isoform X1	**miR-430c-3p**	zinc finger 574-like
miR-181b-3p	Cathepsin S precursor	**miR-430c-3p**	serine threonine- kinase D1-like
miR-181b-3p	PAX-interacting 1-like	**miR-454a**	ubiquitin-conjugating enzyme E2 A
miR-181b-3p	redox-regulatory FAM213A isoform X3	**miR-454a**	phosphoacetylglucosamine mutase-like
miR-181b-3p	forkhead box O3	**miR-454a**	von Hippel-Lindau disease tumor suppressor
miR-181b-3p	transferrin receptor 1-like	**miR-454a**	ADP-ribosylation factor 6
miR-181b-3p	tyrosine- kinase JAK1 isoform X1	**miR-454a**	src substrate p85-like
miR-181b-3p	transcription factor E3-like	**miR-454a**	complement component C7
miR-181b-3p	LSM14 homolog A isoform 3	**miR-454a**	SNF-related serine threonine- kinase-like
miR-181b-3p	BCL2 adenovirus E1B 19 kDa -interacting 3-like	**miR-454a**	S-phase kinase-associated 1
miR-181b-3p	complexin-2	**miR-454a**	Ubiquitin FUBI
miR-181b-3p	voltage-gated potassium channel subunit beta-2-like isoform X2	**miR-454a**	spermine oxidase isoform X1
miR-181b-3p	60S ribosomal L13a	**miR-454a**	calmodulin
miR-181b-3p	40S ribosomal S27	**miR-454a**	transferrin receptor 1-like
miR-182-5p	tyrosine- phosphatase non-receptor type 6	**miR-454a**	sumo-conjugating enzyme ubc9
miR-182-5p	src kinase-associated phospho 2	**miR-454a**	14-3-3 beta alpha
miR-182-5p	stromal cell-derived factor 1-like	**miR-454a**	phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit gamma isoform
miR-182-5p	src substrate p85-like	**miR-454a**	dynein light chain 2, cytoplasmic-like
miR-182-5p	interferon regulatory factor 8	**miR-454a**	nck-associated 1
miR-182-5p	peptidyl-prolyl cis-trans isomerase-like	**miR-454a**	myelin expression factor 2-like
miR-182-5p	c-C motif chemokine 25-like	**miR-454a**	myelin expression factor 2-like
miR-182-5p	F-box only 5-like	**miR-455-2-5p**	tafazzin
miR-182-5p	plasminogen activator inhibitor 1-like	**miR-455-2-5p**	CD83 antigen-like
miR-182-5p	ras-related Rab-32	**miR-455-2-5p**	NDRG1-like isoform X1
miR-182-5p	nucleophosmin-like	**miR-455-2-5p**	ADP-ribosylation factor 1
miR-182-5p	TSC22 domain family 3 isoform X2	**miR-455-2-5p**	40S ribosomal S7
miR-182-5p	tyrosine- kinase FRK-like	**miR-455-2-5p**	dynein light chain 2, cytoplasmic-like
miR-182-5p	BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIBa	**miR-455-2-5p**	dynein light chain 2, cytoplasmic-like

miR-183-5p	F-box only 9-like
miR-183-5p	sorting nexin-3
miR-183-5p	interferon regulatory factor 8
miR-183-5p	cAMP-dependent kinase type I-alpha regulatory subunit
miR-183-5p	nucleophosmin-like
miR-183-5p	NDRG1-like isoform X1
miR-183-5p	apolipo E
miR-183-5p	caspase 3a
miR-183-5p	tyrosine- kinase JAK1 isoform X1
miR-183-5p	proto-oncogene tyrosine- kinase Yrk-like isoform X2
miR-183-5p	sumo-conjugating enzyme ubc9
miR-183-5p	transforming isoform X1
miR-183-5p	MHC class II alpha chain, partial
miR-184	zinc finger 629-like isoform X1
miR-184	activin receptor type-1B isoform X2
