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- (71) **Applicants:** MURDOCH CHILDRENS RESEARCH INSTITUTE [AU/AU]; Royal Children's Hospital, Flemington Road, Parkville, Victoria 3052 (AU). UNIVERSITY OF SYDNEY [AU/AU]; Sydnovate, Level 5, School of Information Technology (J12), University of Sydney, Sydney, New South Wales 2006 (AU).
- (72) **Inventors:** BATEMAN, John Francis; 26 Fowler Street, Box Hill South, Victoria 3128 (AU). KUNG, Louise Hiu-Wai; 2104/318 Russell Street, Melbourne, Victoria 3128 (AU). LITTLE, Christopher Bond; 21/259 Clarence

Street, Sydney, New South Wales 2000 (AU). RAVI, Varshini; 11/ 375-379 Old Northern Rd, Castle Hill, New South Wales 2154 (AU).

- (74) **Agent:** GRIFFITH HACK; GPO Box 1285, Melbourne, Victoria 3001 (AU).

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- (54) **Title:** OSTEOARTHRITIS MIRNAS

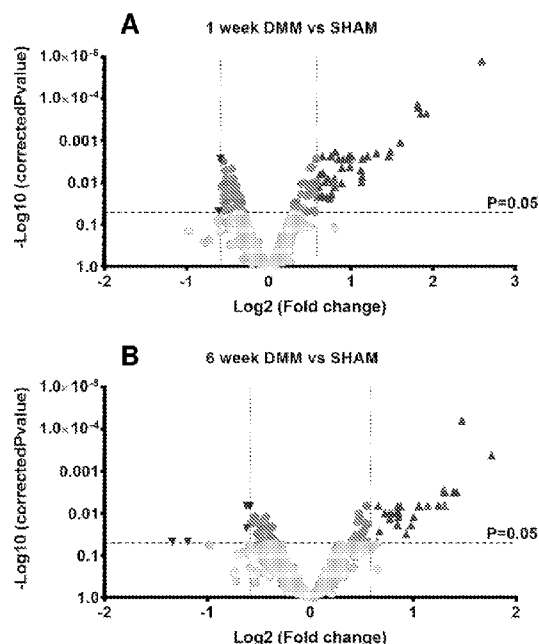


Figure 3.

(57) **Abstract:** The invention relates to an isolated osteoarthritis miRNA, or an ortholog thereof, and to mimics and inhibitors thereof. The invention also relates to use of the osteoarthritis miRNAs, mimics and inhibitors thereof for diagnosing and/or treating osteoarthritis in subject.



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OSTEOARTHRITIS miRNAs**FIELD**

The invention relates to osteoarthritis miRNAs, and to use of
5 such osteoarthritis miRNAs for diagnosing and treating
osteoarthritis.

BACKGROUND

Arthritis is the most prevalent musculoskeletal disease in
10 Australia afflicting nearly 20% of the population, with half of all
cases attributed to osteoarthritis. Osteoarthritis is the most
common form of degenerative joint disease and it results in
considerable disability and health care expenditure worldwide. In
Australia, arthritis cost AU\$24 billion in health care, lost time at
15 work and disability in 2007. Of this cost, osteoarthritis accounted
for over \$4 billion in direct health care costs. The impact of this
disease is growing as the population ages with the number of people
affected expected to double by 2020. Post-traumatic osteoarthritis
that develops after a joint injury accounts for up to 25% of all
20 osteoarthritis cases.

Osteoarthritis is a disease that impacts on all tissues of
the joint. While research continues to focus on defining the
molecular mechanisms of cartilage degeneration in osteoarthritis, it
is becoming increasingly clear that the entire joint, including the
25 subchondral bone, ligaments, menisci and synovial tissues (lining,
fat pad, capsule) actively contribute to the degenerative process.
Nevertheless, osteoarthritis is primarily characterised by the
progressive breakdown of articular cartilage.

However, articular cartilage has a poor reparative capacity
30 and ultimately it is the erosion of this tissue that signifies end-
stage arthritis.

The molecular mechanisms of osteoarthritis include microRNA
(miRNA) modulated gene expression.

A number of miRNAs have been implicated in chondrogenesis
35 (cartilage formation), including miR-145 (possible master regulator
of chondrogenesis), miR-675 (collagen II expression in human
chondrocytes), miR-140 (normal chondrogenesis and cartilage

homeostasis), miR-1 (synthesis of aggrecan), and miR-199a (synthesis of collagen II and COMP). In addition to miR-140, a recent study showed co-expression of another 39 miRNAs in an ATDC5 *in vitro* model of chondrogenesis.

5 To date 50 miRNAs have been shown to be dysregulated in human osteoarthritis cartilage or osteoarthritis-cartilage chondrocytes from joint replacement surgery. Some miRNAs have been identified in osteoarthritis samples, including miR-140 and miR-455 in human osteoarthritis cartilage in one study, in another study miR-22 plus
10 another 15 miRNAs were differentially expressed in human osteoarthritis cartilage, in another study 17 differentially expressed miRNAs were detected in human osteoarthritis cartilage, and in yet another study 7 of 723 miRNAs were differentially expressed in human osteoarthritis chondrocytes. In this last study,
15 only one miRNA was upregulated, miR-483.

 A number of miRNAs (miR-29, miR-141, miR-200a, miR-206, miR-210, miR-2861) have also been associated with osteoblast differentiation. Thirty differentially expressed miRNAs have been identified in osteoarthritis bone, but these have little overlap
20 with those that are changed in cartilage.

 In general, there is little overlap between miRNA expression datasets, for example, only 6 out of 50 miRNAs referred to above were common between any of the studies on human osteoarthritis cartilage or osteoarthritis-cartilage chondrocytes from joint
25 replacement surgery. Furthermore, expression of some miRNAs changed in opposite directions in different studies. For example, miR-140 was reported to be downregulated in osteoarthritis cartilage in some studies, but upregulated in another study. These findings emphasise the variability of available osteoarthritis clinical samples.

30 In addition to changes in miRNA in cartilage and bone in osteoarthritis, miRNA changes have been reported in synovial cells and fluid from osteoarthritis patients and there is growing evidence of miRNA involvement in synovitis/ inflammation.

 Although many disease targets and pathological pathways have
35 been associated with osteoarthritis, diagnosis of osteoarthritis is not definitive and is based largely on observation of symptoms. Moreover, all clinical studies of osteoarthritis to date have relied

on human tissue that can only be obtained at end-stage disease (at joint replacement). Information gathered from these studies provides little information on miRNAs involved in initiation, onset and early progression of osteoarthritis.

5 It follows that diagnosis and treatment of osteoarthritis is difficult in the early stages of osteoarthritis.

Compounding this relatively late window for diagnosis is a paucity of therapeutic options for managing osteoarthritis, let alone reversing osteoarthritis. Presently available osteoarthritis
10 drugs have not demonstrated dramatic success, and in fact, there are no registered therapies that halt osteoarthritis onset or progression.

Clearly, there is a need for improved, in particular earlier, diagnosis of and improved therapy for osteoarthritis. This is
15 because early stage osteoarthritis is a critical time when therapeutic intervention is expected to have the most potential to delay, or reverse, disease progression and improve patient outcomes.

SUMMARY

20 miRNAs are emerging as key cellular regulators which act by fine tuning gene expression patterns during development and in disease. Recent research suggests miRNAs play an important role in cartilage development and homeostasis, but their dysregulation and likely involvement in osteoarthritic joint disease is poorly
25 understood.

Disclosed herein are osteoarthritis miRNAs and their use in diagnosing and treating osteoarthritis.

In a first aspect, the invention provides an isolated osteoarthritis miRNA selected from Tables 1 to 5, or an ortholog
30 thereof.

In one embodiment, the osteoarthritis miRNA of the first aspect initiates and/or progresses early osteoarthritis.

In one embodiment, the osteoarthritis miRNA of the first aspect establishes osteoarthritis and/or progresses established
35 osteoarthritis to end-stage osteoarthritis.

In one embodiment, the osteoarthritis miRNA of the first aspect is represented by any one of SEQ ID NOs: 1 to 139.

In one embodiment, the osteoarthritis miRNA of the first aspect is represented by any one of SEQ ID NOs: 1 to 57.

In one embodiment, the osteoarthritis miRNA of the first aspect is miR-6931, miR-466i, miR-574, miR-3082, miR-1187, miR-669n,
5 miR-468, miR-669l, miR-32, miR-466m, miR-669e or miR-672.

In one embodiment, the osteoarthritis miRNA of the first aspect is represented by any one of SEQ ID NOs: 1 to 12, 140 or 141.

In one embodiment, the osteoarthritis miRNA of the first aspect is produced from a stem-loop represented by any one of SEQ ID
10 NOs: 142 to 155.

In one embodiment, the osteoarthritis miRNA of of the first aspect excludes miR-16-5p, miR-26b-5p, miR-30c-5p, miR-98-5p, miR-149-5p, miR-210-3p, miR-107-3p, miR-185-5p, miR-223-3p, miR-337-3p, miR-342-3p, and miR-377-3p.

15 In a second aspect, the invention provides use of the osteoarthritis miRNA of the first aspect for diagnosing osteoarthritis in a subject.

In a third aspect, the invention provides a method of diagnosing osteoarthritis in a subject, the method comprising:

20 (a) measuring in a sample of the subject expression of the osteoarthritis miRNA of the first aspect;

(b) comparing the measured expression of (a) with expression of the osteoarthritis miRNA in a reference sample; and

(c) when the measured expression of (a) is greater than
25 or lesser than the reference expression of (b) diagnosing osteoarthritis in the subject.

In a fourth aspect, the invention provides a method of treating osteoarthritis in a subject, the method comprising administering to the subject (a) an antagonist that inhibits an
30 activity of an upregulated osteoarthritis miRNA of the first aspect, wherein the subject has been diagnosed as having osteoarthritis by increased expression of the upregulated osteoarthritis miRNA in a sample from the subject relative to a reference sample, or (b) a mimic that mimics an activity of a downregulated osteoarthritis
35 miRNA of the first aspect, wherein the subject has been diagnosed as having osteoarthritis by decreased expression of the downregulated

osteoarthritis miRNA in a sample from the subject relative to a reference sample.

In one embodiment, the sample is synovial fluid or articular cartilage. In one embodiment, the sample comprises a chondrocyte.

5 In one embodiment, the sample comprises a chondrocyte from a mammalian subject.

In one embodiment, the mammalian subject is human.

In one embodiment, the reference sample is from the same subject, a different subject, or a population of subjects.

10 In one embodiment, the antagonist that inhibits an activity of the upregulated osteoarthritis miRNA in the subject is a nucleic acid antagonist or a small molecule. In one embodiment, the nucleic acid antagonist is a peptide nucleic acid, a locked nucleic acid (LNA), a nucleic acid aptamer, an antisense nucleic acid, a
15 phosphorodiamidate morpholino oligomer, a 2'-O-methyl RNA, an antagomir, an antiMir, a miRNA mask, a miRNA sponge, a nucleic acid analogue comprising a 2'-O-methyl nucleotide, 2'-O-allyl nucleotide, 2'-deoxy-2'-fluoro nucleotide, 2'-deoxy nucleotide, 2'-O-methoxyethyl (MOE) nucleotide, or phosphorothioate linkage, a
20 DNzyme, or a ribozyme.

In one embodiment, the mimic that mimics an activity of the downregulated osteoarthritis miRNA in the subject is a peptide nucleic acid, a locked nucleic acid (LNA), a nucleic acid aptamer, a phosphorodiamidate morpholino oligomer, a 2'-O-methyl RNA, a nucleic
25 acid analogue comprising a 2'-O-methyl nucleotide, 2'-O-allyl nucleotide, 2'-deoxy-2'-fluoro nucleotide, 2'-deoxy nucleotide, or 2'-O-methoxyethyl (MOE) nucleotide, or comprises a phosphorothioate linkage.

Additionally or alternatively to the fourth aspect, in a
30 fifth aspect, the invention provides use of (a) an antagonist that inhibits an activity of an upregulated osteoarthritis miRNA of the first aspect or (b) a mimic that mimics an activity of a downregulated osteoarthritis miRNA of the first aspect in the manufacture of a medicament for treating osteoarthritis in the
35 subject, wherein the subject has been diagnosed as having osteoarthritis by increased expression of the upregulated osteoarthritis miRNA or decreased expression of the downregulated

osteoarthritis miRNA in a sample from the subject relative to a reference sample.

Additionally or alternatively to the fourth aspect and fifth aspects, the invention provides (a) an antagonist that inhibits an activity of an upregulated osteoarthritis miRNA of the first aspect or (b) a mimic that mimics an activity of a downregulated osteoarthritis miRNA of the first aspect for treating osteoarthritis in the subject, wherein the subject has been diagnosed as having osteoarthritis by increased expression of the upregulated osteoarthritis miRNA or decreased expression of the downregulated osteoarthritis miRNA in a sample from the subject relative to a reference sample.

In a sixth aspect, the invention provides an isolated nucleic acid antagonist that binds an upregulated osteoarthritis miRNA of the first aspect or binds a target mRNA of the upregulated osteoarthritis miRNA of the first aspect and inhibits an activity of the upregulated osteoarthritis miRNA in a subject.

In one embodiment, the nucleic acid antagonist of the sixth aspect, comprises a reverse complement sequence of any one of SEQ ID NOs: 156 to 183.

In one embodiment, the nucleic acid antagonist of the sixth aspect is a peptide nucleic acid, a locked nucleic acid (LNA), a nucleic acid aptamer, an antisense nucleic acid, a phosphorodiamidate morpholino oligomer, a 2'-O-methyl RNA, an antagomir, an antiMir, a miRNA mask, a miRNA sponge, a nucleic acid analogue comprising a 2'-O-methyl nucleotide, 2'-O-allyl nucleotide, 2'-deoxy-2'-fluoro nucleotide, 2'-deoxy nucleotide, 2'-O-methoxyethyl (MOE) nucleotide, or phosphorothioate linkage, a DNAzyme, or a ribozyme.

In a seventh aspect, the invention provides an isolated nucleic acid mimic that binds a target mRNA of a downregulated osteoarthritis miRNA of the first aspect and mimics an activity of the downregulated osteoarthritis miRNA.

In one embodiment, the isolated nucleic acid mimic of the seventh aspect is a peptide nucleic acid, a locked nucleic acid (LNA), a nucleic acid aptamer, an antisense nucleic acid, a phosphorodiamidate morpholino oligomer, a 2'-O-methyl RNA, an

antagomir, an antiMir, a miRNA mask, a miRNA sponge, a nucleic acid analogue comprising a 2'-O-methyl nucleotide, 2'-O-allyl nucleotide, 2'-deoxy-2'-fluoro nucleotide, 2'-deoxy nucleotide, 2'-O-methoxyethyl (MOE) nucleotide, or phosphorothioate linkage, a
5 DNAzyme, or a ribozyme.

In an eighth aspect, the invention provides a vector encoding the nucleic acid antagonist of the sixth aspect or the nucleic acid mimic of the seventh aspect.

In a ninth aspect, the invention provides a pharmaceutical
10 composition comprising the nucleic acid antagonist of the sixth aspect or the nucleic acid mimic of the seventh aspect.

In a tenth aspect, the invention provides a kit comprising the nucleic acid antagonist of the sixth aspect, the nucleic acid mimic of the seventh aspect, the vector of the eighth aspect, or the
15 pharmaceutical composition of the ninth aspect.

In an eleventh aspect, the invention provides a method of treating osteoarthritis in a subject, the method comprising administering to the subject (a) an antagonist that inhibits an activity of an upregulated osteoarthritis miRNA of the first aspect,
20 or (b) administering to the subject a mimic that mimics an activity of a downregulated osteoarthritis miRNA of the first aspect.

In a twelfth aspect, the invention provides use of (a) an antagonist that inhibits an activity of an upregulated osteoarthritis miRNA of the first aspect or (b) a mimic that mimics an activity of a downregulated osteoarthritis miRNA of the first
25 aspect in the manufacture of a medicament for treating osteoarthritis in the subject.

In a thirteenth aspect, the invention provides a method of treating osteoarthritis in a subject, the method comprising
30 administering to the subject (a) an antagonist that inhibits an activity of an upregulated osteoarthritis miRNA of the first aspect, or (b) administering to the subject a mimic that mimics an activity of a downregulated osteoarthritis miRNA of the first aspect
excluding miR-16-5p, miR-26b-5p, miR-30c-5p, miR-98-5p, miR-149-5p,
35 miR-210-3p, miR-107-3p, miR-185-5p, miR-223-3p, miR-337-3p, miR-342-3p, and miR-377-3p.

In a fourteenth aspect, the invention provides use of (a) an antagonist that inhibits an activity of an upregulated osteoarthritis miRNA of the first aspect or (b) a mimic that mimics an activity of a downregulated osteoarthritis miRNA of the first aspect excluding miR-16-5p, miR-26b-5p, miR-30c-5p, miR-98-5p, miR-149-5p, miR-210-3p, miR-107-3p, miR-185-5p, miR-223-3p, miR-337-3p, miR-342-3p, and miR-377-3p in the manufacture of a medicament for treating osteoarthritis in the subject.

In a fifteenth aspect, the invention provides a method of treating osteoarthritis in a subject, the method comprising administering to the subject (a) an antagonist that inhibits an activity of an upregulated osteoarthritis target mRNA, optionally of Table 10 or Table 11, or an ortholog thereof, or (b) an agonist that promotes an activity of a downregulated osteoarthritis target mRNA, optionally of Table 10 or Table 11, or an ortholog thereof.

Additionally or alternatively to the fifteenth aspect, in a sixteenth aspect, the invention provides use of (a) an antagonist that inhibits an activity of an upregulated osteoarthritis target mRNA, optionally of Table 10 or Table 11, or an ortholog thereof, or (b) an agonist that promotes an activity of a downregulated osteoarthritis target mRNA, optionally of Table 10 or Table 11, or an ortholog thereof in the manufacture of a medicament for treating osteoarthritis in a subject.

Additionally or alternatively to the fifteenth aspect and sixteenth aspects, the invention provides (a) an antagonist that inhibits an activity of an upregulated osteoarthritis target mRNA, optionally of Table 10 or Table 11, or an ortholog thereof, or (b) an agonist that promotes an activity of a downregulated osteoarthritis target mRNA, optionally of Table 10 or Table 11, or an ortholog thereof for treating osteoarthritis in a subject.

In an embodiment of any one of the aspects of the invention, the osteoarthritis is post-traumatic osteoarthritis.

In an embodiment of any one of the aspects of the invention, the osteoarthritis is early osteoarthritis.

In an embodiment of any one of the aspects of the invention, the osteoarthritis is established or end-stage osteoarthritis.

The use of the second aspect or the method of the third aspect for diagnosing osteoarthritis may be performed *in vitro*.

BRIEF DESCRIPTION OF THE DRAWINGS

5 Figure 1 is a plot derived from Example 1 showing one example of verification of microarray data by qPCR of Let-7c-5p at 1 week and 6 weeks post-surgery. HK = Housekeeper; SYN = synovium; SCB = subchondral bone; S1 = Sham at 1 week post-surgery; D1 = DMM at 1 week post-surgery; S6 = Sham at 6 weeks post-surgery; D6 = DMM at
10 6 weeks post-surgery.

Figure 2 provides scatter plots derived from Example 1 comparing miRNA expression between DMM and sham operated mice in (A) synovium (SYN) 6 weeks post-surgery and (B) subchondral bone (SCB) 6 weeks post-surgery. The outer heavy lines represent a fold
15 change of 2 and the middle line represents no change.

Figure 3 provides volcano plots derived from Example 1 showing differentially expressed miRNA in articular cartilage between DMM versus sham operated mice at 1 week post-surgery (A) and 6 weeks post-surgery (B). Differential expression was defined as
20 expression > 1.5 fold change (downregulated left broken line, upregulated right broken line) at an adjusted $P < 0.05$ (horizontal broken line).

Figure 4 provides Venn diagrams derived from Example 1 showing differentially expressed miRNAs in articular cartilage at
25 1 week post-surgery and 6 weeks post-surgery (A) and showing the overlap of the data of Example 1 with previously published miRNA expression data from end-stage human osteoarthritis. Differential expression was defined as expression > 1.5 fold change at an adjusted $P < 0.05$.

30 Figure 5 provides plots derived from Example 1 showing qPCR expression profiles of miRNAs identified in the overlap group of Figure 4B with human osteoarthritis in articular cartilage following surgery.

35 DETAILED DESCRIPTION

The inventors have identified for the first time a specific group of miRNAs that are dysregulated in osteoarthritis. Most

dysregulated miRNAs are upregulated in osteoarthritis, but the invention is not limited to such, because a smaller number of miRNAs are downregulated in osteoarthritis. The inventors have now applied this knowledge to the diagnosis and treatment of osteoarthritis, a sub-type of which is post-traumatic osteoarthritis. In particular, the inventors demonstrate herein that measurement of an osteoarthritis miRNA of the disclosure can be used to diagnose osteoarthritis when the osteoarthritis miRNA expression is greater or lesser in a sample of a subject than that of a normal non-arthritic sample. Given this knowledge, treatment of osteoarthritis is also enabled and encompassed by the invention.

None of the miRNAs identified herein by the inventors, e.g. miR-6931-5p, miR-466i-5p, miR-574-5p, miR-3082-5p, miR-1187, miR-669n, miR-468-3p, miR-669l-5p, miR-32-3p, miR-466m-5p, miR-669e-5p, and miR-672-5p, has been disclosed or suggested to be involved in initiation and early progression of osteoarthritis. The inventors emphasise that all osteoarthritis-associated miRNAs identified to date have been identified in end-stage clinical samples that teach nothing about initiation and early progression of osteoarthritis.

Osteoarthritis-associated miRNAs identified to date in end-stage clinical samples are miR-16-5p, miR-26b-5p, miR-30c-5p, miR-98-5p, miR-149-5p, miR-210-3p, miR-107-3p, miR-185-5p, miR-223-3p, miR-337-3p, miR-342-3p, and miR-377-3p.

As used herein, "osteoarthritis" refers to the breakdown of cartilage in a joint.

One subtype of osteoarthritis is post-traumatic osteoarthritis. As used herein, "post-traumatic osteoarthritis" refers to the breakdown of cartilage in a joint that has suffered physical injury or trauma, e.g. ligament or meniscus damage, bone damage, or articular cartilage damage.

The invention relates to osteoarthritis miRNAs whose expression is dysregulated in initiation and early progression of osteoarthritis, as opposed to miRNAs whose expression is dysregulated in established and end-stage osteoarthritis.

This is not to say that some osteoarthritis miRNAs whose expression is dysregulated in initiation and early progression of osteoarthritis will not continue to be dysregulated as

osteoarthritis is established and possibly progressing to end-stage osteoarthritis.

Furthermore, the invention encompasses use of an osteoarthritis miRNA disclosed herein for treating established or end-stage osteoarthritis, and aspects of the invention are directed to such use.

Osteoarthritis may be diagnosed by physical examination, imaging and/or laboratory (pathology) tests. Physical examination of the affected joint may comprise checking for tenderness, swelling or redness, and for range of motion in the joint. Imaging the affected joint may include X-rays or magnetic resonance imaging (MRI). Cartilage loss appears in X-ray images as narrowing of the space between the bones of the affected joint. X-rays may also reveal bone spurs around the affected joint. X-rays may provide evidence of osteoarthritis in the affected joint before a subject experiences any symptoms. MRI produces detailed images of bone and soft tissues, including cartilage. At present MRI is not commonly used to diagnose osteoarthritis. However, MRI may be more useful for diagnosing initiation and/or early progression of osteoarthritis. Laboratory (pathology) tests include analysis of blood or synovial fluid. Blood analysis may help eliminate other causes of joint pain, such as rheumatoid arthritis. Synovial fluid analysis may eliminate gout or infection as a cause of joint pain.

While not wishing to be bound to theory, and owing to the current clinical difficulty in diagnosing initiation and early progression of osteoarthritis, it follows that initiation and early progression of osteoarthritis may be defined as distinct from established and end-stage osteoarthritis, i.e. non-established and non-end-stage osteoarthritis.

With respect to post-traumatic osteoarthritis, initiation and early progression of osteoarthritis refers to the period immediately following a joint trauma or injury. The period immediately following joint injury or trauma may be 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, 10 days, 11 days, 12 days, 13 days, 14 days, 1 week, 2 weeks, 3 weeks, 4 weeks, 5 weeks, 6 weeks, 7 weeks, 8 weeks, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months,

12 months, 13 months, 14 months, 15 months, 16 months, 17 months, 18 months, 19 months, 20 months, 21 months, 22 months, 23 months, 24 months, 1 year, 2 years, 3 years, 4 years, 5 years or 6 years.

While not wishing to be bound by theory, the inventors
5 consider that at early stages of osteoarthritis, i.e. during initiation and early progression, it is miRNA dysregulation in cartilage that drives osteoarthritis, but not miRNA dysregulation in other joint tissues. And in line with the invention described herein, osteoarthritis may be diagnosed, and treated, based on the
10 detection of dysregulation of an osteoarthritis miRNA of the invention.

"microRNA" or "miRNA" is a recently discovered class of small (~23 nucleotide) noncoding RNAs with important roles in post-transcriptional gene regulation in an expanding number biological
15 systems.

Mature miRNAs range from 21-25 nucleotides in length and are produced from larger precursor miRNAs termed primary miRNAs (or pri-miRNA). Pri-miRNAs are first transcribed by RNA polymerase II to generate the typical stem-loop (hairpin) structure where mature
20 miRNA sequences are embedded. The pri-miRNAs are then processed into shorter precursor miRNAs (pre-miRNAs) by ribonuclease-III (RNase III) Drosha-DGCR8 micro-processing complex. These pre-miRNAs are further processed by Dicer to liberate mature miRNAs that then associate with Argonaut family proteins to form an RNA-induced
25 silencing complex (RISC).

Each precursor can produce two mature miRNAs: one derived from the 5' strand (-5p) and one from the 3' strand (-3p). Related miRNA family members that differ by one or two nucleotides are indicated by additional lower case letters, such as, miR-26a and
30 miR-26b. The RISC effector complexes are guided to target mRNAs where base-pairing of the miRNA to the 3'UTR of target mRNAs results in mRNA decay or translational repression of the target mRNA. miRNAs may also target coding sequences and 5'UTR of mRNAs. Importantly, each miRNA recognises many target mRNAs and mRNAs contain targets
35 for numerous miRNAs creating rich regulatory complexity.

miRNAs are frequently expressed as polycistronic transcripts and about one-third of ~1600 miRNA precursors (miRBase) are located in 156 co-expressed clusters.

As used herein, "ortholog" refers to a miRNA or mRNA in one species with the same function as that of a miRNA or mRNA in another species, respectively, with the "orthologs" arising through speciation. In one embodiment, the orthologs have 90% or more complementarity. In one embodiment, the orthologs have the same nucleic acid sequence (i.e. 100% complementarity). In one embodiment, the miRNA orthologs have the same seed sequence. Without being bound to theory, a "seed sequence" often refers to a minimal sequence of perfect Watson-Crick base pairing between residues 2-8 of the miRNA and its target mRNA.

"Dysregulation" as used herein refers to upregulated or downregulated expression of an osteoarthritis miRNA beyond a specific threshold. The expression threshold for "upregulated" expression is greater than 1.25-fold change increased expression at adjusted $P < 0.05$. The expression threshold for "downregulated" expression is greater than 1.25-fold change decreased expression at adjusted $P < 0.05$. It follows that an "upregulated osteoarthritis miRNA" is a miRNA in any one of Tables 1 to 5 with a positive fold change and a "downregulated osteoarthritis miRNA" is a miRNA in any one of Tables 1 to 5 with a negative fold change.

Fold change may be reported herein as $\log_2$ fold change ($\log_2FC$), where no change is 0, >1.25 fold change is >0.32, >1.5 fold change is >0.58, >2 fold change is >1.

In some embodiments, the osteoarthritis miRNA is represented by any one of SEQ ID NOs: 1 to 139. In some embodiments, the osteoarthritis miRNA is represented by any one of SEQ ID NOs: 1 to 57. In some embodiments, the osteoarthritis miRNA is miR-6931, miR-466i, miR-574, miR-3082, miR-1187, miR-669n, miR-468, miR-669l, miR-32, miR-466m, miR-669e or miR-672. In some embodiments, the osteoarthritis miRNA is represented by any one of SEQ ID NOs: 1 to 12, 140 or 141. In one embodiment, the osteoarthritis miRNA is represented by SEQ ID NO: 140 or SEQ ID NO: 141.

In one embodiment, the osteoarthritis miRNA is produced from a stem-loop represented by any one of SEQ ID NOs: 142 to 155.

In general, miRNA and small interfering RNA (siRNA) are both types of RNA interference (RNAi). However, miRNA differs from siRNA in that miRNA is produced from an RNA transcript folded back on itself to form a stem-loop (hairpin) structure, whereas siRNA is produced from longer regions of double stranded RNA.

As used herein, a miRNA "mimic" is a synthetic nucleic acid that replicates the endogenous function of a miRNA that has been lost or down-regulated. The miRNA mimic may include nucleic acid analogues. The miRNA mimic may be double stranded and chemically modified (e.g. 2'-O-methyl with phosphorothioate modifications), and may be a longer nucleic acid similar to the endogenous miRNA precursor.

In some embodiments, the nucleic acid mimic is a peptide nucleic acid, a locked nucleic acid (LNA), a nucleic acid aptamer, a phosphorodiamidate morpholino oligomer, a 2'-O-methyl RNA, or a nucleic acid analogue comprising a 2'-O-methyl nucleotide, 2'-O-allyl nucleotide, 2'-deoxy-2'-fluoro nucleotide, 2'-deoxy nucleotide or 2'-O-(methoxyethyl (MOE) nucleotide. In some embodiments, the nucleic acid mimic comprises a phosphorothioate linkage.

As used herein, as miRNA generally reduces expression of a target mRNA, an "antagonist that inhibits an activity" of the osteoarthritis miRNAs disclosed herein refers to any nucleic acid or small molecule that is capable of increasing expression of a target mRNA. In some embodiments, the antagonist is a "nucleic acid antagonist", which term excludes small molecules. The increase of target mRNA expression may be caused directly, e.g. a nucleic acid antagonist binding (hybridising) to the osteoarthritis miRNA or its target mRNA, or caused indirectly, e.g. in the case of a small molecule. A nucleic acid antagonist may inhibit formation of the stem-loop from which the osteoarthritis miRNA is produced.

As used herein, a "small molecule" may be an antagonist that inhibits an activity of the osteoarthritis miRNAs disclosed herein. However, based on current knowledge, it is unlikely to bind miRNA. Instead, without wishing to be bound to theory, small molecule inhibitors are thought to modulate expression of miRNAs by targeting signalling pathways that converge on the activation of transcription factors that regulate miRNA encoding genes or to modulate the

machinery that contributes to miRNA maturation and degradation processes.

As used herein, "nucleic acid" refers to single, double or triple stranded DNA, RNA, or modified versions thereof including a peptide nucleic acid or locked nucleic acid (LNA).

A "target mRNA" is an mRNA whose expression is decreased upon binding (hybridisation) of an miRNA, for example to the 3'UTR of the target mRNA.

As used herein, a "nucleic acid aptamer" is a nucleic acid engineered through *in vitro* selection. The nucleic acid aptamer may be DNA, RNA or a nucleic acid analogue. The nucleic acid aptamer may bind the osteoarthritis miRNA or its target mRNA, and thus is a mimic or an antagonist that inhibits an activity of an osteoarthritis miRNA.

As used herein, an "antisense nucleic acid" is a single stranded DNA or RNA that is complementary to a miRNA. Thus, the antisense nucleic acid may bind the osteoarthritis miRNA and is an antagonist that inhibits an activity of an osteoarthritis miRNA. An example of an antisense nucleic acid is an "antimiR".

As used herein, a "locked nucleic acid" or "LNA" is a nucleic acid analogue comprising a bridge between 2' oxygen and 4' carbon that increases the hybridisation properties of an oligonucleotide comprising the LNA. An LNA may be incorporated into DNA or RNA. The LNA may bind the osteoarthritis miRNA or its target mRNA, and thus is a mimic or an antagonist that inhibits an activity of an osteoarthritis miRNA.

As used herein, a "phosphorodiamidate morpholino oligomer" or "PMO" comprises a backbone of methylene morpholine rings and phosphorodiamidate linkages. The PMO is a nucleic acid analogue. The PMO may bind the osteoarthritis miRNA or its target mRNA, and thus is a mimic or an antagonist that inhibits an activity of an osteoarthritis miRNA.

Nucleic acid analogues may find use in the invention. Nucleic acid analogues include 2'-O-methyl nucleotides, 2'-O-allyl nucleotides, 2'-deoxy-2'-fluoro nucleotides, 2'-deoxy nucleotides, 2'-O-(methoxyethyl (MOE) nucleotides, locked nucleic acid (LNA) nucleotides, phosphorothioate (PS) linkages, and combinations

thereof that may be incorporated into a nucleic acid to increase its hybridisation properties and stability against enzymatic degradation compared to natural nucleic acids. For example, "2'-O-methyl RNA" is RNA into which a 2'-O-methyl nucleotide has been incorporated. The
5 nucleic acid analogue may bind the osteoarthritis miRNA or its target mRNA, and thus is a mimic or an antagonist that inhibits an activity of osteoarthritis miRNA.

Other chemically engineered nucleic acids that prevent miRNA binding to a desired site on an mRNA are "antagomirs", often
10 comprising 2'-O-methyl RNA and phosphorothioates, and may be conjugated to cholesterol.

As used herein, a "miRNA mask" consists of a single-stranded 2'-O-methyl-modified antisense oligonucleotide that is fully complementary to miRNA binding sites in the 3' UTR of the target
15 mRNA, thus masking the miRNA binding site to de-repress its target mRNA. The miRNA mask may bind the osteoarthritis miRNA, and thus is an antagonist that inhibits an activity of an osteoarthritis miRNA.

As used herein, a "miRNA sponge" is a competitive inhibitor of miRNA. The miRNA sponge is expressed from a strong promoter and
20 comprises multiple, tandem binding sites to a miRNA. Typically, the miRNA sponge is expressed from a vector. The miRNA sponge may bind the osteoarthritis miRNA, and thus is an antagonist that inhibits an activity of an osteoarthritis miRNA.

In other embodiments, the antagonist that inhibits an
25 activity of the osteoarthritis miRNA in the subject is a nucleic acid selected from the group consisting of antisense RNA, DNA or mixture thereof, DNzyme, or ribozyme.

In some embodiments, the antagonist that inhibits an activity of the osteoarthritis miRNA in the subject is a nucleic acid
30 comprising the reverse complement nucleic acid sequence of the osteoarthritis miRNA. The reverse complement nucleic acid will bind (hybridise) with the osteoarthritis miRNA, as well as the stem-loop sequence from which the mature osteoarthritis miRNAs of the invention are produced. Example stem-loop sequences are provided in
35 Table 7. The reverse complement nucleic acid may be RNA, DNA, and as for any nucleic acid herein, may comprise a nucleic acid analogue.

Example reverse complement sequences for the osteoarthritis miRNAs of the invention are provided in Table 8.

Thus, it will be appreciated by the person skilled in the art that inhibition of a miRNA may occur by binding the miRNA or by
5 binding the target mRNA.

In an embodiment of the invention, a nucleic acid antagonist is represented by any one of SEQ ID NOs: 156 to 183.

In an embodiment of the invention, a nucleic acid antagonist:
is a peptide nucleic acid, a locked nucleic acid (LNA), a nucleic
10 acid aptamer, an antisense nucleic acid, a phosphorodiamidate
morpholino oligomer, a 2'-O-methyl RNA, an antagomir, an miRNA mask,
an miRNA sponge, a nucleic acid analogue comprising a 2'-O-methyl
nucleotide, 2'-O-allyl nucleotide, 2'-deoxy-2'-fluoro nucleotide,
2'-deoxy nucleotide, or 2'-O-(methoxyethyl (MOE) nucleotide, a
15 DNAzyme, or a ribozyme; or comprises a phosphorothioate linkage.

Other examples of, and methods of screening for, antagonists that inhibit an activity of miRNA or mimics that mimic an activity of miRNA are known to the person skilled in the art.

The mimic or antagonist that inhibits an activity of the
20 osteoarthritis miRNA in the subject, where the antagonist is a
nucleic acid, can be obtained using a number of techniques known in
the art. For example, nucleic acids can be chemically synthesized or
recombinantly produced using methods known in the art. For example,
nucleic acids can be chemically synthesized using appropriately
25 protected ribonucleotide phosphoramidites and a conventional RNA/DNA
synthesizer.

In another embodiment, the mimic or antagonist where the
antagonist is a nucleic acid, may be encoded by a second nucleic
acid, which may be inserted into a vector, such as a plasmid or
30 viral vector, to express the mimic or nucleic acid antagonist at the
site of osteoarthritis. Thus, the vector may comprise heterologous
nucleic acids.

