# MicroRNA-128-3p is a novel oncomiR targeting *PHF6* in T-cell acute lymphoblastic leukemia

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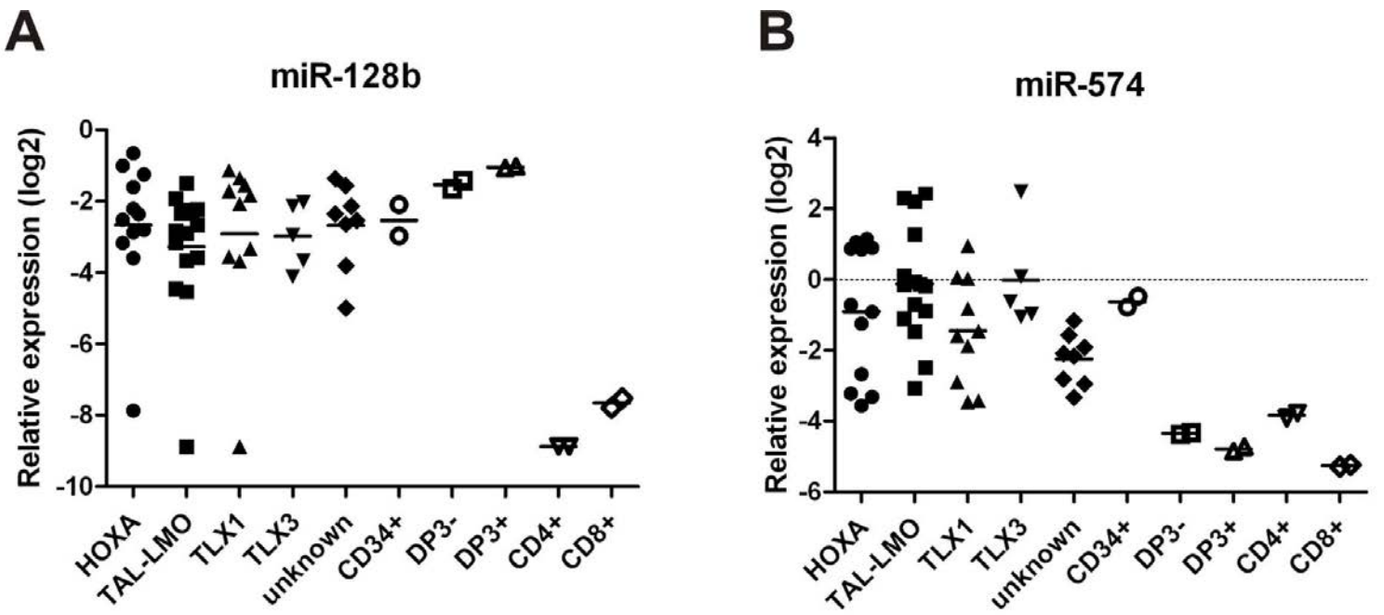
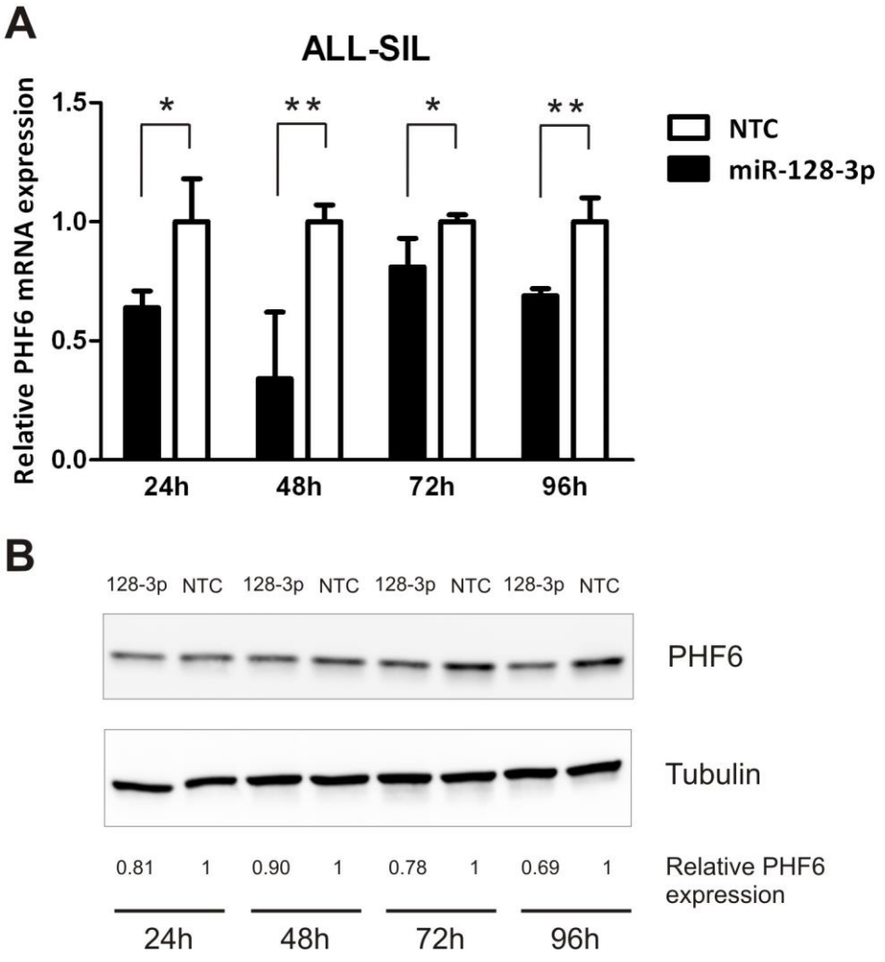
## Supplementary Figures and full Methods