miR-184	ubiquitin-conjugating enzyme E2Q 1
miR-184	sodium potassium-transporting ATPase subunit beta-2-like isoform X2
miR-184	sodium potassium-transporting ATPase subunit alpha-3-like
miR-190b	complement C3
miR-190b	tyrosine- phosphatase non-receptor type 6
miR-190b	cpG-binding -like
miR-190b	transmembrane 14C
miR-190b	plastin-2-like
miR-190b	beta-2-microglobulin precursor
miR-190b	F-box only 9-like
miR-190b	transferrin receptor 1-like
miR-190b	beta-2-microglobulin precursor
miR-190b	Cathepsin S precursor
miR-190b	exosome complex component RRP46
miR-190b	elongation factor 2
miR-190b	cullin-3-like isoform X1
miR-190b	death ligand 3
miR-190b	ras-related Rab-8B
miR-190b	rab5 GDP GTP exchange factor-like isoform X2
miR-190b	redox-regulatory FAM213A
miR-190b	complement C1s subcomponent-like
miR-192	heat shock 70
miR-192	redox-regulatory FAM213A
miR-455-5p	DNA-binding inhibitor ID-2
miR-455-5p	band 3 anion exchange -like
miR-455-5p	NDRG1-like isoform X1
miR-455-5p	proto-oncogene tyrosine- kinase Yrk-like isoform X2
miR-455-5p	c-X-C motif chemokine 14-like
miR-455-5p	c-X-C motif chemokine 14-like
miR-457a	DNA replication licensing factor MCM2
miR-457a	growth factor receptor-bound 2
miR-457a	von Hippel-Lindau disease tumor suppressor
miR-457a	c-C motif chemokine 25-like
miR-457a	PREDICTED: uncharacterized protein C12orf29 homolog isoform X1
miR-457a	ras-related Rab-8B
miR-457a	DNA topoisomerase 2-binding 1-A-like
miR-457a	ETS translocation variant 5-like isoform X2
miR-457a	nck-associated 1-like
miR-457a	complement C3-like
miR-457a	A Chain A, Orally Active 2-Amino Thienopyrimidine Inhibitors Of The Hsp90 Chaperone
miR-457a	probable global transcription activator SNF2L2-like
miR-457a	probable global transcription activator SNF2L2-like
miR-460-5p	cpG-binding -like
miR-460-5p	beta-galactosidase-1 2-like
miR-460-5p	rogdi homolog
miR-460-5p	tyrosine- kinase CSK
miR-460-5p	NDRG1-like isoform X1
miR-460-5p	splicing factor, arginine serine-rich 3
miR-460-5p	Dystrobrevin binding 1a
miR-460-5p	U4 tri-snRNP-associated 1-like
miR-460-5p	mediator of RNA polymerase II transcription subunit 12
miR-460-5p	LIM domain-binding 1 isoform X2
miR-460-5p	phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit gamma isoform
miR-460-5p	complexin-2
miR-460-5p	ras-related R-Ras-like
miR-462	ras-related Rab-10
miR-462	actin-binding anillin
miR-462	MAP kinase-activated kinase 2
miR-462	prefoldin subunit 2
miR-462	basic leucine zipper transcriptional factor ATF-like 3
miR-462	prefoldin subunit 2

miR-193a-3p	DNA mismatch repair Mlh1-like
miR-193a-3p	transcription initiation factor TFIID subunit 3-like
miR-193a-3p	serine arginine-rich splicing factor 3-like isoform X2
miR-193a-3p	cullin-1-like, partial
miR-193a-3p	ubiquitin-conjugating enzyme E2 A isoform X2
miR-193a-3p	band 3 anion exchange -like
miR-193a-5p	interferon regulatory factor 5
miR-193a-5p	anamorsin