Owing to the complementarity of binding (hybridising) between
nucleotides and nucleotide analogues, binding between nucleic acids
35 may be considered in terms of percent complementarity. For example,
the percent complementarity between an osteoarthritis miRNA and its
target mRNA is equivalent to the percentage of base pairs forming

between the osteoarthritis miRNA and its target mRNA. Similarly, percent complementarity between an osteoarthritis miRNA and a nucleic acid antagonist that inhibits an activity of the osteoarthritis miRNA is equivalent to the percentage of base pairs forming between the osteoarthritis miRNA and the nucleic acid antagonist or the percentage of base pairs forming between the nucleic acid antagonist and the target mRNA.

Percent complementarity for the purpose of mimicking or inhibiting an activity of the osteoarthritis miRNA may be 90%, 91%, 92%, 93%, 94%, 94%, 96%, 97%, 98%, 99% or 100%.

Given the nucleic acid sequence of a miRNA, the person skilled in the art will be able to readily identify reverse complement nucleic acid sequences, stem-loops, orthologs, and design any number of mimics or binding antagonists based on complementarity amongst nucleic acids and nucleic acid analogues. The person skilled in the art may use databases (e.g. miRBase) comprising miRNA-related nucleic acid sequences identified by unique accession identifiers.

As used herein, an "antagonist that inhibits an activity of an upregulated osteoarthritis target mRNA" refers to any nucleic acid, peptide, polypeptide (e.g. an antibody), or small molecule that is capable of decreasing expression, transcription or translation of a target mRNA, or is capable of inhibiting activity of the protein encoded by the target mRNA. In some embodiments, the antagonist that inhibits an activity of an upregulated osteoarthritis target mRNA is a "mimic" of an osteoarthritis miRNA as defined above, or other inhibitory RNA (RNAi). That is, the expression and activity of an osteoarthritis miRNA and its target mRNA are inversely related, so promoting activity of an osteoarthritis miRNA can inhibit activity of a target mRNA. The decrease of target mRNA expression, transcription or translation may be caused directly, e.g. a mimic binding (hybridising) to the osteoarthritis miRNA or its target mRNA, or caused indirectly, e.g. in the case of a peptide, polypeptide, or small molecule. An antagonist that inhibits an activity of an upregulated osteoarthritis target mRNA may be a small molecule, peptide or polypeptide (e.g. an antagonist antibody) that inhibits the activity of a protein encoded by the target mRNA.

As used herein, an "agonist that promotes an activity of a downregulated osteoarthritis target mRNA" refers to any nucleic acid, peptide, polypeptide (e.g. an antibody), or small molecule that is capable of increasing expression, transcription or translation of a target mRNA, or is capable of promoting activity of the protein encoded by the target mRNA. In some embodiments, the agonist that promotes an activity of a downregulated osteoarthritis target mRNA is an antagonist of an osteoarthritis miRNA. That is, the expression and activity of an osteoarthritis miRNA and its target mRNA are inversely related, so inhibiting activity of an osteoarthritis miRNA can promote activity of a target mRNA. In one embodiment, the agonist that promotes an activity of a downregulated osteoarthritis target mRNA is a "nucleic acid antagonist" as defined above. The increase of target mRNA expression, transcription or translation may be caused directly, e.g. a nucleic acid antagonist binding (hybridising) to the osteoarthritis miRNA or its target mRNA, or caused indirectly, e.g. in the case of a peptide, polypeptide, or small molecule. An agonist that promotes an activity of a downregulated osteoarthritis target mRNA may be a small molecule, peptide or polypeptide (e.g. an agonist antibody) that promotes the activity of a protein encoded by the target mRNA.

As used herein, a "small molecule", in addition to being an antagonist that inhibits an activity of the osteoarthritis miRNAs disclosed herein as defined above, may modulate expression, transcription or translation of an upregulated or downregulated target mRNA, or may modulate activity of a protein encoded by a target mRNA.

As used herein, the word "antibody" is used in the broadest sense and specifically covers monoclonal antibodies, polyclonal antibodies, multispecific antibodies (e.g. bispecific antibodies) formed from at least one intact antibody, antibody fragments provided that the antibody fragment exhibits the desired biological activity, and peptide aptamers. As used herein, an "antibody fragment" comprises a portion of an intact antibody, preferably the antigen binding and/or the variable region of the intact antibody. Examples of antibody fragments include: Fab, Fab', F(ab')₂ and Fv fragments; diabodies; linear antibodies; single-chain antibody

molecules; and multispecific antibodies formed from antibody fragments. As used herein, the term "intact antibody" refers to an antibody in its substantially intact form, as opposed to an antibody fragment. Specifically, intact antibodies include those with heavy and light chains including an Fc region. The constant domains may be native sequence constant domains (e.g., human native sequence constant domains) or amino acid sequence variants thereof. In some cases, the intact antibody may have one or more effector functions. The term "peptide aptamer" refers to peptides, polypeptides or proteins that interfere with other protein interactions. They consist of a variable peptide loop attached at both ends to a protein scaffold. This double structural constraint greatly increases the binding affinity of the peptide aptamer to levels comparable to an antibody's (nanomolar range).

As used herein, the term "subject" refers to a mammal. The mammal may be a primate, particularly a human, or may be a domestic, zoo, or companion animal. Although it is particularly contemplated that the invention disclosed herein is suitable for medical diagnosis and treatment of humans, it is also applicable to veterinary treatment, including treatment of domestic animals such as horses, cattle and sheep, companion animals such as dogs and cats, or zoo animals such as felids, canids, bovids and ungulates, as well as mice, rats and rabbits, for example.

Generally, the osteoarthritis miRNA is in or from a sample. It follows that, as used herein, a "sample" is of the subject, and more particularly is a sample of a joint of the subject. Thus, the sample may be articular cartilage, subchondral bone, ligaments, menisci or synovial tissues, comprising lining, fat pad, capsule, or fluid. Preferably, the sample is synovial fluid or articular cartilage. In one embodiment, the sample comprises a chondrocyte.

A sample may be obtained by biopsy, including fluid aspirate, or during surgery, for example. Alternatively, the sample may be pre-existing, for example an archived sample.

As used herein, a "reference sample" is a sample of the same type as the sample of interest but derived from a subject or subjects known not to have osteoarthritis, or at least known not to have osteoarthritis in the joint from which the reference sample is

taken. The reference sample may be from the same subject, e.g. another joint not having osteoarthritis, a different subject, or a population of subjects.

Measuring expression of a miRNA may be performed by methods known to the person skilled in the art, for example a two-step process involving reverse transcription and qPCR (yielding quantitative expression) or microarray analysis (yielding relative expression). Commercial reagents and apparatus are available and known to the person skilled in the art.

As used herein with regard to diagnosing or treating osteoarthritis, measured expression of an osteoarthritis miRNA "greater than the reference expression" means greater than a 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 110%, 120%, 130%, 140%, 150%, 160%, 170%, 180%, 190%, 200%, 225%, 250%, 275%, 300% or greater increase. For the avoidance of doubt, a 100% increase is equivalent to a doubling or 2-fold increase in expression, a 200% increase is a tripling or 3-fold increase in expression and so on. In some embodiments, measured expression of an osteoarthritis miRNA "greater than the reference expression" means >1.25, >1.5, or >2 fold change increased expression at adjusted $P < 0.05$.

As used herein with regard to diagnosing or treating osteoarthritis, measured expression of an osteoarthritis miRNA "lesser than the reference expression" means greater than a 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 110%, 120%, 130%, 140%, 150%, 160%, 170%, 180%, 190%, 200%, 225%, 250%, 275%, 300% or greater decrease. For the avoidance of doubt, a 100% decrease is equivalent to complete ablation of expression, and a 50% decrease is equivalent to one-half or 0.5-fold expression and so on. In some embodiments, measured expression of an osteoarthritis miRNA "lesser than the reference expression" means >1.25, >1.5, or >2 fold decreased expression at adjusted $P < 0.05$.

The mimic or antagonist that inhibits an activity of the osteoarthritis miRNA in the subject will be formulated, dosed, and administered in a fashion consistent with good medical practice. It

will be appreciated by the person skilled in the art that the exact manner of formulating, dosing and administering to a subject a therapeutically effective amount of a mimic or an antagonist that inhibits an activity of the osteoarthritis miRNA in the subject will be at the discretion of a medical practitioner. The mode of administration, including dosage, combination with other agents, timing and frequency of administration, and the like, may be affected by the diagnosis of a subject's likely responsiveness to treatment with the mimic or antagonist, as well as the subject's condition and history. Other relevant factors may include body size, body weight, age, health, sex of the subject, the site of administration, the method of administration, the scheduling of administration, possible side-effects and other factors known to medical practitioners. The therapeutically effective amount of the mimic or antagonist to be administered will be governed by such considerations.

The mimic or antagonist that inhibits an activity of the osteoarthritis miRNA in the subject, or a pharmaceutical composition comprising the mimic or antagonist, may be administered to a subject by any suitable method including parenteral (e.g. intravenous (IV) or intraarterial administration), intramuscular, intraperitoneal, intracerebrospinal, subcutaneous (SC), intraarticular, intrasynovial, intrathecal, oral, topical and inhalation routes (e.g. intrapulmonary). Parenteral infusions include intramuscular, IV, intraarterial, intraperitoneal and SC administration. Preferably, the mimic or antagonist, or a pharmaceutical composition comprising the mimic or antagonist, is administered to the subject intraarticularly or intrasynovially.

"Intraarticular" refers to administration into a joint affected by osteoarthritis. "Intrasynovial" refers to administration within the synovial lining of a joint.

The term "therapeutically effective amount" refers to an amount of a mimic or an antagonist that inhibits an activity of the osteoarthritis miRNA in the subject effective to treat osteoarthritis in the subject.

Viral and non-viral strategies have been developed for formulating and administering miRNAs. Non-viral strategies include

nucleic acids with chemical modifications, liposomes, polymers, hydrogels and nanoparticles, including encapsulation.

The most widely studied nucleic acid modification is the replacement of each non-bridging oxygen in the ribose backbone with a sulfur atom, thereby forming a phosphorothioate, which possess an improved *in vivo* half-life relative to naked miRNAs.

Encapsulation may be achieved using biodegradable polymers such as polylactide-polyglycolide, poly(orthoesters) and poly(anhydrides), anucleated bacterial minicells, a microemulsion, or liposomes. Liposomes may be, for example, a cationic liposome, e.g. DOTAP, LIPOFECTIN or LIPOFECTAMINE. The biodegradable polymer may be a sustained-release polymer. The mimic or antagonist may be formulated with a nanoparticle, microsphere or hydrogel.

If intraarticular or intrasynovial administration (e.g. injection) is deemed advantageous, miRNAs may be directly injected, thereby avoiding potential formulation issues.

The mimic or antagonist that inhibits an activity of the osteoarthritis miRNA in the subject may be formulated as a pharmaceutical composition. For example, the mimic or antagonist may be formulated with a pharmaceutically acceptable carrier. Methods for the formulation of compounds with pharmaceutical carriers are known in the art.

As used herein, the term "pharmaceutical composition" refers to a composition comprising a mimic or an antagonist that inhibits an activity of the osteoarthritis miRNA in the subject as described herein that has been formulated for administration to a subject. Preferably, the pharmaceutical composition is sterile. In one embodiment, the therapeutic composition is pyrogen-free.

The pharmaceutical composition may comprise the mimic or antagonist in any concentration that allows the administered mimic or antagonist to achieve a concentration in the range of from 0.1 µg/kg to 100 mg/kg. In some embodiments, the mimic or antagonist is administered to achieve a concentration of 0.1 µg/kg, 1 µg/kg, 10 µg/kg, 100 µg/kg, 1 mg/kg, 2 mg/kg, 3 mg/kg, 4 mg/kg, 5 mg/kg, 6 mg/kg, 7 mg/kg, 8 mg/kg, 9 mg/kg, 10 mg/kg, 11 mg/kg, 12 mg/kg, 13 mg/kg, 14 mg/kg, 15 mg/kg, 20 mg/kg, 25 mg/kg, 30 mg/kg, 35 mg/kg, 40 mg/kg, 45 mg/kg, 50 mg/kg, 55 mg/kg, 60 mg/kg, 65 mg/kg,

70 mg/kg, 75 mg/kg, 80 mg/kg, 85 mg/kg, 90 mg/kg, 95 mg/kg, or 100 mg/kg. The pharmaceutical compositions may comprise the mimic or antagonist in an amount of from 0.1% to 99.9% by weight. The mimic, nucleic acid antagonist or pharmaceutical composition may be
5 provided in at a concentration of, for example, from about 1 nM to about 100 nM, from about 2 nM to about 50 nM, from 2 nM to about 10 nM, or 1 nM, 10 nM, 100 nM, 1 μ M, 10 μ M, 100 μ M, 1 mM, 10 mM, or 100 mM of mimic or nucleic acid antagonist.

Pharmaceutically acceptable carriers include water, buffered
10 water, saline solutions such as, for example, normal saline or balanced saline solutions such as Hank's or Earle's balanced solutions, glycine, and hyaluronic acid.

The pharmaceutical composition may be formulated for parenteral administration. Pharmaceutical compositions for
15 parenteral administration may comprise pharmaceutically acceptable sterile aqueous or nonaqueous solutions, dispersions, suspensions or emulsions as well as sterile powders for reconstitution into sterile injectable solutions or dispersions. Examples of suitable aqueous and nonaqueous carriers, solvents, diluents or vehicles include
20 water, ethanol, polyols (such as glycerol, propylene glycol, polyethylene glycol), carboxymethylcellulose and mixtures thereof, vegetable oils (such as olive oil), injectable organic esters (e.g. ethyl oleate).

The pharmaceutical composition may comprise the mimic or
25 antagonist in an encapsulated form, as described above.

The pharmaceutical composition may be formulated for oral administration. Solid dosage forms for oral administration may include, for example, tablets, dragees, capsules, pills, and granules. In such solid dosage forms, the composition may comprise
30 at least one pharmaceutically acceptable carrier such as sodium citrate and/or dicalcium phosphate and/or fillers or extenders such as starches, lactose, sucrose, glucose, mannitol, and silicic acid; binders such as carboxymethylcellulose, alginates, gelatin, polyvinylpyrrolidone, sucrose and acacia; humectants such as
35 glycerol; disintegrating agents such as agar-agar, calcium carbonate, potato or tapioca starch, alginic acid, silicates, and sodium carbonate; wetting agents such as acetyl alcohol, glycerol

monostearate; absorbants such as kaolin and bentonite clay; and/or lubricants such as talc, calcium stearate, magnesium stearate, solid polyethylene glycol, sodium lauryl sulfate, and mixtures thereof.

Liquid dosage forms for oral administration may include, for
5 example, pharmaceutically acceptable emulsions, solutions, suspensions, syrups and elixirs. Liquid dosages may include inert diluents such as water or other solvents, solubilizing agents and/or emulsifiers such as ethyl alcohol, isopropyl alcohol, ethyl carbonate, ethyl acetate, benzyl alcohol, benzyl benzoate, propylene
10 glycol, 1,3-butylene glycol, dimethyl formamide, oils (such as, for example, cottonseed oil, corn oil, germ oil, castor oil, olive oil, sesame oil), glycerol, tetrahydrofurfuryl alcohol, polyethylene glycols and fatty acid esters of sorbitan, and mixtures thereof.

The pharmaceutical composition may comprise penetration
15 enhancers to enhance their delivery of agent. Penetration enhancers may include fatty acids such as oleic acid, lauric acid, capric acid, myristic acid, palmitic acid, stearic acid, linoleic acid, linolenic acid, dicaprate, reclineate, monoolein, dilaurin, caprylic acid, arachidonic acid, glyceryl 1-monocaprate, mono and di-
20 glycerides and physiologically acceptable salts thereof.

The pharmaceutical composition may further include chelating agents such as, for example, ethylenediaminetetraacetic acid (EDTA), citric acid, salicylates (e.g. sodium salicylate, 5-methoxysalicylate, homovanilate).

25 The mimic or nucleic acid antagonist may be administered by administering cells which comprise the mimic or antagonist, where the antagonist is a nucleic acid. Cells that comprise the nucleic acid may be cells into which the nucleic acid has been directly introduced, or may be cells into which a second nucleic acid that
30 encodes that mimic or nucleic acid antagonist has been introduced. The cell comprising the mimic or nucleic acid antagonist may be a stem cell, such as an embryonic stem cell, an adult stem cell, or an induced pluripotent stem cell (iPSC). The cells may be obtained from the subject (i.e. ex vivo) or from an alternative source. Methods
35 for the preparation of stem cells, differentiated cells and precursors thereof, are well known in the art. Methods suitable for the transfer of nucleic acids into mammalian cells *in vitro* are

known in the art and include the use of liposomes, electroporation, microinjection, cell fusion, DEAE-dextran, the calcium phosphate precipitation method, nanoparticles or minicells.

The mimic or nucleic acid antagonist may be introduced into
5 cells by conjugating a moiety to enhance its cellular absorption, as well as in some cases targeting it to a particular tissue or facilitating uptake by specific types of cells. For example, a hydrophobic ligand conjugated to the nucleic acid may facilitate direct permeation of the cellular membrane, or a ligand or moiety
10 may be attached which facilitates targeting or receptor-mediated endocytosis or cellular uptake. Examples of such ligand or moieties include: cholesterol; other lipophilic compounds such as: 1-pyrene butyric acid, 1,3-bis-O-(hexadecyl)glycerol, and menthol; folic acid; polyethylene glycols; carbohydrate clusters; cross-linking
15 agents; porphyrin conjugates; delivery peptides; monoclonal antibodies against a target molecule; aptamers capable of binding to a target molecule.

As noted above, the mimic or nucleic acid antagonist may be formulated and administered, including introduced into cells, using
20 recombinant viral vectors. The recombinant viral vectors typically comprise sequences encoding the mimic or nucleic acid antagonist and any suitable promoter for expressing the mimic or nucleic acid antagonist. Suitable promoters are known in the art and their selection is well within the person skilled in the art. Any viral
25 vector capable of accepting the coding sequence for the mimic or nucleic acid antagonist to be expressed can be used, for example, vectors derived from adenovirus (AV); adeno-associated virus (AAV); retroviruses (e.g. lentiviruses (LV), Rhabdoviruses, murine leukemia virus); herpes virus, and the like. Selection of recombinant viral
30 vectors suitable for use in the invention, methods for inserting nucleic acid sequences for expressing the mimic or nucleic acid antagonist into the vector, and methods of delivering the viral vector to the cells of interest are within those skilled in the art.

Also provided is an article of manufacture and a kit,
35 comprising a container comprising the mimic, antagonist that inhibits an activity of the osteoarthritis miRNA in the subject, or pharmaceutical composition comprising the mimic or antagonist. The

container may be a bottle or vial comprising the mimic, antagonist or pharmaceutical composition in oral or parenteral dosage form, each dosage form comprising a unit dose of the mimic, antagonist or pharmaceutical composition. For example, the mimic or nucleic acid antagonist may be in the form of an injectable solution in a disposable container. The article of manufacture or kit may further comprise printed instructions and/or a label or the like, indicating treatment of a subject according to the method disclosed herein.

The mimic, antagonist or pharmaceutical composition may be administered in combination with a second pharmaceutical substance, for example, acetaminophen (paracetamol), a non-steroidal anti-inflammatory (NSAID), a COX2 inhibitor, an oral opioid, or glucocorticoid. Administering "in combination" includes administration before, at the same time, or after the mimic, antagonist or pharmaceutical composition.

The terms "treat", "treating" or "treatment" refer to both therapeutic treatment and prophylactic or preventative measures, wherein the aim is to prevent or ameliorate osteoarthritis in a subject or slow down (lessen) progression of osteoarthritis. Subjects in need of treatment include those already with osteoarthritis as well as those in which osteoarthritis is to be prevented.

The terms "preventing", "prevention", "preventative" or "prophylactic" refer to keeping from occurring, or to hinder, defend from, or protect from the occurrence of osteoarthritis, including an abnormality or symptom. A subject in need of prevention may be prone to develop osteoarthritis.

In one embodiment, prevention of osteoarthritis refers to prevention of post-traumatic osteoarthritis.

The terms "ameliorate" or "amelioration" refer to a decrease, reduction or elimination of osteoarthritis, including an abnormality or symptom. A subject in need of treatment may already have osteoarthritis, or may be prone to have osteoarthritis, or may be in whom osteoarthritis is to be prevented.

The terms "diagnose", "diagnosing" or "diagnosis" refer to the identification of osteoarthritis in a subject.

It is to be noted that the term "a" or "an" refers to one or more, for example, "a molecule," is understood to represent one or more molecules. As such, the terms "a" or "an", "one or more," and "at least one" may be used interchangeably herein.

5 In the claims which follow and in the description of the invention, except where the context requires otherwise due to express language or necessary implication, the word "comprise" or variations such as "comprises" or "comprising" is used in an inclusive sense, i.e. to specify the presence of the stated features
10 but not to preclude the presence or addition of further features in various embodiments of the invention.

It is to be understood that if any prior art publication is referred to herein, such reference does not constitute an admission that the publication forms a part of the common general knowledge in
15 the art in Australia or any other country.

EXAMPLES

Example 1. miRNA microarray expression profiling during onset and progression of post-traumatic osteoarthritis (wild-type mice)

20 **Method.** Osteoarthritis was induced in 10-12 week old male wild-type mice by bilateral surgical destabilization of the medial meniscus (DMM). Total RNA was isolated from microdissected synovium and laser capture microdissected medial tibial plateau subchondral bone and articular cartilage of DMM and sham-operated mice at 1 week
25 and 6 weeks post-surgery. For synovium and subchondral bone, n=4 mice (DMM and sham) were used and for articular cartilage, n=3 each of 3 pooled mice (DMM and sham) were used.

Global miRNA expression profiling was performed using Agilent Mouse miRNA microarrays (Release 21.0, example microarray probes are
30 identified in Table 9). miRNAs differentially expressed in DMM compared to sham control determined using established bioinformatic analytics. Differential expression (i.e. dysregulation) was defined as adjusted $P < 0.05$. The severity of chondrocyte hypertrophy, proteoglycan loss, and structural damage in the tibial articular
35 cartilage of the contralateral medial femoro-tibial joint was scored by one observer blinded to surgical intervention and post-operative time.

Microarray data was validated by qPCR of multiple miRNAs, an example of which, Let-7c-5p in synovium and subchondral bone at 1 week and 6 weeks, is shown in Figure 1.

Results. Chondrocyte hypertrophy was considerably more extensive in tibial articular cartilage of DMM compared with sham-operated joints at both 1 and 6 weeks ($p = 0.002$ and $p = 0.004$, respectively), but did not differ with time in either surgical group. There was no articular cartilage proteoglycan loss in either surgical group at 1 week, but significant proteoglycan loss was observed in the DMM group with time ($P < 0.001$) and in DMM versus sham-operated group at 6 weeks ($P < 0.001$). Similarly, maximal and total articular cartilage structural damage scores did not differ between DMM and sham-operated groups at 1 week, but both scores progressed with time in DMM ($P < 0.003$) and in DMM versus sham-operated groups at 6 weeks ($P < 0.001$).

The sensitivity of the microarrays to detect statistically valid miRNA expression changes was demonstrated by the identification of 584 miRNAs differentially expressed between synovium and subchondral bone (adjusted $P < 0.05$). Moreover, 341 and 150 miRNAs were significantly dysregulated between 1 week and 6 week time points (fold change > 1.25 ; adjusted $P < 0.05$) in synovium and subchondral bone, respectively.

Although these data show both tissue specific miRNA expression patterns and temporal changes, there were **no changes in miRNA expression in either the synovium or subchondral bone between DMM and sham mice at either 1 week or 6 weeks post-surgery** (Figure 2A, 2B). Since this model represents early osteoarthritis, these data indicate that miRNA changes in subchondral bone detected by others in late disease are not involved in osteoarthritis initiation and progression.

In marked contrast to synovium and subchondral bone, significant dysregulation of many miRNAs in post-traumatic osteoarthritis articular cartilage compared to the sham-operated control were detected (Figure 3A, 3B). The most highly dysregulated (>2 -fold change, adjusted $P < 0.05$) osteoarthritis miRNAs at both 1 week and 6 weeks post-surgery were increased rather than decreased (Figure 3A, 3B).

miRNA expression profiling identified at 1 week post-surgery 122 osteoarthritis miRNAs (Table 1) and at 6 weeks post-surgery 74 osteoarthritis miRNAs (Table 2) dysregulated in articular cartilage that were differentially expressed (adjusted $P < 0.05$) in DMM versus sham-operated groups (Figure 4A).

Table 1. Osteoarthritis miRNAs in articular cartilage differentially expressed at 1 week post-surgery in DMM versus sham mice. Fold change is reported as $\log_2$ with threshold adjusted P < 0.05. miRNA sequences are provided in Tables 3 to 5.

miRNA	Log ₂ FC	adj. P	miRBase Accession	SEQ ID NO:
mmu-miR-6931-5p	2.6	0.000	MIMAT0027762	1
mmu-miR-1187	1.9	0.000	MIMAT0005837	2
mmu-miR-3082-5p	1.8	0.000	MIMAT0014872	3
mmu-miR-574-5p	1.8	0.000	MIMAT0004893	4
mmu-miR-466i-5p	1.8	0.000	MIMAT0017325	5
mmu-miR-669n	1.6	0.001	MIMAT0009427	6
mmu-miR-468-3p	1.5	0.002	MIMAT0002109	7
mmu-miR-32-3p	1.5	0.002	MIMAT0017050	8
mmu-miR-669l-5p	1.3	0.002	MIMAT0009418	9
mmu-miR-466m-5p	1.2	0.002	MIMAT0014882	10
mmu-miR-669e-5p	1.1	0.003	MIMAT0005853	11
mmu-miR-672-5p	1.1	0.005	MIMAT0003735	12
mmu-miR-6348	1.1	0.007	MIMAT0025091	13
mmu-miR-6918-5p	1.1	0.010	MIMAT0027736	14
mmu-miR-466f-5p	1.0	0.002	MIMAT0004881	15
mmu-miR-669o-5p	1.0	0.002	MIMAT0009421	16
mmu-miR-466h-5p	1.0	0.004	MIMAT0004884	17
mmu-miR-466j	1.0	0.003	MIMAT0005848	18
mmu-miR-669b-5p	1.0	0.002	MIMAT0003476	19
mmu-miR-466c-5p	0.9	0.003	MIMAT0004877	20
mmu-miR-467c-5p	0.9	0.004	MIMAT0004885	21
mmu-miR-31-5p	0.9	0.010	MIMAT0000538	22
mmu-miR-669f-5p	0.8	0.003	MIMAT0017327	23
mmu-miR-5126	0.8	0.002	MIMAT0020637	58
mmu-miR-195a-3p	0.8	0.008	MIMAT0017000	24
mmu-miR-6904-5p	0.8	0.012	MIMAT0027708	25
mmu-miR-669k-5p	0.8	0.010	MIMAT0017323	26
mmu-miR-7682-3p	0.8	0.018	MIMAT0029885	59
mmu-miR-3960	0.8	0.002	MIMAT0019336	60
mmu-miR-7118-5p	0.8	0.002	MIMAT0028133	27
mmu-miR-7218-5p	0.7	0.024	MIMAT0028404	61
mmu-miR-6546-5p	0.7	0.008	MIMAT0029792	62
mmu-miR-504-3p	0.7	0.022	MIMAT0017277	63
mmu-miR-6959-5p	0.7	0.010	MIMAT0027818	64
mmu-miR-16-1-3p	0.7	0.006	MIMAT0004625	28
mmu-miR-8110	0.6	0.002	MIMAT0031416	65
mmu-miR-8095	0.6	0.020	MIMAT0031396	66
mmu-miR-6769b-5p	0.6	0.006	MIMAT0028040	67
mmu-miR-7030-5p	0.6	0.010	MIMAT0027964	29
mmu-miR-7082-3p	0.6	0.022	MIMAT0028071	30
mmu-miR-1895	0.6	0.012	MIMAT0007867	68
mmu-miR-297c-5p	0.6	0.010	MIMAT0004865	31
mmu-miR-7038-5p	0.6	0.010	MIMAT0027980	32

miRNA	Log ₂ FC	adj. P	miRBase Accession	SEQ ID NO:
mmu-miR-3101-3p	0.6	0.003	MIMAT0014922	33
mmu-miR-1927	0.6	0.049	MIMAT0009390	69
mmu-let-7j	0.5	0.018	MIMAT0025123	34
mmu-miR-1930-3p	0.5	0.019	MIMAT0017340	70
mmu-miR-499-3p	0.5	0.010	MIMAT0017254	71
mmu-miR-129b-5p	0.5	0.046	MIMAT0029862	72
mmu-miR-206-3p	0.5	0.011	MIMAT0000239	35
mmu-miR-214-5p	0.5	0.014	MIMAT0004664	73
mmu-miR-222-3p	0.5	0.011	MIMAT0000670	74
mmu-miR-1224-5p	0.5	0.004	MIMAT0005460	75
mmu-miR-1306-3p	0.5	0.004	MIMAT0009411	36
mmu-miR-700-5p	0.5	0.012	MIMAT0017256	37
mmu-miR-294-3p	0.5	0.049	MIMAT0000372	76
mmu-miR-15a-3p	0.5	0.020	MIMAT0004624	38
mmu-miR-5622-3p	0.5	0.050	MIMAT0022372	77
mmu-miR-3098-3p	0.4	0.010	MIMAT0014918	39
mmu-miR-5099	0.4	0.042	MIMAT0020606	40
mmu-miR-346-5p	0.4	0.019	MIMAT0000597	41
mmu-miR-7034-5p	0.4	0.011	MIMAT0027972	78
mmu-miR-16-2-3p	0.4	0.040	MIMAT0017018	79
mmu-miR-696	0.4	0.048	MIMAT0003483	80
mmu-miR-99b-3p	0.3	0.049	MIMAT0004525	81
mmu-miR-6538	0.3	0.030	MIMAT0025583	82
mmu-miR-7018-5p	0.3	0.042	MIMAT0027940	83
mmu-miR-7036a-5p	0.3	0.033	MIMAT0027976	84
mmu-miR-1897-5p	0.3	0.050	MIMAT0007864	85
mmu-miR-149-5p	-0.3	0.049	MIMAT0000159	86
mmu-miR-99a-5p	-0.3	0.031	MIMAT0000131	87
mmu-miR-210-3p	-0.3	0.049	MIMAT0000658	42
mmu-miR-26b-5p	-0.3	0.025	MIMAT0000534	43
mmu-miR-331-3p	-0.3	0.024	MIMAT0000571	88
mmu-miR-29b-1-5p	-0.3	0.049	MIMAT0004523	89
mmu-miR-30e-5p	-0.4	0.034	MIMAT0000248	90
mmu-miR-29c-5p	-0.4	0.019	MIMAT0004632	91
mmu-miR-128-3p	-0.4	0.019	MIMAT0000140	44
mmu-miR-148b-3p	-0.4	0.019	MIMAT0000580	92
mmu-miR-136-5p	-0.4	0.024	MIMAT0000148	45
mmu-miR-337-3p	-0.4	0.049	MIMAT0000578	93
mmu-let-7f-5p	-0.4	0.050	MIMAT0000525	94
mmu-miR-151-5p	-0.4	0.012	MIMAT0004536	46
mmu-miR-22-5p	-0.4	0.019	MIMAT0004629	95
mmu-miR-6972-5p	-0.4	0.017	MIMAT0027846	96
mmu-miR-455-5p	-0.4	0.046	MIMAT0003485	97
mmu-miR-101c	-0.4	0.025	MIMAT0019349	98
mmu-miR-495-3p	-0.4	0.014	MIMAT0003456	99
mmu-miR-28c	-0.4	0.014	MIMAT0019339	47
mmu-miR-434-5p	-0.4	0.025	MIMAT0001421	100
mmu-miR-28a-5p	-0.4	0.008	MIMAT0000653	48

miRNA	Log ₂ FC	adj. P	miRBase Accession	SEQ ID NO:
mmu-miR-329-3p	-0.4	0.041	MIMAT0000567	49
mmu-miR-181a-1-3p	-0.5	0.005	MIMAT0000660	101
mmu-miR-181c-5p	-0.5	0.008	MIMAT0000674	102
mmu-miR-196a-5p	-0.5	0.019	MIMAT0000518	103
mmu-miR-30a-3p	-0.5	0.012	MIMAT0000129	104
mmu-let-7b-5p	-0.5	0.012	MIMAT0000522	105
mmu-miR-377-3p	-0.5	0.019	MIMAT0000741	50
mmu-miR-224-5p	-0.5	0.012	MIMAT0000671	106
mmu-let-7a-5p	-0.5	0.019	MIMAT0000521	107
mmu-miR-337-5p	-0.5	0.019	MIMAT0004644	108
mmu-miR-1839-5p	-0.5	0.014	MIMAT00009456	51
mmu-miR-30e-3p	-0.5	0.010	MIMAT0000249	109
mmu-miR-376b-5p	-0.5	0.011	MIMAT0003388	52
mmu-miR-361-5p	-0.5	0.012	MIMAT0000704	110
mmu-let-7c-5p	-0.5	0.010	MIMAT0000523	111
mmu-miR-466g	-0.5	0.020	MIMAT0004883	112
mmu-miR-411-5p	-0.5	0.018	MIMAT0004747	113
mmu-miR-98-5p	-0.5	0.008	MIMAT0000545	114
mmu-miR-379-5p	-0.5	0.024	MIMAT0000743	115
mmu-miR-425-5p	-0.5	0.008	MIMAT0004750	116
mmu-miR-669f-3p	-0.5	0.022	MIMAT0005839	117
mmu-miR-379-3p	-0.5	0.005	MIMAT0017080	53
mmu-miR-466f-3p	-0.5	0.032	MIMAT0004882	118
mmu-miR-376c-3p	-0.5	0.010	MIMAT0003183	54
mmu-miR-299b-5p	-0.5	0.020	MIMAT0022836	55
mmu-miR-30c-5p	-0.5	0.014	MIMAT0000514	119
mmu-miR-466i-3p	-0.5	0.046	MIMAT0005834	120
mmu-miR-374c-5p	-0.6	0.003	MIMAT0014953	121
mmu-miR-411-3p	-0.6	0.012	MIMAT0001093	56
mmu-miR-196b-5p	-0.6	0.003	MIMAT0001081	57
mmu-miR-6954-5p	-0.6	0.048	MIMAT0027808	122

Table 2. Osteoarthritis miRNAs differentially expressed in articular cartilage at 6 weeks post-surgery in DMM versus sham mice.

Fold change is reported as log₂ with threshold adjusted P < 0.05.