### Supplementary Figure 1



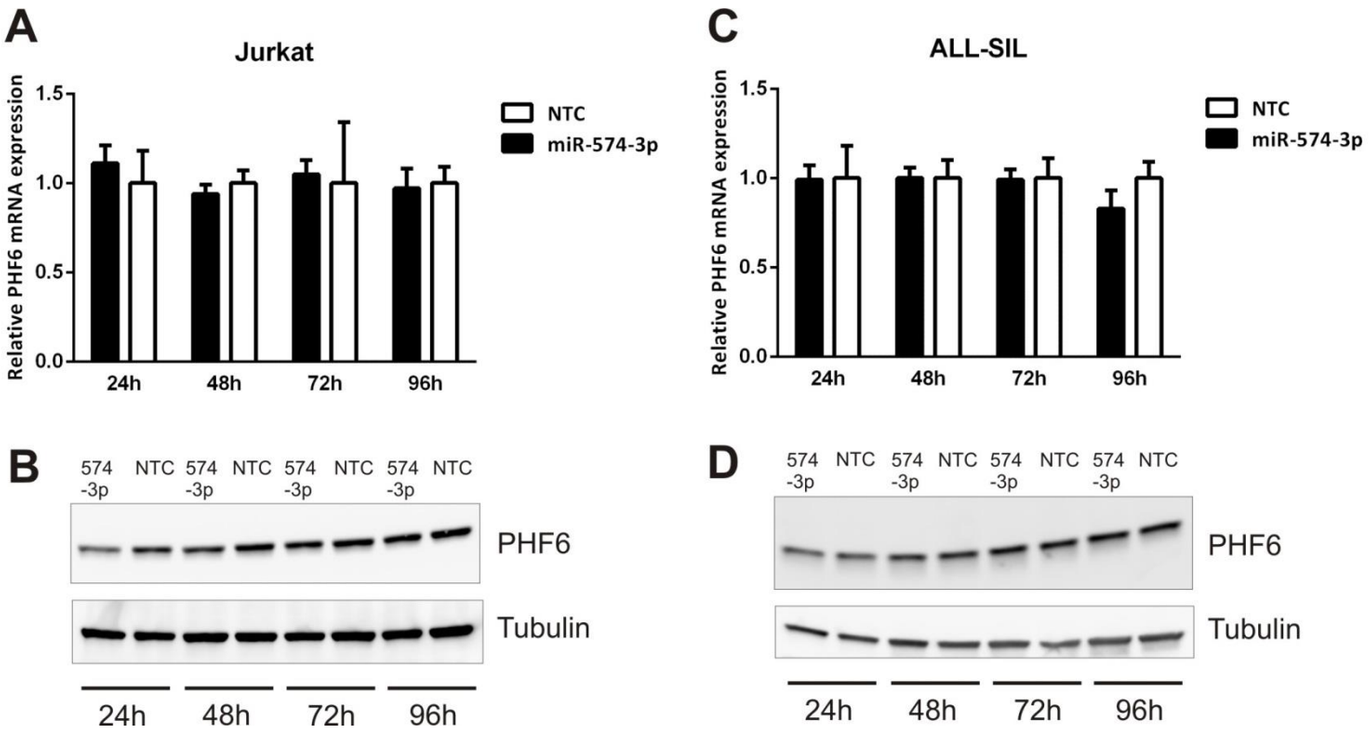

**Supplementary Figure 1**. **MicroRNA-128b and miR-574 expression profiles in T-ALL samples and normal thymocyte subsets**. Relative expression levels for **(A)** miR-128b (later annotated as miR-128-3p) and **(B)** miR-574 (later annotated as miR-574-3p) are indicated for the T-ALL patient samples in the different T-ALL subgroups (HOXA, TAL-LMO, TLX1, TLX3 and unknown cases), and for the normal thymocyte subsets (immature $CD34^+$, DP3- ($CD4^+CD8^+CD3$-), DP3+ ($CD4^+CD8^+CD3^+$), and mature $CD4^+$ or $CD8^+$ stages).