miR-193a-5p	heat shock 70
miR-193a-5p	adenosine deaminase CECR1-A-like
miR-193a-5p	DNA mismatch repair Mlh1-like
miR-193b-3p	tyrosine- phosphatase non-receptor type 6
miR-193b-3p	transcription initiation factor TFIID subunit 3-like
miR-193b-3p	cellular tumor antigen p53
miR-193b-3p	serine arginine-rich splicing factor 3-like isoform X2
miR-193b-3p	cullin-1-like, partial
miR-193b-3p	ubiquitin-conjugating enzyme E2 A isoform X2
miR-193b-3p	A Chain A, Orally Active 2-Amino Thienopyrimidine Inhibitors Of The Hsp90 Chaperone
miR-194a	pituitary tumor-transforming gene 1 -interacting -like
miR-194a	src kinase-associated phospho 2
miR-194a	complement C1q subcomponent subunit C
miR-194a	probable BRICK1-like
miR-194a	armadillo repeat-containing 6-like
miR-194a	beta-catenin-interacting 1
miR-194a	c-C motif chemokine 25-like
miR-194a	PREDICTED: uncharacterized protein C12orf29 homolog isoform X1
miR-194a	basic leucine zipper transcriptional factor ATF-like 3
miR-194a	heat shock 70
miR-194a	Dystrobrevin binding 1a
miR-194a	beta-actin
miR-194a	guanine nucleotide-binding subunit alpha-13
miR-194a	calcineurin subunit B type 1
miR-196a-5p	translocator
miR-196a-5p	stromal cell-derived factor 1-like
miR-196a-5p	rogdi homolog
miR-196a-5p	mediator of RNA polymerase II transcription subunit 12
miR-196a-5p	cornichon homolog
miR-19a-3p	ubiquitin-conjugating enzyme E2 A
miR-462	mitogen-activated kinase 7-like
miR-727-3p	complement C3
miR-727-3p	SAM and SH3 domain-containing 3-like
miR-727-3p	beta-2-microglobulin precursor
miR-727-3p	beta-catenin-interacting 1
miR-727-3p	beta-2-microglobulin precursor
miR-727-3p	plasminogen activator inhibitor 1-like
miR-727-3p	apolipo E
miR-727-3p	insulin-like growth factor 1 receptor 1
miR-727-3p	unc-93 homolog B1-like
miR-729	transmembrane 14C
miR-729	Interleukin enhancer binding factor 2
miR-729	nucleophosmin-like
miR-729	calmodulin
miR-729	eva-1 homolog C-like isoform X2
miR-729	ras-related Rab-6A isoform X1
miR-729	phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit gamma isoform
miR-729	MHC class I antigen, partial
miR-729	phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2B-like
miR-729	WD repeat and FYVE domain-containing 1-like
miR-729	MHC class I alpha chain, partial
miR-729	zinc finger Gfi-1b-like
miR-735-3p	ubiquitin-conjugating enzyme E2 D3
miR-735-3p	Red
miR-735-3p	c-C motif chemokine 25-like
miR-735-3p	GA-binding alpha chain
miR-735-3p	WAS WASL-interacting family member 1
miR-735-5p	CCAAT enhancer-binding alpha
miR-735-5p	Dual oxidase 1
miR-737-5p	Ras-related C3 botulinum toxin substrate 2 precursor
miR-737-5p	stromal cell-derived factor 1-like
miR-737-5p	hsp90 co-chaperone Cdc37-like 1
miR-737-5p	beta-galactosidase-1 2-like
miR-737-5p	SAM and SH3 domain-containing 3-like
miR-737-5p	argonaute-3 isoform X2
miR-737-5p	CCAAT enhancer-binding alpha
miR-737-5p	26S protease regulatory subunit 7
miR-737-5p	zinc finger 629-like isoform X1