5 miRNA sequences are provided in Tables 3 to 5.

miRNA	Log ₂ FC	adj. P	miRBase Accession	SEQ ID NO:
mmu-miR-6931-5p	1.8	0.000	MIMAT0027762	1
mmu-miR-5099	1.5	0.000	MIMAT0020606	40
mmu-miR-1187	1.4	0.003	MIMAT0005837	2
mmu-miR-3082-5p	1.4	0.003	MIMAT0014872	3
mmu-miR-574-5p	1.3	0.003	MIMAT0004893	4
mmu-miR-32-3p	1.3	0.006	MIMAT0017050	8
mmu-miR-669n	1.3	0.006	MIMAT0009427	6
mmu-miR-466i-5p	1.3	0.003	MIMAT0017325	5
mmu-miR-468-3p	1.2	0.006	MIMAT0002109	7

miRNA	Log ₂ FC	adj. P	miRBase Accession	SEQ ID NO:
mmu-miR-669l-5p	1.1	0.006	MIMAT0009418	9
mmu-miR-466m-5p	1.1	0.007	MIMAT0014882	10
mmu-miR-669e-5p	1.1	0.006	MIMAT0005853	11
mmu-miR-672-5p	1.0	0.012	MIMAT0003735	12
mmu-miR-6348	1.0	0.019	MIMAT0025091	13
mmu-miR-6918-5p	0.9	0.030	MIMAT0027736	14
mmu-miR-466f-5p	0.9	0.007	MIMAT0004881	15
mmu-miR-466h-5p	0.9	0.012	MIMAT0004884	17
mmu-miR-466j	0.9	0.010	MIMAT0005848	18
mmu-miR-669b-5p	0.8	0.007	MIMAT0003476	19
mmu-miR-467c-5p	0.8	0.009	MIMAT0004885	21
mmu-miR-31-5p	0.8	0.018	MIMAT0000538	22
mmu-miR-669o-5p	0.8	0.010	MIMAT0009421	16
mmu-miR-195a-3p	0.8	0.013	MIMAT0017000	24
mmu-miR-466c-5p	0.8	0.010	MIMAT0004877	20
mmu-miR-669f-5p	0.7	0.010	MIMAT0017327	23
mmu-miR-669k-5p	0.7	0.026	MIMAT0017323	26
mmu-miR-7118-5p	0.7	0.006	MIMAT0028133	27
mmu-miR-6904-5p	0.6	0.046	MIMAT0027708	25
mmu-miR-16-1-3p	0.6	0.018	MIMAT0004625	28
mmu-miR-7082-3p	0.6	0.047	MIMAT0028071	30
mmu-miR-3101-3p	0.5	0.006	MIMAT0014922	33
mmu-miR-206-3p	0.5	0.017	MIMAT0000239	35
mmu-miR-7038-5p	0.5	0.025	MIMAT0027980	32
mmu-miR-7030-5p	0.5	0.031	MIMAT0027964	29
mmu-miR-3098-3p	0.5	0.012	MIMAT0014918	39
mmu-let-7j	0.5	0.046	MIMAT0025123	34
mmu-miR-1306-3p	0.5	0.010	MIMAT0009411	36
mmu-miR-346-5p	0.5	0.016	MIMAT0000597	41
mmu-miR-297c-5p	0.5	0.041	MIMAT0004865	31
mmu-miR-15a-3p	0.5	0.036	MIMAT0004624	38
mmu-miR-3470a	0.4	0.032	MIMAT0015640	123
mmu-miR-700-5p	0.4	0.042	MIMAT0017256	37
mmu-miR-196b-5p	-0.3	0.046	MIMAT0001081	57
mmu-let-7d-5p	-0.4	0.040	MIMAT0000383	124
mmu-miR-28a-5p	-0.4	0.021	MIMAT0000653	48
mmu-miR-376b-5p	-0.4	0.038	MIMAT0003388	52
mmu-miR-128-3p	-0.4	0.022	MIMAT0000140	44
mmu-miR-28c	-0.4	0.026	MIMAT0019339	47
mmu-miR-376c-3p	-0.4	0.046	MIMAT0003183	54
mmu-miR-377-3p	-0.4	0.041	MIMAT0000741	50
mmu-miR-379-3p	-0.4	0.018	MIMAT0017080	53
mmu-miR-151-5p	-0.4	0.012	MIMAT0004536	46
mmu-miR-136-5p	-0.4	0.022	MIMAT0000148	45
mmu-miR-26b-5p	-0.4	0.013	MIMAT0000534	43
mmu-miR-10a-5p	-0.5	0.026	MIMAT0000648	125
mmu-miR-300-3p	-0.5	0.041	MIMAT0000378	126
mmu-miR-411-3p	-0.5	0.046	MIMAT0001093	56

miRNA	Log ₂ FC	adj. P	miRBase Accession	SEQ ID NO:
mmu-miR-382-3p	-0.5	0.021	MIMAT00004691	127
mmu-miR-185-5p	-0.5	0.046	MIMAT00000214	128
mmu-miR-299b-5p	-0.5	0.046	MIMAT0022836	55
mmu-miR-329-3p	-0.5	0.042	MIMAT0000567	49
mmu-miR-154-5p	-0.5	0.032	MIMAT0000164	129
mmu-miR-1839-5p	-0.5	0.016	MIMAT0009456	51
mmu-miR-486a-5p	-0.5	0.028	MIMAT0003130	130
mmu-miR-100-5p	-0.5	0.029	MIMAT0000655	131
mmu-miR-15b-5p	-0.5	0.012	MIMAT0000124	132
mmu-miR-15a-5p	-0.5	0.012	MIMAT0000526	133
mmu-miR-342-3p	-0.6	0.017	MIMAT0000590	134
mmu-miR-210-3p	-0.6	0.007	MIMAT0000658	42
mmu-miR-107-3p	-0.6	0.006	MIMAT0000647	135
mmu-miR-434-3p	-0.6	0.022	MIMAT0001422	136
mmu-miR-129-2-3p	-0.6	0.006	MIMAT0000544	137
mmu-miR-223-3p	-1.2	0.046	MIMAT0000665	138
mmu-miR-451a	-1.3	0.046	MIMAT0001632	139

Of the osteoarthritis miRNAs listed in Table 1, 65
 osteoarthritis miRNAs were dysregulated only at 1 week post-surgery
 (Table 3 and Figure 4A), and of the osteoarthritis miRNAs listed in
 5 Table 2, 17 osteoarthritis miRNAs were dysregulated only at 6 weeks
 post-surgery (Table 4 and Figure 4A).

Of the dysregulated osteoarthritis miRNAs listed in Tables 1
 and 2, 57 osteoarthritis miRNAs were common to both 1 and 6 week
 time points (Table 5 and Figure 4A).

Table 3. Osteoarthritis miRNAs in articular cartilage differentially expressed only at 1 week post-surgery in DM versus sham mice. Fold change is reported as log₂ with threshold adjusted P < 0.05.

miRNA	log ₂ FC	adj. P	miRBase Accession	SEQ ID NO:	Sequence
mmu-miR-5126	0.8	0.002	MIMAT0020637	58	GCGGGCGGGCCGGGGGGGG
mmu-miR-7682-3p	0.8	0.018	MIMAT0029885	59	CCUGUGGGUUGGUUGGCUUU
mmu-miR-3960	0.8	0.002	MIMAT0019336	60	GGCGGGCGGGAGGCGGGGG
mmu-miR-7218-5p	0.7	0.024	MIMAT0028404	61	UGCAGGUUUAGUAGAGGG
mmu-miR-6546-5p	0.7	0.008	MIMAT0029792	62	AGCGCCUCUGAGCUUGUCUUGU
mmu-miR-504-3p	0.7	0.022	MIMAT0017277	63	AGGAGAGCAGGGCAGGGUUUC
mmu-miR-6959-5p	0.7	0.010	MIMAT0027818	64	UGGAAACCUUGUCGGGCUUG
mmu-miR-8110	0.6	0.002	MIMAT0031416	65	AAGCGUGAUUGGGGGGGGG
mmu-miR-8095	0.6	0.020	MIMAT0031396	66	AAAGGAUUCUGUCUGUCUCC
mmu-miR-6769b-5p	0.6	0.006	MIMAT0028040	67	CCUGGUGGGUGGGGAAGAGC
mmu-miR-1895	0.6	0.012	MIMAT0007867	68	CCCCGAGGAGGACGAGGAGGA
mmu-miR-1927	0.6	0.049	MIMAT0009390	69	GACCUCUGGAUUAAGGACUGA
mmu-miR-1930-3p	0.5	0.019	MIMAT0017340	70	GGUGCAGUACUGUGGCUUGG
mmu-miR-499-3p	0.5	0.010	MIMAT0017254	71	GAACAUCACAGCAAGUCUGUCU
mmu-miR-129b-5p	0.5	0.046	MIMAT0029862	72	GUUUUUGGGUAAGGCUUCC
mmu-miR-214-5p	0.5	0.014	MIMAT0004664	73	UGCCUGUCUACACUUGCUGGC
mmu-miR-222-3p	0.5	0.011	MIMAT0000670	74	AGCUACAUCUGGCUACUGGGU
mmu-miR-1224-5p	0.5	0.004	MIMAT0005460	75	GUGAGGACUGGGGAGGUGGAG
mmu-miR-294-3p	0.5	0.049	MIMAT0000372	76	AAAGUCUUCUUUUUGUGUGU
mmu-miR-5622-3p	0.5	0.050	MIMAT0022372	77	CUUAGCUGGUAGUGGUGGUC
mmu-miR-7034-5p	0.4	0.011	MIMAT0027972	78	UCCGGGAGGAUGGAUGUCU
mmu-miR-16-2-3p	0.4	0.040	MIMAT0017018	79	ACCAUAUUAUUGUCUGCUUU
mmu-miR-696	0.4	0.048	MIMAT0003483	80	GGUGUGCUUGCUGUGGG
mmu-miR-99b-3p	0.3	0.049	MIMAT0004525	81	CAAGCUCGUGUCUGUGGUCG
mmu-miR-6538	0.3	0.030	MIMAT0025583	82	CGCGGGUCCGGGGCGGCG
mmu-miR-7018-5p	0.3	0.042	MIMAT0027940	83	GUGAGCAGACAGGAGUGGUGGG
mmu-miR-7036a-5p	0.3	0.033	MIMAT0027976	84	AGCGGGGUUGGUGGGGAAGAGA
mmu-miR-1897-5p	0.3	0.050	MIMAT0007864	85	CUUUGGAUGGAGAAAGAGGGG
mmu-miR-149-5p	-0.3	0.049	MIMAT0000159	86	UCUGGCUCCGUGUCUACUCCC

miRNA	log ₂ FC	adj. P	miRBase Accession	SEQ ID NO:	Sequence
nmu-miR-99a-5p	-0.3	0.031	MIMAT0000131	87	AACCCGUAGAUCCGAUCUUGUG
nmu-miR-331-3p	-0.3	0.024	MIMAT0000571	88	GCCCCUGGGCCUAUCCUAGAA
nmu-miR-29b-1-5p	-0.3	0.049	MIMAT0004523	89	GCUGGUUUCAUAGGUGGUUUA
nmu-miR-30e-5p	-0.4	0.034	MIMAT0000248	90	UGUAAACAUCUUGACUGGAAG
nmu-miR-29c-5p	-0.4	0.019	MIMAT0004632	91	UGACCGAUUUCUCCUGGUGUUC
nmu-miR-148b-3p	-0.4	0.019	MIMAT0000580	92	UCAGUGCAUCACAGAACUUUGU
nmu-miR-337-3p	-0.4	0.049	MIMAT0000578	93	UCAGCUCCUAUAGAUAGCCUUU
nmu-let-7f-5p	-0.4	0.050	MIMAT0000525	94	UGAGGUAGUAGAUUGUAUAGUU
nmu-miR-22-5p	-0.4	0.019	MIMAT0004629	95	AGUUCUUCAGUGGCAAGCUUUA
nmu-miR-6972-5p	-0.4	0.017	MIMAT0027846	96	GCUGGAGGCACAGGGCAGACAG
nmu-miR-455-5p	-0.4	0.046	MIMAT0003485	97	UAUGUGCCUUUGGACUACAUCG
nmu-miR-101c	-0.4	0.025	MIMAT0019349	98	ACAGUACUGUGAUAAACUGA
nmu-miR-495-3p	-0.4	0.014	MIMAT0003456	99	AAACAAACAUGGUGCAUUUCUU
nmu-miR-434-5p	-0.4	0.025	MIMAT0001421	100	GCUCGACUCAUGGUUUGAACCA
nmu-miR-181a-1-3p	-0.5	0.005	MIMAT0000660	101	ACCAUCGACCGUGAUUUGUACC
nmu-miR-181c-5p	-0.5	0.008	MIMAT0000674	102	AACAUUCAACCGUGCGGUGAGU
nmu-miR-196a-5p	-0.5	0.019	MIMAT0000518	103	UAGGUAGUUCAUGUUGUUGGG
nmu-miR-30a-3p	-0.5	0.012	MIMAT0000129	104	CUUUCAGUCGGAUGUUUGCAGC
nmu-let-7b-5p	-0.5	0.012	MIMAT0000522	105	UGAGGUAGUAGGUUGUGUGGUU
nmu-miR-224-5p	-0.5	0.012	MIMAT0000671	106	UAAGUCACUAGUGGUUCCGUU
nmu-let-7a-5p	-0.5	0.019	MIMAT0000521	107	UGAGGUAGUAGGUUGUAUAGUU
nmu-miR-337-5p	-0.5	0.019	MIMAT0004644	108	CGGCGUCAUGGAGGAGUUGAUU
nmu-miR-30e-3p	-0.5	0.010	MIMAT0000249	109	CUUUCAGUCGGAUGUUUACAGC
nmu-miR-361-5p	-0.5	0.012	MIMAT0000704	110	UUUUCAGAAUCCUCCAGGGGUAC
nmu-let-7c-5p	-0.5	0.010	MIMAT0000523	111	UGAGGUAGUAGGUUGUAUGGUU
nmu-miR-466g	-0.5	0.020	MIMAT0004883	112	AUACAGACACAUGCACACACA
nmu-miR-411-5p	-0.5	0.018	MIMAT0004747	113	UAGUAGACCGUAUAGCGUACG
nmu-miR-98-5p	-0.5	0.008	MIMAT0000545	114	UGAGGUAGUAAGUUGUAUUGUU
nmu-miR-379-5p	-0.5	0.024	MIMAT0000743	115	UGGUAGACUAUGGAACGJAGG
nmu-miR-425-5p	-0.5	0.008	MIMAT0004750	116	AAUGACACGAUACUCCCGUUGA
nmu-miR-669f-3p	-0.5	0.022	MIMAT0005839	117	CAUUAUACAUACACACACACGUAU
nmu-miR-466f-3p	-0.5	0.032	MIMAT0004882	118	CAUACACACACACAUACACAC

miRNA	log ₂ FC	adj. P	miRBase Accession	SEQ ID NO:	Sequence
mmu-miR-30c-5p	-0.5	0.014	MIMAT0000514	119	UGUAAACAUCUACACUCUCAGC
mmu-miR-4661-3p	-0.5	0.046	MIMAT00005834	120	AUACACACACACAUACACACUA
mmu-miR-374c-5p	-0.6	0.003	MIMAT0014953	121	AUAUACACACUGCUAAGUG
mmu-miR-6954-5p	-0.6	0.048	MIMAT0027808	122	UGGGGAGUUCUGGGGGCAGAU

Table 4. Osteoarthritis miRNAs in articular cartilage differentially expressed only at 6 weeks post-surgery in DMM versus sham mice. Fold change is reported as log₂ with threshold adjusted P < 0.05.

miRNA	log ₂ FC	adj. P	miRBase Accession	SEQ ID NO:	Sequence
mmu-miR-3470a	0.4	0.032	MIMAT0015640	123	UCACUUUGUAGACCAGGCUUG
mmu-let-7d-5p	-0.4	0.040	MIMAT0000383	124	AGAGGUAGUAGGUUGCAUAGUU
mmu-miR-10a-5p	-0.5	0.026	MIMAT0000648	125	UACCCUGUAGAUCGGAUUUGUG
mmu-miR-300-3p	-0.5	0.041	MIMAT0000378	126	UAUGCAAGGGCAAGCUCUCUUC
mmu-miR-382-3p	-0.5	0.021	MIMAT0004691	127	UCAUUCACGGACACACUUUUU
mmu-miR-185-5p	-0.5	0.046	MIMAT0000214	128	UGGAGAGAAAGGCAGUUCUGA
mmu-miR-154-5p	-0.5	0.032	MIMAT0000164	129	UAGGUUAUCCGUGUUGCCUUCG
mmu-miR-486a-5p	-0.5	0.028	MIMAT0003130	130	UCCUGUACUGAGCUGCCCCGAG
mmu-miR-100-5p	-0.5	0.029	MIMAT0000655	131	AACCCGUAGAUCGGAACUUGUG
mmu-miR-15b-5p	-0.5	0.012	MIMAT0000124	132	UAGCAGCACAUCAUGGUUUACA
mmu-miR-15a-5p	-0.5	0.012	MIMAT0000526	133	UAGCAGCACAUAAUUGGUUUUG
mmu-miR-342-3p	-0.6	0.017	MIMAT0000590	134	UCUCACACAGAAAUCGCACCCGU
mmu-miR-107-3p	-0.6	0.006	MIMAT0000647	135	AGCAGCAUUGUACAGGGCUAUA
mmu-miR-434-3p	-0.6	0.022	MIMAT0001422	136	UUUGAACCAUCACUCGACUCCU
mmu-miR-129-2-3p	-0.6	0.006	MIMAT0000544	137	AAGCCUUUACCCCAAAAGCAU
mmu-miR-223-3p	-1.2	0.046	MIMAT0000665	138	UGUCAGUUUGUCAAUACCCCA
mmu-miR-451a	-1.3	0.046	MIMAT0001632	139	AAACCGUUAACCAUUAUCUGAGUU

Table 5. Osteoarthritis miRNAs in articular cartilage differentially expressed at 1 week post-surgery and 6 weeks post-surgery in DMM versus sham mice. Fold change is reported as log₂ with threshold adjusted P < 0.05.

miRNA	1 week log ₂ FC	1 week adj. P	6 weeks log ₂ FC	6 weeks adj. P	miRBase Accession	SEQ ID NO:	Sequence
mmu-miR-6931-5p	2.6	0.000	1.8	0.000	MIMAT0027762	1	UGGGUGGGGAGUGGGGACU
mmu-miR-1187	1.9	0.000	1.4	0.003	MIMAT0005837	2	UAUGUGUGUGUAUGUGUGUAA
mmu-miR-3082-5p	1.8	0.000	1.4	0.003	MIMAT0014872	3	GACAGAGUGUGUGUCUGUGU
mmu-miR-574-5p	1.8	0.000	1.3	0.003	MIMAT0004893	4	UGAGUGUGUGUGUGAGUGUGU
mmu-miR-4661-5p	1.8	0.000	1.3	0.003	MIMAT0017325	5	UGUGUGUGUGUGUGUGUGUG
mmu-miR-669n	1.6	0.001	1.3	0.006	MIMAT0009427	6	AUUUGUGUGGAGUGUGUGU
mmu-miR-468-3p	1.5	0.002	1.2	0.006	MIMAT0002199	7	UAUGACUGAUGUGCGUGUGUCUG
mmu-miR-32-3p	1.5	0.002	1.3	0.006	MIMAT0017050	8	CAAUUUAGUGUGUGAGUAUU
mmu-miR-6691-5p	1.3	0.002	1.1	0.006	MIMAT0009418	9	AGUUGUGUGGCAUGUAUUGU
mmu-miR-466n-5p	1.2	0.002	1.1	0.007	MIMAT0014882	10	UGUGUGCAUGUGCAUGUGUGAU
mmu-miR-669e-5p	1.1	0.003	1.1	0.006	MIMAT0005853	11	UGUCUUGUGUGUGCAUGUUCAU
mmu-miR-672-5p	1.1	0.005	1.0	0.012	MIMAT0003735	12	UGAGGUUGGUGUACUGUGUGA
mmu-miR-6348	1.1	0.007	1.0	0.019	MIMAT0025091	13	UCAGCCUUUAUAGGUGUGUGU
mmu-miR-6918-5p	1.1	0.010	0.9	0.030	MIMAT0027736	14	UGCUGAGGACGGGAUUAGGUUCU
mmu-miR-466f-5p	1.0	0.002	0.9	0.007	MIMAT0004881	15	UACGUGUGUGUGCAUGUGCAUG
mmu-miR-669o-5p	1.0	0.002	0.8	0.010	MIMAT0009421	16	UAGUUGUGUGUGCAUGUUUAUGU
mmu-miR-466h-5p	1.0	0.004	0.9	0.012	MIMAT0004884	17	UGUGUGCAUGUGUCUUGUGUGUA
mmu-miR-466j	1.0	0.003	0.9	0.010	MIMAT0005848	18	UGUGUGCAUGUGUGCAUGUGUAA
mmu-miR-669b-5p	1.0	0.002	0.8	0.007	MIMAT0003476	19	AGUUUUGUGUGCAUGUGCAUGU
mmu-miR-466c-5p	0.9	0.003	0.8	0.010	MIMAT0004877	20	UGAUGUGUGUGUGCAUGUACAUAU
mmu-miR-467c-5p	0.9	0.004	0.8	0.009	MIMAT0004885	21	UAAGUGCGGUGCAUGUAUAUGUG
mmu-miR-31-5p	0.9	0.010	0.8	0.018	MIMAT0000538	22	AGGCAAGAUGUGGCAUAGCUG
mmu-miR-669f-5p	0.8	0.003	0.7	0.010	MIMAT0017327	23	AGUUGUGUGUGCAUGUGCAUGUGU
mmu-miR-195a-3p	0.8	0.008	0.8	0.013	MIMAT0017000	24	CCAAUAUUGGUGUGUGUCUCC
mmu-miR-6904-5p	0.8	0.012	0.6	0.046	MIMAT0027708	25	UCCUGGGGUAGAGUUGAGUGG
mmu-miR-669k-5p	0.8	0.010	0.7	0.026	MIMAT0017323	26	UGUGCAUGUGUGUAUAGUUGUGUC
mmu-miR-7118-5p	0.8	0.002	0.7	0.006	MIMAT0028133	27	UGGGGAAGCGGAGAGAGGAAC

miRNA	1 week log ₂ FC	1 week adj. p	6 weeks log ₂ FC	6 weeks adj. p	miRBase Accession	SEQ ID NO:	Sequence
mmu-miR-16-1-3p	0.7	0.006	0.6	0.018	MIMAT0004625	28	CCAGUAUUGACUGUGCUGUGA
mmu-miR-7030-5p	0.6	0.010	0.5	0.031	MIMAT0027964	29	UGGGAGGUGGUGUGUGCUAGUC
mmu-miR-7082-3p	0.6	0.022	0.6	0.047	MIMAT0028071	30	GGCCCCUGGUGUGUGUGUCUCC
mmu-miR-297c-5p	0.6	0.010	0.5	0.041	MIMAT0004865	31	AUGUAUGUGUGAUGUACAUGU
mmu-miR-7038-5p	0.6	0.010	0.5	0.025	MIMAT0027980	32	UGUAGAAGGAAGGUGUGUGUG
mmu-miR-3101-3p	0.6	0.003	0.5	0.006	MIMAT0014922	33	UAGCUUUGGUGAUGGUGUUU
mmu-let-7j	0.5	0.018	0.5	0.046	MIMAT0025123	34	UGAGGUAUUAGUUUGUGUGUUAU
mmu-miR-206-3p	0.5	0.011	0.5	0.017	MIMAT0000239	35	UGGAUGUAAGGAAGUGUGUGG
mmu-miR-1306-3p	0.5	0.004	0.5	0.010	MIMAT0009411	36	ACGUUGGUCUGGUGUGUGAUG
mmu-miR-700-5p	0.5	0.012	0.4	0.042	MIMAT0017256	37	UAAGGCUCCUCCUGUGUGUGG
mmu-miR-15a-3p	0.5	0.020	0.5	0.036	MIMAT0004624	38	CAGGCCAUACUGUGUGUGCCUCA
mmu-miR-3098-3p	0.4	0.010	0.5	0.012	MIMAT0014918	39	UUCUGUGCCUGCCUUUUAAGGA
mmu-miR-5099	0.4	0.042	1.5	0.000	MIMAT0020606	40	UUAGAUCGAUGUGGUGGUCC
mmu-miR-346-5p	0.4	0.019	0.5	0.016	MIMAT0000597	41	UGUCUGCCCGAGUGCCUGCCUCU
mmu-miR-210-3p	-0.3	0.049	-0.6	0.007	MIMAT0000658	42	CUGUGCGUGUGACAGCGGCGUGA
mmu-miR-26b-5p	-0.3	0.025	-0.4	0.013	MIMAT0000534	43	UUCAAGUAUUACAGGAUAGGU
mmu-miR-128-3p	-0.4	0.019	-0.4	0.022	MIMAT0000140	44	UCACAGUAAACCGGUCUCUUU
mmu-miR-136-5p	-0.4	0.024	-0.4	0.022	MIMAT0000148	45	ACUCCAUUUGUUUUGAUGAUGG
mmu-miR-151-5p	-0.4	0.012	-0.4	0.012	MIMAT0004536	46	UCGAGGAGCUCACAGUCUAGU
mmu-miR-28c	-0.4	0.014	-0.4	0.026	MIMAT0019339	47	AGGAGCUCACAGUCUUAUUGA
mmu-miR-28a-5p	-0.4	0.008	-0.4	0.021	MIMAT0000653	48	AAGGAGCUCACAGUCUUAUUGAG
mmu-miR-329-3p	-0.4	0.041	-0.5	0.042	MIMAT0000567	49	AACACACCCAGCUAAACCUUUU
mmu-miR-377-3p	-0.5	0.019	-0.4	0.041	MIMAT0000741	50	AUCACACAAAGGCAACUUUUUGU
mmu-miR-1839-5p	-0.5	0.014	-0.5	0.016	MIMAT0009456	51	AAGGUAGUAAGAACAGGUCUUG
mmu-miR-376b-5p	-0.5	0.011	-0.4	0.038	MIMAT0003388	52	GUGGAUUAUCCUUCUAUGGUUA
mmu-miR-379-3p	-0.5	0.005	-0.4	0.018	MIMAT0017090	53	UAUGUAACAUGGUGCCACUAACU
mmu-miR-376c-3p	-0.5	0.010	-0.4	0.046	MIMAT0003183	54	AACAUAAGAGGAAAUUUCACGU
mmu-miR-299b-5p	-0.5	0.020	-0.5	0.046	MIMAT0022836	55	GGUUUACCGUCCACACUAACU
mmu-miR-411-3p	-0.6	0.012	-0.5	0.046	MIMAT0001093	56	UAUGUAACACGGGCCACUAACC
mmu-miR-196b-5p	-0.6	0.003	-0.3	0.046	MIMAT0001081	57	UAGGUAGUUUCCUGUGUGUGGG

Amongst the 57 dysregulated osteoarthritis miRNAs listed in Table 5 with adjusted $p < 0.05$, 12 osteoarthritis miRNAs were identified with a fold change > 2.0 and, including miR-6931-5p, miR-1187, miR-3082-5p, miR-574-5p, miR-466i-5p, miR-669n, miR-468-3p, miR-32-3p, miR-669l-5p, miR-466m-5p, miR-669e-5p, and miR-672-5p. Mature miRNA sequences, stem-loop sequences, reverse complement RNA and DNA sequences, and probe sequences for the 12 osteoarthritis miRNAs listed in Table 5 with a fold change > 2.0 are provided in Tables 6 to 9, respectively.

Table 6. Mature miRNA sequences of miRNAs with fold change > 2 listed in Table 5

miRNA	Sequence	SEQ ID NO:
mmu-miR-6931-5p	UGGGGUGGGGAGUGGGGGACU	1
mmu-miR-466i-5p	UGUGUGUGUGUGUGUGUGUG	5
mmu-miR-574-5p	UGAGUGUGUGUGUGAGUGUGU	4
mmu-miR-3082-5p	GACAGAGUGUGUGUCUGUGU	3
mmu-miR-1187	UAUGUGUGUGUAUGUGUGUAA	2
mmu-miR-669n	AUUUGUGUGGGAUGUGUGU	6
mmu-miR-468-3p	UAUGACUGAUGUGCGUGUGUCUG	7
mmu-miR-669l-5p	AGUUGUGUGUGCAUGUAUAUGU	9
mmu-miR-32-3p	CAAUUAGUGUGUGAUUU	8
mmu-miR-466m-5p	UGUGUGCAUGUGCAUGUGUAU	10
mmu-miR-669e-5p	UGUCUUGUGUGCAUGUUCAU	11
mmu-miR-672-5p	UGAGGUUGGUGUACUGUGUGUGA	12
hsa-miR-574-5p	UGAGUGUGUGUGAGUGUGU	140
hsa-miR-32-3p	CAAUUAGUGUGUGAUUU	141

Table 7. Stem-loop sequences of miRNAs with fold change > 2 listed in Table 5

miRNA	Stem-loop sequence	SEQ ID NO:
mmu-miR-6931	GUCACUGGGGUGGGGAGUGGGGGACUUCUGAAUCACUAGAGGC UCUGGAAUGACCCAACCUCUUCAUACCCAG	142
mmu-miR-466i	AGAGAUCAUGUCAGUGAACUGCCACAUUUUUGAUUAUAUUA UGUAUGUAUGUGUGUGUGUGUGUGUGUGUAUAUAUAUACA CACACACAUACACACUACAUGUAUGCAACAUUAUAC	143
mmu-miR-574	UGCGGGCGUGUGAGUGUGUGUGUGAGUGUGUGUGCGUCCA AGUCCACGCUCAUGCACACCCACACGCCCCGCACG	144
mmu-miR-3082	GGACAGAGUGUGUGUCUGUGUGGAGACAGGAGUUGCCCAC ACAUGGCACUACACUCUGCAGG	145
mmu-miR-1187	UCAUAUAGUAUUAACCGAACUGUUUCCUUAUAGACACAAU UUUUUUUACACACACACACACAUUAUAUAUAUUAUGU GUGUGUGUAUGUGUGUAAUAACAAUGUAAAAUAGUA	146
mmu-miR-669n	UACAUUUGUGUGGGAUGUGUGUGUAAUUGUAUGUGCAUCCC	147

miRNA	Stem-loop sequence	SEQ ID NO:
	ACAGCACAUGUG	
mmu-miR-468	AUAAGAAACUUGGCGUGUCGUGACUGAUGUACUGAUAAAGAAA CUCAGUGUGAUUAGACUGAUGUGCGUGUGUCUGUCU	148
mmu-miR-669l	GUUUGUGCAUGUGCGUAUAGUUGUGUGUGCAUGUAUUAUGUGU GUAUAUGAAUAUACAUAUACAUAACACACCCAUUAUUAACACGC AUUCAUAUGAACAC	149
mmu-miR-32	GGAGAUUAUUGCACAUAUACUAAGUUGCAUGUUGUCACGGCCUC AAUGCAAUUUAGUGUGUGUGAUUUUUU	150
mmu-miR-466m	UGUGUGUGUUCUUGUGUGUGCAUGUGCAUGUGUGUAUAUGAA UAUACAUAUACAUAACACACAUAACACACGCACGUACACACACA	151
mmu-miR-669e	GCCUGGGAUUAUGGGGUGUACCCUAUAUAUGGGCAGGUGUG UGUCUUGUGUGUGCAUGUUCAUUUUGUGUAUAUGAAUAUGAAU AUACACACACUUAACACACUCAUGCACACACACACA	152
mmu-miR-672	GAUGGUGAUCUAGCCCUUUAGUUUUUGAGGUUGGUGUACUGUG UGUGAGUAUACAUAUUUAUCACACACAGUCACUAUCUUCGAA AGUGAGGGUGCACAUC	153
hsa-miR-574	GGGACCUGCCUGGGUGCGGGCGUGUGAGUGUGUGUGUGUGAG UGUGUGUCGCUCCGGGUCCACGCUCAUGCACACACCCACACG CCCACACUCAGG	154
hsa-miR-32	GGAGAUUAUUGCACAUAUACUAAGUUGCAUGUUGUCACGGCCUC AAUGCAAUUUAGUGUGUGUGAUUUUUU	155

Table 8. Reverse complement RNA and DNA sequences of miRNAs with fold change > 2 listed in Table 5

miRNA	SEQ ID NO:	RNA Sequence	SEQ ID NO:
		DNA Sequence	
mmu-miR-6931-5p	1	AGUCCCCCACCUCACCCCA	156
		AGTCCCCCACTCCCCACCCCA	170
mmu-miR-466i-5p	2	CACACACACACACACACACA	157
		CACACACACACACACACACA	171
mmu-miR-574-5p	3	ACACACUCACACACACACUCA	158
		ACACACTCACACACACACACTCA	172
mmu-miR-3082-5p	4	ACACAGACACACACACUCUGUC	159
		ACACAGACACACACACTCTGTC	173
mmu-miR-1187	5	UUACACACAUAACACACACACUA	160
		TTACACACATACACACACACATA	174
mmu-miR-669n	6	ACACACAUCCACACACAAAU	161
		ACACACATCCACACACAAAT	175
mmu-miR-468-3p	7	CAGACACACGCACAUCAGUCAUA	162
		CAGACACACGCACATCAGTCATA	176
mmu-miR-669l-5p	8	ACAUAUACAUGCACACACAACU	163
		ACATATACATGCACACACAACU	177
mmu-miR-32-3p	9	AAUAUCACACACACUAAAUUG	164
		AATATCACACACACTAAATTG	178
mmu-miR-466m-5p	10	AUACACACAUGCACAUGCACACA	165
		ATACACACATGCACATGCACACA	179
mmu-miR-669e-5p	11	AUGAACAUUGCACACACAAGACA	166
		ATGAACATGCACACACAAGACA	180
mmu-miR-672-5p	12	UCACACACAGUACACCAACCUCA	167
		TCACACACAGTACACCAACCTCA	181
hsa-miR-574-5p	140	ACACACUCACACACACACUCA	168

miRNA	SEQ ID NO:	RNA Sequence	SEQ ID NO:
		DNA Sequence	
		ACACACTCACACACACACTCA	182
hsa-miR-32-3p	141	AAAUAUACACACACUAAAUUG	169
		AAATATCACACACACTAAATTG	183

Table 9. miRNA probe sequences of miRNAs with fold change > 2 listed in Table 5

miRNA	Probe name	Sequence	SEQ ID NO:
mmu-miR-6931-5p	A_54_P00006306	AGTCCCCCACTCC	184
mmu-miR-4661-5p	A_54_P00005053	CACACACACACACACA	185
mmu-miR-574-5p	A_54_P3154	ACACACTCACACACACAC	186
mmu-miR-3082-5p	A_54_P00004829	ACACAGACACACACA	187
mmu-miR-1187	A_54_P00004436	TTACACACATACACACAC	188
mmu-miR-669n	A_54_P2015	ACACACATCCACACACA	189
mmu-miR-468-3p	A_54_P1660	CAGACACACGCACATCA	190
mmu-miR-6691-5p	A_54_P00004591	ACATATACATGCACACAC	191
mmu-miR-32-3p	A_54_P00004821	AATATCACACACACTAAATT	192
mmu-miR-466m-5p	A_54_P00004975	ATACACACATGCACATG	193
mmu-miR-669e-5p	A_54_P00004466	ATGAACATGCACACAC	194
mmu-miR-672-5p	A_54_P2883	TCACACACAGTACACC	195

5 The miRNA microarray data were validated by qPCR of 20 miRNAs (examples are shown in Figure 5A to 5H). Of these examples, the cartilage-specific miR-140 was significantly down-regulated in DMM (Figure 5A, 5B).

10 Fifty dysregulated miRNAs have been reported in human osteoarthritis cartilage. Of these, a group of 12 (adjusted $P < 0.05$) overlapped with this example (Figure 4B), including miR-16 family member miR-15a-5p (SEQ ID NO: 133, Figure 5C), miR-16-5p, miR-26b-5p (SEQ ID NO: 43, Figure 5D), miR-30c-5p (SEQ ID NO: 119, Figure 5E), miR-98-5p (SEQ ID NO: 114, Figure 5F), miR-149-5p (SEQ ID NO: 86, Figure 5G), miR-210-3p (SEQ ID NO: 42, Figure 5H), miR-107-3p (SEQ ID NO: 135), miR-185-5p (SEQ ID NO: 128), miR-223-3p (SEQ ID NO: 138), miR-337-3p (SEQ ID NO: 93), miR-342-3p (SEQ ID NO: 134), and miR-377-3p (SEQ ID NO: 50). However, as noted above, previous studies using end-stage osteoarthritis samples are not necessarily related to initiation and early progression of osteoarthritis. This group of 12 osteoarthritis miRNAs is different from the group of 12 osteoarthritis miRNAs with >2 fold change identified in Table 5.

Conclusions. Typical osteoarthritis pathological features were demonstrated in the articular cartilage of DMM-operated mice compared with sham-operated mice, some of which were time dependent (proteoglycan loss and structural damage). Microarray data revealed dynamic changes in miRNA expression profiles between normal (sham-operated) and osteoarthritis cartilage (DMM). Interestingly, changes in miRNA expression that mirrored the temporal changes in proteoglycan loss and structural damage were observed. Similarly, changes in miRNA expression were also demonstrated that were independent of time, reflecting the chondrocyte hypertrophy scores that were also static. In conclusion, miRNA regulators of osteoarthritis initiation and progression in articular cartilage that have not been previously associated with osteoarthritis have been identified. Future studies are now focused on determining their role in osteoarthritis disease progression and identifying miRNA gene targets.

Example 2. miRNA microarray expression profiling during onset and progression of post-traumatic osteoarthritis (wild-type and *Adamts5* Δ cat mice)

ADAMTS5 as the major aggrecanase in arthritic mouse cartilage, which was demonstrated by producing genetically modified mice where the ADAMTS5 catalytic domain was deleted and the enzyme was thus proteolytically inactive. In the *Adamts5* Δ cat mice, ablation of ADAMTS5 activity is sufficient to protect against aggrecan loss and subsequent cartilage erosion in arthritis. *Adamts5* Δ cat mice are used to discriminate between miRNA expression changes that occur upstream and downstream of aggrecan degradation.

Differentially expressed miRNAs in both wild-type and *Adamts5* Δ cat mice represent early osteoarthritis disease processes independent of ADAMTS5 activity and aggrecan breakdown. In contrast, miRNAs identified only in wild-type mice are likely to be involved with progressive cartilage degeneration and be relevant to targets in established human disease where cartilage degeneration has occurred by the time of clinical determination.

Consequently, the following examples 2 and 3 will confirm the findings of example 1, i.e. that miR-6931-5p, miR-466i-5p, miR-574-5p, miR-3082-5p, miR-1187, miR-669n, miR-468-3p, miR-669l-5p,

miR-32-3p, miR-466m-5p, miR-669e-5p, and miR-672-5p are osteoarthritis miRNAs, and will distinguish early from later osteoarthritis miRNAs. In this way, early and later therapies may be targeted to a subject depending on the stage of disease at diagnosis.

2.1 Induction of arthritis and dissection of joint tissues.

Skeletally mature (10 week old) male C57BL6 mice and *Adamts5* Δ cat mice undergo surgical DMM or sham operation of the right knee. In sham operations, the meniscotibial ligament is exposed but not cut. Animals are sacrificed at 1, 2 and 6 weeks post-surgery (n=4 per time-point) representing early to progressive cartilage degeneration.