**Supplementary Figure 2**



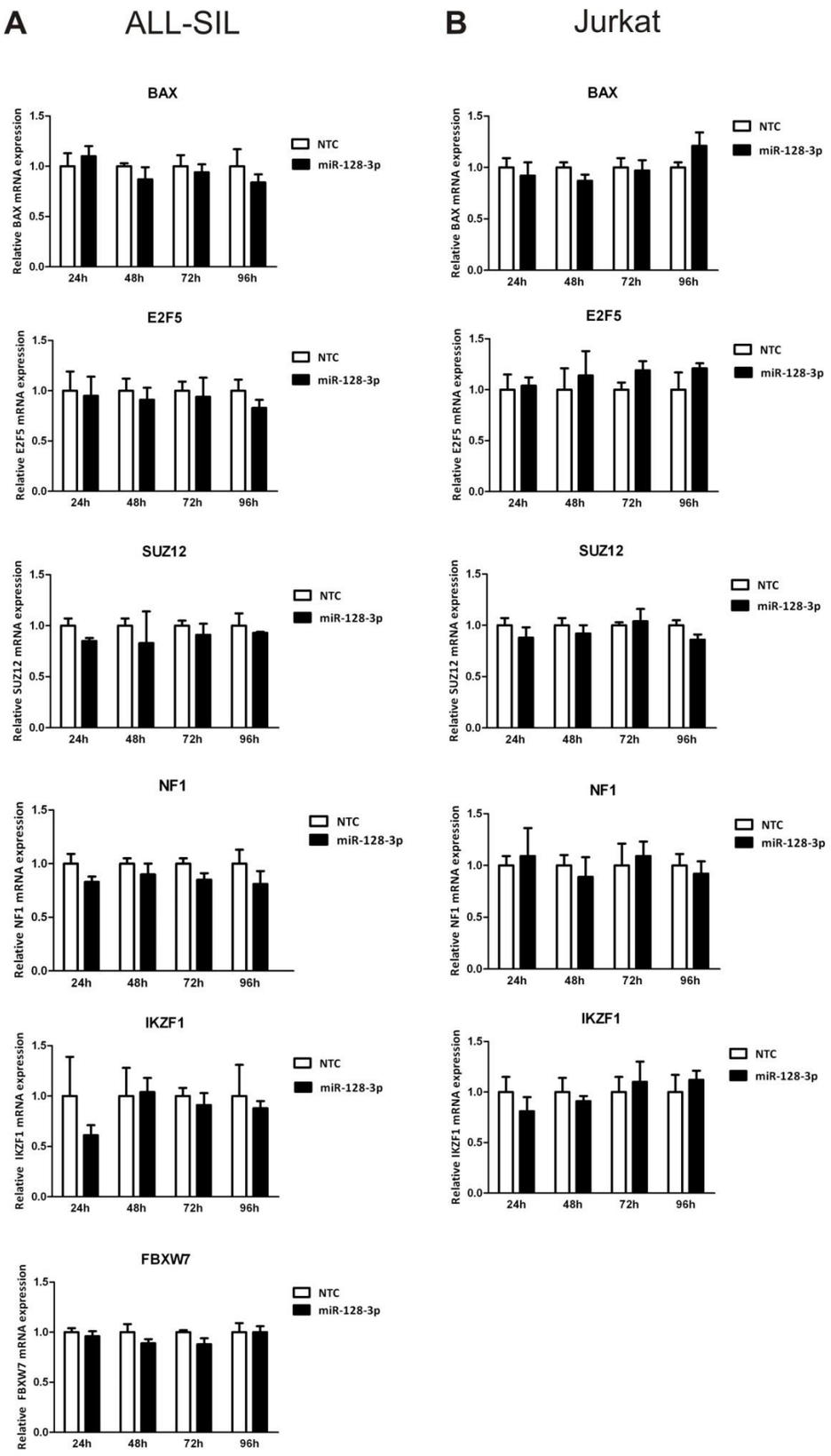

**Supplementary Figure 2**. **MicroRNA-128-3p is able to regulate *PHF6* expression in ALL-SIL cells**. Twenty-four, 48, 72, and 96 hours post-electroporation of ALL-SIL with miR-128-3p mimics, RNA and protein fractions were isolated. Following, RT-qPCR and western blot analysis were performed to evaluate the effects of miRNA overexpression on PHF6 mRNA (A) and protein (B) levels, respectively (see Methods). Results are shown from one experiment, representative for two independent biological replicates. **(A)** Each data point represents the mean (+/- SD) of 4 independent electroporation reactions (performed in parallel for each time point and for miR-128-3p/NTC). PHF6 mRNA expression was normalized against 3 reference genes (see Methods) and compared to relative PHF6 expression in the NTC controls for each time point. Significance levels (t-test): *p<0.05; **p<0.01. **(B)** PHF6 protein levels were quantified using Image J software, normalized to α-Tubulin levels, and compared to relative PHF6 levels in the NTC controls for each time point.