miR-19a-3p	DNA-directed RNA polymerases I, II, and III subunit RPABC3
miR-19a-3p	serine threonine- kinase PAK 4-like
miR-19a-3p	ADP-ribosylation factor 6
miR-19a-3p	SAM and SH3 domain-containing 3-like
miR-19a-3p	complement component C7
miR-19a-3p	SNF-related serine threonine- kinase-like
miR-19a-3p	MHC class I alpha chain
miR-19a-3p	c-C motif chemokine 25-like
miR-19a-3p	PRELI domain-containing 1, mitochondrial-like
miR-19a-3p	40S ribosomal S7
miR-19a-3p	spermine oxidase isoform X1
miR-19a-3p	dynein light chain 2, cytoplasmic-like
miR-19a-3p	transferrin receptor 1-like
miR-19a-3p	cullin-1-like, partial
miR-19a-3p	serine threonine kinase raf1
miR-19a-3p	guanine nucleotide exchange factor VAV3 isoform X1
miR-19a-3p	tyrosine- kinase FRK-like
miR-19a-5p	cell division cycle 5
miR-19a-5p	cytoplasmic NCK1 isoform X1
miR-19a-5p	translocator
miR-19a-5p	stromal cell-derived factor 1-like
miR-19a-5p	MAP kinase-activated kinase 2
miR-19a-5p	cpG-binding -like
miR-19a-5p	transmembrane 14C
miR-19a-5p	plastin-2-like
miR-19a-5p	ADP-ribosylation factor 6
miR-19a-5p	SAM and SH3 domain-containing 3-like
miR-19a-5p	activin receptor type-1B isoform X2
miR-19a-5p	DNA topoisomerase 2-binding 1-A-like
miR-19a-5p	tumor suppressor candidate 2-like
miR-19a-5p	nck-associated 1-like
miR-19a-5p	proto-oncogene tyrosine- kinase Yrk-like isoform X2
miR-19a-5p	MHC class I alpha chain, partial
miR-19b-3p	ubiquitin-conjugating enzyme E2 A
miR-19b-3p	ubiquitin-conjugating enzyme E2 D3
miR-19b-3p	DNA-directed RNA polymerases I, II, and III subunit RPABC3
miR-19b-3p	complement component C6
miR-19b-3p	serine threonine- kinase PAK 4-like
miR-737-5p	S-phase kinase-associated 1
miR-737-5p	Ubiquitin FUBI
miR-737-5p	actin-related 2 isoform X2
miR-737-5p	plasminogen activator inhibitor 1-like
miR-737-5p	actin-related 3
miR-737-5p	ADP-ribosylation factor 1
miR-737-5p	E3 ubiquitin- ligase pellino homolog 1
miR-737-5p	AP-2 complex subunit mu-A-like isoform X2
miR-737-5p	bA2 globin
miR-737-5p	cullin-1
miR-737-5p	transport Sec61 subunit gamma
miR-737-5p	Proteasome (prosome, macropain) 26S subunit, ATPase, 6
miR-737-5p	calmodulin
miR-737-5p	proto-oncogene tyrosine- kinase Yrk-like isoform X2
miR-737-5p	beta-galactosidase-1 2-like
miR-737-5p	ras-related Rab-33A-like
miR-737-5p	leptin receptor gene-related -like
miR-737-5p	MHC class I alpha chain, partial
miR-737-5p	phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit gamma isoform
miR-737-5p	chromobox homolog 1
miR-737-5p	sulfotransferase 6B1
miR-737-5p	amyloid beta A4 precursor -binding family B member 1-interacting
miR-737-5p	mitogen-activated kinase 9 isoform X2
miR-737-5p	cell division control 42 homolog isoform X1
miR-737-5p	MHC class I alpha chain, partial
miR-737-5p	twisted gastrulation homolog 1-A-like
miR-737-5p	zinc finger Gfi-1b-like
miR-737-5p	ras-related C3 botulinum toxin substrate 2
miR-738	Red
miR-738	chromobox homolog 1