Immediately after euthanasia, the synovial tissues (joint capsule + synovial membrane + infra-patellar fat pad) are dissected free of muscle and the remainder of the joint, placed in RNALater (Ambion) and stored at -80°C for later RNA extraction. Exposed tibial epiphyses are isolated, placed in RNALater containing 20% EDTA, decalcified for 72 hours and embedded in OCT. Serial 7 μ m coronal cryo-sections (30-45 per joint) are fixed in ethanol, air-dried and non-calcified medial tibial plateau articular cartilage and underlying subchondral bone from previously assigned areas of cartilage fibrillation and loss of toluidine blue staining are harvested separately by laser microdissection (Arcturus).

2.2 miRNA isolation and differential expression. Total RNA is

isolated from pooled microdissected sections of cartilage and bone pooled from each DMM or sham-operated knee, e.g. using the miRCURY RNA isolation kit (Exiqon), to obtain 7-10 ng total RNA from microdissected tibial cartilage of a single mouse joint. To avoid amplification steps that would be necessary for microarray-based approaches, PCR detection methods that can quantify miRNA from these low levels of total RNA without amplification are employed. cDNA is generated, e.g. using the miRCURY LNA Universal RT miRNA system (Exiqon). Quantitative PCR (qPCR) using pre-validated miRNA primers to the 748 mouse miRNAs (miRBase vl 9) is performed, e.g. using a Roche LightCycler 480.

Greater than 5 μ g RNA is obtained from synovial tissue samples, so miRNA microarray approach such as miRCURY LNA array

(Exiqon) is used. DMM and sham-operated tissue samples from different time-points are analysed, e.g. at 1 and 6 weeks. These samples will identify the crucial miRNAs at early and later stages, and these differentially expressed miRNAs are measured by targeted

5 PCR (Exiqon miRCURY LNA Universal RT PCR panels with custom LNA miRNA selection) in the wild-type and *Adamts5* Δ cat at all time-points, e.g. 1, 2 and 6 weeks. This provides complete coverage of the post-traumatic osteoarthritis-related miRNAs since all these will be identified in the wild-type samples, with the *Adamts5* Δ cat

10 mouse data providing the refining data by identifying those that are dependent or independent of ADAMTS5 activity. Significant differences in expression levels of miRNAs between DMM and Sham-operated mouse samples from microarray data is performed using the statistical program R, using the package "limma", which utilises

15 linear models to identify differentially expressed miRNA. The data is background corrected (normexp) and normalised (quantile) within limma. miRNA qPCR data is analysed using the using the GenEx qPCR analysis software package (Exiqon).

2.3 In situ hybridisation. Differentially expressed miRNA is

20 validated and localised to cartilage versus other joint tissues (meniscus, joint capsule, bone) and specific chondrocyte populations (superficial versus deep; lesion versus surrounding cartilage) by *in situ* hybridisation. DMM and sham operated joints are fixed in 4% paraformaldehyde, decalcified in 10% EDTA and paraffin-embedded.

25 Hybridisation is performed using validated miRNA LNA probes (Exiqon).

Example 3. Confirmation of the role of osteoarthritis miRNAs on osteoarthritis initiation and progression in vivo

3.1 Generation of osteoarthritis miRNA cartilage-specific

30 **knockout mice by CRISPR/Cas9 genome editing.** CRISPR/Cas9 genome editing technology is used to generate conditional floxed miRNAs of osteoarthritis miRNAs. The CRISPR system has been used to generate miRNA knockouts *in vivo*, including silencing miRNAs (miR-126a and miRNA gene cluster miR-17a-2 to miR-92a-2) in zebrafish, and

35 deletion of the maternally expressed lncRNA gene, Rian in mice. Because the osteoarthritis miRNAs may also have roles in early cartilage development and in other developmental processes, an

inducible cartilage-specific system is used to allow normal development and cartilage maturation before inducing miRNA knockdown prior to and during post-traumatic osteoarthritis initiation (DMM surgery).

5 The floxed miRNA mice are crossed with Col2a1-Cre-ERT mice (JAX #006774) to generate mice (Col2a1-Cre-ERT:miRfl/fl) where cartilage specific knockout can be induced in mature mice by tamoxifen injection.

10 **3.2 Confirmation of the resultant miRNA knockdown in articular cartilage.** To confirm cartilage-specific knockdown, male Col2a1-Cre-ERT:miRfl/fl mice are injected daily with tamoxifen (intraperitoneal injection, 50mg/kg) at 8-10 weeks of age and after 7-10 days, knee joints are harvested. Frozen sections are used to assess localised Cre-recombinase activity. Fixed, decalcified and
15 paraffin embedded joints are used for *in situ* hybridisation using validated miRNA LNA probes (Exiqon). Osteoarthritis miRNA knockdown is confirmed by cartilage microdissection, RNA extraction, and miRNA expression assessed by qPCR (Qiagen miScript RT qPCR Kit) in
20 tamoxifen-injected and control mice.

20 Histopathology is used to determine if the induction of osteoarthritis miRNA knockdown in mature cartilage brings about pathology in unchallenged joints at 4, 8 and 16 weeks post miRNA knockdown (n=16/group). Differences in histopathological scoring of OA pathology in mouse knee joints of 20-40% (depending on tissue and
25 parameter) can be detected with >85% power with n=16 per group.

30 **3.3 Effect of candidate miRNA knockdown on OA initiation and progression.** Articular cartilage osteoarthritis miRNA knockdown is induced in skeletally mature male Col2a1-Cre-ERT:miRfl/fl mice at 8-10 weeks of age by daily tamoxifen injection. Ten days later, DMM surgery is performed to induce post-traumatic osteoarthritis. For
35 these experiments, both sham and naïve controls are used.

 In parallel experiments, to determine the role of the osteoarthritis miRNAs in osteoarthritis progression, miRNA knockdown is induced with tamoxifen at 1 week and 4 weeks post DMM surgery.
35 Male Col2a1-Cre-ERT:miRfl/fl mice and control mice are harvested at 4, 8 and 16 weeks post DMM surgery (n=16/group; power calculation as above) representing early, progressive, and late osteoarthritis.

Sections of the knee joints are stained with toluidine blue to visualise proteoglycans and the structural integrity of the cartilage. Stained sections are scored in a blind fashion using a semi-quantitative scoring system that assesses chondrocyte hypertrophy, proteoglycan loss, and structural damage in the tibial articular cartilage of the medial femoro-tibial joints.

Example 4. Modulating cartilage osteoarthritis miRNAs for therapy.

Example 3 is confirmed *in vivo* using intra-articular viral delivery to modulate miRNA expression. This approach has been used in pre-clinical models including the mouse to overexpress or knock down miRNA, and is clinically applicable. A variety of vectors have been used, but adeno-associated-virus (AAV) provides optimal transfection of chondrocytes with prolonged expression after a single injection and limited inflammatory response in infected cells. Intra-articular viral injection minimises systemic exposure and off-target effects on other tissues.

4.1 Administration of an AAV expressing a miRNA antagonist or miRNA mimic to DMM-operated mice. Osteoarthritis miRNAs are targeted by intra-articular injection of an AAV expressing a miRNA antagonist (for knockdown) or miRNA mimic (for over-expression). Osteoarthritis miRNA sequences are cloned into AAV expression vectors with a mCherry reporter (Vector BioLabs) to allow simultaneous verification of miRNA expression and transfection efficiency via fluorescent microscopy. A single intra-articular injection of 10^{11} vg/joint is administered immediately (preventative) or 4 weeks (therapeutic) after DMM surgery.

4.2 Confirmation of the osteoarthritis miRNA knockdown or overexpression. To determine successful knockdown or overexpression of the osteoarthritis miRNA at 4, 8 and 16 weeks post-DMM surgery, knee joints are dissected to collect tibial plateau articular cartilage and epiphyseal subchondral bone and RNA extracted as described above. Approximately ~250-500µg total RNA is obtained from subchondral bone and articular cartilage of each joint. Osteoarthritis miRNAs are measured by RT qPCR (Qiagen miScript RT qPCR Kit). As controls, RNA is isolated from tissues (e.g. liver, muscle, kidneys) that have not been directly injected with AAV. In

situ hybridisation is also performed on sections of the knee joints to visualise the location of the osteoarthritis miRNA within the joint (meniscus, joint capsule, bone) and specific chondrocyte populations (superficial, middle, deep zones) where AAV induced miRNA expression occurs.

4.3 Effect of miRNA therapy on osteoarthritis initiation and progression. Knee joints are examined histologically at 4, 8 and 16 weeks after DMM surgery and AAV injection (n=16). DMM-operated animals injected with empty AAV are used as controls (n=16). The knee joints are fixed, decalcified, processed, sectioned and chondrocyte hypertrophy, proteoglycan loss, cartilage structural damage, subchondral bone sclerosis and synovitis scored as described above (Example 3.3).

Example 5. Paired miRNA:mRNA expression data analysis reveals target mRNAs

As described previously (Bateman *et al.* *Arthritis and Rheumatism* 2013;65(6):1547-60), mRNA expression profiling was performed in cartilage from wild-type (mice and *Adamts5* Δ cat mice, each with surgically induced osteoarthritis. In *Adamts5* Δ cat mice, ADAMTS5 activity is lacking and aggrecan loss and cartilage erosion are inhibited, which distinguishes mRNA expression changes that are independent of ADAMTS5 activity and cartilage breakdown. Mechanical instability was introduced into the knee joints of 10 week old male mice via DMM surgery. Cartilage from the developing lesion in the destabilized medial meniscus and corresponding regions in sham-operated mice was harvested by microdissection at 1, 2, and 6 weeks post-surgery, and RNA was extracted, amplified, and hybridized to whole-genome microarrays.

The mRNA expression data from 1 week and 6 weeks DMM vs sham-operated mice and corresponding miRNA expression data from example 1 were analysed using the microRNA Target Filter module within Ingenuity Pathway Analysis to identify target mRNAs and biological effects of dysregulated osteoarthritis miRNAs. By combining in vivo expression data of miRNAs and mRNAs using a paired analysis, target mRNAs have been identified (Tables 10 and 11). Target mRNAs and their biological pathways provide additional therapeutic options for preventing and/or treating osteoarthritis, by inhibiting or

promoting transcription (e.g. via miRNAs), and/or by inhibiting or promoting translation, and/or by inhibiting or activating proteins encoded by the target mRNAs.

5

Table 10. Osteoarthritis miRNAs in articular cartilage and target mRNAs differentially expressed at 1 week post-surgery in DMM versus sham mice with dysregulated expression.

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	AARSD1	ENSMUSG00000075528	2.924
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	ABL2	ENSMUSG00000026596	2.158
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	ARL6IP6	ENSMUSG00000026960	3.519
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	ATP2A2	ENSMUSG00000029467	3.343
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	CACFD1	ENSMUSG00000015488	2.201
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	CALU	ENSMUSG00000029767	3.067
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	CDV3	ENSMUSG00000032803	2.604
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	CHD9	ENSMUSG00000056608	2.565
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	CHSY3	ENSMUSG00000058152	6.220
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	DCN	ENSMUSG00000019929	3.130
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	DPH3	ENSMUSG00000021905	2.462
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	FAM118A	ENSMUSG00000022434	2.135
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	GALNT1	ENSMUSG00000000420	3.568
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	GAREM	ENSMUSG00000042680	2.160
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	GJB4	ENSMUSG00000046623	3.956
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	HBEGF	ENSMUSG00000024486	4.754
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	HK2	ENSMUSG00000000628	2.493

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	HMG1	ENSMUSG00000078249	4.019
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	Hmga2	ENSMUSG00000056758	4.405
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	HS2ST1	ENSMUSG00000040151	2.657
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	IFRD1	ENSMUSG00000001627	2.145
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	LAMP2	ENSMUSG00000016534	2.003
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	LDLRAD4	ENSMUSG00000024544	2.708
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	LOXL3	ENSMUSG00000000693	2.601
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	MAP3K2	ENSMUSG00000024383	2.315
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	MAP4K3	ENSMUSG00000024242	2.447
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	MFAP3L	ENSMUSG000000031647	2.764
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	MTPN	ENSMUSG00000029840	2.850
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	NGF	ENSMUSG00000027859	4.807
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	NXT2	ENSMUSG00000042271	2.525
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	OPA3	ENSMUSG000000052214	2.066
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	OSMR	ENSMUSG00000022146	2.289
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	PTGS2	ENSMUSG000000032487	19.160
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	RAB11FIP4	ENSMUSG000000017639	2.585
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	RGPD4 (includes others)	ENSMUSG000000003226	2.528
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	RGS16	ENSMUSG00000026475	4.031
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	SLC1A4	ENSMUSG000000020142	2.449
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	SLC30A4	ENSMUSG000000005802	2.768

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	SLC4A7	ENSMUSG00000021733	2.774
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	SPRYD7	ENSMUSG00000021930	2.326
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	STARD3NL	ENSMUSG00000003062	2.225
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	SUCLG2	ENSMUSG000000061838	3.114
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	SULF1	ENSMUSG000000016918	2.979
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	SYPL1	ENSMUSG000000020570	2.880
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	TRIB1	ENSMUSG000000032501	2.711
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	WDR37	ENSMUSG000000021147	4.184
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	YOD1	ENSMUSG000000046404	2.776
mmu-miR-98-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.494	ZNF275	ENSMUSG000000031365	2.601
mmu-miR-206-3p	miR-1-3p (and other miRNAs w/seed GGAAUGU)	0.527	ARHGEF18	ENSMUSG000000004568	-3.167
mmu-miR-206-3p	miR-1-3p (and other miRNAs w/seed GGAAUGU)	0.527	EIF4E	ENSMUSG000000028156	-3.143
mmu-miR-206-3p	miR-1-3p (and other miRNAs w/seed GGAAUGU)	0.527	EMILIN3	ENSMUSG000000050700	-2.944
mmu-miR-206-3p	miR-1-3p (and other miRNAs w/seed GGAAUGU)	0.527	HS3ST3B1	ENSMUSG000000070407	-4.356
mmu-miR-206-3p	miR-1-3p (and other miRNAs w/seed GGAAUGU)	0.527	MAP2	ENSMUSG000000015222	-2.560
mmu-miR-206-3p	miR-1-3p (and other miRNAs w/seed GGAAUGU)	0.527	OSBPL7	ENSMUSG000000038534	-2.560
mmu-miR-206-3p	miR-1-3p (and other miRNAs w/seed GGAAUGU)	0.527	SGIP1	ENSMUSG000000028524	-3.034
mmu-miR-206-3p	miR-1-3p (and other miRNAs w/seed GGAAUGU)	0.527	SNAI2	ENSMUSG000000022676	-2.118
mmu-miR-206-3p	miR-1-3p (and other miRNAs w/seed GGAAUGU)	0.527	TRANK1	ENSMUSG000000062296	-2.219
mmu-miR-99a-5p	miR-100-5p (and other miRNAs w/seed ACCCGUA)	-0.331	GPRC5B	ENSMUSG000000008734	3.220
mmu-miR-99a-5p	miR-100-5p (and other miRNAs w/seed ACCCGUA)	-0.331	SLC44A1	ENSMUSG000000028412	2.782

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-99a-5p	miR-100-5p (and other miRNAs w/seed ACCCGUA)	-0.331	TRIB1	ENSMUSG00000032501	2.711
mmu-miR-1224-5p	miR-1224-5p (and other miRNAs w/seed UGAGGAC)	0.518	COL6A2	ENSMUSG00000056174	-5.252
mmu-miR-1224-5p	miR-1224-5p (and other miRNAs w/seed UGAGGAC)	0.518	GOLGA3	ENSMUSG00000029502	-4.640
mmu-miR-1224-5p	miR-1224-5p (and other miRNAs w/seed UGAGGAC)	0.518	GSTM5	ENSMUSG00000058135	-2.732
mmu-miR-1224-5p	miR-1224-5p (and other miRNAs w/seed UGAGGAC)	0.518	IL18BP	ENSMUSG00000070427	-2.178
mmu-miR-1224-5p	miR-1224-5p (and other miRNAs w/seed UGAGGAC)	0.518	MAOB	ENSMUSG00000040147	-3.568
mmu-miR-1224-5p	miR-1224-5p (and other miRNAs w/seed UGAGGAC)	0.518	MAP2K6	ENSMUSG00000020623	-2.579
mmu-miR-1224-5p	miR-1224-5p (and other miRNAs w/seed UGAGGAC)	0.518	NCAM1	ENSMUSG00000039542	-3.709
mmu-miR-1224-5p	miR-1224-5p (and other miRNAs w/seed UGAGGAC)	0.518	PRRX1	ENSMUSG00000026586	-2.910
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	ABL2	ENSMUSG00000026596	2.158
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	ANGPT2	ENSMUSG00000031465	4.675
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	C5orf15	ENSMUSG00000036275	2.167
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	CEM1P	ENSMUSG00000052353	3.630
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	CISD2	ENSMUSG00000028165	3.029
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	CSRNP1	ENSMUSG00000032515	2.565
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	DDAH1	ENSMUSG00000028194	2.848
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	DHX32	ENSMUSG00000030986	4.003
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	DTNA	ENSMUSG00000024302	5.102
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	EFR3A	ENSMUSG00000015002	2.341

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
	w/seed CACAGUG)				
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	EIF5	ENSMUSG00000021282	2.056
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	ENPEP	ENSMUSG00000028024	4.231
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	EPB41L1	ENSMUSG00000027624	3.202
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	ERLEC1	ENSMUSG00000020311	2.088
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	F3	ENSMUSG00000028128	5.234
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	FELN2	ENSMUSG00000064080	3.145
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	GALNT7	ENSMUSG00000031608	3.832
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	GAREM	ENSMUSG00000042680	2.160
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	GCC2	ENSMUSG00000038039	2.542
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	GCNT2	ENSMUSG00000021360	2.186
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	GIGYF2	ENSMUSG00000048000	2.588
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	GNA13	ENSMUSG00000020611	2.657
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	GPD2	ENSMUSG00000026827	2.365
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	GPX8	ENSMUSG00000021760	2.208
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	GSPT1	ENSMUSG00000062203	2.621
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	HAPLN1	ENSMUSG00000021613	4.727
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	HBEGF	ENSMUSG00000024486	4.754
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	HEATR5A	ENSMUSG00000035181	2.129
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	IL13RA1	ENSMUSG00000017057	4.260
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	KLF3	ENSMUSG00000029178	2.514
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	KPNA3	ENSMUSG00000021929	2.132

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
	w/seed CACAGUG)				
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	LAPTM4B	ENSMUSG00000022257	2.242
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	LIN7C	ENSMUSG00000027162	2.691
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	LUM	ENSMUSG00000036446	4.857
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	M1AP	ENSMUSG00000030041	2.817
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	MAP3K2	ENSMUSG00000024383	2.315
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	MRPL42	ENSMUSG00000062981	2.786
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	NCS1	ENSMUSG00000062661	2.286
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	NETO1	ENSMUSG00000050321	2.208
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	NHS	ENSMUSG00000059493	3.326
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	NXT2	ENSMUSG00000042271	2.525
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	PAIP2	ENSMUSG00000037058	2.059
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	PCNX	ENSMUSG00000021140	2.398
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	PDS5B	ENSMUSG00000034021	2.152
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	PITHD1	ENSMUSG00000028669	2.493
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	PLPP3	ENSMUSG00000028517	2.892
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	PNO1	ENSMUSG00000020116	2.497
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	RARB	ENSMUSG00000017491	4.056
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	RGPD4 (includes others)	ENSMUSG00000003226	2.528
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	RPF1	ENSMUSG00000028187	3.758
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	RUNX1	ENSMUSG00000022952	2.410
mmu-miR-128-3p	miR-128-3p (and	-0.376	SLC5A3	ENSMUSG000000089774	4.078

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
	other miRNAs w/seed CACAGUG)				
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	SMURF2	ENSMUSG00000018363	2.852
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	SOC55	ENSMUSG00000037104	2.471
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	SP4	ENSMUSG00000025323	2.296
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	SPRY2	ENSMUSG00000022114	3.254
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	STK38L	ENSMUSG00000001630	4.290
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	TAPT1	ENSMUSG00000046985	2.318
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	TMX1	ENSMUSG00000021072	2.916
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	TSPAN6	ENSMUSG00000067377	4.053
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	TUSC3	ENSMUSG00000039530	4.411
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	UBE2K	ENSMUSG00000029203	2.362
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	VPS4B	ENSMUSG00000009907	2.110
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	ZFP36L1	ENSMUSG00000021127	3.521
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.376	ZZZ3	ENSMUSG00000039068	3.706
mmu-miR-1306-3p	miR-1306-3p (miRNAs w/seed CGUUGGC)	0.505	MCERP1	ENSMUSG00000013974	-2.619
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUAU)	-0.389	ACTC1	ENSMUSG00000068614	2.373
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUAU)	-0.389	CD28	ENSMUSG00000026012	2.657
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUAU)	-0.389	CYP51A1	ENSMUSG00000001467	3.378
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUAU)	-0.389	DSTN	ENSMUSG00000015932	3.550
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUAU)	-0.389	FN1	ENSMUSG00000026193	9.107
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUAU)	-0.389	GCNT2	ENSMUSG00000021360	2.186
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUAU)	-0.389	MID2	ENSMUSG00000000266	2.346

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
	CUCCAUU)				
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUU)	-0.389	MINOS1-NBL1/NBL1	ENSMUSG00000041120	3.543
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUU)	-0.389	MLLT11	ENSMUSG00000053192	2.755
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUU)	-0.389	MSH3	ENSMUSG00000014850	2.236
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUU)	-0.389	MTPN	ENSMUSG00000029840	2.850
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUU)	-0.389	PGM3	ENSMUSG00000056131	3.036
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUU)	-0.389	RADIL	ENSMUSG00000029576	2.043
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUU)	-0.389	SMOC2	ENSMUSG00000023886	4.155
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUU)	-0.389	SNAPC1	ENSMUSG00000021113	2.464
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUU)	-0.389	STXBP3	ENSMUSG00000027882	2.034
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUU)	-0.389	SUCLG2	ENSMUSG00000061838	3.114
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUU)	-0.389	TIMM17A	ENSMUSG00000062580	2.530
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUU)	-0.389	TRAPPC6B	ENSMUSG00000020993	2.544
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUU)	-0.389	TRIB1	ENSMUSG00000032501	2.711
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUU)	-0.389	TSPAN3	ENSMUSG00000032324	3.800
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUU)	-0.389	TWSG1	ENSMUSG00000024098	3.740
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUU)	-0.389	UBE2D3	ENSMUSG00000078578	2.581
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUU)	-0.389	UBE3D	ENSMUSG00000032415	2.160
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUU)	-0.389	ZCCHC14	ENSMUSG00000061410	2.791
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	ABL2	ENSMUSG00000026596	2.158
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	ACVR1	ENSMUSG00000026836	2.661

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	AMOTL2	ENSMUSG00000032531	3.583
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	ANGEL2	ENSMUSG00000026634	2.092
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	ANGPT2	ENSMUSG00000031465	4.675
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	ATP2A2	ENSMUSG00000029467	3.343
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	CAV2	ENSMUSG00000000058	3.050
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	CDK8	ENSMUSG00000029635	2.761
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	CHD9	ENSMUSG00000056608	2.565
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	CHMP3	ENSMUSG00000053119	2.505
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	COL10A1	ENSMUSG00000039462	9.680
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	COL6A3	ENSMUSG00000048126	5.728
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	DDAH1	ENSMUSG00000028194	2.848
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	EMP1	ENSMUSG00000030208	5.836
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	EPB41L1	ENSMUSG00000027624	3.202
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	EPN2	ENSMUSG00000001036	2.745
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	ERRFI1	ENSMUSG00000028967	6.000
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	ETS1	ENSMUSG00000032035	2.457

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	F3	ENSMUSG00000028128	5.234
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	FEZ2	ENSMUSG00000056121	2.412
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	GPRC5B	ENSMUSG00000008734	3.220
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	HSPA4L	ENSMUSG00000025757	4.350
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	LAMP2	ENSMUSG00000016534	2.003
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	MAP2K1	ENSMUSG00000004936	2.373
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	MAP3K2	ENSMUSG00000024383	2.315
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	NCS1	ENSMUSG00000062661	2.286
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	NETO1	ENSMUSG00000059321	2.208
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	NHS	ENSMUSG00000059493	3.326
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	PLPP3	ENSMUSG00000028517	2.892
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	PRKG2	ENSMUSG00000029334	4.627
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	RTN4	ENSMUSG00000020458	3.229
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	SLC5A3	ENSMUSG00000089774	4.078
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	SLC7A2	ENSMUSG00000031596	4.389
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	SOC3	ENSMUSG00000053113	2.299

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	SPRYD7	ENSMUSG00000021930	2.326
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	SSR1	ENSMUSG00000021427	2.709
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	STK38L	ENSMUSG00000001630	4.290
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	STT3A	ENSMUSG00000032116	4.147
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	SULF1	ENSMUSG00000016918	2.979
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	TMCC3	ENSMUSG00000020023	7.961
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	TMEM128	ENSMUSG00000067365	2.646
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	UBE2D3	ENSMUSG00000078578	2.581
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	UBE2K	ENSMUSG00000029203	2.362
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	USP33	ENSMUSG00000025437	2.294
mmu-miR-148b-3p	miR-148a-3p (and other miRNAs w/seed CAGUGCA)	-0.385	ZBTB18	ENSMUSG00000063659	2.014
mmu-miR-149-5p	miR-149-5p (miRNAs w/seed CUGGCUC)	-0.308	AEBP1	ENSMUSG00000020473	2.866
mmu-miR-149-5p	miR-149-5p (miRNAs w/seed CUGGCUC)	-0.308	AMOTL2	ENSMUSG00000032531	3.583
mmu-miR-149-5p	miR-149-5p (miRNAs w/seed CUGGCUC)	-0.308	APPL2	ENSMUSG00000020263	2.342
mmu-miR-149-5p	miR-149-5p (miRNAs w/seed CUGGCUC)	-0.308	ATP2A2	ENSMUSG00000029467	3.343
mmu-miR-149-5p	miR-149-5p (miRNAs w/seed CUGGCUC)	-0.308	BAIAP2L1	ENSMUSG00000038859	2.511
mmu-miR-149-5p	miR-149-5p (miRNAs w/seed CUGGCUC)	-0.308	CCDC142	ENSMUSG00000079511	2.189
mmu-miR-149-5p	miR-149-5p (miRNAs w/seed CUGGCUC)	-0.308	CDK17	ENSMUSG00000020015	2.170

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
	CUGGCUC)				
mmu-miR-149-5p	miR-149-5p (miRNAs w/seed CUGGCUC)	-0.308	CNIH4	ENSMUSG00000062169	2.342
mmu-miR-149-5p	miR-149-5p (miRNAs w/seed CUGGCUC)	-0.308	DAP	ENSMUSG00000039168	2.586
mmu-miR-149-5p	miR-149-5p (miRNAs w/seed CUGGCUC)	-0.308	DDAH1	ENSMUSG00000028194	2.848
mmu-miR-149-5p	miR-149-5p (miRNAs w/seed CUGGCUC)	-0.308	DLD	ENSMUSG00000020664	2.428
mmu-miR-149-5p	miR-149-5p (miRNAs w/seed CUGGCUC)	-0.308	DLL1	ENSMUSG00000014773	5.359
mmu-miR-149-5p	miR-149-5p (miRNAs w/seed CUGGCUC)	-0.308	EIF5	ENSMUSG00000021282	2.056
mmu-miR-149-5p	miR-149-5p (miRNAs w/seed CUGGCUC)	-0.308	EPB41L1	ENSMUSG00000027624	3.202
mmu-miR-149-5p	miR-149-5p (miRNAs w/seed CUGGCUC)	-0.308	FAM118A	ENSMUSG00000022434	2.135
mmu-miR-149-5p	miR-149-5p (miRNAs w/seed CUGGCUC)	-0.308	FOSL1	ENSMUSG00000024912	4.708
mmu-miR-149-5p	miR-149-5p (miRNAs w/seed CUGGCUC)	-0.308	FOXO1	ENSMUSG00000050295	2.359
mmu-miR-149-5p	miR-149-5p (miRNAs w/seed CUGGCUC)	-0.308	GAREM	ENSMUSG00000042680	2.160
mmu-miR-149-5p	miR-149-5p (miRNAs w/seed CUGGCUC)	-0.308	IL11	ENSMUSG00000004371	22.880
mmu-miR-149-5p	miR-149-5p (miRNAs w/seed CUGGCUC)	-0.308	LMCD1	ENSMUSG00000057604	2.301
mmu-miR-149-5p	miR-149-5p (miRNAs w/seed CUGGCUC)	-0.308	LTBP2	ENSMUSG00000002020	4.793
mmu-miR-149-5p	miR-149-5p (miRNAs w/seed CUGGCUC)	-0.308	MAP3K2	ENSMUSG00000024383	2.315
mmu-miR-149-5p	miR-149-5p (miRNAs w/seed CUGGCUC)	-0.308	NPR3	ENSMUSG00000022206	7.306
mmu-miR-149-5p	miR-149-5p (miRNAs w/seed CUGGCUC)	-0.308	PLPP3	ENSMUSG00000028517	2.892
mmu-miR-149-5p	miR-149-5p (miRNAs w/seed CUGGCUC)	-0.308	PNO1	ENSMUSG00000020116	2.497
mmu-miR-149-5p	miR-149-5p (miRNAs w/seed CUGGCUC)	-0.308	RNF11	ENSMUSG00000028557	2.278
mmu-miR-149-5p	miR-149-5p (miRNAs w/seed CUGGCUC)	-0.308	RNF2	ENSMUSG00000026484	2.544
mmu-miR-149-5p	miR-149-5p (miRNAs w/seed CUGGCUC)	-0.308	SRPX2	ENSMUSG00000031253	2.795

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
	CUGGCUC)				
mmu-miR-149-5p	miR-149-5p (miRNAs w/seed CUGGCUC)	-0.308	TNFRSF12A	ENSMUSG00000023905	5.946
mmu-miR-149-5p	miR-149-5p (miRNAs w/seed CUGGCUC)	-0.308	ZNF275	ENSMUSG00000031365	2.601
mmu-miR-151-5p	miR-151-5p (and other miRNAs w/seed CGAGGAG)	-0.396	HAS1	ENSMUSG00000003665	5.063
mmu-miR-151-5p	miR-151-5p (and other miRNAs w/seed CGAGGAG)	-0.396	IQGAP1	ENSMUSG00000030536	2.850
mmu-miR-151-5p	miR-151-5p (and other miRNAs w/seed CGAGGAG)	-0.396	SUCLG2	ENSMUSG00000061838	3.114
mmu-miR-151-5p	miR-151-5p (and other miRNAs w/seed CGAGGAG)	-0.396	TXNDC12	ENSMUSG00000028567	2.474
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	ABL2	ENSMUSG00000026596	2.158
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	ABTB2	ENSMUSG00000032724	2.723
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	APOO	ENSMUSG00000079508	2.072
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	APPL2	ENSMUSG00000020263	2.342
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	ATP2A2	ENSMUSG00000029467	3.343
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	CCDC117	ENSMUSG00000020482	2.347
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	CDK8	ENSMUSG00000029635	2.761
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	CHD9	ENSMUSG00000056608	2.565
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	CHMP3	ENSMUSG00000053119	2.505
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	CYR61	ENSMUSG00000028195	6.512
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	DCN	ENSMUSG00000019929	3.130

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	DIP2C	ENSMUSG00000048264	2.975
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	DNAJA4	ENSMUSG00000032285	2.408
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	DTNA	ENSMUSG00000024302	5.102
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	ENPP1	ENSMUSG00000037370	3.224
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	EPN2	ENSMUSG00000001036	2.745
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	ETS1	ENSMUSG00000032035	2.457
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	EVI2A	ENSMUSG00000078771	3.735
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	FOS	ENSMUSG00000021250	10.091
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	GCC2	ENSMUSG00000038039	2.542
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	GCNT2	ENSMUSG00000021360	2.186
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	GHITM	ENSMUSG00000041028	3.310
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	GPD2	ENSMUSG00000026827	2.365
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	HAPLN1	ENSMUSG00000021613	4.727
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	HS2ST1	ENSMUSG00000040151	2.657
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	KANK1	ENSMUSG00000032702	3.326
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	KCTD3	ENSMUSG00000026608	2.488

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	KLF3	ENSMUSG00000029178	2.514
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	LIN7C	ENSMUSG00000027162	2.691
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	MAP2K1	ENSMUSG00000004936	2.373
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	MAP3K2	ENSMUSG00000024383	2.315
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	MBNL2	ENSMUSG00000022139	3.213
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	MEX3B	ENSMUSG00000057706	4.383
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	MFAP3L	ENSMUSG00000031647	2.764
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	MID2	ENSMUSG00000000266	2.346
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	MTPN	ENSMUSG00000029840	2.850
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	PLEKHA3	ENSMUSG00000002733	4.374
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	PLPP3	ENSMUSG00000028517	2.892
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	RNF2	ENSMUSG00000026484	2.544
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	RNF6	ENSMUSG00000029634	2.654
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	RUNX1	ENSMUSG00000022952	2.410
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	SACM1L	ENSMUSG00000025240	2.599
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	SLC38A2	ENSMUSG00000022462	3.065

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	SLC7A2	ENSMUSG00000031596	4.389
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	SOC33	ENSMUSG00000053113	2.299
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	STC2	ENSMUSG00000020303	2.504
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	TIMP3	ENSMUSG00000020044	3.853
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	TMEM33	ENSMUSG00000037720	2.711
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	TNFRSF11B	ENSMUSG00000063727	6.320
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	TNS3	ENSMUSG00000020422	2.570
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	TULP4	ENSMUSG00000034377	2.207
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	TUSC3	ENSMUSG00000039530	4.411
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	TXNDC12	ENSMUSG00000028567	2.474
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	USP33	ENSMUSG00000025437	2.294
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	VBPI	ENSMUSG00000031197	2.301
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	WDR37	ENSMUSG00000021147	4.184
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	YOD1	ENSMUSG00000046404	2.776
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	YWHAG	ENSMUSG00000051391	2.462
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	ZCCHC14	ENSMUSG00000061410	2.791

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	ZFP36L1	ENSMUSG00000021127	3.521
mmu-miR-181c-5p	miR-181a-5p (and other miRNAs w/seed ACAUUCA)	-0.450	ZZZ3	ENSMUSG00000039068	3.706
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.468	ARL4A	ENSMUSG00000047446	2.789
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.468	AVP11	ENSMUSG00000018821	2.061
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.468	CHCHD4	ENSMUSG00000034203	2.354
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.468	COX16	ENSMUSG00000091803	2.377
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.468	DCN	ENSMUSG00000019929	3.130
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.468	DPH3	ENSMUSG00000021905	2.462
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.468	FOS	ENSMUSG00000021250	10.091
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.468	HSPA4L	ENSMUSG00000025757	4.350
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.468	IDH3A	ENSMUSG00000032279	3.869
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.468	LAMP2	ENSMUSG00000016534	2.003
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.468	MAP3K2	ENSMUSG00000024383	2.315
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.468	MTMR7	ENSMUSG00000039431	4.064
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.468	PFN2	ENSMUSG00000027805	2.558
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.468	RAB11FIP4	ENSMUSG00000017639	2.585

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.468	RARB	ENSMUSG00000017491	4.056
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.468	RNF149	ENSMUSG00000048234	2.464
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.468	SEPT7	ENSMUSG00000001833	2.378
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.468	SMURF2	ENSMUSG00000018363	2.852
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.468	SPRYD7	ENSMUSG00000021930	2.326
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.468	TSPAN6	ENSMUSG00000067377	4.053
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.590	ABL2	ENSMUSG00000026596	2.158
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.590	CDV3	ENSMUSG00000032803	2.604
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.590	GSPT1	ENSMUSG00000062203	2.621
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.590	HMGAI	ENSMUSG00000078249	4.019
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.590	LAPTM4B	ENSMUSG00000022257	2.242
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.590	MAP4K3	ENSMUSG00000024242	2.447
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.590	MBNL2	ENSMUSG00000022139	3.213
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.590	NCS1	ENSMUSG00000062661	2.286
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.590	NHS	ENSMUSG00000059493	3.326
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.590	OPA3	ENSMUSG00000052214	2.066

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.590	OSMR	ENSMUSG00000022146	2.289
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.590	PTTG1IP	ENSMUSG00000009291	2.365
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.590	SARAF	ENSMUSG000000031532	2.118
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.590	SDCBP	ENSMUSG00000028249	2.245
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.590	SNX24	ENSMUSG000000024535	2.592
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.590	SSR1	ENSMUSG000000021427	2.709
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.590	TMEM33	ENSMUSG000000037720	2.711
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.590	TMX1	ENSMUSG000000021072	2.916
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.590	WDR37	ENSMUSG000000021147	4.184
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.590	YOD1	ENSMUSG000000046404	2.776
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.590	ZNF385B	ENSMUSG000000027016	5.404
mmu-let-7j	miR-202-3p (and other miRNAs w/seed GAGGUAAU)	0.550	ADAMTS14	ENSMUSG000000059901	-2.334
mmu-let-7j	miR-202-3p (and other miRNAs w/seed GAGGUAAU)	0.550	ADCY9	ENSMUSG000000005580	-2.161
mmu-let-7j	miR-202-3p (and other miRNAs w/seed GAGGUAAU)	0.550	DENND6A	ENSMUSG000000040818	-2.013
mmu-let-7j	miR-202-3p (and other miRNAs w/seed GAGGUAAU)	0.550	GHR	ENSMUSG000000055737	-2.650
mmu-let-7j	miR-202-3p (and other miRNAs w/seed GAGGUAAU)	0.550	LRRN3	ENSMUSG000000036295	-3.269
mmu-let-7j	miR-202-3p (and other miRNAs w/seed GAGGUAAU)	0.550	MGLL	ENSMUSG000000033174	-3.899
mmu-let-7j	miR-202-3p (and other miRNAs w/seed GAGGUAAU)	0.550	PIK3IP1	ENSMUSG000000034614	-3.184