**Supplementary Figure 3**



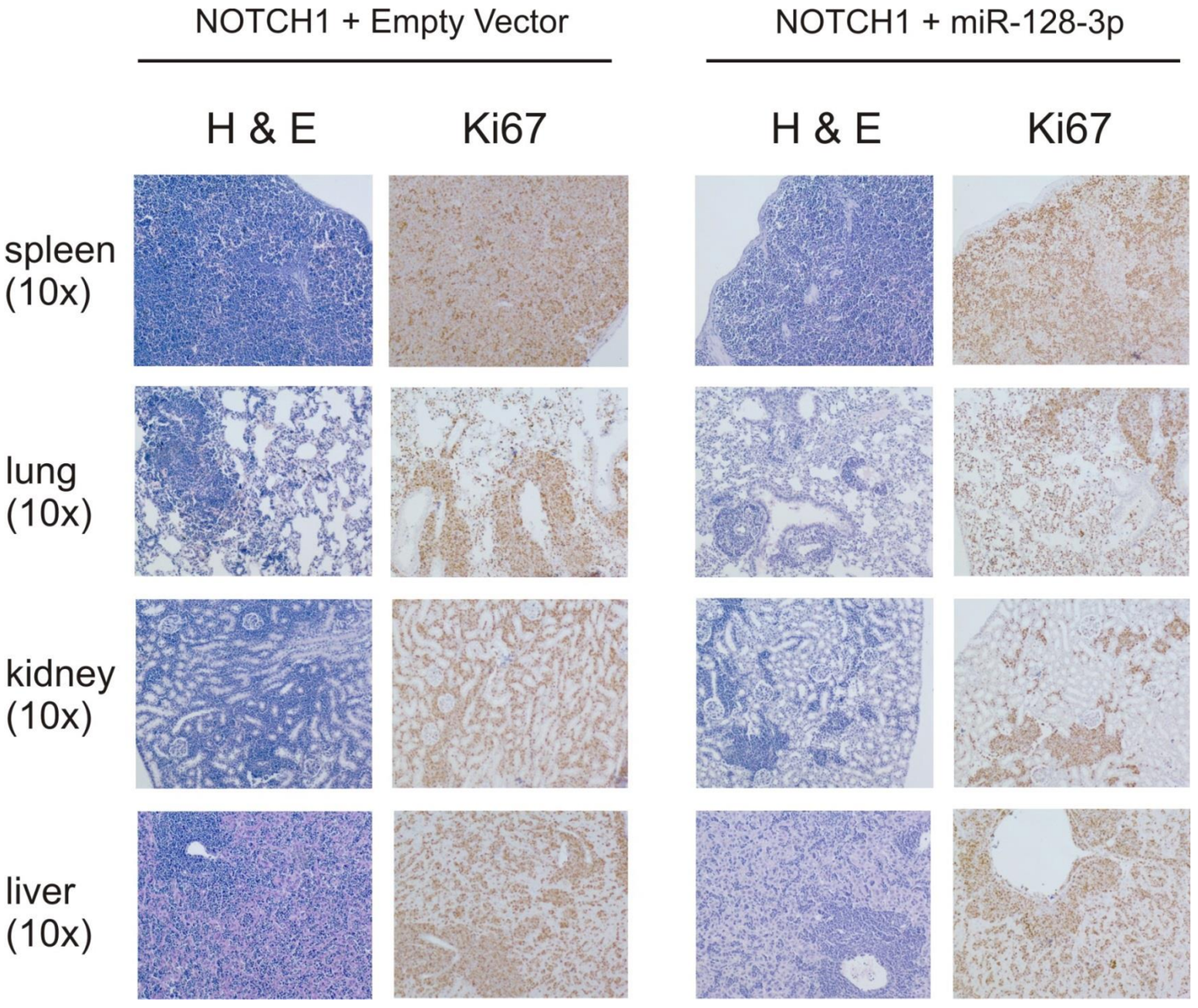

**Supplementary Figure 3**. **MicroRNA-574-3p does not significantly repress *PHF6* expression in T-ALL cells**. Twenty-four, 48, 72, and 96 hours post-electroporation of Jurkat **(A, B)** or ALL-SIL **(C, D)** cells with miR-574-3p mimics, RNA and protein fractions were isolated in parallel. Following, RT-qPCR and western blot analysis were performed to evaluate the effects of miR-574-3p overexpression on PHF6 mRNA **(A, C)** and protein **(B, D)** levels, respectively. Results are shown from one experiment for each cell line, representative for two independent biological replicates for each cell line. **(A, C)** Each data point represents the mean (+/- SD) of 4 independent electroporation reactions (performed in parallel for each time point and for miR-574-3p/NTC). PHF6 mRNA expression was normalized against 3 reference genes (see Methods) and compared to relative PHF6 expression in the NTC controls for each time point. **(B, D)** PHF6 protein levels were quantified using Image J software, normalized to α-Tubulin levels, and compared to relative PHF6 levels in the NTC controls for each time point.