miR-92a-5p	cpG-binding -like
miR-92a-5p	DNA-directed RNA polymerases I, II, and III subunit RPABC1
miR-92a-5p	40S ribosomal S14
miR-92a-5p	ATP-dependent RNA helicase DHX8
miR-92a-5p	mitogen-activated kinase 9 isoform X2
miR-92a-5p	complexin-2
miR-92b-3p	tubulin beta chain
miR-92b-3p	stromal cell-derived factor 1-like

miR-19b-3p	ADP-ribosylation factor 6
miR-19b-3p	src substrate p85-like
miR-19b-3p	complement component C7
miR-19b-3p	transferrin receptor 1-like
miR-19b-3p	SNF-related serine threonine- kinase-like
miR-19b-3p	MHC class I alpha chain
miR-19b-3p	spermine oxidase isoform X1
miR-19b-3p	dynein light chain 2, cytoplasmic-like
miR-19b-3p	transferrin receptor 1-like
miR-19b-3p	serine threonine kinase raf1
miR-19b-3p	guanine nucleotide exchange factor VAV3 isoform X1
miR-19b-3p	dynein light chain 2, cytoplasmic-like
miR-19b-3p	myelin expression factor 2-like
miR-19b-3p	tyrosine- kinase FRK-like
miR-19b-3p	myelin expression factor 2-like
miR-19c-3p	ubiquitin-conjugating enzyme E2 A
miR-19c-3p	ubiquitin-conjugating enzyme E2 D3
miR-19c-3p	complement component C6
miR-19c-3p	serine threonine- kinase PAK 4-like
miR-19c-3p	ADP-ribosylation factor 6
miR-19c-3p	SAM and SH3 domain-containing 3-like
miR-19c-3p	src substrate p85-like
miR-19c-3p	complement component C7
miR-19c-3p	transferrin receptor 1-like
miR-19c-3p	SNF-related serine threonine- kinase-like
miR-19c-3p	MHC class I alpha chain
miR-19c-3p	PRELI domain-containing 1, mitochondrial-like
miR-19c-3p	40S ribosomal S7
miR-19c-3p	dynein light chain 2, cytoplasmic-like
miR-19c-3p	transferrin receptor 1-like
miR-19c-3p	U4 tri-snRNP-associated 1-like
miR-19c-3p	serine threonine kinase raf1
miR-19c-3p	guanine nucleotide exchange factor VAV3 isoform X1
miR-19c-3p	dynein light chain 2, cytoplasmic-like
miR-19c-3p	myelin expression factor 2-like
miR-19c-3p	tyrosine- kinase FRK-like
miR-19c-3p	myelin expression factor 2-like
miR-19d-3p	ubiquitin-conjugating enzyme E2 A
miR-92b-3p	MHC class II antigen beta chain
miR-92b-3p	AP-2 complex subunit mu-A-like isoform X2
miR-9-3p	interleukin-10 receptor subunit beta-like
miR-9-3p	MAP kinase-activated kinase 2
miR-9-3p	rogdi homolog
miR-9-3p	SAM and SH3 domain-containing 3-like
miR-9-3p	src substrate p85-like
miR-9-3p	sorting nexin-3
miR-9-3p	26S protease regulatory subunit 6B
miR-9-3p	catenin beta-1
miR-9-3p	LSM14 homolog A isoform X3
miR-9-3p	microtubule-associated 1A
miR-9-3p	catenin beta-1
miR-9-3p	C-type lectin domain family 4 member F-like
miR-9-3p	mitogen-activated kinase 9 isoform X2
miR-9-3p	notch-regulated ankyrin repeat-containing
miR-9-3p	Indoleamine 2,3-dioxygenase 1
miR-9-4-3p	interleukin-10 receptor subunit beta-like
miR-9-4-3p	MAP kinase-activated kinase 2
miR-9-4-3p	cpG-binding -like
miR-9-4-3p	rogdi homolog
miR-9-4-3p	SAM and SH3 domain-containing 3-like
miR-9-4-3p	sorting nexin-3
miR-9-4-3p	26S protease regulatory subunit 6B