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
	w/seed GAGGUAU)				
mmu-let-7j	miR-202-3p (and other miRNAs w/seed GAGGUAU)	0.550	PRRX1	ENSMUSG00000026586	-2.910
mmu-let-7j	miR-202-3p (and other miRNAs w/seed GAGGUAU)	0.550	TRANK1	ENSMUSG00000062296	-2.219
mmu-miR-210-3p	miR-210-3p (miRNAs w/seed UGUGCGU)	-0.334	PITHD1	ENSMUSG00000028669	2.493
mmu-miR-210-3p	miR-210-3p (miRNAs w/seed UGUGCGU)	-0.334	PXDC1	ENSMUSG00000021411	2.385
mmu-miR-210-3p	miR-210-3p (miRNAs w/seed UGUGCGU)	-0.334	TRIB1	ENSMUSG00000032501	2.711
mmu-miR-222-3p	miR-221-3p (and other miRNAs w/seed GCUACAU)	0.522	CAMKK1	ENSMUSG00000020785	-2.048
mmu-miR-222-3p	miR-221-3p (and other miRNAs w/seed GCUACAU)	0.522	KLHL18	ENSMUSG00000054792	-2.175
mmu-miR-222-3p	miR-221-3p (and other miRNAs w/seed GCUACAU)	0.522	NCAM1	ENSMUSG00000039542	-3.709
mmu-miR-222-3p	miR-221-3p (and other miRNAs w/seed GCUACAU)	0.522	OSBPL7	ENSMUSG00000038534	-2.560
mmu-miR-224-5p	miR-224-5p (miRNAs w/seed AAGUCAC)	-0.459	ANGPT2	ENSMUSG00000031465	4.675
mmu-miR-224-5p	miR-224-5p (miRNAs w/seed AAGUCAC)	-0.459	ATL2	ENSMUSG00000059811	2.395
mmu-miR-224-5p	miR-224-5p (miRNAs w/seed AAGUCAC)	-0.459	CCDC117	ENSMUSG00000020482	2.347
mmu-miR-224-5p	miR-224-5p (miRNAs w/seed AAGUCAC)	-0.459	COBLL1	ENSMUSG00000034903	2.479
mmu-miR-224-5p	miR-224-5p (miRNAs w/seed AAGUCAC)	-0.459	DTNA	ENSMUSG00000024302	5.102
mmu-miR-224-5p	miR-224-5p (miRNAs w/seed AAGUCAC)	-0.459	EIF2AK3	ENSMUSG00000031668	2.161
mmu-miR-224-5p	miR-224-5p (miRNAs w/seed AAGUCAC)	-0.459	EIF5	ENSMUSG00000021282	2.056
mmu-miR-224-5p	miR-224-5p (miRNAs w/seed AAGUCAC)	-0.459	FHL2	ENSMUSG00000008136	3.350
mmu-miR-224-5p	miR-224-5p (miRNAs w/seed AAGUCAC)	-0.459	GIGYF2	ENSMUSG00000048000	2.588
mmu-miR-224-5p	miR-224-5p (miRNAs w/seed AAGUCAC)	-0.459	GTF3C4	ENSMUSG00000035666	2.289
mmu-miR-224-5p	miR-224-5p (miRNAs w/seed AAGUCAC)	-0.459	IL11	ENSMUSG00000004371	22.880
mmu-miR-224-5p	miR-224-5p (miRNAs w/seed AAGUCAC)	-0.459	ITM2B	ENSMUSG00000022108	2.136

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
	AAGUCAC)				
mmu-miR-224-5p	miR-224-5p (miRNAs w/seed AAGUCAC)	-0.459	LIN7C	ENSMUSG00000027162	2.691
mmu-miR-224-5p	miR-224-5p (miRNAs w/seed AAGUCAC)	-0.459	MBNL2	ENSMUSG00000022139	3.213
mmu-miR-224-5p	miR-224-5p (miRNAs w/seed AAGUCAC)	-0.459	MRPL42	ENSMUSG000000062981	2.786
mmu-miR-224-5p	miR-224-5p (miRNAs w/seed AAGUCAC)	-0.459	NCS1	ENSMUSG000000062661	2.286
mmu-miR-224-5p	miR-224-5p (miRNAs w/seed AAGUCAC)	-0.459	NUP153	ENSMUSG000000021374	2.553
mmu-miR-224-5p	miR-224-5p (miRNAs w/seed AAGUCAC)	-0.459	PCNX	ENSMUSG000000021140	2.398
mmu-miR-224-5p	miR-224-5p (miRNAs w/seed AAGUCAC)	-0.459	PHLPP1	ENSMUSG000000044340	2.247
mmu-miR-224-5p	miR-224-5p (miRNAs w/seed AAGUCAC)	-0.459	PLPP3	ENSMUSG000000028517	2.892
mmu-miR-224-5p	miR-224-5p (miRNAs w/seed AAGUCAC)	-0.459	SLMAP	ENSMUSG000000021870	2.110
mmu-miR-224-5p	miR-224-5p (miRNAs w/seed AAGUCAC)	-0.459	TMBIM1	ENSMUSG000000006301	2.230
mmu-miR-224-5p	miR-224-5p (miRNAs w/seed AAGUCAC)	-0.459	TMEM128	ENSMUSG000000067365	2.646
mmu-miR-224-5p	miR-224-5p (miRNAs w/seed AAGUCAC)	-0.459	TMX1	ENSMUSG000000021072	2.916
mmu-miR-224-5p	miR-224-5p (miRNAs w/seed AAGUCAC)	-0.459	TNS3	ENSMUSG000000020422	2.570
mmu-miR-224-5p	miR-224-5p (miRNAs w/seed AAGUCAC)	-0.459	TULP4	ENSMUSG000000034377	2.207
mmu-miR-224-5p	miR-224-5p (miRNAs w/seed AAGUCAC)	-0.459	UBE2D3	ENSMUSG000000078578	2.581
mmu-miR-224-5p	miR-224-5p (miRNAs w/seed AAGUCAC)	-0.459	UBE2G1	ENSMUSG000000020794	2.075
mmu-miR-224-5p	miR-224-5p (miRNAs w/seed AAGUCAC)	-0.459	YOD1	ENSMUSG000000046404	2.776
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	ABL2	ENSMUSG000000026596	2.158
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	ARL6IP6	ENSMUSG000000026960	3.519
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	CDK2AP1	ENSMUSG000000078154	2.233
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	CDK8	ENSMUSG000000029635	2.761

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
	w/seed UCAAGUA)				
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	CDV3	ENSMUSG00000032803	2.604
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	COL10A1	ENSMUSG00000039462	9.680
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	EIF5	ENSMUSG00000021282	2.056
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	ENPEP	ENSMUSG00000028024	4.231
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	FAM118A	ENSMUSG00000022434	2.135
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	GALNT7	ENSMUSG00000031608	3.832
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	GNA13	ENSMUSG00000020611	2.657
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	GPX8	ENSMUSG00000021760	2.208
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	HAPLN1	ENSMUSG00000021613	4.727
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	HEATR5A	ENSMUSG00000035181	2.129
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	HMGAI	ENSMUSG00000078249	4.019
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	HS2ST1	ENSMUSG00000040151	2.657
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	KPNA3	ENSMUSG00000021929	2.132
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	MAP3K2	ENSMUSG00000024383	2.315
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	MEX3B	ENSMUSG00000057706	4.383
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	MFAP3L	ENSMUSG00000031647	2.764
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	MSH3	ENSMUSG00000014850	2.236
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	MTPN	ENSMUSG00000029840	2.850
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	MTX2	ENSMUSG00000027099	2.259
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	NETO1	ENSMUSG00000050321	2.208
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	NHS	ENSMUSG00000059493	3.326

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
	w/seed UCAAGUA)				
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	NUP153	ENSMUSG00000021374	2.553
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	PCNX	ENSMUSG00000021140	2.398
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	PTGS2	ENSMUSG00000032487	19.160
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	PTP4A1	ENSMUSG00000026064	2.910
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	RNF6	ENSMUSG00000029634	2.654
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	SAR1B	ENSMUSG00000020386	3.415
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	SGMS2	ENSMUSG00000050931	3.816
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	SH2D5	ENSMUSG00000045349	2.509
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	SLC35A3	ENSMUSG00000027957	2.114
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	SLC38A2	ENSMUSG00000022462	3.065
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	SMAD1	ENSMUSG00000031681	2.821
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	SULF1	ENSMUSG00000016918	2.979
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	TMEM33	ENSMUSG00000037720	2.711
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	UBE2G1	ENSMUSG00000020794	2.075
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	UBE2K	ENSMUSG00000029203	2.362
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	YWHAE	ENSMUSG00000020849	2.027
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	ZBTB18	ENSMUSG00000063659	2.014
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	ZNF275	ENSMUSG00000031365	2.601
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.344	ZNF385B	ENSMUSG00000027016	5.404
mmu-miR-294-3p	miR-291a-3p (and other miRNAs w/seed AAGUGCU)	0.469	ADAMTS18	ENSMUSG00000053399	-6.088

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-294-3p	miR-291a-3p (and other miRNAs w/seed AAGUGCU)	0.469	ARHGEF18	ENSMUSG00000004568	-3.167
mmu-miR-294-3p	miR-291a-3p (and other miRNAs w/seed AAGUGCU)	0.469	EIF4B	ENSMUSG000000058655	-2.339
mmu-miR-294-3p	miR-291a-3p (and other miRNAs w/seed AAGUGCU)	0.469	HABP4	ENSMUSG000000021476	-2.082
mmu-miR-294-3p	miR-291a-3p (and other miRNAs w/seed AAGUGCU)	0.469	IRF1	ENSMUSG000000018899	-2.949
mmu-miR-294-3p	miR-291a-3p (and other miRNAs w/seed AAGUGCU)	0.469	KAT2B	ENSMUSG000000000708	-3.095
mmu-miR-294-3p	miR-291a-3p (and other miRNAs w/seed AAGUGCU)	0.469	KLHL18	ENSMUSG000000054792	-2.175
mmu-miR-294-3p	miR-291a-3p (and other miRNAs w/seed AAGUGCU)	0.469	NIN	ENSMUSG000000021068	-3.385
mmu-miR-294-3p	miR-291a-3p (and other miRNAs w/seed AAGUGCU)	0.469	PRRX1	ENSMUSG000000026586	-2.910
mmu-miR-294-3p	miR-291a-3p (and other miRNAs w/seed AAGUGCU)	0.469	RASSF2	ENSMUSG000000027339	-2.930
mmu-miR-294-3p	miR-291a-3p (and other miRNAs w/seed AAGUGCU)	0.469	RELL1	ENSMUSG000000047881	-2.321
mmu-miR-294-3p	miR-291a-3p (and other miRNAs w/seed AAGUGCU)	0.469	RTN1	ENSMUSG000000021087	-2.461
mmu-miR-294-3p	miR-291a-3p (and other miRNAs w/seed AAGUGCU)	0.469	SLAIN1	ENSMUSG000000055717	-2.148
mmu-miR-294-3p	miR-291a-3p (and other miRNAs w/seed AAGUGCU)	0.469	SYDE1	ENSMUSG000000032714	-2.013
mmu-miR-294-3p	miR-291a-3p (and other miRNAs w/seed AAGUGCU)	0.469	TAOK2	ENSMUSG000000059981	-2.656
mmu-miR-294-3p	miR-291a-3p (and other miRNAs w/seed AAGUGCU)	0.469	TBC1D2	ENSMUSG000000039813	-3.413
mmu-miR-294-3p	miR-291a-3p (and other miRNAs w/seed AAGUGCU)	0.469	TSHZ2	ENSMUSG000000047907	-2.415

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-294-3p	miR-291a-3p (and other miRNAs w/seed AAGUGCU)	0.469	ZNF362	ENSMUSG00000028799	-2.430
mmu-miR-297c-5p	miR-297a-5p (and other miRNAs w/seed UGUUAUGU)	0.591	EIF4E	ENSMUSG00000028156	-3.143
mmu-miR-297c-5p	miR-297a-5p (and other miRNAs w/seed UGUUAUGU)	0.591	NDNF	ENSMUSG00000049001	-3.196
mmu-miR-297c-5p	miR-297a-5p (and other miRNAs w/seed UGUUAUGU)	0.591	SCARA3	ENSMUSG00000034463	-3.097
mmu-miR-3082-5p	miR-3082-5p (and other miRNAs w/seed ACAGAGU)	1.849	CAMKK2	ENSMUSG00000029471	-2.570
mmu-miR-3082-5p	miR-3082-5p (and other miRNAs w/seed ACAGAGU)	1.849	EIF4E	ENSMUSG00000028156	-3.143
mmu-miR-3082-5p	miR-3082-5p (and other miRNAs w/seed ACAGAGU)	1.849	KAZALD1	ENSMUSG00000025213	-2.211
mmu-miR-3082-5p	miR-3082-5p (and other miRNAs w/seed ACAGAGU)	1.849	MAP2	ENSMUSG00000015222	-2.560
mmu-miR-3082-5p	miR-3082-5p (and other miRNAs w/seed ACAGAGU)	1.849	NCAM1	ENSMUSG00000039542	-3.709
mmu-miR-3082-5p	miR-3082-5p (and other miRNAs w/seed ACAGAGU)	1.849	VIT	ENSMUSG00000024076	-3.211
mmu-miR-30e-3p	miR-30a-3p (and other miRNAs w/seed UUUCAGU)	-0.468	CYR61	ENSMUSG00000028195	6.512
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	ABCC9	ENSMUSG00000030249	2.333
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	ABL2	ENSMUSG00000026596	2.158
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	ACTC1	ENSMUSG00000068614	2.373
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	ACVR1	ENSMUSG00000026836	2.661
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	ADGRA3	ENSMUSG00000029090	2.113
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	AMOTL2	ENSMUSG00000032531	3.583
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	ARL4A	ENSMUSG00000047446	2.789

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	ARL6IP6	ENSMUSG00000026960	3.519
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	ATL2	ENSMUSG00000059811	2.395
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	ATP2A2	ENSMUSG00000029467	3.343
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	B3GALNT2	ENSMUSG00000039242	2.553
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	BMP7	ENSMUSG00000008999	4.864
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	CALU	ENSMUSG00000029767	3.067
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	CCDC117	ENSMUSG00000020482	2.347
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	CHD9	ENSMUSG00000056608	2.565
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	DDAH1	ENSMUSG00000028194	2.848
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	DDX46	ENSMUSG00000021500	2.048
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	DIP2C	ENSMUSG00000048264	2.975
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	DLD	ENSMUSG00000020664	2.428
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	DTNA	ENSMUSG00000024302	5.102
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	EFR3A	ENSMUSG00000015002	2.341
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	EIF5	ENSMUSG00000021282	2.056
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	EPN2	ENSMUSG00000001036	2.745
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	ERRFI1	ENSMUSG00000028967	6.000
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	FAM210B	ENSMUSG00000027495	3.182
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	GALNT1	ENSMUSG00000000420	3.568
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	GALNT7	ENSMUSG00000031608	3.832
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	GAREM	ENSMUSG00000042680	2.160

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	GCNT2	ENSMUSG00000021360	2.186
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	GIGYF2	ENSMUSG00000048000	2.588
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	GJA1	ENSMUSG00000050953	2.530
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	GNA13	ENSMUSG00000020611	2.657
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	GPD2	ENSMUSG00000026827	2.365
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	HTRA3	ENSMUSG00000029096	3.023
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	IFRD1	ENSMUSG00000001627	2.145
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	KCTD3	ENSMUSG00000026608	2.488
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	KPNA3	ENSMUSG00000021929	2.132
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	LIN7C	ENSMUSG00000027162	2.691
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	M1AP	ENSMUSG00000030041	2.817
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	MAP3K2	ENSMUSG00000024383	2.315
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	MBNL2	ENSMUSG00000022139	3.213
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	MEX3B	ENSMUSG00000057706	4.383
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	MFAP3L	ENSMUSG00000031647	2.764
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	MID2	ENSMUSG00000000266	2.346
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	MYO10	ENSMUSG00000022272	4.045
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	NCS1	ENSMUSG00000062661	2.286
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	NHS	ENSMUSG00000059493	3.326
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	NOV	ENSMUSG00000037362	3.787
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	NPR3	ENSMUSG00000022206	7.306

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	NT5E	ENSMUSG00000032420	14.162
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	P4HA1	ENSMUSG00000019916	3.792
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	PBRM1	ENSMUSG00000042323	2.425
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	PFN2	ENSMUSG00000027805	2.558
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	PGM3	ENSMUSG00000056131	3.036
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	PTP4A1	ENSMUSG00000026064	2.910
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	RARB	ENSMUSG00000017491	4.056
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	RGPD4 (include s others)	ENSMUSG00000003226	2.528
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	RUNX1	ENSMUSG00000022952	2.410
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	SEC61A2	ENSMUSG00000025816	2.277
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	SEPT7	ENSMUSG00000001833	2.378
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	SERINC3	ENSMUSG00000017707	3.171
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	SGMS2	ENSMUSG00000050931	3.816
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	SLC30A4	ENSMUSG00000005802	2.768
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	SLC38A2	ENSMUSG00000022462	3.065
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	SLC4A7	ENSMUSG00000021733	2.774
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	SLC5A3	ENSMUSG00000089774	4.078
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	SMAD1	ENSMUSG00000031681	2.821
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	SOCS3	ENSMUSG000000053113	2.299
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	SP4	ENSMUSG00000025323	2.296
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	SSR3	ENSMUSG00000027828	3.406

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
	w/seed GUAAACA)				
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	STK38L	ENSMUSG00000001630	4.290
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	SUCLG2	ENSMUSG000000061838	3.114
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	SYPL1	ENSMUSG000000020570	2.880
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	TIMP3	ENSMUSG000000020044	3.853
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	TM4SF1	ENSMUSG000000027800	4.155
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	TMEM59	ENSMUSG000000028618	2.514
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	TULP4	ENSMUSG000000034377	2.207
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	TUSC3	ENSMUSG000000039530	4.411
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	UAP1	ENSMUSG000000026670	2.639
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	UBE2D3	ENSMUSG000000078578	2.581
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	UBE2G1	ENSMUSG000000020794	2.075
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	UBE2K	ENSMUSG000000029203	2.362
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	WNT7B	ENSMUSG000000022382	2.166
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	YOD1	ENSMUSG000000046404	2.776
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	ZBTB18	ENSMUSG000000063659	2.014
mmu-miR-30c-5p	miR-30c-5p (and other miRNAs w/seed GUAAACA)	-0.542	ZCCHC14	ENSMUSG000000061410	2.791
mmu-miR-31-5p	miR-31-5p (and other miRNAs w/seed GGCAAGA)	0.887	CORO7/CO RO7-PAM16	ENSMUSG000000039637	-2.807
mmu-miR-31-5p	miR-31-5p (and other miRNAs w/seed GGCAAGA)	0.887	IRF1	ENSMUSG000000018899	-2.949
mmu-miR-31-5p	miR-31-5p (and other miRNAs w/seed GGCAAGA)	0.887	RAB6B	ENSMUSG000000032549	-2.856
mmu-miR-31-5p	miR-31-5p (and other miRNAs w/seed GGCAAGA)	0.887	SYDE1	ENSMUSG000000032714	-2.013
mmu-miR-31-5p	miR-31-5p (and other miRNAs w/seed GGCAAGA)	0.887	TEP1	ENSMUSG000000006281	-2.344

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
	w/seed GGCAAGA)				
mmu-miR-31-5p	miR-31-5p (and other miRNAs w/seed GGCAAGA)	0.887	TSHZ2	ENSMUSG00000047907	-2.415
mmu-miR-31-5p	miR-31-5p (and other miRNAs w/seed GGCAAGA)	0.887	ZNF362	ENSMUSG00000028799	-2.430
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.449	ABL2	ENSMUSG00000026596	2.158
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.449	ARL4A	ENSMUSG00000047446	2.789
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.449	ATP1B3	ENSMUSG00000032412	3.029
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.449	BMP7	ENSMUSG00000008999	4.864
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.449	CLTB	ENSMUSG00000047547	2.858
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.449	DTNA	ENSMUSG00000024302	5.102
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.449	KIAA0040	ENSMUSG00000090394	2.507
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.449	MTUS2	ENSMUSG00000029651	2.507
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.449	NHS	ENSMUSG00000059493	3.326
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.449	NOM1	ENSMUSG00000001569	2.025
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.449	PLEKHA3	ENSMUSG00000002733	4.374
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.449	RAB1A	ENSMUSG00000020149	2.844
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.449	SLC23A2	ENSMUSG00000027340	3.665
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.449	SLC44A1	ENSMUSG00000028412	2.782
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.449	SLC5A3	ENSMUSG00000089774	4.078
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.449	SLC7A2	ENSMUSG00000031596	4.389
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.449	SMNDC1	ENSMUSG00000025024	2.774
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.449	SP4	ENSMUSG00000025323	2.296
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.449	SSR1	ENSMUSG00000021427	2.709

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
	w/seed ACACACC)				
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.449	TGFB1	ENSMUSG00000035493	4.727
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.449	VPS4B	ENSMUSG00000009907	2.110
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.449	ZBTB18	ENSMUSG000000063659	2.014
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.449	ZZZ3	ENSMUSG00000039068	3.706
mmu-miR-331-3p	miR-331-3p (miRNAs w/seed CCCUGG)	-0.345	ABL2	ENSMUSG00000026596	2.158
mmu-miR-331-3p	miR-331-3p (miRNAs w/seed CCCUGG)	-0.345	ABTB2	ENSMUSG00000032724	2.723
mmu-miR-331-3p	miR-331-3p (miRNAs w/seed CCCUGG)	-0.345	ALOX12	ENSMUSG00000000320	2.621
mmu-miR-331-3p	miR-331-3p (miRNAs w/seed CCCUGG)	-0.345	AMOTL2	ENSMUSG00000032531	3.583
mmu-miR-331-3p	miR-331-3p (miRNAs w/seed CCCUGG)	-0.345	C14orf79	ENSMUSG00000037594	2.390
mmu-miR-331-3p	miR-331-3p (miRNAs w/seed CCCUGG)	-0.345	C1SD2	ENSMUSG000000028165	3.029
mmu-miR-331-3p	miR-331-3p (miRNAs w/seed CCCUGG)	-0.345	COL6A2	ENSMUSG00000020241	2.940
mmu-miR-331-3p	miR-331-3p (miRNAs w/seed CCCUGG)	-0.345	FAM210B	ENSMUSG00000027495	3.182
mmu-miR-331-3p	miR-331-3p (miRNAs w/seed CCCUGG)	-0.345	FXYP3	ENSMUSG00000057092	2.626
mmu-miR-331-3p	miR-331-3p (miRNAs w/seed CCCUGG)	-0.345	GJB4	ENSMUSG00000046623	3.956
mmu-miR-331-3p	miR-331-3p (miRNAs w/seed CCCUGG)	-0.345	GTF3C4	ENSMUSG00000035666	2.289
mmu-miR-331-3p	miR-331-3p (miRNAs w/seed CCCUGG)	-0.345	KANK1	ENSMUSG00000032702	3.326
mmu-miR-331-3p	miR-331-3p (miRNAs w/seed CCCUGG)	-0.345	NCS1	ENSMUSG00000062661	2.286
mmu-miR-331-3p	miR-331-3p (miRNAs w/seed CCCUGG)	-0.345	NFATC1	ENSMUSG00000033016	2.608
mmu-miR-331-3p	miR-331-3p (miRNAs w/seed CCCUGG)	-0.345	OPA3	ENSMUSG00000052214	2.066
mmu-miR-331-3p	miR-331-3p (miRNAs w/seed CCCUGG)	-0.345	PHLPP1	ENSMUSG00000044340	2.247
mmu-miR-331-3p	miR-331-3p (miRNAs w/seed CCCUGG)	-0.345	PITHD1	ENSMUSG00000028669	2.493

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
	CCCCUGG)				
mmu-miR-331-3p	miR-331-3p (miRNAs w/seed CCCCUGG)	-0.345	PITPNA	ENSMUSG00000017781	2.698
mmu-miR-331-3p	miR-331-3p (miRNAs w/seed CCCCUGG)	-0.345	PTGES	ENSMUSG00000050737	3.313
mmu-miR-331-3p	miR-331-3p (miRNAs w/seed CCCCUGG)	-0.345	RAB11FIP4	ENSMUSG00000017639	2.585
mmu-miR-331-3p	miR-331-3p (miRNAs w/seed CCCCUGG)	-0.345	RUNX1	ENSMUSG00000022952	2.410
mmu-miR-331-3p	miR-331-3p (miRNAs w/seed CCCCUGG)	-0.345	SERINC2	ENSMUSG00000023232	2.981
mmu-miR-331-3p	miR-331-3p (miRNAs w/seed CCCCUGG)	-0.345	SLC1A4	ENSMUSG00000020142	2.449
mmu-miR-331-3p	miR-331-3p (miRNAs w/seed CCCCUGG)	-0.345	SLC23A2	ENSMUSG00000027340	3.665
mmu-miR-331-3p	miR-331-3p (miRNAs w/seed CCCCUGG)	-0.345	SOC3	ENSMUSG00000053113	2.299
mmu-miR-331-3p	miR-331-3p (miRNAs w/seed CCCCUGG)	-0.345	SSR3	ENSMUSG00000027828	3.406
mmu-miR-331-3p	miR-331-3p (miRNAs w/seed CCCCUGG)	-0.345	TADA2A	ENSMUSG00000018651	2.216
mmu-miR-331-3p	miR-331-3p (miRNAs w/seed CCCCUGG)	-0.345	TMCC3	ENSMUSG00000020023	7.961
mmu-miR-331-3p	miR-331-3p (miRNAs w/seed CCCCUGG)	-0.345	TNFRSF12A	ENSMUSG00000023905	5.946
mmu-miR-331-3p	miR-331-3p (miRNAs w/seed CCCCUGG)	-0.345	YOD1	ENSMUSG00000046404	2.776
mmu-miR-346-5p	miR-346 (and other miRNAs w/seed GUCUGCC)	0.399	CA7	ENSMUSG00000031883	-2.110
mmu-miR-346-5p	miR-346 (and other miRNAs w/seed GUCUGCC)	0.399	CERCAM	ENSMUSG00000039787	-2.485
mmu-miR-346-5p	miR-346 (and other miRNAs w/seed GUCUGCC)	0.399	GSTM5	ENSMUSG00000058135	-2.732
mmu-miR-346-5p	miR-346 (and other miRNAs w/seed GUCUGCC)	0.399	IQCE	ENSMUSG00000036555	-2.512
mmu-miR-346-5p	miR-346 (and other miRNAs w/seed GUCUGCC)	0.399	KLF15	ENSMUSG00000030087	-3.260
mmu-miR-346-5p	miR-346 (and other miRNAs w/seed GUCUGCC)	0.399	KLHL18	ENSMUSG00000054792	-2.175
mmu-miR-346-5p	miR-346 (and other miRNAs w/seed GUCUGCC)	0.399	LIMCH1	ENSMUSG00000037736	-2.628
mmu-miR-346-5p	miR-346 (and other miRNAs w/seed GUCUGCC)	0.399	NIN	ENSMUSG00000021068	-3.385

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
	w/seed GUCUGCC)				
mmu-miR-346-5p	miR-346 (and other miRNAs w/seed GUCUGCC)	0.399	PIK3IP1	ENSMUSG00000034614	-3.184
mmu-miR-346-5p	miR-346 (and other miRNAs w/seed GUCUGCC)	0.399	RASSF2	ENSMUSG00000027339	-2.930
mmu-miR-346-5p	miR-346 (and other miRNAs w/seed GUCUGCC)	0.399	RCOR2	ENSMUSG00000024968	-2.275
mmu-miR-346-5p	miR-346 (and other miRNAs w/seed GUCUGCC)	0.399	ZNF362	ENSMUSG00000028799	-2.430
mmu-miR-361-5p	miR-361-5p (miRNAs w/seed UAUCAGA)	-0.473	ACTC1	ENSMUSG00000068614	2.373
mmu-miR-361-5p	miR-361-5p (miRNAs w/seed UAUCAGA)	-0.473	BEND6	ENSMUSG00000042182	2.641
mmu-miR-361-5p	miR-361-5p (miRNAs w/seed UAUCAGA)	-0.473	DPF3	ENSMUSG00000021221	2.811
mmu-miR-361-5p	miR-361-5p (miRNAs w/seed UAUCAGA)	-0.473	EIF1AX	ENSMUSG00000057561	2.255
mmu-miR-361-5p	miR-361-5p (miRNAs w/seed UAUCAGA)	-0.473	GIGYF2	ENSMUSG00000048000	2.588
mmu-miR-361-5p	miR-361-5p (miRNAs w/seed UAUCAGA)	-0.473	GNA13	ENSMUSG00000020611	2.657
mmu-miR-361-5p	miR-361-5p (miRNAs w/seed UAUCAGA)	-0.473	IL13RA1	ENSMUSG00000017057	4.260
mmu-miR-361-5p	miR-361-5p (miRNAs w/seed UAUCAGA)	-0.473	MTX2	ENSMUSG00000027099	2.259
mmu-miR-361-5p	miR-361-5p (miRNAs w/seed UAUCAGA)	-0.473	NHS	ENSMUSG00000059493	3.326
mmu-miR-361-5p	miR-361-5p (miRNAs w/seed UAUCAGA)	-0.473	NUP153	ENSMUSG00000021374	2.553
mmu-miR-361-5p	miR-361-5p (miRNAs w/seed UAUCAGA)	-0.473	PGM3	ENSMUSG00000056131	3.036
mmu-miR-361-5p	miR-361-5p (miRNAs w/seed UAUCAGA)	-0.473	RNF11	ENSMUSG00000028557	2.278
mmu-miR-361-5p	miR-361-5p (miRNAs w/seed UAUCAGA)	-0.473	SDCBP	ENSMUSG00000028249	2.245
mmu-miR-361-5p	miR-361-5p (miRNAs w/seed UAUCAGA)	-0.473	SEC61A2	ENSMUSG00000025816	2.277
mmu-miR-361-5p	miR-361-5p (miRNAs w/seed UAUCAGA)	-0.473	SLC1A3	ENSMUSG00000005360	2.066
mmu-miR-361-5p	miR-361-5p (miRNAs w/seed UAUCAGA)	-0.473	SLC41A1	ENSMUSG00000013275	2.304
mmu-miR-361-5p	miR-361-5p (miRNAs w/seed UAUCAGA)	-0.473	SNX3	ENSMUSG00000019804	2.445

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
	UAUCAGA)				
mmu-miR-361-5p	miR-361-5p (miRNAs w/seed UAUCAGA)	-0.473	UBE2K	ENSMUSG00000029203	2.362
mmu-miR-361-5p	miR-361-5p (miRNAs w/seed UAUCAGA)	-0.473	VBP1	ENSMUSG00000031197	2.301
mmu-miR-361-5p	miR-361-5p (miRNAs w/seed UAUCAGA)	-0.473	ZBTB18	ENSMUSG00000063659	2.014
mmu-miR-374c-5p	miR-374c-5p (and other miRNAs w/seed UAAUACA)	-0.560	ABCC9	ENSMUSG00000030249	2.333
mmu-miR-374c-5p	miR-374c-5p (and other miRNAs w/seed UAAUACA)	-0.560	APOO	ENSMUSG00000079508	2.072
mmu-miR-374c-5p	miR-374c-5p (and other miRNAs w/seed UAAUACA)	-0.560	ATL2	ENSMUSG00000059811	2.395
mmu-miR-374c-5p	miR-374c-5p (and other miRNAs w/seed UAAUACA)	-0.560	BTG1	ENSMUSG00000036478	5.832
mmu-miR-374c-5p	miR-374c-5p (and other miRNAs w/seed UAAUACA)	-0.560	CALU	ENSMUSG00000029767	3.067
mmu-miR-374c-5p	miR-374c-5p (and other miRNAs w/seed UAAUACA)	-0.560	CDK2AP1	ENSMUSG00000078154	2.233
mmu-miR-374c-5p	miR-374c-5p (and other miRNAs w/seed UAAUACA)	-0.560	CGGBP1	ENSMUSG00000054604	2.204
mmu-miR-374c-5p	miR-374c-5p (and other miRNAs w/seed UAAUACA)	-0.560	CHSY3	ENSMUSG00000058152	6.220
mmu-miR-374c-5p	miR-374c-5p (and other miRNAs w/seed UAAUACA)	-0.560	EPR3A	ENSMUSG00000015002	2.341
mmu-miR-374c-5p	miR-374c-5p (and other miRNAs w/seed UAAUACA)	-0.560	F3	ENSMUSG00000028128	5.234
mmu-miR-374c-5p	miR-374c-5p (and other miRNAs w/seed UAAUACA)	-0.560	GPD2	ENSMUSG00000026827	2.365
mmu-miR-374c-5p	miR-374c-5p (and other miRNAs w/seed UAAUACA)	-0.560	ITGB1	ENSMUSG00000025809	2.509
mmu-miR-374c-5p	miR-374c-5p (and other miRNAs w/seed UAAUACA)	-0.560	KLF3	ENSMUSG00000029178	2.514
mmu-miR-374c-5p	miR-374c-5p (and other	-0.560	NETO1	ENSMUSG00000050321	2.208

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
	miRNAs w/seed UAAUACA)				
mmu-miR-374c-5p	miR-374c-5p (and other miRNAs w/seed UAAUACA)	-0.560	NOM1	ENSMUSG00000001569	2.025
mmu-miR-374c-5p	miR-374c-5p (and other miRNAs w/seed UAAUACA)	-0.560	PDGFC	ENSMUSG000000028019	2.715
mmu-miR-374c-5p	miR-374c-5p (and other miRNAs w/seed UAAUACA)	-0.560	PLPP3	ENSMUSG000000028517	2.892
mmu-miR-374c-5p	miR-374c-5p (and other miRNAs w/seed UAAUACA)	-0.560	PRDX1	ENSMUSG000000028691	2.696
mmu-miR-374c-5p	miR-374c-5p (and other miRNAs w/seed UAAUACA)	-0.560	RGPD4 (includes others)	ENSMUSG00000003226	2.528
mmu-miR-374c-5p	miR-374c-5p (and other miRNAs w/seed UAAUACA)	-0.560	TSPAN6	ENSMUSG000000067377	4.053
mmu-miR-374c-5p	miR-374c-5p (and other miRNAs w/seed UAAUACA)	-0.560	YOD1	ENSMUSG000000046404	2.776
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.532	ABCC9	ENSMUSG000000030249	2.333
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.532	ACTC1	ENSMUSG000000068614	2.373
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.532	ATP1B3	ENSMUSG000000032412	3.029
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.532	DCN	ENSMUSG000000019929	3.130
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.532	DLL1	ENSMUSG000000014773	5.359
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.532	ENPEP	ENSMUSG000000028024	4.231
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.532	HAPLN1	ENSMUSG000000021613	4.727
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.532	HBEGF	ENSMUSG000000024486	4.754
mmu-miR-376c-3p	miR-376c-3p (and other	-0.532	RANK1	ENSMUSG000000032702	3.326

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
	miRNAs w/seed ACAUAGA)				
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.532	LDLRAD4	ENSMUSG00000024544	2.708
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.532	MFAP3L	ENSMUSG00000031647	2.764
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.532	MLLT11	ENSMUSG00000053192	2.755
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.532	OPA3	ENSMUSG00000052214	2.066
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.532	PDGFC	ENSMUSG00000028019	2.715
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.532	PHLDA2	ENSMUSG00000010760	28.562
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.532	PLPP3	ENSMUSG00000028517	2.892
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.532	PARB	ENSMUSG00000017491	4.056
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.532	SLC38A2	ENSMUSG00000022462	3.065
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.532	SLC7A2	ENSMUSG00000031596	4.389
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.532	TMEM33	ENSMUSG00000037720	2.711
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.532	TNS3	ENSMUSG00000020422	2.570
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	ANGEL2	ENSMUSG00000026634	2.092
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	ANKH	ENSMUSG00000022265	5.472
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	ATL2	ENSMUSG00000059811	2.395
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	B3GALNT2	ENSMUSG00000039242	2.553