**Supplementary Figure 4**



**Supplementary Figure 4**. **MicroRNA-128-3p does not significantly repress expression of *BAX*, *E2F5*, *SUZ12*, *NF1*, *IKZF1* and *FBXW7* in T-ALL cells**. Twenty-four, 48, 72, and 96 hours post-electroporation of ALL-SIL **(A)** or Jurkat **(B)** cells with miR-128-3p mimics, RNA fractions were isolated. Following, RT-qPCR analysis was performed to evaluate the effects of miR-128-3p overexpression on the expression levels of *BAX*, *E2F5*, *SUZ12*, *NF1*, *IKZF1* and *FBXW7*. Results are shown from one experiment for each cell line. The mRNA expression levels for each gene were normalized against 3 reference genes (see Methods) and compared to relative mRNA expression in the NTC controls for each time point.

**Supplementary Figure 5**




**Supplementary Figure 5. Pathological examination of T-ALL mice.** Pathological examination of leukemic mice shows infiltration of lymphoblasts in spleen, lung, kidney and liver tissues. Microphotographs (10x magnification) after H & E staining and IHC for Ki67 are shown for one control mouse (NOTCH1 + Empty Vector) and one miR-128-3p (NOTCH1 + miR-128-3p) overexpressing mouse, representative for two examined mice per group.

# Supplementary full Methods

### Cell lines

The HEK293T cell line and the T-ALL cell lines Jurkat and ALL-SIL were obtained from DSMZ and were cultured in RPMI-1640 (Gibco, Life Technologies, Carlsbad, CA, USA), supplemented with 10% FCS, L-glutamine (10 ml/L), penicillin (100 µg/ml) and streptomycine (100 µg/ml), in a controlled environment (37 °C, 5% $CO_2$).

### MicroRNA profiling of T-ALL samples and normal thymocyte subsets

MicroRNA expression profiles from 50 diagnostic T-ALL samples and T-cell subsets at different stages of T-cell differentiation, used in this study, have been previously described (1). This study (2008/531) was approved by the Medical Ethical Commission of Ghent University Hospital (Belgium, registration B67020084745), as reported before in our prior publication (1). MicroRNA profiling was performed using reverse transcription (RT) qPCR analysis according to Mestdagh et al. (2). This assay consists of 2 steps, making use of stem-loop (3) specific RT primers followed by limited cycle sample pre-amplification and final TaqMan singleplex qPCR quantification (Applied Biosystems, Life Technologies, Carlsbad, CA, USA). Concisely, 20 ng of total RNA was reverse transcribed by use of the MegaPlex reverse transcriptase stem-loop primer pool for cDNA synthesis of 430 miRNAs and 18 small RNA controls (custom design). The sequences of the miRNAs in this library can be found in Supplementary Table 2. cDNA pre-amplification was performed in a 14-cycle PCR reaction by use of TaqMan PreAmp Master Mix (2×) and PreAmp Primer Mix (5×) (Applied Biosystems). This primer mix consists of a miRNA-specific forward primer and a universal reverse primer (2). By use of a 40-cycle PCR protocol, the 448 small RNAs were profiled. SDS software version 2.1 was used to calculate the raw Cq values, using automatic base line settings and a threshold of 0.05. Normalization of the qPCR data of the miRNA expression profiles was performed according to the global mean normalization method (calculation of the average expression value of all expressed miRNAs in a given sample as the normalization factor). MicroRNAs with a Cq value >32 were considered not expressed (4).

### *PHF6* 3'UTR-miRNA library screens

HEK293T cells were seeded at a density of 10,000 cells/well in 96-well plates. Twenty-four hours after seeding, cells were co-transfected with 100 ng of a reporter vector containing the wild-type *PHF6* 3'UTR cloned downstream of the Firefly luciferase gene (SwitchGear Genomics, Menlo Park, CA, USA) and 20 ng of the pRL-TK control vector containing the Renilla luciferase gene (Promega, Madison, WI, USA) together with a library of 470 miRNA mimics (2.5 pmol) (Ambion's Pre-miR miRNA Precursor Library - Human V3, design based on miRBase release 9.2 with exclusion of hsa-miR-122a, Life Technologies, Carlsbad, CA, USA). Lipid based transfections were performed using 0.4 µl Dharmafect Duo reagent (Dharmacon, Thermo Scientific, Waltham, MA, USA). Forty-eight hours post-transfection, luciferase reporter gene activities were assayed using the Dual-Luciferase Reporter assay system (Promega) according to the manufacturer's protocol with minor changes (LARII and Stop & Glo buffer volumes were reduced to 50 µl). Firefly reporter gene activities were normalized to Renilla values, then log-transformed and subsequently robust z-scores were calculated and median centered to the distribution of robust z-scores of 36 analogous screens for other genes on a per miRNA basis in order to remove potential systematic bias. The resulting interaction scores are thus more negative for miRNAs that interact with the 3'UTR. In order to determine the interaction score cutoff that separates interactions from non-interactions, the scores for a set of miRNA interactions validated in literature and re-evaluated in the analogous screens were used together with the scores for a set of negative control interactions from an empty 3'UTR vector miRNA library screen to perform ROC-curve analysis and determine the point of highest accuracy (interaction score cutoff= -1.94, accuracy= 91%, specificity = 99%, sensitivity = 51%). *PHF6* 3'UTR-miRNA library screen results were replicated in three independent experiments. For

a more detailed description of the 3'UTR-miRNA library screen setup and data-analysis we refer to Van Peer et al. (in preparation).