miR-9-4-3p	LSM14 homolog A isoform X3
miR-9-4-3p	microtubule-associated 1A
miR-9-4-3p	nck-associated 1-like
miR-9-4-3p	catenin beta-1
miR-9-4-3p	C-type lectin domain family 4 member F-like
miR-9-4-3p	mitogen-activated kinase 9 isoform X2
miR-9-4-3p	notch-regulated ankyrin repeat-containing
miR-9-5p	tubulin beta chain
miR-9-5p	von Hippel-Lindau disease tumor suppressor
miR-9-5p	Wiskott-Aldrich syndrome homolog
miR-9-5p	beta-galactosidase-1 2-like
miR-9-5p	serine threonine- kinase PAK 4-like
miR-9-5p	beta-2-microglobulin precursor
miR-9-5p	Red

miR-19d-3p	DNA-directed RNA polymerases I, II, and III subunit RPABC3	**miR-9-5p**	dynactin subunit 5
miR-19d-3p	cleavage and polyadenylation specificity factor subunit 1-like	**miR-9-5p**	tumor necrosis factor receptor superfamily member 14-like
miR-19d-3p	complement component C6	**miR-9-5p**	plasminogen activator inhibitor 1-like
miR-19d-3p	src substrate p85-like	**miR-9-5p**	TSC22 domain family 3 isoform X2
miR-19d-3p	transferrin receptor 1-like	**miR-9-5p**	NEDD8-conjugating enzyme Ubc12
miR-19d-3p	SNF-related serine threonine- kinase-like	**miR-9-5p**	Golgi phospho 3
miR-19d-3p	MHC class I alpha chain	**miR-9-5p**	twisted gastrulation homolog 1-A-like
miR-19d-3p	c-C motif chemokine 25-like	**miR-9-5p**	adenosine kinase
miR-19d-3p	spermine oxidase isoform X1	**miR-9-7-3p**	interleukin-10 receptor subunit beta-like
miR-19d-3p	dynein light chain 2, cytoplasmic-like	**miR-9-7-3p**	MAP kinase-activated kinase 2
miR-19d-3p	sodium potassium-transporting ATPase subunit alpha-3-like	**miR-9-7-3p**	cpG-binding -like
miR-19d-3p	guanine nucleotide exchange factor VAV3 isoform X1	**miR-9-7-3p**	rogdi homolog
miR-19d-3p	dynein light chain 2, cytoplasmic-like	**miR-9-7-3p**	SAM and SH3 domain-containing 3-like
miR-19d-3p	myelin expression factor 2-like	**miR-9-7-3p**	src substrate p85-like
miR-19d-3p	tyrosine- kinase FRK-like	**miR-9-7-3p**	26S protease regulatory subunit 6B
miR-19d-3p	myelin expression factor 2-like	**miR-9-7-3p**	splicing factor, arginine serine-rich 3
miR-19d-5p	ubiquitin-conjugating enzyme E2 A	**miR-9-7-3p**	probable ATP-dependent RNA helicase DDX41
miR-19d-5p	transmembrane 203	**miR-9-7-3p**	LSM14 homolog A isoform X3
miR-19d-5p	rogdi homolog	**miR-9-7-3p**	nck-associated 1-like
miR-19d-5p	beta-catenin-interacting 1	**miR-9-7-3p**	catenin beta-1
miR-19d-5p	plasminogen activator inhibitor 1-like	**miR-9-7-3p**	C-type lectin domain family 4 member F-like
miR-19d-5p	dynein light chain 2, cytoplasmic-like	**miR-9-7-3p**	mitogen-activated kinase 9 isoform X2
miR-19d-5p	mediator of RNA polymerase II transcription subunit 12	**miR-9-7-3p**	notch-regulated ankyrin repeat-containing
miR-200a-3p	transcription elongation factor SPT6	**miR-9-7-3p**	Indoleamine 2,3-dioxygenase 1
miR-200a-3p	cytoplasmic NCK1 isoform X1	**miR-99**	kinase C alpha type
miR-200a-3p	stromal cell-derived factor 1-like	**miR-99**	complement factor B