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	BMP7	ENSMUSG00000008999	4.864
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	CCDC117	ENSMUSG00000020482	2.347
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	CDV3	ENSMUSG00000032803	2.604
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	DCN	ENSMUSG00000019929	3.130
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	DPH3	ENSMUSG00000021905	2.462
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	ETS1	ENSMUSG00000032035	2.457
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	FUT8	ENSMUSG00000021065	4.249
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	GSPT1	ENSMUSG00000062203	2.621
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	HEATR5A	ENSMUSG00000035181	2.129
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	HS2ST1	ENSMUSG00000040151	2.657
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	KMT2E	ENSMUSG00000029004	2.479
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	LAMP2	ENSMUSG00000016534	2.003
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	NETO1	ENSMUSG00000050321	2.208
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	NT5E	ENSMUSG00000032420	14.162
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	NUP153	ENSMUSG00000021374	2.553
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	NXT2	ENSMUSG00000042271	2.525
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	PAIP2	ENSMUSG00000037058	2.059
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	PGM3	ENSMUSG00000056131	3.036
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	PN01	ENSMUSG00000020116	2.497
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	PTGES	ENSMUSG00000050737	3.313
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	RUNX1	ENSMUSG00000022952	2.410

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	SARAF	ENSMUSG00000031532	2.118
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	SDCBP	ENSMUSG00000028249	2.245
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	SEMA3E	ENSMUSG00000063531	5.370
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	SGK1	ENSMUSG00000019970	7.008
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	SLC4A7	ENSMUSG00000021733	2.774
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	SLC7A2	ENSMUSG00000031596	4.389
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	SMIM14	ENSMUSG00000037822	2.195
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	SNX13	ENSMUSG00000020590	2.466
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	SULF1	ENSMUSG00000016918	2.979
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	TAPT1	ENSMUSG00000046985	2.318
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	TMCC3	ENSMUSG00000020023	7.961
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	TMEM33	ENSMUSG00000037720	2.711
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	TMX1	ENSMUSG00000021072	2.916
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	TRAPPC6B	ENSMUSG00000020993	2.544
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	UBA3	ENSMUSG00000030061	2.452
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	UBE2K	ENSMUSG00000029203	2.362
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	UTP23	ENSMUSG00000022313	2.565
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	WDR37	ENSMUSG00000021147	4.184
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	ZFP36L1	ENSMUSG00000021127	3.521
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.458	ZZZ3	ENSMUSG00000039068	3.706
mmu-miR-379-5p	miR-379-5p (and other miRNAs w/seed GGUAGAC)	-0.501	ABCB4	ENSMUSG00000042476	3.506

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-379-5p	miR-379-5p (and other miRNAs w/seed GGUAGAC)	-0.501	ARL4A	ENSMUSG00000047446	2.789
mmu-miR-379-5p	miR-379-5p (and other miRNAs w/seed GGUAGAC)	-0.501	CACFD1	ENSMUSG00000015488	2.201
mmu-miR-379-5p	miR-379-5p (and other miRNAs w/seed GGUAGAC)	-0.501	CALU	ENSMUSG00000029767	3.067
mmu-miR-379-5p	miR-379-5p (and other miRNAs w/seed GGUAGAC)	-0.501	CAPZA2	ENSMUSG00000015733	2.066
mmu-miR-379-5p	miR-379-5p (and other miRNAs w/seed GGUAGAC)	-0.501	FOXF2	ENSMUSG00000038402	4.308
mmu-miR-379-5p	miR-379-5p (and other miRNAs w/seed GGUAGAC)	-0.501	GAREM	ENSMUSG00000042680	2.160
mmu-miR-379-5p	miR-379-5p (and other miRNAs w/seed GGUAGAC)	-0.501	GPD2	ENSMUSG00000026827	2.365
mmu-miR-379-5p	miR-379-5p (and other miRNAs w/seed GGUAGAC)	-0.501	HBEGF	ENSMUSG00000024486	4.754
mmu-miR-379-5p	miR-379-5p (and other miRNAs w/seed GGUAGAC)	-0.501	HSPA4L	ENSMUSG00000025757	4.350
mmu-miR-379-5p	miR-379-5p (and other miRNAs w/seed GGUAGAC)	-0.501	IDH3A	ENSMUSG00000032279	3.869
mmu-miR-379-5p	miR-379-5p (and other miRNAs w/seed GGUAGAC)	-0.501	MAP3K2	ENSMUSG00000024383	2.315
mmu-miR-379-5p	miR-379-5p (and other miRNAs w/seed GGUAGAC)	-0.501	MRPL42	ENSMUSG00000062981	2.786
mmu-miR-379-5p	miR-379-5p (and other miRNAs w/seed GGUAGAC)	-0.501	MYO10	ENSMUSG00000022272	4.045
mmu-miR-379-5p	miR-379-5p (and other miRNAs w/seed GGUAGAC)	-0.501	PLEKHB1	ENSMUSG00000030701	3.084
mmu-miR-379-5p	miR-379-5p (and other miRNAs w/seed GGUAGAC)	-0.501	RARB	ENSMUSG00000017491	4.056
mmu-miR-379-5p	miR-379-5p (and other miRNAs w/seed GGUAGAC)	-0.501	RNF6	ENSMUSG00000029634	2.654
mmu-miR-379-5p	miR-379-5p (and other miRNAs w/seed GGUAGAC)	-0.501	TIMP3	ENSMUSG00000020044	3.853
mmu-miR-379-5p	miR-379-5p (and other miRNAs w/seed GGUAGAC)	-0.501	TMCC3	ENSMUSG00000020023	7.961
mmu-miR-4661-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	BMP2	ENSMUSG00000027358	4.797
mmu-miR-4661-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	CAV2	ENSMUSG00000000058	3.050
mmu-miR-4661-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	CYP51A1	ENSMUSG00000001467	3.378

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-466i-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	GCC2	ENSMUSG00000038039	2.542
mmu-miR-466i-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	GNA14	ENSMUSG00000024697	7.846
mmu-miR-466i-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	HK2	ENSMUSG00000000628	2.493
mmu-miR-466i-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	KIAA0040	ENSMUSG00000090394	2.507
mmu-miR-466i-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	MTUS2	ENSMUSG00000029651	2.507
mmu-miR-466i-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	MYO10	ENSMUSG00000022272	4.045
mmu-miR-466i-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	NHS	ENSMUSG00000059493	3.326
mmu-miR-466i-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	NT5E	ENSMUSG00000032420	14.162
mmu-miR-466i-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	PROS1	ENSMUSG00000022912	4.028
mmu-miR-466i-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	PTGES	ENSMUSG00000050737	3.313
mmu-miR-466i-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	PTP4A1	ENSMUSG00000026064	2.910
mmu-miR-466i-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	RAB1A	ENSMUSG00000020149	2.844
mmu-miR-466i-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	RGPD4 (includes others)	ENSMUSG00000003226	2.528
mmu-miR-466i-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	RNF11	ENSMUSG00000028557	2.278
mmu-miR-466i-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	RUNX1	ENSMUSG00000022952	2.410
mmu-miR-466i-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	SDCBP	ENSMUSG00000028249	2.245
mmu-miR-466i-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	SGMS2	ENSMUSG00000050931	3.816
mmu-miR-466i-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	SLC1A4	ENSMUSG00000020142	2.449
mmu-miR-466i-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	SLC35A3	ENSMUSG00000027957	2.114
mmu-miR-466i-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	SLC44A1	ENSMUSG00000028412	2.782
mmu-miR-466i-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	SLC7A2	ENSMUSG00000031596	4.389

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
	w/seed UACACAC)				
mmu-miR-466i-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	SP4	ENSMUSG00000025323	2.296
mmu-miR-466i-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	SSR1	ENSMUSG00000021427	2.709
mmu-miR-466i-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	STXBP3	ENSMUSG00000027882	2.034
mmu-miR-466i-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	TMCC3	ENSMUSG00000020023	7.961
mmu-miR-466i-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	TRAPPC6B	ENSMUSG00000020993	2.544
mmu-miR-466i-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	TRIB1	ENSMUSG00000032501	2.711
mmu-miR-466i-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	USP39	ENSMUSG00000056305	2.028
mmu-miR-466i-3p	miR-3941 (and other miRNAs w/seed UACACAC)	-0.543	VPS4B	ENSMUSG00000009907	2.110
mmu-miR-3960	miR-3960 (and other miRNAs w/seed GCGGCGG)	0.760	ADAMTSL2	ENSMUSG00000036040	-6.467
mmu-miR-3960	miR-3960 (and other miRNAs w/seed GCGGCGG)	0.760	ADAP1	ENSMUSG00000056413	-2.592
mmu-miR-3960	miR-3960 (and other miRNAs w/seed GCGGCGG)	0.760	ARHGEF18	ENSMUSG00000004568	-3.167
mmu-miR-3960	miR-3960 (and other miRNAs w/seed GCGGCGG)	0.760	ATP2A3	ENSMUSG00000020788	-2.020
mmu-miR-3960	miR-3960 (and other miRNAs w/seed GCGGCGG)	0.760	CORO7/CO RO7-PAM16	ENSMUSG00000039637	-2.807
mmu-miR-3960	miR-3960 (and other miRNAs w/seed GCGGCGG)	0.760	MAP2K7	ENSMUSG00000002948	-2.576
mmu-miR-411-5p	miR-411-5p (and other miRNAs w/seed AGUAGAC)	-0.494	ABCC9	ENSMUSG00000030249	2.333
mmu-miR-411-5p	miR-411-5p (and other miRNAs w/seed AGUAGAC)	-0.494	EIF1AX	ENSMUSG00000057561	2.255
mmu-miR-411-5p	miR-411-5p (and other miRNAs w/seed AGUAGAC)	-0.494	GATAD1	ENSMUSG00000007415	3.845
mmu-miR-411-5p	miR-411-5p (and other miRNAs w/seed AGUAGAC)	-0.494	MAP2K1	ENSMUSG00000004936	2.373
mmu-miR-411-5p	miR-411-5p (and other miRNAs w/seed AGUAGAC)	-0.494	MLLT11	ENSMUSG00000053192	2.755
mmu-miR-411-5p	miR-411-5p (and other miRNAs w/seed AGUAGAC)	-0.494	PTGS2	ENSMUSG00000032487	19.160
mmu-miR-411-5p	miR-411-5p (and other miRNAs w/seed AGUAGAC)	-0.494	PXDC1	ENSMUSG00000021411	2.385

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
	w/seed AGUAGAC)				
mmu-miR-411-5p	miR-411-5p (and other miRNAs w/seed AGUAGAC)	-0.494	RNF149	ENSMUSG00000048234	2.464
mmu-miR-411-5p	miR-411-5p (and other miRNAs w/seed AGUAGAC)	-0.494	SLC4A7	ENSMUSG00000021733	2.774
mmu-miR-411-5p	miR-411-5p (and other miRNAs w/seed AGUAGAC)	-0.494	TM4SF1	ENSMUSG00000027800	4.155
mmu-miR-411-5p	miR-411-5p (and other miRNAs w/seed AGUAGAC)	-0.494	TMCC3	ENSMUSG00000020023	7.961
mmu-miR-425-5p	miR-425-5p (and other miRNAs w/seed AUGACAC)	-0.509	BCAS2	ENSMUSG00000005687	2.247
mmu-miR-425-5p	miR-425-5p (and other miRNAs w/seed AUGACAC)	-0.509	CDADC1	ENSMUSG00000021982	2.151
mmu-miR-425-5p	miR-425-5p (and other miRNAs w/seed AUGACAC)	-0.509	DIP2C	ENSMUSG00000048264	2.975
mmu-miR-425-5p	miR-425-5p (and other miRNAs w/seed AUGACAC)	-0.509	EPN2	ENSMUSG00000001036	2.745
mmu-miR-425-5p	miR-425-5p (and other miRNAs w/seed AUGACAC)	-0.509	ERLEC1	ENSMUSG00000020311	2.088
mmu-miR-425-5p	miR-425-5p (and other miRNAs w/seed AUGACAC)	-0.509	GHITM	ENSMUSG000000041028	3.310
mmu-miR-425-5p	miR-425-5p (and other miRNAs w/seed AUGACAC)	-0.509	HS2ST1	ENSMUSG000000040151	2.657
mmu-miR-425-5p	miR-425-5p (and other miRNAs w/seed AUGACAC)	-0.509	HSPH1	ENSMUSG00000029657	2.444
mmu-miR-425-5p	miR-425-5p (and other miRNAs w/seed AUGACAC)	-0.509	IL11	ENSMUSG00000004371	22.880
mmu-miR-425-5p	miR-425-5p (and other miRNAs w/seed AUGACAC)	-0.509	KLF3	ENSMUSG00000029178	2.514
mmu-miR-425-5p	miR-425-5p (and other miRNAs w/seed AUGACAC)	-0.509	LAMP2	ENSMUSG00000016534	2.003
mmu-miR-425-5p	miR-425-5p (and other miRNAs w/seed AUGACAC)	-0.509	LIN7C	ENSMUSG00000027162	2.691
mmu-miR-425-5p	miR-425-5p (and other miRNAs w/seed AUGACAC)	-0.509	MRPS6	ENSMUSG00000039680	2.277
mmu-miR-425-5p	miR-425-5p (and other miRNAs w/seed AUGACAC)	-0.509	NOV	ENSMUSG00000037362	3.787
mmu-miR-425-5p	miR-425-5p (and other miRNAs w/seed AUGACAC)	-0.509	RNF11	ENSMUSG00000028557	2.278
mmu-miR-425-5p	miR-425-5p (and other miRNAs w/seed AUGACAC)	-0.509	SLITRK6	ENSMUSG00000045871	4.056
mmu-miR-425-5p	miR-425-5p (and other miRNAs w/seed AUGACAC)	-0.509	UBE2G1	ENSMUSG00000020794	2.075

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
	w/seed AUGACAC)				
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.755	ADAMTS14	ENSMUSG00000059901	-2.334
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.755	ADCY9	ENSMUSG0000005580	-2.161
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.755	ALDH3B1	ENSMUSG00000024885	-2.172
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.755	CA7	ENSMUSG00000031883	-2.110
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.755	CNN2	ENSMUSG00000004665	-2.932
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.755	FAM109A	ENSMUSG00000044134	-2.172
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.755	FOXRED2	ENSMUSG00000016552	-2.338
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.755	GLUL	ENSMUSG00000026473	-3.655
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.755	GSTM5	ENSMUSG00000058135	-2.732
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.755	JMJD8	ENSMUSG00000025736	-2.723
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.755	LYPD6B	ENSMUSG00000026765	-3.942
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.755	NKD1	ENSMUSG00000031661	-3.618
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.755	OSBPL7	ENSMUSG00000038534	-2.560
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.755	PADI2	ENSMUSG00000028927	-7.765
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.755	PDZK1IP1	ENSMUSG00000028716	-2.180
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.755	SAT2	ENSMUSG00000069835	-2.856
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.755	SFXN4	ENSMUSG00000063698	-2.253
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.755	SKI	ENSMUSG00000029050	-2.095
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.755	SORT1	ENSMUSG00000068747	-2.464
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.755	TBC1D2	ENSMUSG00000039813	-3.413
mmu-miR-6769b-5p	miR-4456 (and other miRNAs	0.628	ADAMTS14	ENSMUSG00000059901	-2.334

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
	w/seed CUGGUGG)				
mmu-miR-6769b-5p	miR-4456 (and other miRNAs w/seed CUGGUGG)	0.628	ADAP1	ENSMUSG00000056413	-2.592
mmu-miR-6769b-5p	miR-4456 (and other miRNAs w/seed CUGGUGG)	0.628	C19orf66	ENSMUSG00000038884	-2.556
mmu-miR-6769b-5p	miR-4456 (and other miRNAs w/seed CUGGUGG)	0.628	CSDC2	ENSMUSG00000042109	-3.036
mmu-miR-6769b-5p	miR-4456 (and other miRNAs w/seed CUGGUGG)	0.628	CYS1	ENSMUSG00000062563	-3.937
mmu-miR-6769b-5p	miR-4456 (and other miRNAs w/seed CUGGUGG)	0.628	DEF6	ENSMUSG00000002257	-2.488
mmu-miR-6769b-5p	miR-4456 (and other miRNAs w/seed CUGGUGG)	0.628	FOXRED2	ENSMUSG00000016552	-2.338
mmu-miR-6769b-5p	miR-4456 (and other miRNAs w/seed CUGGUGG)	0.628	LGALS3BP	ENSMUSG00000033880	-2.821
mmu-miR-6769b-5p	miR-4456 (and other miRNAs w/seed CUGGUGG)	0.628	PCK2	ENSMUSG00000040618	-2.038
mmu-miR-455-5p	miR-455-5p (and other miRNAs w/seed AUGUGCC)	-0.400	BAG1	ENSMUSG00000028416	2.734
mmu-miR-455-5p	miR-455-5p (and other miRNAs w/seed AUGUGCC)	-0.400	CDV3	ENSMUSG00000032803	2.604
mmu-miR-455-5p	miR-455-5p (and other miRNAs w/seed AUGUGCC)	-0.400	DSTN	ENSMUSG00000015932	3.550
mmu-miR-455-5p	miR-455-5p (and other miRNAs w/seed AUGUGCC)	-0.400	EPN2	ENSMUSG00000001036	2.745
mmu-miR-455-5p	miR-455-5p (and other miRNAs w/seed AUGUGCC)	-0.400	ERLEC1	ENSMUSG00000020311	2.088
mmu-miR-455-5p	miR-455-5p (and other miRNAs w/seed AUGUGCC)	-0.400	ETS1	ENSMUSG00000032035	2.457
mmu-miR-455-5p	miR-455-5p (and other miRNAs w/seed AUGUGCC)	-0.400	GPD2	ENSMUSG00000026827	2.365
mmu-miR-455-5p	miR-455-5p (and other miRNAs w/seed AUGUGCC)	-0.400	KPNA3	ENSMUSG00000021929	2.132
mmu-miR-455-5p	miR-455-5p (and other miRNAs w/seed AUGUGCC)	-0.400	LDLRAD4	ENSMUSG00000024544	2.708
mmu-miR-455-5p	miR-455-5p (and other miRNAs w/seed AUGUGCC)	-0.400	MFAP3L	ENSMUSG00000031647	2.764
mmu-miR-455-5p	miR-455-5p (and other miRNAs w/seed AUGUGCC)	-0.400	NCK2	ENSMUSG00000066877	2.274
mmu-miR-455-5p	miR-455-5p (and other miRNAs w/seed AUGUGCC)	-0.400	RNF149	ENSMUSG00000048234	2.464
mmu-miR-455-5p	miR-455-5p (and other miRNAs w/seed AUGUGCC)	-0.400	SOC3	ENSMUSG00000053113	2.299

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
	w/seed AUGUGCC)				
mmu-miR-455-5p	miR-455-5p (and other miRNAs w/seed AUGUGCC)	-0.400	TJP1	ENSMUSG00000030516	2.661
mmu-miR-455-5p	miR-455-5p (and other miRNAs w/seed AUGUGCC)	-0.400	TMEM33	ENSMUSG00000037720	2.711
mmu-miR-455-5p	miR-455-5p (and other miRNAs w/seed AUGUGCC)	-0.400	TSPAN6	ENSMUSG00000067377	4.053
mmu-miR-455-5p	miR-455-5p (and other miRNAs w/seed AUGUGCC)	-0.400	UBE2K	ENSMUSG00000029203	2.362
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGUGG)	2.593	ADCY9	ENSMUSG00000005580	-2.161
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGUGG)	2.593	ARHGEF18	ENSMUSG00000004568	-3.167
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGUGG)	2.593	ARVCF	ENSMUSG00000000325	-3.132
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGUGG)	2.593	CAMKK2	ENSMUSG00000029471	-2.570
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGUGG)	2.593	COL8A2	ENSMUSG00000056174	-5.252
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGUGG)	2.593	CSDC2	ENSMUSG00000042109	-3.036
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGUGG)	2.593	EDNRA	ENSMUSG00000031616	-2.626
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGUGG)	2.593	FOXRED2	ENSMUSG00000016552	-2.338
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGUGG)	2.593	GALNT16	ENSMUSG00000021130	-6.021
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGUGG)	2.593	GLUL	ENSMUSG00000026473	-3.655
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGUGG)	2.593	IMPDH1	ENSMUSG00000003500	-2.043
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGUGG)	2.593	IVD	ENSMUSG00000027332	-2.180
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGUGG)	2.593	JMJD8	ENSMUSG00000025736	-2.723
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGUGG)	2.593	KLF15	ENSMUSG00000030087	-3.260
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGUGG)	2.593	KLHL18	ENSMUSG000000054792	-2.175
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGUGG)	2.593	LRRC3B	ENSMUSG000000045201	-2.166

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	2.593	MAP2K7	ENSMUSG00000002948	-2.576
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	2.593	MYH14	ENSMUSG000000030739	-3.299
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	2.593	MYO7A	ENSMUSG000000030761	-2.045
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	2.593	NCAM1	ENSMUSG000000039542	-3.709
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	2.593	NKD1	ENSMUSG000000031661	-3.618
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	2.593	OSBPL7	ENSMUSG000000038534	-2.560
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	2.593	PADI2	ENSMUSG000000028927	-7.765
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	2.593	PFKFB4	ENSMUSG000000025648	-2.776
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	2.593	PIGZ	ENSMUSG000000045625	-2.462
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	2.593	PRRX1	ENSMUSG000000026586	-2.910
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	2.593	PUM2	ENSMUSG000000020594	-2.130
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	2.593	SARDH	ENSMUSG000000009614	-3.042
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	2.593	SCARA3	ENSMUSG000000034463	-3.097
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	2.593	SFXN5	ENSMUSG000000033720	-2.558
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	2.593	SKAP1	ENSMUSG000000057058	-2.321
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	2.593	SKI	ENSMUSG000000029050	-2.095
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	2.593	SSTR2	ENSMUSG000000047904	-2.008
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	2.593	TRANK1	ENSMUSG000000062296	-2.219
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	2.593	TXNL4B	ENSMUSG000000031723	-2.097
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	2.593	VIT	ENSMUSG000000024076	-3.211
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	2.593	ZNF362	ENSMUSG000000028799	-2.430

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	AEBP1	ENSMUSG00000020473	2.866
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	BMP2	ENSMUSG00000027358	4.797
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	C14orf79	ENSMUSG00000037594	2.390
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	CACFD1	ENSMUSG00000015488	2.201
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	CD14	ENSMUSG00000051439	3.745
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	CDA	ENSMUSG00000028755	3.141
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	CEMIP	ENSMUSG00000052353	3.630
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	CHMP3	ENSMUSG00000053119	2.505
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	COL6A2	ENSMUSG00000020241	2.940
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	COL6A3	ENSMUSG00000048126	5.728
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	CSRNPI	ENSMUSG00000032515	2.565
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	CTSK	ENSMUSG00000028111	3.202
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	DAP	ENSMUSG00000039168	2.586
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	DIXDC1	ENSMUSG00000032064	2.563
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	DLD	ENSMUSG00000020664	2.428
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	DLL1	ENSMUSG00000014773	5.359
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	DOK4	ENSMUSG00000040631	4.475
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	EPN2	ENSMUSG00000001036	2.745
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	GJB4	ENSMUSG00000046623	3.956
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	GTF3C4	ENSMUSG00000035666	2.289
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	HMGAL	ENSMUSG00000078249	4.019

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	HTRA3	ENSMUSG00000029096	3.023
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	IDH3A	ENSMUSG00000032279	3.869
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	KCNK5	ENSMUSG00000023243	4.299
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	LRTM2	ENSMUSG00000055003	5.673
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	MMGT1	ENSMUSG00000061273	2.415
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	MTCH2	ENSMUSG00000027282	2.004
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	MTUS2	ENSMUSG00000029651	2.507
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	NCS1	ENSMUSG00000062661	2.286
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	NPR3	ENSMUSG00000022206	7.306
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	OPA3	ENSMUSG000000052214	2.066
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	PFKP	ENSMUSG00000021196	3.430
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	PHLPP1	ENSMUSG00000044340	2.247
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	PITPNA	ENSMUSG00000017781	2.698
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	PXDC1	ENSMUSG00000021411	2.385
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	RAB11FIP4	ENSMUSG00000017639	2.585
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	RGS16	ENSMUSG00000026475	4.031
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	SAR1B	ENSMUSG00000020386	3.415
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	SERINC2	ENSMUSG00000023232	2.981
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	SFN	ENSMUSG00000047281	2.912
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	SGCG	ENSMUSG00000035296	4.084
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	SLC41A1	ENSMUSG00000013275	2.304

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	SNX13	ENSMUSG00000020590	2.466
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	TIMP3	ENSMUSG00000020044	3.853
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	TULP4	ENSMUSG00000034377	2.207
mmu-miR-6954-5p	miR-486-3p (and other miRNAs w/seed GGGGCAG)	-0.610	VWA1	ENSMUSG00000042116	2.769
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	ACTC1	ENSMUSG00000068614	2.373
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	ADGRA3	ENSMUSG00000029090	2.113
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	AMOTL2	ENSMUSG00000032531	3.583
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	ATL2	ENSMUSG00000059811	2.395
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	B3GALNT2	ENSMUSG00000039242	2.553
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	BMP7	ENSMUSG00000008999	4.864
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	BTG1	ENSMUSG00000036478	5.832
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	COP58	ENSMUSG00000034432	2.715
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	DLL1	ENSMUSG00000014773	5.359
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	EIF1AX	ENSMUSG00000057561	2.255
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	ETS1	ENSMUSG00000032035	2.457
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	FOXC1	ENSMUSG00000050295	2.359
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	GALNT1	ENSMUSG00000000420	3.568
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	GCC2	ENSMUSG00000038039	2.542
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	HBEGF	ENSMUSG00000024486	4.754
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	LAMP2	ENSMUSG00000016534	2.003
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	LDLRAD3	ENSMUSG00000048058	3.231

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	LDLRAD4	ENSMUSG00000024544	2.708
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	LRTM2	ENSMUSG00000055003	5.673
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	MAP3K2	ENSMUSG00000024383	2.315
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	MBNL2	ENSMUSG00000022139	3.213
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	MGAT2	ENSMUSG00000043998	2.892
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	MID2	ENSMUSG00000000266	2.346
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	MYO10	ENSMUSG00000022272	4.045
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	NDFIP2	ENSMUSG00000053253	3.027
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	NETO1	ENSMUSG00000050321	2.208
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	PAIP2	ENSMUSG00000037058	2.059
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	PBRM1	ENSMUSG00000042323	2.425
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	PFN2	ENSMUSG00000027805	2.558
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	PSMD5	ENSMUSG00000026869	2.325
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	PTP4A1	ENSMUSG00000026064	2.910
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	RADIL	ENSMUSG00000029576	2.043
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	SEPT7	ENSMUSG00000001833	2.378
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	SGK1	ENSMUSG00000019970	7.008
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	SLC44A1	ENSMUSG00000028412	2.782
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	SMNDC1	ENSMUSG00000025024	2.774
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	SPRYD7	ENSMUSG00000021930	2.326
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	SSR1	ENSMUSG00000021427	2.709

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	STK38L	ENSMUSG00000001630	4.290
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	TMEM128	ENSMUSG000000067365	2.646
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	TNFRSF21	ENSMUSG000000023915	3.696
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	TUSC3	ENSMUSG000000039530	4.411
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	ZBTB18	ENSMUSG000000063659	2.014
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	ZCCHC14	ENSMUSG000000061410	2.791
mmu-miR-495-3p	miR-495-3p (and other miRNAs w/seed AACAAAC)	-0.413	ZFP36L1	ENSMUSG000000021127	3.521
mmu-miR-6546-5p	miR-566 (and other miRNAs w/seed GGCGCCU)	0.719	ADORA1	ENSMUSG000000042429	-4.392
mmu-miR-6546-5p	miR-566 (and other miRNAs w/seed GGCGCCU)	0.719	CNN2	ENSMUSG000000004665	-2.932
mmu-miR-6546-5p	miR-566 (and other miRNAs w/seed GGCGCCU)	0.719	ECSIT	ENSMUSG000000066839	-2.053
mmu-miR-6546-5p	miR-566 (and other miRNAs w/seed GGCGCCU)	0.719	MGLL	ENSMUSG000000033174	-3.899
mmu-miR-6546-5p	miR-566 (and other miRNAs w/seed GGCGCCU)	0.719	TXNL4B	ENSMUSG000000031723	-2.097
mmu-miR-574-5p	miR-574-5p (miRNAs w/seed GAGUGUG)	1.823	AATK	ENSMUSG000000025375	-5.840
mmu-miR-574-5p	miR-574-5p (miRNAs w/seed GAGUGUG)	1.823	CAMKK1	ENSMUSG000000020785	-2.048
mmu-miR-574-5p	miR-574-5p (miRNAs w/seed GAGUGUG)	1.823	JMJDE	ENSMUSG000000025736	-2.723
mmu-miR-574-5p	miR-574-5p (miRNAs w/seed GAGUGUG)	1.823	MAOB	ENSMUSG000000040147	-3.568
mmu-miR-574-5p	miR-574-5p (miRNAs w/seed GAGUGUG)	1.823	MCPH1	ENSMUSG000000039842	-2.275
mmu-miR-574-5p	miR-574-5p (miRNAs w/seed GAGUGUG)	1.823	NCAM1	ENSMUSG000000039542	-3.709
mmu-miR-574-5p	miR-574-5p (miRNAs w/seed GAGUGUG)	1.823	PFKFB4	ENSMUSG000000025648	-2.776
mmu-miR-574-5p	miR-574-5p (miRNAs w/seed GAGUGUG)	1.823	PIK3IP1	ENSMUSG000000034614	-3.184
mmu-miR-28a-5p	miR-708-5p (and other miRNAs w/seed AGGAGCU)	-0.430	AMOTL2	ENSMUSG000000032531	3.583

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-28a-5p	miR-708-5p (and other miRNAs w/seed AGGAGCU)	-0.430	ATL2	ENSMUSG00000059811	2.395
mmu-miR-28a-5p	miR-708-5p (and other miRNAs w/seed AGGAGCU)	-0.430	BAG1	ENSMUSG00000028416	2.734
mmu-miR-28a-5p	miR-708-5p (and other miRNAs w/seed AGGAGCU)	-0.430	BTG1	ENSMUSG00000036478	5.832
mmu-miR-28a-5p	miR-708-5p (and other miRNAs w/seed AGGAGCU)	-0.430	CHSY3	ENSMUSG00000058152	6.220
mmu-miR-28a-5p	miR-708-5p (and other miRNAs w/seed AGGAGCU)	-0.430	DAP	ENSMUSG00000039168	2.586

Table 11. Osteoarthritis miRNAs in articular cartilage and target mRNAs differentially expressed at 6 weeks post-surgery in DMM versus sham mice with dysregulated expression.

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-let-7d-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.366	ABL2	ENSMUSG00000026596	2.094
mmu-let-7d-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.366	ACP1	ENSMUSG00000044573	2.745
mmu-let-7d-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.366	AGO3	ENSMUSG00000028842	2.346
mmu-let-7d-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.366	AKR1B10	ENSMUSG00000029762	2.286
mmu-let-7d-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.366	ATP2A2	ENSMUSG00000029467	2.144
mmu-let-7d-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.366	CBX5	ENSMUSG00000009575	2.239
mmu-let-7d-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.366	CFLAR	ENSMUSG00000026031	2.797
mmu-let-7d-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.366	DCN	ENSMUSG00000019929	2.542
mmu-let-7d-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.366	DNAJA2	ENSMUSG000000031701	2.120
mmu-let-7d-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.366	DNAJB9	ENSMUSG00000014905	3.676
mmu-let-7d-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.366	DPYSL3	ENSMUSG00000024501	2.360
mmu-let-7d-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.366	DSP	ENSMUSG00000054889	3.441
mmu-let-7d-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.366	EIF4G2	ENSMUSG00000005610	2.043

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-let-7d-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.366	ETNK1	ENSMUSG00000030275	3.249
mmu-let-7d-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.366	GABPA	ENSMUSG00000008976	2.774
mmu-let-7d-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.366	RLF9	ENSMUSG00000033863	2.650
mmu-let-7d-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.366	KPNA1	ENSMUSG00000022905	2.196
mmu-let-7d-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.366	KRAS	ENSMUSG00000030265	2.071
mmu-let-7d-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.366	NDUFA4	ENSMUSG00000029632	2.041
mmu-let-7d-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.366	PTGS2	ENSMUSG00000032487	32.809
mmu-let-7d-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.366	SCD	ENSMUSG00000037071	3.883
mmu-let-7d-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.366	SEMA4F	ENSMUSG00000000627	2.369
mmu-let-7d-5p	let-7a-5p (and other miRNAs w/seed GAGGUAG)	-0.366	TSPAN2	ENSMUSG00000027858	2.910
mmu-miR-206-3p	miR-1-3p (and other miRNAs w/seed GGAAUGU)	0.527	AGRN	ENSMUSG00000041936	-2.455
mmu-miR-206-3p	miR-1-3p (and other miRNAs w/seed GGAAUGU)	0.527	ARHGEF18	ENSMUSG00000004568	-3.373
mmu-miR-206-3p	miR-1-3p (and other miRNAs w/seed GGAAUGU)	0.527	CCND2	ENSMUSG00000000184	-3.473
mmu-miR-206-3p	miR-1-3p (and other miRNAs w/seed GGAAUGU)	0.527	DGKB	ENSMUSG00000036095	-2.365
mmu-miR-206-3p	miR-1-3p (and other miRNAs w/seed GGAAUGU)	0.527	HELZ2	ENSMUSG00000027580	-2.455
mmu-miR-206-3p	miR-1-3p (and other miRNAs w/seed GGAAUGU)	0.527	HS3ST3B1	ENSMUSG00000070407	-6.264
mmu-miR-206-3p	miR-1-3p (and other miRNAs w/seed GGAAUGU)	0.527	IQGAP3	ENSMUSG00000028068	-3.249
mmu-miR-206-3p	miR-1-3p (and other miRNAs w/seed GGAAUGU)	0.527	LRP1	ENSMUSG00000040249	-3.964
mmu-miR-206-3p	miR-1-3p (and other miRNAs w/seed GGAAUGU)	0.527	NFAT5	ENSMUSG0000003847	-2.904
mmu-miR-206-3p	miR-1-3p (and other miRNAs w/seed GGAAUGU)	0.527	PLCG1	ENSMUSG00000016933	-2.864
mmu-miR-206-3p	miR-1-3p (and other miRNAs w/seed GGAAUGU)	0.527	PTPN1	ENSMUSG00000027540	-2.681

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-206-3p	miR-1-3p (and other miRNAs w/seed GGAAUGU)	0.527	PTPRS	ENSMUSG00000013236	-2.013
mmu-miR-206-3p	miR-1-3p (and other miRNAs w/seed GGAAUGU)	0.527	SLC16A3	ENSMUSG00000025161	-2.949
mmu-miR-206-3p	miR-1-3p (and other miRNAs w/seed GGAAUGU)	0.527	SMARCC1	ENSMUSG00000032481	-2.236
mmu-miR-206-3p	miR-1-3p (and other miRNAs w/seed GGAAUGU)	0.527	SOX5	ENSMUSG00000041540	-2.302
mmu-miR-206-3p	miR-1-3p (and other miRNAs w/seed GGAAUGU)	0.527	TAOK3	ENSMUSG00000061288	-2.058
mmu-miR-206-3p	miR-1-3p (and other miRNAs w/seed GGAAUGU)	0.527	VEGFA	ENSMUSG00000023951	-2.301
mmu-miR-100-5p	miR-100-5p (and other miRNAs w/seed ACCCGUA)	-0.514	EMPR2	ENSMUSG00000067336	3.499
mmu-miR-100-5p	miR-100-5p (and other miRNAs w/seed ACCCGUA)	-0.514	PPP1CB	ENSMUSG00000014956	2.198
mmu-miR-100-5p	miR-100-5p (and other miRNAs w/seed ACCCGUA)	-0.514	RAP1B	ENSMUSG00000052681	2.202
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	ABL2	ENSMUSG00000026596	2.094
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	AGO3	ENSMUSG00000028842	2.346
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	ATF6	ENSMUSG00000026663	2.031
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	BHLHE40	ENSMUSG00000030103	3.031
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	CHST11	ENSMUSG00000034612	2.418
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	DLL1	ENSMUSG00000014773	3.580
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	DNAJB4	ENSMUSG00000028035	2.498
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	DNAJC12	ENSMUSG00000036764	2.886
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	DPYSL3	ENSMUSG00000024501	2.360
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	DSEL	ENSMUSG00000038702	2.015
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	DUSP14	ENSMUSG00000018648	2.053
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	EIF1AX	ENSMUSG00000057561	2.244

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	ETNK1	ENSMUSG00000030275	3.249
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	FOXCl	ENSMUSG00000050295	2.291
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	GNAI3	ENSMUSG00000000001	2.247
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	GOSR2	ENSMUSG00000020946	2.147
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	IL15	ENSMUSG00000031712	2.117
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	IQGAP1	ENSMUSG00000030536	2.301
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	KPNA1	ENSMUSG00000022905	2.196
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	LATS2	ENSMUSG00000021959	2.051
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	LRRK2	ENSMUSG00000036273	2.683
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	NEDD9	ENSMUSG00000021365	2.542
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	NFIB	ENSMUSG00000008575	2.007
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	NPR3	ENSMUSG00000022206	9.254
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	PLAGL1	ENSMUSG00000019817	2.623
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	REST	ENSMUSG00000029249	2.113
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	SDCBP	ENSMUSG00000028249	2.811
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	SGMS2	ENSMUSG00000050931	3.850
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	SPRY1	ENSMUSG00000037211	2.745
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	UBE2Q1	ENSMUSG00000042572	2.323
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	USP6NL	ENSMUSG00000039046	2.189
mmu-miR-107-3p	miR-103-3p (and other miRNAs w/seed GCAGCAU)	-0.617	VCL	ENSMUSG00000021823	2.193
mmu-miR-10a-5p	miR-10a-5p (and other miRNAs w/seed ACCUGU)	-0.452	ABL2	ENSMUSG00000026596	2.094