**Single 3'UTR-miRNA reporter gene assays and rescue experiments**

The Site-Directed Mutagenesis Kit (Stratagene, Agilent Technologies, Santa Clara, CA, USA) was used to generate *PHF6* 3'UTR reporter constructs in which miR-128-3p target sites were mutated. Sanger sequencing was used to confirm successful mutagenesis in the mutant constructs. Primer sequences used for mutagenesis:

| | |
|---|---|
| 7mer-m8 (1) | FW: AAAATGTAACAGGTGGAAAATTAAAAGTTGCTTAATGACTGATTT |
| | REV: AAATCAGTCATTAAGCAACTTTTAATTTTCCACCTGTTACATTTT |
| 7mer-m8 (2) | FW: TCCTTAAAGCcAGGTGTCTAGATCATTTTTTACATTGTGTGCC |
| | REV: GGCACACAATGTAAAAAATGATCTAGACACCTGGCTTTAAGGA |
| 7mer-m8 (3) | FW: ACTACCTGTTTTTCGCCAGGTGGTGTGATTGGCT |
| | REV: AGCCAATCACACCACCTGGCGAAAAACAGGTAGT |
| 6mer off-set | FW: GACATCCATAACTACTATTCTTTTGTACATGTTTTCTAAAATC |
| | REV: GATTTTAGAAAACATGTACAAAAGAATAGTAGTTATGGATGTC |

HEK-293T cells were co-transfected with the wild-type/mutant 3'UTR vector of *PHF6* (SwitchGear Genomics) and a pRL-TK control vector (Promega) together with either the miRNA mimic of interest (Ambion, PM11746, 4427975) or a scrambled, non-targeting control (NTC) miRNA mimic (Ambion, AM17111). Transfections and luciferase measurements were performed as described above.

**Transfection/electroporation of miRNA mimics or LNAs in cell lines**

HEK-293T cells were seeded in 6-well culture plates at a density of 200,000 cells per well, 24 hours prior to transfection. Cells were transfected using Dharmafect2 (Thermo Scientific) at a final concentration of 0.4 % and a final concentration of 100 nM miRNA mimics (Ambion). T-ALL cell lines ALL-SIL and Jurkat were transfected with miRNA mimics by electroporation. Briefly, for each electroporation, 16 $x10^6$ cells were suspended in 500 µl RPMI medium. MicroRNA mimics were then added to the cell suspension (final concentration 600 nM). Next, cells were transferred to an electroporation tube and electroporated (0.250 kV and 1 mF) with the Gene Pulser II (Bio-Rad). Cells from one electroporation were then divided over four 12-well plates to a final cell suspension of 3.2 $x10^6$ cells in 2 ml RPMI-1640 + 15% FCS. Cells were incubated at 37°C and collected for protein and RNA isolation after 24, 48, 72 and 96 hours (see further). For miR-128-3p knock down studies, Jurkat cells were electroporated with miR-128 specific LNAs (miRCURY LNA™ microRNA Power inhibitor, #426742-00, Exiqon, Vedbaeck, Denmark) or non-targeting control LNAs (Power control A, #500150). LNAs (final concentration 400 nM) were electroporated at 0.300 kV and 1 mF with the Gene Pulser II.

**RNA isolation, cDNA synthesis and RT-qPCR**

Total RNA was isolated with the miRNeasy Mini Kit (Qiagen, Hilden, Germany) and DNase-treated (RNase-Free DNase Set, Qiagen) according to the manufacturer's protocol. RNA concentration and purity was measured using the Nanodrop instrument (Thermo Scientific, Waltham, MA, USA). cDNA synthesis was performed on 500 ng total RNA with 4 µl of iScript reaction mix and 1 µl of iScript reverse transcriptase (iScript, Bio-Rad, Hercules, CA, USA) in a final volume of 20 µl. Subsequently, this mix was incubated for 5′ at 25°C, 30′ at 42°C and 5′ at 85°C using the iCycler (Bio-Rad).

RT-qPCR gene expression quantifications were performed and reported according to the MIQE guidelines where appropriate (5). All reactions were performed in 384-well plates using 5 ng cDNA, 2.5 µl of SsoAdvanced (Bio-Rad) mastermix and 250 nM primers in a total volume of 5 µl. The readout was performed by use of the LightCycler 480

instrument (Roche, Basel , Switzerland). All qPCR reactions were performed in duplicate and Cq values were averaged.

Expression levels were normalized against at least three out of four stably expressed reference genes per experiment (for HEK293T: *HMBS*, *SDC4*, *SDHA*, *TBP*; for ALL-SIL: *UBC*, *YWHAZ*, *HMBS*, *HPRT1*; for Jurkat: *B2M*, *SDC4*, *SDHA*, *TBP*; for mouse samples: *tbp, ubc* and *ppia*) and analyzed using qbase+ software (http://www.biogazelle.com). All qPCR assays were extensively validated *in silico* using the primerXL (http://www.primerxl.org/) pipeline and empirically validated, checking both primer efficiency and specificity.

Primer sequences used for RT-qPCR assays in these studies, listed per gene (* mouse genes; rest are human):

| Gene | Forward primer sequence | Reverse primer sequence |
|---|---|---|
| ***phf6**** | **GTGGGACAGAGAGAGTTAGA** | **GGCAGTTCAATGAAGGATCT** |
| ***ikzf1**** | **GCTAGCCTTACCCAAATTCA** | **GCTAAGGATGAGTGAGCAAA** |
| ***nf1**** | **ATTCGATACACTTGCGGAAA** | **CTCATCCCACTGAGAACAAG** |
| ***pten**** | **GTAATCAAGGCCAGTGCTAA** | **CACATGAAGCATCCACAGTA** |
| ***bax**** | **GAGATGAACTGGACAGCAAT** | **GAAGTTGCCATCAGCAAAC** |
| ***fbxw7**** | **AGCATGTCCACGTTAGAATC** | **GTGCCGTAGAAACCCATATT** |
| ***e2f5**** | **ACACAGCTGGAAGTACCTAT** | **AACCACTGGCTTAGATGAAC** |
| ***suz12**** | **ACTGTATAGCTTACTCAAACATCT** | **CTCCGACATGCTTGCTTT** |
| ***tbp**** | **CCCCACAACTCTTCCATTCT** | **GCAGGAGTGATAGGGGTCAT** |
| ***ubc**** | **GCAGATCTTTGTGAAGACCC** | **GAAGGTACGTCTGTCTTCCT** |
| ***ppia**** | **CAGACGCCACTGTCGCTTT** | **TGTCTTTGGAACTTTGTCTGCAA** |
| ***PHF6*** | AAAAGGGCCTACAAGACAG | ACAATGGCACAAAGAACAC |
| ***IKZF1*** | ACCCGAGGATCAGTCTTG | TCCATGGTCCTCAGGTTAT |
| ***NF1*** | AGCACAACAAGGAATGTCTAA | GCTTCTCCAAATATTCTCATATTGTT |
| ***PTEN*** | CCGAAAGGTTTTGCTACCATTCT | AAAATTATTTCCTTTCTGAGCATTCC |
| ***BAX*** | GATGCGTCCACCAAGAAGCT | CGGCCCCAGTTGAAGTTG |
| ***FBXW7*** | TGGGATATCAAAACAGGACAGTGT | TAAACAGGTCACAGCACTCTGATG |
| ***E2F5*** | CCTGTTCCCCCACCTGATG | TTTCTGTGGAGTCACTGGAGTCA |
| ***SUZ12*** | AACAGCCATATGGTGAAGTC | CTGGAAGCTCTTCATTGACA |
| ***HMBS*** | GGCAATGCGGCTGCAA | GGGTACCCACGCGAATCAC |

| | | |
|---|---|---|
| ***SDHA*** | TGGGAACAAGAGGGCATCTG | CCACCACTGCATCAAATTCATG |
| ***TBP*** | CACGAACCACGGCACTGATT | TTTTCTTGCTGCCAGTCTGGAC |
| ***UBC*** | ATTTGGGTCGCGGTTCTTG | TGCCTTGACATTCTCGATGGT |
| ***YWHAZ*** | ACTTTTGGTACATTGTGGCTTCAA | CCGCCAGGACAAACCAGTAT |
| ***HPRT1*** | TGACACTGGCAAAACAATGCA | GGTCCTTTTCACCAGCAAGCT |
| ***B2M*** | TGCTGTCTCCATGTTTGATGTATCT | TCTCTGCTCCCCACCTCTAAGT |