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-10a-5p	miR-10a-5p (and other miRNAs w/seed ACCUGU)	-0.452	ATP5F1	ENSMUSG00000000563	2.608
mmu-miR-10a-5p	miR-10a-5p (and other miRNAs w/seed ACCUGU)	-0.452	BDH1	ENSMUSG00000046598	2.435
mmu-miR-10a-5p	miR-10a-5p (and other miRNAs w/seed ACCUGU)	-0.452	CBX5	ENSMUSG00000009575	2.239
mmu-miR-10a-5p	miR-10a-5p (and other miRNAs w/seed ACCUGU)	-0.452	CFLAR	ENSMUSG00000026031	2.797
mmu-miR-10a-5p	miR-10a-5p (and other miRNAs w/seed ACCUGU)	-0.452	CREB1	ENSMUSG00000025958	2.764
mmu-miR-10a-5p	miR-10a-5p (and other miRNAs w/seed ACCUGU)	-0.452	H3F3A/H3 F3B	ENSMUSG00000016559	2.079
mmu-miR-10a-5p	miR-10a-5p (and other miRNAs w/seed ACCUGU)	-0.452	NDUFA4	ENSMUSG00000029632	2.041
mmu-miR-10a-5p	miR-10a-5p (and other miRNAs w/seed ACCUGU)	-0.452	NDUFB6	ENSMUSG00000071014	2.495
mmu-miR-10a-5p	miR-10a-5p (and other miRNAs w/seed ACCUGU)	-0.452	NR2F2	ENSMUSG00000030551	2.586
mmu-miR-10a-5p	miR-10a-5p (and other miRNAs w/seed ACCUGU)	-0.452	REBP7	ENSMUSG00000031353	2.082
mmu-miR-10a-5p	miR-10a-5p (and other miRNAs w/seed ACCUGU)	-0.452	RNGTT	ENSMUSG00000028274	2.617
mmu-miR-10a-5p	miR-10a-5p (and other miRNAs w/seed ACCUGU)	-0.452	SNRPB2	ENSMUSG00000008333	2.354
mmu-miR-10a-5p	miR-10a-5p (and other miRNAs w/seed ACCUGU)	-0.452	TWSG1	ENSMUSG00000024098	2.488
mmu-miR-10a-5p	miR-10a-5p (and other miRNAs w/seed ACCUGU)	-0.452	UAP1	ENSMUSG00000026670	2.160
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	ABL2	ENSMUSG00000026596	2.094
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	BMPR2	ENSMUSG00000067336	3.499
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	CBX5	ENSMUSG00000009575	2.239
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	CCNG1	ENSMUSG00000020326	2.425
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	CREB1	ENSMUSG00000025958	2.764
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	ENAH	ENSMUSG00000022995	2.442
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	ENPEP	ENSMUSG00000028024	2.888

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	GNA13	ENSMUSG00000020611	2.505
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	GOSR2	ENSMUSG00000020946	2.147
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	GPD2	ENSMUSG00000026827	2.526
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	GPX8	ENSMUSG00000021760	2.216
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	H3F3A/H3F3B	ENSMUSG00000016559	2.079
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	IL13RA1	ENSMUSG00000017057	2.672
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	JAG1	ENSMUSG00000027276	2.578
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	MAP2K4	ENSMUSG00000033352	2.315
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	MET	ENSMUSG00000009376	3.742
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	NCS1	ENSMUSG00000062661	2.041
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	NFIB	ENSMUSG00000008575	2.007
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	NR2F2	ENSMUSG00000030551	2.586
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	PAICS	ENSMUSG00000029247	2.830
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	PDGFRA	ENSMUSG00000029231	4.314
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	PLAGL1	ENSMUSG00000019817	2.623
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	RAP1B	ENSMUSG00000052681	2.202
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	RARB	ENSMUSG00000017491	5.626
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	RND3	ENSMUSG00000017144	3.396
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	RNGTT	ENSMUSG00000028274	2.617
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	SCD	ENSMUSG00000037071	3.883
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	SOC5	ENSMUSG00000037104	2.547

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	SOC6	ENSMUSG00000056153	2.285
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	SPRY2	ENSMUSG00000022114	5.249
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	TJP2	ENSMUSG00000024812	2.427
mmu-miR-128-3p	miR-128-3p (and other miRNAs w/seed CACAGUG)	-0.394	TSPAN6	ENSMUSG00000067377	3.482
mmu-miR-129-2-3p	miR-129-1-3p (and other miRNAs w/seed AGCCCUU)	-0.623	ACSBG1	ENSMUSG00000032281	5.491
mmu-miR-129-2-3p	miR-129-1-3p (and other miRNAs w/seed AGCCCUU)	-0.623	BMPR2	ENSMUSG00000067336	3.499
mmu-miR-129-2-3p	miR-129-1-3p (and other miRNAs w/seed AGCCCUU)	-0.623	CDC42EP3	ENSMUSG00000036533	2.130
mmu-miR-129-2-3p	miR-129-1-3p (and other miRNAs w/seed AGCCCUU)	-0.623	DOK4	ENSMUSG00000040631	3.290
mmu-miR-129-2-3p	miR-129-1-3p (and other miRNAs w/seed AGCCCUU)	-0.623	DYRK3	ENSMUSG00000016526	6.277
mmu-miR-129-2-3p	miR-129-1-3p (and other miRNAs w/seed AGCCCUU)	-0.623	GJA1	ENSMUSG00000050953	3.399
mmu-miR-129-2-3p	miR-129-1-3p (and other miRNAs w/seed AGCCCUU)	-0.623	GNAI3	ENSMUSG00000020611	2.505
mmu-miR-129-2-3p	miR-129-1-3p (and other miRNAs w/seed AGCCCUU)	-0.623	H3F3A/H3F3B	ENSMUSG00000016559	2.079
mmu-miR-129-2-3p	miR-129-1-3p (and other miRNAs w/seed AGCCCUU)	-0.623	HSPA4	ENSMUSG00000020361	2.152
mmu-miR-129-2-3p	miR-129-1-3p (and other miRNAs w/seed AGCCCUU)	-0.623	MAP2K4	ENSMUSG00000033352	2.315
mmu-miR-129-2-3p	miR-129-1-3p (and other miRNAs w/seed AGCCCUU)	-0.623	PERP	ENSMUSG00000019851	3.004
mmu-miR-129-2-3p	miR-129-1-3p (and other miRNAs w/seed AGCCCUU)	-0.623	PPM1D	ENSMUSG00000020525	2.066
mmu-miR-129-2-3p	miR-129-1-3p (and other miRNAs w/seed AGCCCUU)	-0.623	PRPF40A	ENSMUSG00000061136	2.542

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-129-2-3p	miR-129-1-3p (and other miRNAs w/seed AGCCCUU)	-0.623	RAP1B	ENSMUSG00000052681	2.202
mmu-miR-129-2-3p	miR-129-1-3p (and other miRNAs w/seed AGCCCUU)	-0.623	VTI1A	ENSMUSG00000024983	2.031
mmu-miR-1306-3p	miR-1306-3p (miRNAs w/seed CGUUGGC)	0.468	AHCYL2	ENSMUSG00000029772	-2.155
mmu-miR-1306-3p	miR-1306-3p (miRNAs w/seed CGUUGGC)	0.468	ARFIP2	ENSMUSG00000030881	-2.083
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUAU)	-0.440	APC	ENSMUSG00000005871	2.949
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUAU)	-0.440	ATP5F1	ENSMUSG00000000563	2.608
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUAU)	-0.440	BMPR2	ENSMUSG000000067336	3.499
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUAU)	-0.440	ENAH	ENSMUSG000000022995	2.442
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUAU)	-0.440	GDI2	ENSMUSG000000021218	2.183
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUAU)	-0.440	HS3ST1	ENSMUSG000000051022	2.430
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUAU)	-0.440	HSPA13	ENSMUSG000000032932	2.190
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUAU)	-0.440	MAP2K4	ENSMUSG000000033352	2.315
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUAU)	-0.440	NDUFA4	ENSMUSG000000029632	2.041
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUAU)	-0.440	NFIB	ENSMUSG000000008575	2.007
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUAU)	-0.440	NR2F2	ENSMUSG000000030551	2.586
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUAU)	-0.440	PTPRK	ENSMUSG000000019889	3.050
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUAU)	-0.440	RNGTT	ENSMUSG000000028274	2.617
mmu-miR-136-5p	miR-136-5p (miRNAs w/seed CUCCAUAU)	-0.440	TWSG1	ENSMUSG000000024098	2.488
mmu-miR-151-5p	miR-151-5p (and other miRNAs w/seed CGAGGAG)	-0.433	HS3ST1	ENSMUSG000000051022	2.430
mmu-miR-151-5p	miR-151-5p (and other miRNAs w/seed CGAGGAG)	-0.433	IQGAP1	ENSMUSG000000030536	2.301
mmu-miR-154-5p	miR-154-5p (miRNAs w/seed)	-0.490	CLTC	ENSMUSG000000047126	2.604

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
	AGGUUAU)				
mmu-miR-154-5p	miR-154-5p (miRNAs w/seed AGGUUAU)	-0.490	F2R	ENSMUSG00000048376	2.615
mmu-miR-154-5p	miR-154-5p (miRNAs w/seed AGGUUAU)	-0.490	NT5E	ENSMUSG00000032420	5.649
mmu-miR-154-5p	miR-154-5p (miRNAs w/seed AGGUUAU)	-0.490	PLAGL1	ENSMUSG00000019817	2.623
mmu-miR-154-5p	miR-154-5p (miRNAs w/seed AGGUUAU)	-0.490	SULT1E1	ENSMUSG00000029272	3.278
mmu-miR-154-5p	miR-154-5p (miRNAs w/seed AGGUUAU)	-0.490	UBE2A	ENSMUSG00000016308	2.073
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	ABL2	ENSMUSG00000026596	2.094
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	ACSBG1	ENSMUSG00000032281	5.491
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	ADSS	ENSMUSG00000015961	3.114
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	ATF6	ENSMUSG00000026663	2.031
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	BAIAP2	ENSMUSG00000025372	2.417
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	CBX5	ENSMUSG00000009575	2.239
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	DDX3X	ENSMUSG00000000787	2.250
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	DLL1	ENSMUSG00000014773	3.580
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	DMPK	ENSMUSG00000030409	2.017
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	DNAJA2	ENSMUSG00000031701	2.120
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	DNAJB4	ENSMUSG00000028035	2.498
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	DSEL	ENSMUSG00000038702	2.015
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	DUSP10	ENSMUSG00000039384	3.222
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	EIF1AX	ENSMUSG00000057561	2.244
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	EIF4G2	ENSMUSG0000005610	2.043
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	ENAH	ENSMUSG00000022995	2.442

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
	w/seed AGCAGCA}				
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	ETNK1	ENSMUSG00000030275	3.249
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	FGF1	ENSMUSG00000036585	5.095
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	FOSL1	ENSMUSG00000024912	3.373
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	GABPA	ENSMUSG00000008976	2.774
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	GNA13	ENSMUSG00000020611	2.505
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	GNAI3	ENSMUSG00000000001	2.247
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	H3F3A/H3 F3B	ENSMUSG00000016559	2.079
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	HSPA4L	ENSMUSG00000025757	5.184
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	IDH3A	ENSMUSG00000032279	2.423
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	IL15	ENSMUSG00000031712	2.117
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	KPNA1	ENSMUSG00000022905	2.196
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	KRAS	ENSMUSG00000030265	2.071
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	LATS2	ENSMUSG00000021959	2.051
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	MAP2K1	ENSMUSG00000004936	2.173
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	MAP2K4	ENSMUSG00000033352	2.315
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	MCL1	ENSMUSG00000038612	3.779
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	NCOA4	ENSMUSG00000056234	2.163
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	NCS1	ENSMUSG00000062661	2.041
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	NEDD9	ENSMUSG00000021365	2.542
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	NPR3	ENSMUSG00000022206	9.254
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	PLAGL1	ENSMUSG00000019817	2.623

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
	w/seed AGCAGCA)				
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	PPM1D	ENSMUSG00000020525	2.066
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	PTGS2	ENSMUSG00000032487	32.809
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	RARB	ENSMUSG00000017491	5.626
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	RFK	ENSMUSG00000024712	2.120
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	RTN4	ENSMUSG00000020458	2.207
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	SEMA3D	ENSMUSG00000040254	4.093
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	SEPT11	ENSMUSG00000058013	2.283
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	SGK1	ENSMUSG00000019970	2.706
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	SIAH1	ENSMUSG00000036840	2.464
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	SNRPB2	ENSMUSG00000008333	2.354
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	SOC6	ENSMUSG00000056153	2.285
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	SPTLC1	ENSMUSG00000021468	2.148
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	UBE2Q1	ENSMUSG00000042572	2.323
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	UGP2	ENSMUSG00000001891	2.457
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	USP6NL	ENSMUSG00000039046	2.189
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	VCL	ENSMUSG00000021823	2.193
mmu-miR-15a-5p	miR-16-5p (and other miRNAs w/seed AGCAGCA)	-0.550	VTI1A	ENSMUSG00000024983	2.031
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.499	CFLAR	ENSMUSG00000026031	2.797
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.499	DCN	ENSMUSG00000019929	2.542
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.499	DNAJA2	ENSMUSG00000031701	2.120

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.499	EIF4G2	ENSMUSG00000005610	2.043
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.499	FOS	ENSMUSG000000021250	10.974
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.499	HSPA4L	ENSMUSG000000025757	5.184
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.499	IDH3A	ENSMUSG000000032279	2.423
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.499	PFN2	ENSMUSG000000027805	2.440
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.499	RARB	ENSMUSG000000017491	5.626
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.499	SEPT7	ENSMUSG000000001833	2.942
mmu-miR-1839-5p	miR-1839-5p (and other miRNAs w/seed AGGUAGA)	-0.499	TSPAN6	ENSMUSG000000067377	3.482
mmu-miR-185-5p	miR-185-5p (and other miRNAs w/seed GGAGAGA)	-0.475	ABCG1	ENSMUSG000000024030	6.417
mmu-miR-185-5p	miR-185-5p (and other miRNAs w/seed GGAGAGA)	-0.475	ABL2	ENSMUSG000000026596	2.094
mmu-miR-185-5p	miR-185-5p (and other miRNAs w/seed GGAGAGA)	-0.475	ATP2A2	ENSMUSG000000029467	2.144
mmu-miR-185-5p	miR-185-5p (and other miRNAs w/seed GGAGAGA)	-0.475	BDH1	ENSMUSG000000046598	2.435
mmu-miR-185-5p	miR-185-5p (and other miRNAs w/seed GGAGAGA)	-0.475	BMPR2	ENSMUSG000000067336	3.499
mmu-miR-185-5p	miR-185-5p (and other miRNAs w/seed GGAGAGA)	-0.475	CBX5	ENSMUSG000000009575	2.239
mmu-miR-185-5p	miR-185-5p (and other miRNAs w/seed GGAGAGA)	-0.475	CFLAR	ENSMUSG000000026031	2.797
mmu-miR-185-5p	miR-185-5p (and other miRNAs w/seed GGAGAGA)	-0.475	ENAH	ENSMUSG000000022995	2.442
mmu-miR-185-5p	miR-185-5p (and other miRNAs w/seed GGAGAGA)	-0.475	F13A1	ENSMUSG000000039109	2.902
mmu-miR-185-5p	miR-185-5p (and other miRNAs w/seed GGAGAGA)	-0.475	GJA1	ENSMUSG000000050953	3.399

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-185-5p	miR-185-5p (and other miRNAs w/seed GGAGAGA)	-0.475	GNA13	ENSMUSG00000020611	2.505
mmu-miR-185-5p	miR-185-5p (and other miRNAs w/seed GGAGAGA)	-0.475	GOSR2	ENSMUSG00000020946	2.147
mmu-miR-185-5p	miR-185-5p (and other miRNAs w/seed GGAGAGA)	-0.475	GPX8	ENSMUSG00000021760	2.216
mmu-miR-185-5p	miR-185-5p (and other miRNAs w/seed GGAGAGA)	-0.475	HSPA4	ENSMUSG00000020361	2.152
mmu-miR-185-5p	miR-185-5p (and other miRNAs w/seed GGAGAGA)	-0.475	IQGAP1	ENSMUSG00000030536	2.301
mmu-miR-185-5p	miR-185-5p (and other miRNAs w/seed GGAGAGA)	-0.475	LRRK2	ENSMUSG00000036273	2.683
mmu-miR-185-5p	miR-185-5p (and other miRNAs w/seed GGAGAGA)	-0.475	NFIB	ENSMUSG00000008575	2.007
mmu-miR-185-5p	miR-185-5p (and other miRNAs w/seed GGAGAGA)	-0.475	RAB7A	ENSMUSG00000079477	2.036
mmu-miR-185-5p	miR-185-5p (and other miRNAs w/seed GGAGAGA)	-0.475	RHOA	ENSMUSG00000007815	2.225
mmu-miR-185-5p	miR-185-5p (and other miRNAs w/seed GGAGAGA)	-0.475	RRAS2	ENSMUSG000000055723	2.623
mmu-miR-185-5p	miR-185-5p (and other miRNAs w/seed GGAGAGA)	-0.475	SEL1L	ENSMUSG00000020964	2.894
mmu-miR-185-5p	miR-185-5p (and other miRNAs w/seed GGAGAGA)	-0.475	SEMA3D	ENSMUSG00000040254	4.093
mmu-miR-185-5p	miR-185-5p (and other miRNAs w/seed GGAGAGA)	-0.475	USP6NL	ENSMUSG00000039046	2.189
mmu-miR-185-5p	miR-185-5p (and other miRNAs w/seed GGAGAGA)	-0.475	VTI1A	ENSMUSG00000024983	2.031
mmu-miR-185-5p	miR-185-5p (and other miRNAs w/seed GGAGAGA)	-0.475	YWHAG	ENSMUSG000000051391	2.172
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.345	ABL2	ENSMUSG00000026596	2.094
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.345	ANXA1	ENSMUSG00000024659	2.840
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.345	IMPAD1	ENSMUSG00000066324	3.758
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.345	NCS1	ENSMUSG00000062661	2.041
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.345	NDUFB6	ENSMUSG00000071014	2.495

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
	AGGUAGU)				
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.345	PDGFRA	ENSMUSG00000029231	4.314
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.345	PPP1CB	ENSMUSG00000014956	2.198
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.345	PRMT3	ENSMUSG00000030505	2.215
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.345	SDCBP	ENSMUSG00000028249	2.811
mmu-miR-196b-5p	miR-196a-5p (and other miRNAs w/seed AGGUAGU)	-0.345	SLC25A5	ENSMUSG00000016319	2.187
mmu-let-7j	miR-202-3p (and other miRNAs w/seed GAGGUAU)	0.471	ADCY9	ENSMUSG00000005580	-2.809
mmu-let-7j	miR-202-3p (and other miRNAs w/seed GAGGUAU)	0.471	CCND2	ENSMUSG00000000184	-3.473
mmu-let-7j	miR-202-3p (and other miRNAs w/seed GAGGUAU)	0.471	FGF11	ENSMUSG00000042826	-2.586
mmu-let-7j	miR-202-3p (and other miRNAs w/seed GAGGUAU)	0.471	GALE	ENSMUSG00000028671	-2.069
mmu-let-7j	miR-202-3p (and other miRNAs w/seed GAGGUAU)	0.471	GHR	ENSMUSG000000055737	-3.063
mmu-let-7j	miR-202-3p (and other miRNAs w/seed GAGGUAU)	0.471	GLI2	ENSMUSG00000048402	-4.087
mmu-let-7j	miR-202-3p (and other miRNAs w/seed GAGGUAU)	0.471	HMMR	ENSMUSG00000020330	-2.285
mmu-let-7j	miR-202-3p (and other miRNAs w/seed GAGGUAU)	0.471	LIMK2	ENSMUSG00000020451	-2.121
mmu-let-7j	miR-202-3p (and other miRNAs w/seed GAGGUAU)	0.471	MGLL	ENSMUSG00000033174	-4.457
mmu-let-7j	miR-202-3p (and other miRNAs w/seed GAGGUAU)	0.471	NRTN	ENSMUSG00000039481	-4.231
mmu-let-7j	miR-202-3p (and other miRNAs w/seed GAGGUAU)	0.471	POU2F1	ENSMUSG00000026565	-2.418
mmu-miR-210-3p	miR-210-3p (miRNAs w/seed UGUGCGU)	-0.588	KPNA1	ENSMUSG00000022905	2.196
mmu-miR-210-3p	miR-210-3p (miRNAs w/seed UGUGCGU)	-0.588	NDUFA4	ENSMUSG00000029632	2.041
mmu-miR-210-3p	miR-210-3p (miRNAs w/seed UGUGCGU)	-0.588	PPP1CB	ENSMUSG00000014956	2.198

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-210-3p	miR-210-3p (miRNAs w/seed UGUGCGU)	-0.588	RAB7A	ENSMUSG00000079477	2.036
mmu-miR-210-3p	miR-210-3p (miRNAs w/seed UGUGCGU)	-0.588	RHOQ	ENSMUSG00000024143	2.392
mmu-miR-210-3p	miR-210-3p (miRNAs w/seed UGUGCGU)	-0.588	SDHD	ENSMUSG00000000171	2.272
mmu-miR-210-3p	miR-210-3p (miRNAs w/seed UGUGCGU)	-0.588	USP6NL	ENSMUSG00000039046	2.189
mmu-miR-223-3p	miR-223-3p (miRNAs w/seed GUCAGUU)	-1.191	ACSL3	ENSMUSG00000032883	2.199
mmu-miR-223-3p	miR-223-3p (miRNAs w/seed GUCAGUU)	-1.191	APC	ENSMUSG00000005871	2.949
mmu-miR-223-3p	miR-223-3p (miRNAs w/seed GUCAGUU)	-1.191	CBX5	ENSMUSG00000009575	2.239
mmu-miR-223-3p	miR-223-3p (miRNAs w/seed GUCAGUU)	-1.191	CD44	ENSMUSG00000005087	4.121
mmu-miR-223-3p	miR-223-3p (miRNAs w/seed GUCAGUU)	-1.191	DSEL	ENSMUSG00000038702	2.015
mmu-miR-223-3p	miR-223-3p (miRNAs w/seed GUCAGUU)	-1.191	DUSP10	ENSMUSG00000039384	3.222
mmu-miR-223-3p	miR-223-3p (miRNAs w/seed GUCAGUU)	-1.191	GNA13	ENSMUSG00000020611	2.505
mmu-miR-223-3p	miR-223-3p (miRNAs w/seed GUCAGUU)	-1.191	GPX8	ENSMUSG00000021760	2.216
mmu-miR-223-3p	miR-223-3p (miRNAs w/seed GUCAGUU)	-1.191	KPNA1	ENSMUSG00000022905	2.196
mmu-miR-223-3p	miR-223-3p (miRNAs w/seed GUCAGUU)	-1.191	LNPEP	ENSMUSG00000023845	2.238
mmu-miR-223-3p	miR-223-3p (miRNAs w/seed GUCAGUU)	-1.191	NCS1	ENSMUSG00000062661	2.041
mmu-miR-223-3p	miR-223-3p (miRNAs w/seed GUCAGUU)	-1.191	NFIB	ENSMUSG00000008575	2.007
mmu-miR-223-3p	miR-223-3p (miRNAs w/seed GUCAGUU)	-1.191	PFN2	ENSMUSG00000027805	2.440
mmu-miR-223-3p	miR-223-3p (miRNAs w/seed GUCAGUU)	-1.191	RRAS2	ENSMUSG00000055723	2.623
mmu-miR-223-3p	miR-223-3p (miRNAs w/seed GUCAGUU)	-1.191	SGMS2	ENSMUSG00000050931	3.850
mmu-miR-223-3p	miR-223-3p (miRNAs w/seed GUCAGUU)	-1.191	SIAH1	ENSMUSG00000036840	2.464
mmu-miR-223-3p	miR-223-3p (miRNAs w/seed GUCAGUU)	-1.191	SLC23A2	ENSMUSG00000027340	3.091

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-223-3p	miR-223-3p (miRNAs w/seed GUCAGUU)	-1.191	TSPAN6	ENSMUSG00000067377	3.482
mmu-miR-223-3p	miR-223-3p (miRNAs w/seed GUCAGUU)	-1.191	UBE2A	ENSMUSG00000016308	2.073
mmu-miR-223-3p	miR-223-3p (miRNAs w/seed GUCAGUU)	-1.191	USP6NL	ENSMUSG00000039046	2.189
mmu-miR-223-3p	miR-223-3p (miRNAs w/seed GUCAGUU)	-1.191	VTI1A	ENSMUSG00000024983	2.031
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	ABL2	ENSMUSG00000026596	2.094
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	ACSL3	ENSMUSG000000032883	2.199
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	BHLHE40	ENSMUSG000000030103	3.031
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	CDH4	ENSMUSG000000000305	3.378
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	COX5A	ENSMUSG000000000088	2.193
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	CREB1	ENSMUSG000000025958	2.764
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	DDX3X	ENSMUSG000000000787	2.250
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	DNAJA2	ENSMUSG000000031701	2.120
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	EIF4G2	ENSMUSG000000005610	2.043
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	ENPEP	ENSMUSG000000028024	2.888
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	ETNK1	ENSMUSG000000030275	3.249
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	GNA13	ENSMUSG000000020611	2.505
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	GPX8	ENSMUSG000000021760	2.216
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	HSPA13	ENSMUSG000000032932	2.190
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	IMPAD1	ENSMUSG000000066324	3.758
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	JAG1	ENSMUSG000000027276	2.578
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	KPNA1	ENSMUSG000000022905	2.196

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	LEF1	ENSMUSG00000027985	3.110
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	MCL1	ENSMUSG00000038612	3.779
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	MED23	ENSMUSG00000019984	3.078
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	NCOA4	ENSMUSG00000056234	2.163
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	NDUFA4	ENSMUSG00000029632	2.041
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	PTGS2	ENSMUSG00000032487	32.809
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	PTP4A1	ENSMUSG00000026064	3.015
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	RAB11A	ENSMUSG00000004771	2.354
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	RDH14	ENSMUSG00000020621	2.459
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	REST	ENSMUSG00000029249	2.113
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	RFK	ENSMUSG00000024712	2.120
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	RHOQ	ENSMUSG00000024143	2.392
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	SGMS2	ENSMUSG00000050931	3.850
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	SOC6	ENSMUSG00000056153	2.285
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	TANK	ENSMUSG00000064289	2.412
mmu-miR-26b-5p	miR-26a-5p (and other miRNAs w/seed UCAAGUA)	-0.442	TJP2	ENSMUSG00000024812	2.427
mmu-miR-297c-5p	miR-297a-5p (and other miRNAs w/seed UGUAUGU)	0.458	TCF3	ENSMUSG00000020167	-2.051
mmu-miR-297c-5p	miR-297a-5p (and other miRNAs w/seed UGUAUGU)	0.458	VEGFA	ENSMUSG00000023951	-2.301
mmu-miR-3082-5p	miR-3082-5p (and other miRNAs w/seed ACAGAGU)	1.393	ARHGAP8/PRR5-ARHGAP8	ENSMUSG00000078954	-2.048
mmu-miR-3082-5p	miR-3082-5p (and other miRNAs w/seed ACAGAGU)	1.393	CAMKK2	ENSMUSG00000029471	-2.518

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-3082-5p	miR-3082-5p (and other miRNAs w/seed ACAGAGU)	1.393	DCTN4	ENSMUSG00000024603	-2.449
mmu-miR-31-5p	miR-31-5p (and other miRNAs w/seed GGCAAGA)	0.846	AGRN	ENSMUSG00000041936	-2.455
mmu-miR-31-5p	miR-31-5p (and other miRNAs w/seed GGCAAGA)	0.846	AGT	ENSMUSG00000031980	-2.307
mmu-miR-31-5p	miR-31-5p (and other miRNAs w/seed GGCAAGA)	0.846	ARHGEF2	ENSMUSG00000028059	-2.467
mmu-miR-31-5p	miR-31-5p (and other miRNAs w/seed GGCAAGA)	0.846	GLI2	ENSMUSG00000048402	-4.087
mmu-miR-31-5p	miR-31-5p (and other miRNAs w/seed GGCAAGA)	0.846	GRB10	ENSMUSG00000020176	-2.088
mmu-miR-31-5p	miR-31-5p (and other miRNAs w/seed GGCAAGA)	0.846	GTF2E1	ENSMUSG00000022828	-2.294
mmu-miR-31-5p	miR-31-5p (and other miRNAs w/seed GGCAAGA)	0.846	NFAT5	ENSMUSG00000003847	-2.904
mmu-miR-31-5p	miR-31-5p (and other miRNAs w/seed GGCAAGA)	0.846	P4HTM	ENSMUSG00000006675	-2.462
mmu-miR-31-5p	miR-31-5p (and other miRNAs w/seed GGCAAGA)	0.846	POU2F1	ENSMUSG00000026565	-2.418
mmu-miR-31-5p	miR-31-5p (and other miRNAs w/seed GGCAAGA)	0.846	PTPN1	ENSMUSG00000027540	-2.681
mmu-miR-31-5p	miR-31-5p (and other miRNAs w/seed GGCAAGA)	0.846	SIN3B	ENSMUSG00000031622	-2.142
mmu-miR-31-5p	miR-31-5p (and other miRNAs w/seed GGCAAGA)	0.846	TEP1	ENSMUSG00000006281	-2.181
mmu-miR-31-5p	miR-31-5p (and other miRNAs w/seed GGCAAGA)	0.846	TNS1	ENSMUSG00000055322	-5.238
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.486	ABCG1	ENSMUSG00000024030	6.417
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.486	ABL2	ENSMUSG00000026596	2.094
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.486	ACP1	ENSMUSG00000044573	2.745
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.486	BCL10	ENSMUSG00000028191	2.713
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.486	BHLHE40	ENSMUSG00000030103	3.031
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.486	BMP7	ENSMUSG00000008999	2.385
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.486	BMPR2	ENSMUSG00000067336	3.499

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.486	DPYSL2	ENSMUSG00000022048	3.089
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.486	DPYSL3	ENSMUSG00000024501	2.360
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.486	DUSP10	ENSMUSG00000039384	3.222
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.486	H3F3A/H3F3B	ENSMUSG00000016559	2.079
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.486	MET	ENSMUSG00000009376	3.742
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.486	NDUFA4	ENSMUSG00000029632	2.041
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.486	PERP	ENSMUSG00000019851	3.004
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.486	PLEKHA3	ENSMUSG00000002733	2.819
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.486	PRPF40A	ENSMUSG00000061136	2.542
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.486	REST	ENSMUSG00000029249	2.113
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.486	RFK	ENSMUSG00000024712	2.120
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.486	SIAH1	ENSMUSG00000036840	2.464
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.486	SLC23A2	ENSMUSG00000027340	3.091
mmu-miR-329-3p	miR-329-3p (and other miRNAs w/seed ACACACC)	-0.486	SOC6	ENSMUSG000000056153	2.285
mmu-miR-342-3p	miR-342-3p (miRNAs w/seed CUCACAC)	-0.574	BMP7	ENSMUSG00000008999	2.385
mmu-miR-342-3p	miR-342-3p (miRNAs w/seed CUCACAC)	-0.574	BMPR2	ENSMUSG00000067336	3.499
mmu-miR-342-3p	miR-342-3p (miRNAs w/seed CUCACAC)	-0.574	CEX5	ENSMUSG00000009575	2.239
mmu-miR-342-3p	miR-342-3p (miRNAs w/seed CUCACAC)	-0.574	DDX3X	ENSMUSG00000000787	2.250
mmu-miR-342-3p	miR-342-3p (miRNAs w/seed CUCACAC)	-0.574	GJA1	ENSMUSG000000050953	3.399
mmu-miR-342-3p	miR-342-3p (miRNAs w/seed CUCACAC)	-0.574	GOSR2	ENSMUSG00000020946	2.147
mmu-miR-342-3p	miR-342-3p (miRNAs w/seed CUCACAC)	-0.574	IL11	ENSMUSG00000004371	12.389

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-342-3p	miR-342-3p (miRNAs w/seed CUCACAC)	-0.574	LATS2	ENSMUSG00000021959	2.051
mmu-miR-342-3p	miR-342-3p (miRNAs w/seed CUCACAC)	-0.574	MAP1LC3B	ENSMUSG00000031812	2.136
mmu-miR-342-3p	miR-342-3p (miRNAs w/seed CUCACAC)	-0.574	PDGFRA	ENSMUSG00000029231	4.314
mmu-miR-342-3p	miR-342-3p (miRNAs w/seed CUCACAC)	-0.574	PFN2	ENSMUSG00000027805	2.440
mmu-miR-342-3p	miR-342-3p (miRNAs w/seed CUCACAC)	-0.574	SEPT11	ENSMUSG00000058013	2.283
mmu-miR-342-3p	miR-342-3p (miRNAs w/seed CUCACAC)	-0.574	SGMS2	ENSMUSG00000050931	3.850
mmu-miR-346-5p	miR-346 (and other miRNAs w/seed GUCUGCC)	0.463	DCTN4	ENSMUSG00000024603	-2.449
mmu-miR-346-5p	miR-346 (and other miRNAs w/seed GUCUGCC)	0.463	DGKB	ENSMUSG00000036095	-2.365
mmu-miR-346-5p	miR-346 (and other miRNAs w/seed GUCUGCC)	0.463	EKBP5	ENSMUSG00000024222	-3.240
mmu-miR-346-5p	miR-346 (and other miRNAs w/seed GUCUGCC)	0.463	GSTM5	ENSMUSG00000058135	-2.079
mmu-miR-346-5p	miR-346 (and other miRNAs w/seed GUCUGCC)	0.463	IRF8	ENSMUSG00000041515	-3.864
mmu-miR-346-5p	miR-346 (and other miRNAs w/seed GUCUGCC)	0.463	PDE4A	ENSMUSG00000032177	-2.713
mmu-miR-346-5p	miR-346 (and other miRNAs w/seed GUCUGCC)	0.463	POU2F1	ENSMUSG00000026565	-2.418
mmu-miR-346-5p	miR-346 (and other miRNAs w/seed GUCUGCC)	0.463	TNS1	ENSMUSG00000055322	-5.238
mmu-miR-346-5p	miR-346 (and other miRNAs w/seed GUCUGCC)	0.463	UBTF	ENSMUSG00000020923	-2.076
mmu-miR-346-5p	miR-346 (and other miRNAs w/seed GUCUGCC)	0.463	USP40	ENSMUSG00000055501	-2.523
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.404	ANXA1	ENSMUSG00000024659	2.840
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.404	APC	ENSMUSG0000005871	2.949
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.404	CREB1	ENSMUSG00000025958	2.764
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.404	CREM	ENSMUSG00000063889	2.486

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.404	DCN	ENSMUSG00000019929	2.542
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.404	DLL1	ENSMUSG00000014773	3.580
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.404	DNAJA2	ENSMUSG000000031701	2.120
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.404	ENPEP	ENSMUSG00000028024	2.888
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.404	ETNK1	ENSMUSG000000030275	3.249
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.404	NFIB	ENSMUSG00000008575	2.007
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.404	NR2F2	ENSMUSG000000030551	2.586
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.404	NUDT4	ENSMUSG000000020029	2.065
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.404	PDGFC	ENSMUSG000000028019	4.353
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.404	PPP2CE	ENSMUSG000000009630	2.086
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.404	RARB	ENSMUSG000000017491	5.626
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.404	SPRY1	ENSMUSG000000037211	2.745
mmu-miR-376c-3p	miR-376c-3p (and other miRNAs w/seed ACAUAGA)	-0.404	TANK	ENSMUSG000000064289	2.412
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	ACSL3	ENSMUSG000000032883	2.199
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	ARID4B	ENSMUSG000000039219	2.288
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	AZIN1	ENSMUSG000000037458	2.161
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	BMP7	ENSMUSG000000008999	2.385

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	CUL1	ENSMUSG00000029686	2.610
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	DCN	ENSMUSG00000019929	2.542
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	DNAJB9	ENSMUSG00000014905	3.676
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	EIF4G2	ENSMUSG00000005610	2.043
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	ENAH	ENSMUSG00000022995	2.442
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	ETNK1	ENSMUSG00000030275	3.249
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	ETS1	ENSMUSG00000032035	2.730
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	GNAI3	ENSMUSG00000000001	2.247
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	GOSR2	ENSMUSG00000020946	2.147
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	H3F3A/H3 F3B	ENSMUSG00000016559	2.079
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	IDS	ENSMUSG00000035847	2.255
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	JAG1	ENSMUSG00000027276	2.578
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	LIG4	ENSMUSG00000049717	3.615
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	MAT2B	ENSMUSG00000042032	3.072
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	NFIB	ENSMUSG00000008575	2.007
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	NR2F2	ENSMUSG00000030551	2.586
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	NT5E	ENSMUSG00000032420	5.649
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	PDGFRA	ENSMUSG00000029231	4.314
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	PIAS1	ENSMUSG00000032405	2.282
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	RFK	ENSMUSG00000024712	2.120
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	SDCBP	ENSMUSG00000028249	2.811

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	SEMA3D	ENSMUSG00000040254	4.093
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	SEMA3E	ENSMUSG00000063531	4.494
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	SEPT11	ENSMUSG00000058013	2.283
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	SGK1	ENSMUSG00000019970	2.706
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	SOCS6	ENSMUSG00000056153	2.285
mmu-miR-377-3p	miR-377-3p (miRNAs w/seed UCACACA)	-0.426	SPTLC1	ENSMUSG000000021468	2.148
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.661	ADCY9	ENSMUSG00000005580	-2.809
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.661	AGRN	ENSMUSG000000041936	-2.455
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.661	AHCYL2	ENSMUSG000000029772	-2.155
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.661	ARHGEF2	ENSMUSG000000028059	-2.467
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.661	ARHGEF6	ENSMUSG000000031133	-4.488
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.661	DGKB	ENSMUSG000000036095	-2.365
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.661	FKBP5	ENSMUSG000000024222	-3.240
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.661	GLI2	ENSMUSG000000048402	-4.087
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.661	GSTM5	ENSMUSG000000058135	-2.079
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.661	HTT	ENSMUSG000000029104	-2.473
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.661	IQGAP3	ENSMUSG000000028068	-3.249
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.661	LIMS2	ENSMUSG000000024395	-2.293
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.661	MARK2	ENSMUSG000000024969	-2.674
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.661	MEF2D	ENSMUSG00000001419	-2.059
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.661	PADI2	ENSMUSG000000028927	-4.296

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.661	PTPN1	ENSMUSG00000027540	-2.681
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.661	SLC6A1	ENSMUSG00000030310	-2.471
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.661	TAOK3	ENSMUSG00000061288	-2.058
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.661	THRA	ENSMUSG00000058756	-2.267
mmu-miR-7118-5p	miR-4271 (and other miRNAs w/seed GGGGAAG)	0.661	TNS1	ENSMUSG00000055322	-5.238
mmu-miR-451a	miR-451a (and other miRNAs w/seed AACCGUU)	-1.342	DPYSL3	ENSMUSG00000024501	2.360
mmu-miR-451a	miR-451a (and other miRNAs w/seed AACCGUU)	-1.342	NEDD9	ENSMUSG00000021365	2.542
mmu-miR-451a	miR-451a (and other miRNAs w/seed AACCGUU)	-1.342	PAB5A	ENSMUSG00000017831	2.245
mmu-miR-451a	miR-451a (and other miRNAs w/seed AACCGUU)	-1.342	SGK1	ENSMUSG00000019970	2.706
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	ACSS1	ENSMUSG00000027452	-3.399
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	ADCY9	ENSMUSG00000005580	-2.809
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	AGRN	ENSMUSG00000041936	-2.455
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	ARHGDIA	ENSMUSG00000025132	-2.091
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	ARHGEF18	ENSMUSG00000004568	-3.373
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	CABIN1	ENSMUSG00000020196	-3.415
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	CAMKK2	ENSMUSG00000029471	-2.518
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	COL11A2	ENSMUSG00000024330	-2.317
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	COL20A1	ENSMUSG00000016356	-2.992
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	COL5A3	ENSMUSG00000004098	-2.823
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	COL8A2	ENSMUSG00000056174	-3.755
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	DNM1	ENSMUSG00000026825	-2.473

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	EDNRA	ENSMUSG00000031616	-2.858
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	ENTPD2	ENSMUSG00000015085	-2.894
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	EKBP5	ENSMUSG00000024222	-3.240
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	GYS1	ENSMUSG00000003865	-3.089
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	HDAC10	ENSMUSG00000062906	-2.293
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	HELZ2	ENSMUSG00000027580	-2.455
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	INHA	ENSMUSG00000032968	-2.556
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	LMNA	ENSMUSG00000028063	-2.500
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	LRP1	ENSMUSG00000040249	-3.964
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	MAP2K7	ENSMUSG00000002948	-2.967
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	MAPK8IP3	ENSMUSG00000024163	-3.220
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	MARK2	ENSMUSG00000024969	-2.674
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	MEF2D	ENSMUSG00000001419	-2.059
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	PABPN1	ENSMUSG00000022194	-2.713
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	PADI2	ENSMUSG00000028927	-4.296
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	PDE4A	ENSMUSG00000032177	-2.713
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	PFKFB4	ENSMUSG00000025648	-2.648
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	PLXNA3	ENSMUSG00000031398	-2.509
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	PLXNB2	ENSMUSG00000036606	-2.154
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	POU2F1	ENSMUSG00000026565	-2.418
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	PTPRS	ENSMUSG00000013236	-2.013

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	SCARB1	ENSMUSG00000037936	-2.038
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	SLC16A3	ENSMUSG00000025161	-2.949
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	SMARCC1	ENSMUSG00000032481	-2.236
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	TAB1	ENSMUSG00000022414	-2.626
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	TCF7L2	ENSMUSG00000024985	-2.420
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	TNS1	ENSMUSG00000055322	-5.238
mmu-miR-6931-5p	miR-4651 (and other miRNAs w/seed GGGGUGG)	1.762	UBTF	ENSMUSG00000020923	-2.076
mmu-miR-486a-5p	miR-486-5p (and other miRNAs w/seed CCUGUAC)	-0.504	ARID4B	ENSMUSG00000039219	2.288
mmu-miR-486a-5p	miR-486-5p (and other miRNAs w/seed CCUGUAC)	-0.504	F2R	ENSMUSG00000048376	2.615
mmu-miR-486a-5p	miR-486-5p (and other miRNAs w/seed CCUGUAC)	-0.504	GPX8	ENSMUSG00000021760	2.216
mmu-miR-486a-5p	miR-486-5p (and other miRNAs w/seed CCUGUAC)	-0.504	H3F3A/H3F3B	ENSMUSG00000016559	2.079
mmu-miR-486a-5p	miR-486-5p (and other miRNAs w/seed CCUGUAC)	-0.504	LSM8	ENSMUSG00000044155	2.338
mmu-miR-486a-5p	miR-486-5p (and other miRNAs w/seed CCUGUAC)	-0.504	MDH1	ENSMUSG00000020321	2.321
mmu-miR-486a-5p	miR-486-5p (and other miRNAs w/seed CCUGUAC)	-0.504	NPR3	ENSMUSG00000022206	9.254
mmu-miR-486a-5p	miR-486-5p (and other miRNAs w/seed CCUGUAC)	-0.504	PDGFC	ENSMUSG00000028019	4.353
mmu-miR-486a-5p	miR-486-5p (and other miRNAs w/seed CCUGUAC)	-0.504	SEMA3E	ENSMUSG00000063531	4.494
mmu-miR-486a-5p	miR-486-5p (and other miRNAs w/seed CCUGUAC)	-0.504	SIAH1	ENSMUSG00000036840	2.464
mmu-miR-486a-5p	miR-486-5p (and other miRNAs w/seed CCUGUAC)	-0.504	SNRPD1	ENSMUSG00000002477	2.585
mmu-miR-486a-5p	miR-486-5p (and other miRNAs w/seed CCUGUAC)	-0.504	VTIL1A	ENSMUSG00000024983	2.031
mmu-miR-574-5p	miR-574-5p (miRNAs w/seed GAGUGUG)	1.305	FGF11	ENSMUSG00000042826	-2.586
mmu-miR-574-5p	miR-574-5p (miRNAs w/seed GAGUGUG)	1.305	MEF2D	ENSMUSG00000001419	-2.059

miRNA	miRNA family name with seed sequence	miRNA Exp Log Ratio	Gene Symbol	Ensemble Gene ID	mRNA Exp Fold Change
mmu-miR-574-5p	miR-574-5p (miRNAs w/seed GAGUGUG)	1.305	PFKFB4	ENSMUSG00000025648	-2.648
mmu-miR-574-5p	miR-574-5p (miRNAs w/seed GAGUGUG)	1.305	PHKA2	ENSMUSG00000031295	-3.795
mmu-miR-28a-5p	miR-708-5p (and other miRNAs w/seed AGGAGCU)	-0.371	AS3MT	ENSMUSG00000003559	2.124
mmu-miR-28a-5p	miR-708-5p (and other miRNAs w/seed AGGAGCU)	-0.371	BHLHE40	ENSMUSG00000030103	3.031
mmu-miR-28a-5p	miR-708-5p (and other miRNAs w/seed AGGAGCU)	-0.371	BTG1	ENSMUSG00000036478	3.845
mmu-miR-28a-5p	miR-708-5p (and other miRNAs w/seed AGGAGCU)	-0.371	C9orf3	ENSMUSG00000021458	2.998
mmu-miR-28a-5p	miR-708-5p (and other miRNAs w/seed AGGAGCU)	-0.371	CBX5	ENSMUSG00000009575	2.239
mmu-miR-28a-5p	miR-708-5p (and other miRNAs w/seed AGGAGCU)	-0.371	CREB1	ENSMUSG00000025958	2.764
mmu-miR-28a-5p	miR-708-5p (and other miRNAs w/seed AGGAGCU)	-0.371	DSEL	ENSMUSG00000038702	2.015
mmu-miR-28a-5p	miR-708-5p (and other miRNAs w/seed AGGAGCU)	-0.371	ENAH	ENSMUSG00000022995	2.442
mmu-miR-28a-5p	miR-708-5p (and other miRNAs w/seed AGGAGCU)	-0.371	FGF1	ENSMUSG00000036585	5.095
mmu-miR-28a-5p	miR-708-5p (and other miRNAs w/seed AGGAGCU)	-0.371	H3F3A/H3 F3B	ENSMUSG00000016559	2.079
mmu-miR-28a-5p	miR-708-5p (and other miRNAs w/seed AGGAGCU)	-0.371	IQGAP1	ENSMUSG00000030536	2.301
mmu-miR-28a-5p	miR-708-5p (and other miRNAs w/seed AGGAGCU)	-0.371	LRRK2	ENSMUSG00000036273	2.683
mmu-miR-28a-5p	miR-708-5p (and other miRNAs w/seed AGGAGCU)	-0.371	NFE2L2	ENSMUSG00000015839	2.296
mmu-miR-28a-5p	miR-708-5p (and other miRNAs w/seed AGGAGCU)	-0.371	NT5E	ENSMUSG00000032420	5.649
mmu-miR-28a-5p	miR-708-5p (and other miRNAs w/seed AGGAGCU)	-0.371	RAP1B	ENSMUSG000000052681	2.202
mmu-miR-28a-5p	miR-708-5p (and other miRNAs w/seed AGGAGCU)	-0.371	SEMA4F	ENSMUSG00000000627	2.369
mmu-miR-28a-5p	miR-708-5p (and other miRNAs w/seed AGGAGCU)	-0.371	UBE2A	ENSMUSG00000016308	2.073

CLAIMS

1. Use of an osteoarthritis miRNA for diagnosing osteoarthritis in a subject, wherein the osteoarthritis miRNA is:
 - selected from Tables 1 to 5, or an ortholog thereof;
 - represented by any one of SEQ ID NOs: 1 to 139;
 - represented by any one of SEQ ID NOs: 1 to 57;
 - selected from the group consisting of miR-6931, miR-466i, miR-574, miR-3082, miR-1187, miR-669n, miR-468, miR-669l, miR-32, miR-466m, miR-669e and miR-672;
 - represented by any one of SEQ ID NOs: 1 to 12, 140 or 141; or
 - produced from a stem-loop represented by any one of SEQ ID NOs: 142 to 155.
2. Use of (a) an antagonist that inhibits an activity of an upregulated osteoarthritis miRNA or (b) a mimic that mimics an activity of a downregulated osteoarthritis miRNA in the manufacture of a medicament for treating osteoarthritis in the subject, wherein the subject has been diagnosed as having osteoarthritis by increased expression of the upregulated osteoarthritis miRNA or decreased expression of the downregulated osteoarthritis miRNA in a sample from the subject relative to a reference sample, wherein the osteoarthritis miRNA is:
 - selected from Tables 1 to 5, or an ortholog thereof;
 - represented by any one of SEQ ID NOs: 1 to 139;
 - represented by any one of SEQ ID NOs: 1 to 57;
 - selected from the group consisting of miR-6931, miR-466i, miR-574, miR-3082, miR-1187, miR-669n, miR-468, miR-669l, miR-32, miR-466m, miR-669e and miR-672;
 - represented by any one of SEQ ID NOs: 1 to 12, 140 or 141; or
 - produced from a stem-loop represented by any one of SEQ ID NOs: 142 to 155.
3. Use of (a) an antagonist that inhibits an activity of an upregulated osteoarthritis target mRNA, optionally of Table 10 or Table 11, or an ortholog thereof, or (b) an agonist that promotes an activity of a downregulated osteoarthritis target mRNA, optionally of Table 10 or Table 11, or an ortholog thereof in the manufacture of a medicament for treating osteoarthritis in a subject.

4. An isolated osteoarthritis miRNA selected from Tables 1 to 5, or an ortholog thereof.

5. The osteoarthritis miRNA of claim 4 represented by any one of SEQ ID NOs: 1 to 139.

6. The osteoarthritis miRNA of claim 4 represented by any one of SEQ ID NOs: 1 to 57.

7. The osteoarthritis miRNA of claim 4 selected from the group consisting of miR-6931, miR-466i, miR-574, miR-3082, miR-1187, miR-669n, miR-468, miR-669l, miR-32, miR-466m, miR-669e and miR-672.

8. The osteoarthritis miRNA of any one of claims 4 to 7, represented by any one of SEQ ID NOs: 1 to 12, 140 or 141.

9. The osteoarthritis miRNA of any one of claims 4 to 8, produced from a stem-loop represented by any one of SEQ ID NOs: 142 to 155.

10. The osteoarthritis miRNA of any one of claims 4 to 9 that initiates and/or progresses early osteoarthritis.

11. The osteoarthritis miRNA of any one of claims 4 to 9 that establishes osteoarthritis and/or progresses established osteoarthritis to end-stage osteoarthritis.

12. An isolated nucleic acid antagonist that binds an upregulated osteoarthritis miRNA or binds a target mRNA of the upregulated osteoarthritis miRNA and inhibits an activity of the upregulated osteoarthritis miRNA of any one of claims 4 to 11 in a subject.

13. The nucleic acid antagonist of claim 12, comprising a reverse complement sequence of any one of SEQ ID NOs: 156 to 183.

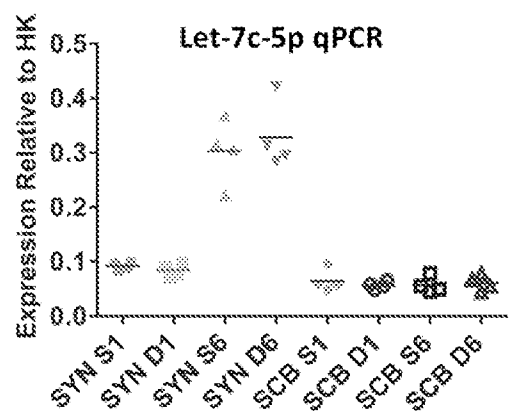


Figure 1

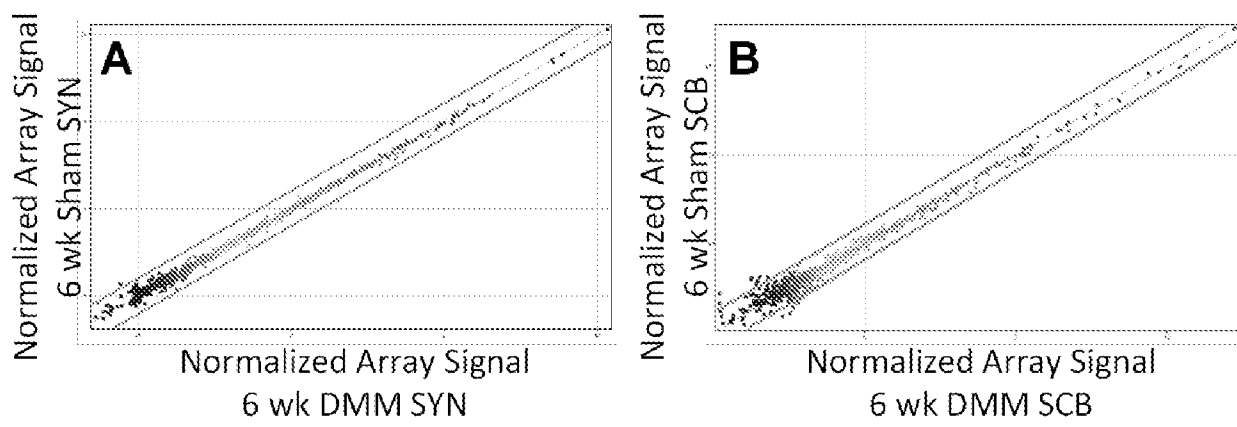


Figure 2

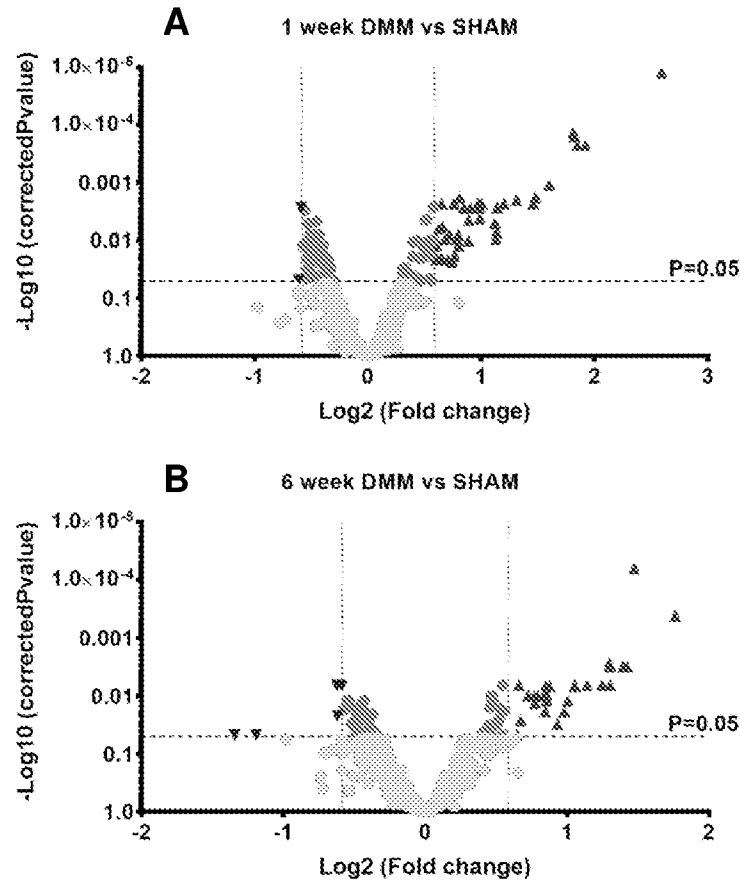


Figure 3.

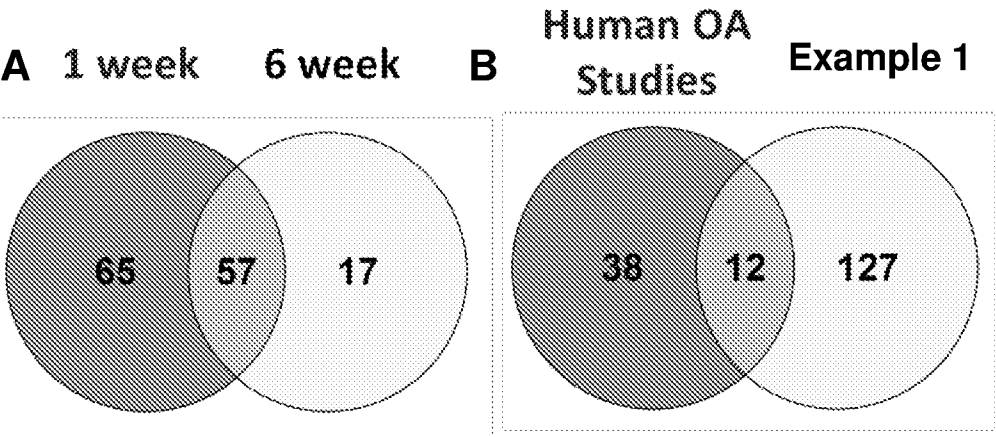


Figure 4

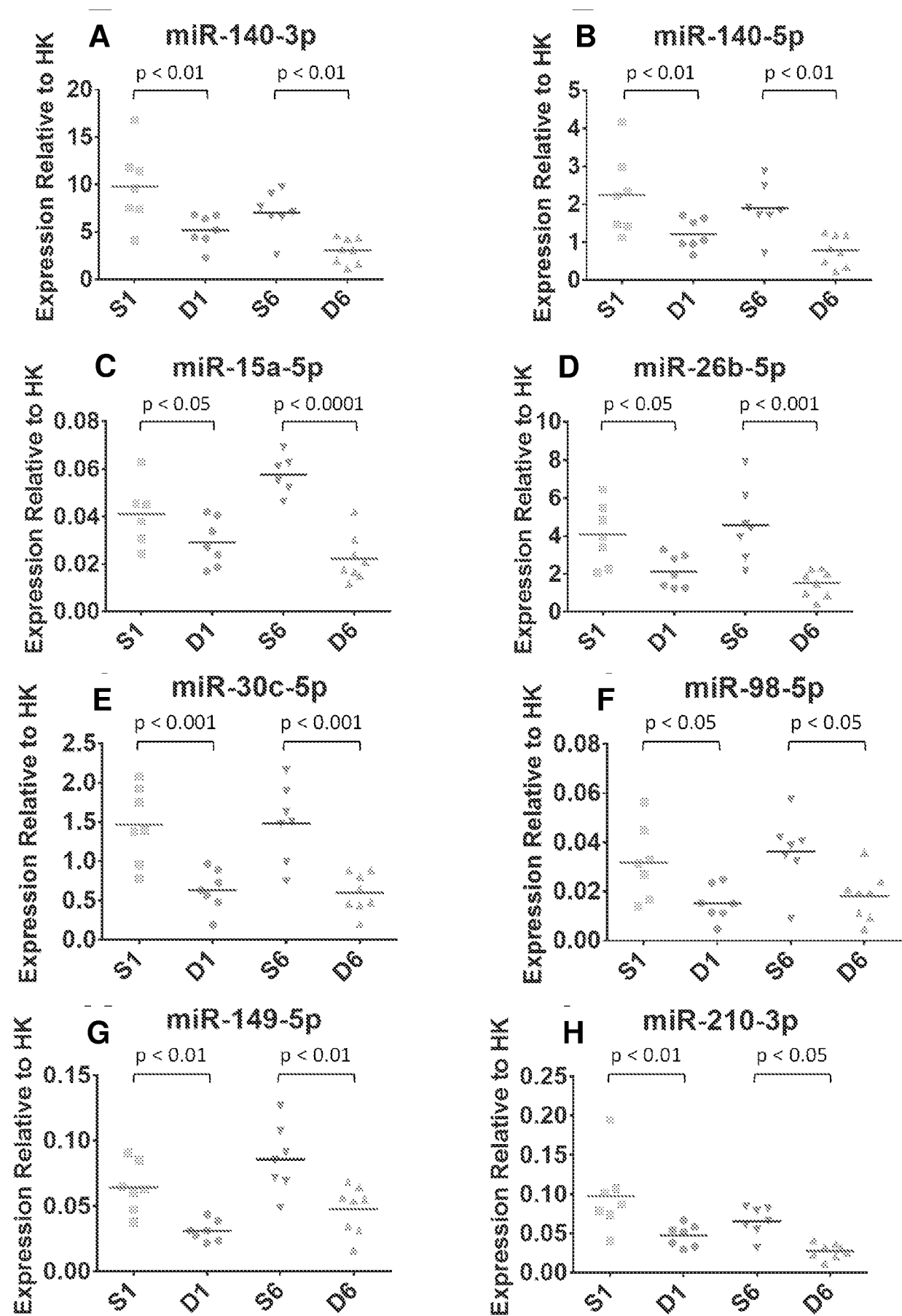


Figure 5

INTERNATIONAL SEARCH REPORT

International application No.
PCT/AU2017/050241

A. CLASSIFICATION OF SUBJECT MATTER

C12Q 1/68 (2006.01) A61K 31/7088 (2006.01)

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EPOQUE: PATENW. STN: CAPLUS, MEDLINE, EMBASE, BIOSIS. Searched for keywords: MICRORNA, OSTEOARTHRITIS, MIR-6391, MIR-3082, MIR-1187, MIR-31, MIR-32, MIR-574, LET-7D and like terms.

GENOME QUEST: SEQ ID NOs 1, 2, 3, 22, 124, 140 and 141 were searched at 90% sequence identity. Results were filtered for keywords: osteoarthritis, antagomir, antimir and like terms.

THE LENS, GOOGLE SCHOLAR and internal databases provided by IP Australia. Searched for applicant and inventor names.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
	Documents are listed in the continuation of Box C	

☒ Further documents are listed in the continuation of Box C

☒ See patent family annex

* "A"	Special categories of cited documents: document defining the general state of the art which is not considered to be of particular relevance	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"E"	earlier application or patent but published on or after the international filing date	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O"	document referring to an oral disclosure, use, exhibition or other means	"&"	document member of the same patent family
"P"	document published prior to the international filing date but later than the priority date claimed		
Date of the actual completion of the international search 30 May 2017		Date of mailing of the international search report 30 May 2017	
Name and mailing address of the ISA/AU AUSTRALIAN PATENT OFFICE PO BOX 200, WODEN ACT 2606, AUSTRALIA Email address: pct@ipaustalia.gov.au		Authorised officer Kelly Hitchens AUSTRALIAN PATENT OFFICE (ISO 9001 Quality Certified Service) Telephone No. +6262223604	

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing filed or furnished:
 - a. (means)
☐ on paper
☒ in electronic form
 - b. (time)
☐ in the international application as filed
☒ together with the international application in electronic form
☐ subsequently to this Authority for the purposes of search
2. ☐ In addition, in the case that more than one version or copy of a sequence listing has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that in the application as filed or does not go beyond the application as filed, as appropriate, were furnished.
3. Additional comments:
Sequencing listing was used for searching purposes.

INTERNATIONAL SEARCH REPORT C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		International application No. PCT/AU2017/050241
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DE-UGARTE, L., ET AL., "MiRNA profiling of whole trabecular bone: identification of osteoporosis-related changes in MiRNAs in human hip bones.", BMC Medical Genomics, 2015, vol. 8, article 75. Abstract, Table S1	4, 7-11
X	KIM, D., ET AL., "Peroxisomal dysfunction is associated with up-regulation of apoptotic cell death via miR-223 induction in knee osteoarthritis patients with type 2 diabetes mellitus.", Bone, 2014, vol. 64, pages 124-131. Figure 3	4-5, 7-11
X	XIA, Z., ET AL., "Altered function in cartilage derived mesenchymal stem cell leads to OA-related cartilage erosion.", American Journal Of Translational Research, 2016 (Published Online: 15 February), vol. 8, no. 2, pages 433-446. Abstract, Table 4	1, 4-11
X	WO 2014/013258 A1 (RENEURON LIMITED) 23 January 2014 Example 4, Tables 4, 5, and 7-9	4-11
X	GenBank Accession No. NR_105896 20 November 2014. ncRNA	4-11
X	GenBank Accession No. NR_035415 21 May 2015. ncRNA	4-11
X	GenBank Accession No. NR_037243 21 May 2015. ncRNA	4-11
X	WO 2014/195693 A1 (ISIS INNOVATION LIMITED) 11 December 2014 Abstract, Claims 1 and 8-10, Example 4	4-6, 10-12
X	WO 2005/079397 A2 (ROCKEFELLER UNIVERSITY) 01 September 2005 Abstract, Table 1	4-6, 10-12
X	JONES, S., ET AL., "The identification of differentially expressed microRNA in osteoarthritic tissue that modulate the production of TNF- α and MMP13.", Osteoarthritis and Cartilage, 2009, vol. 17, no. 4, pages 464-472. Abstract, Table 1, Page 472 column 1 paragraph 3	1-2
X	FILKOVA, M., ET AL., "MicroRNAs in Rheumatoid Arthritis.", BioDrugs, 2012, vol. 26, no. 3, pages 131-141. Abstract, Page 136 column 2 paragraphs 2-4 and Page 137 column 1 paragraph 2	12-13
P,X	KUNG, L., ET AL., "Utility of circulating serum miRNAs as biomarkers of early cartilage degeneration in animal models of post-traumatic osteoarthritis and inflammatory arthritis.", Osteoarthritis and Cartilage, 2016 (Published online: 09 September), vol. 25, no. 3, pages 426-434. Abstract, Figures 3-5	1-2 and 4-12
P,X	KUNG, L., ET AL., "Cartilage microRNA dysregulation in mouse osteoarthritis overlaps with patient disease candidates." BioRxiv, 2017 (Published online: 3 March), article 113456. Abstract, Tables 1, 2, S2 and S3	1-2 and 4-12
Form PCT/ISA/210 (fifth sheet) (July 2009)		

INTERNATIONAL SEARCH REPORT C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		International application No. PCT/AU2017/050241
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	KUNG, L., ET AL., "MicroRNA expression profiling of articular cartilage from a mouse model of post-traumatic OA." Osteoarthritis and Cartilage, 2016 (April), vol. 24, supplement 1, pages S345-S346, abstract 567. Abstract	1-2 and 4-12
A	US 2004/0013663 A1 (CHOONG-CHIN, ET AL.) 22 January 2004	
A	CN 102038959 B (SHANGHAI INSTITUTES FOR BIOLOGICAL SCIENCES, CAS) 19 December 2012, English abstract retrieved from EPODOC database	

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
the subject matter listed in Rule 39 on which, under Article 17(2)(a)(i), an international search is not required to be carried out, including
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

See Supplemental Box for Details

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-2 and 4-13 (in part)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- ☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- ☐ No protest accompanied the payment of additional search fees.

Supplemental Box**Continuation of: Box III**

This International Application does not comply with the requirements of unity of invention because it does not relate to one invention or to a group of inventions so linked as to form a single general inventive concept.

This Authority has found that there are different inventions based on the following features that separate the claims into distinct groups:

Group A

Invention 1. Claims 1-2 and 4-13 (in part) are directed to the miRNA mmu-miR-6931-5p (SEQ ID NO 1) and the pre-miRNA comprising said miRNA (mmu-miR6931: SEQ ID 142); their use in diagnosing osteoarthritis; antagonists or mimics of said miRNAs (including those comprising SEQ ID NOs 156 and 170); and treating osteoarthritis using antagonists or mimics of said miRNAs.

Invention 2. Claims 1-2 and 4-13 (in part) are directed to the miRNA mmu-miR-1187 (SEQ ID NO 2) and the pre-miRNA comprising said miRNA (SEQ ID NO 146); their use in diagnosing osteoarthritis; antagonists or mimics of said miRNAs (including those comprising SEQ ID NOs 160 and 174); and treating osteoarthritis using antagonists or mimics of said miRNAs.

Invention 3. Claims 1-2 and 4-13 (in part) are directed to the miRNA mmu-miR-3082-5p (SEQ ID NO 3) and the pre-miRNA comprising said miRNA (mmu-miR-3082: SEQ ID NO 145); their use in diagnosing osteoarthritis; antagonists or mimics of said miRNAs (including those comprising SEQ ID NOs 159 and 173); and treating osteoarthritis using antagonists or mimics of said miRNAs.

Invention 4. Claims 1-2 and 4-13 (in part) are directed to the miRNAs mmu-miR-574-5p (SEQ ID NO 4) and hsa-miR-574-5p (SEQ ID NO 140), and the pre-miRNA comprising said miRNA (mmu-miR574: SEQ ID NO 144; hsa-miR-574: SEQ ID NO 154); their use in diagnosing osteoarthritis; antagonists or mimics of said miRNAs (including those comprising SEQ ID NOs 158, 168, 172, and 182); treating osteoarthritis using antagonists or mimics of said miRNAs.

Invention 5. Claims 1-2 and 4-13 (in part) are directed to the miRNA mmu-miR-466i-5p (SEQ ID NO 5) and the pre-miRNA comprising said miRNA (mmu-miR466i: SEQ ID NO 143); their use in diagnosing osteoarthritis; antagonists or mimics of said miRNAs (including those comprising SEQ ID NOs 157 and 171); and treating osteoarthritis using antagonists or mimics of said miRNAs.

Invention 6. Claims 1-2 and 4-13 (in part) are directed to the miRNA mmu-miR-669n (SEQ ID NO 6) and the pre-miRNA comprising said miRNA (SEQ ID NO 147); their use in diagnosing osteoarthritis; antagonists or mimics of said miRNAs (including those comprising SEQ ID NOs 166 and 180); and treating osteoarthritis using antagonists or mimics of said miRNAs.

Invention 7. Claims 1-2 and 4-13 (in part) are directed to the miRNA mmu-miR-468-3p (SEQ ID NO 7) and the pre-miRNA comprising said miRNA (mmu-miR-468: SEQ ID NO 148); their use in diagnosing osteoarthritis; antagonists or mimics of said miRNAs (including those comprising SEQ ID NOs 162 and 176); and treating osteoarthritis using antagonists or mimics of said miRNAs.

Inventions 8-139. As inventions 1-6, but for each of the other miRNAs listed in Tables 1 to 5 (e.g. SEQ ID NOs 8-139), wherein each miRNA represents a separate invention. Said inventions encompass, where appropriate: the associated pre-miRNA (e.g. SEQ ID NOs 149-153); antagonists comprising SEQ ID NOs 163-167, 169, 174-181 and 183; and/or the corresponding human miRNA (e.g. mmu-miRNA-32-3p and hsa-miRNA-32-3p are one invention).

Group B

Claim 3 is directed to treating osteoarthritis using antagonists or agonists of the osteoarthritis target mRNAs. Please note that the meaning of "osteoarthritis target mRNAs" is unclear and for the purposes of this report is considered to mRNAs that are targeted by miRNAs differentially regulated in osteoarthritis. As such these claims encompass an extremely large number of possible mRNAs, that may be targets of multiple miRNAs, and therefore an incalculable number of inventions. Furthermore, treatment of osteoarthritis using antagonists or agonists of target mRNAs, including the mRNAs of Tables 10 and 11, is not supported by the specification and is considered to be speculative.

Supplemental Box

PCT Rule 13.2, first sentence, states that unity of invention is only fulfilled when there is a technical relationship among the claimed inventions involving one or more of the same or corresponding special technical features. PCT Rule 13.2, second sentence, defines a special technical feature as a feature which makes a contribution over the prior art.

When there is no special technical feature common to all the claimed inventions there is no unity of invention.

In the above groups of claims, the identified features may have the potential to make a contribution over the prior art but are not common to all the claimed inventions and therefore cannot provide the required technical relationship. The only feature common to all of the claimed inventions are miRNAs that are associated with osteoarthritis and mRNAs targeted by said miRNAs. However these feature does not make a contribution over the prior art because it is disclosed in:

Linh, T.T.L., et al. "Review: the role of microRNAs in osteoarthritis and chondrogenesis." *Arthritis & Rheumatology* 65.8 (2013): 1963-1974.

Linh et al discloses numerous miRNA biomarkers of osteoarthritis, including miR-146a, and their target mRNAs, and suggests manipulating the levels of the miRNAs as a means of treating osteoarthritis (see Figure 2, Pg. 1971 Cl. 2 para. 1-3, 'MicroRNAs in osteoarthritis' Pg. 1969-1970).

Yu, X.-M., et al. "MicroRNAs' involvement in osteoarthritis and the prospects for treatments." *Evidence-Based Complementary and Alternative Medicine* 2015 (2015): Article ID 236179.

Yu et al discloses numerous miRNA associated with osteoarthritis, including miRs-146a, -155, -181a, and -223, and their targets, and further suggests miRNAs as a target for treating osteoarthritis (see Table 1, Figures 1 and 2, 'Role of miRNAs in OA' Pg. 6-8, 'miRNAs in the Diagnosis and Therapy of OA' Pg 8-9).

Therefore in the light of this document this common feature cannot be a special technical feature. Therefore there is no special technical feature common to all the claimed inventions and the requirements for unity of invention are consequently not satisfied *a posteriori*.

Due to the large number of inventions, significant search effort would be required to search all the claims and thus additional fees were requested.

In response to the request for additional search fees the Applicant elected 7 Group A (Claims 1-2 and 4-13) inventions to be searched and examined: specifically the miRNAs relating to SEQ ID NOs: 1, 2, 3, 22, 124, 140 and 141.

INTERNATIONAL SEARCH REPORT		International application No.			
Information on patent family members		PCT/AU2017/050241			
This Annex lists known patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.					
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