**Protein isolation and Western blot**

Cells were washed with ice-cold PBS and snap-frozen in liquid nitrogen. Cells were lysed in RIPA lysis buffer (32 mM $Na^+$-DOC, 150 mM NaCl, 50 mM TrisHCl (pH 7.5), 0.1 % SDS en 1 % NP-40) supplemented with protease inhibitors (Complete Protease Inhibitor Cocktail Tablets, Roche), incubated for minimum 30 minutes at 4 °C under rotating conditions, and finally centrifuged (8000 g, 10 minutes, 4 °C) to obtain cleared lysate fractions. Per fraction, 20 µl lysate was combined with 5µl of a denaturation buffer mix (5x laemmli buffer (25 ml 10 % SDS-solution, 20 ml 100 % glycerol, 7.75 ml 1 M TrisHCl pH 6.8 en 1.25 ml 1 % Bromo Phenol Blue solution), 1:7 40x β-mercaptoethanol), and incubated at 95°C for 10 min in a shaker. Denatured fractions were subsequently loaded on precast gels (Bio-Rad; 10% SDS) and subjected to SDS-PAGE (100 V and 0.25 A, 1-2 hours). Proteins were then transferred onto a nitrocellulose membrane (nitrocellulose/Filter Paper Sandwiches 0.2µm, Bio-Rad) (100 V, 0.25 A, 1-2 hours). Membranes were blocked with a solution of 5% non-fat milk in 1x TBST for 1 hour and then probed with primary antibodies dissolved in 5% milk/TBST by overnight incubation at 4°C. Primary antibodies used in this study are anti-PHF6 (rabbit, Cell Signaling (Danvers, MA, USA), 7076S, dilution 1/2000; rabbit, Sigma, HPA001023, dilution 1/2000), anti-α-tubuline (mouse, Sigma (St. Louis, MI, USA, T5168, dilution 1/5000) and anti-β-actin (mouse, Sigma, A5316, dilution 1/5000). Membranes were then 3 times washed for 5 minutes with 1x TBST and probed with HRP-linked secondary antibodies dissolved in 5% milk/TBST for 1 hour. Secondary antibodies used in this study are HRP-linked anti-mouse and anti-rabbit (Cell Signaling, dilution 1/5000). Finally, membranes were washed 3 times for 5 min with 1xTBST, incubated with luminal/enhancer buffer (SuperSignal West Dura Extended Duration Substrate, Thermo Scientific) and developed by chemiluminescent detection using the UCP chemiDoc-it® 500 Imaging System (UVP). To remove antibodies from the blots, membranes were incubated with stripping buffer (Restore PLUS Western Blot Stripping Buffer, Thermo Scientific) for 15 minutes, washed for 5 times (5 minutes per wash) with 1x TBST, and blocked with 5% milk/TBST before probing with another primary antibody.

**Rank Products analysis**

MicroRNAs differentially expressed (pfp-value <0.05) between T-ALL patient samples and normal thymocyte subsets were identified using Rank Products analysis (RankProd package) in the R statistical programming environment (version 3.0.1).

**MicroRNA nomenclature and annotation**

During the course of this study, official nomenclature an sequence annotation as put forward by the miRBase database (http://www.mirbase.org/) changed for the miRNAs investigated here. At the start of our study, miR-574 (mature sequence CACGCUCAUGCACACACCCAC) and both miR-128a (mature sequence UCACAGUGAACCGGUCUCUUUU) and miR-128b (mature sequence UCACAGUGAACCGGUCUCUUUC) were

annotated in miRBase (release 9.2), and all three were included in the miRNA library for the PHF6 3'UTR screens and the library for miRNA profiling of the T-ALL patient samples and normal thymocytes. In the miRNA library screens for *PHF6*, miR-574 and miR-128b were found to be hits (see Supplementary Table 1). However, at the start of our validation studies, miRBase merged the records of miR-128a and miR-128b into a single record, miR-128 (accession number MIMAT0000424), with a mature sequence (UCACAGUGAACCGGUCUCUUU) that is one nucleotide shorter than the sequences of the previously annotated miR-128a and miR-128b. Also miR-574 was re-annotated to miR-574-3p (mature sequence CACGCUCAUGCACACACCCAC), which is one nucleotide longer at the 3' end. Therefore, we used these newly annotated miR-128 and miR-574-3p sequences in our follow-up experiments, including the validation luciferase (and rescue) assays in HEK293T (Figure 3), and the miRNA overexpression experiments in HEK293T (Figure 4) and T-ALL cell lines (Figure 5 and Supplementary Figures 2-4). We speculated that, since the sequence changes occurred 3' of the miRNA's sequences, it is likely that the newly annotated miR-128 and miR-574-3p sequences are functionally redundant, as the seed regions remain unchanged. We could indeed confirm in follow-up experiments that *PHF6* is equally regulated by miR-128 and miR-574-3p in HEK293T. In the most recent release of miRBase (release 20), the human mature miR-128 sequence (UCACAGUGAACCGGUCUCUUU) was renamed miR-128-3p. In this manuscript, we use the most up-to-date names at time of publication for the miRNAs under investigation, miR-128-3p and miR-574-3p. For the miRNA overexpression studies in mouse, the human pre-miR-128-2 sequence was used, which gives rise to mature miR-128-3p.

**T-ALL mouse model**

For the mouse work, the institutional and national guide for the care and use of laboratory animals was followed. Fetal liver cells from mice were isolated at embryonic day 13-14 and retrovirally transduced with ICN1 (active NOTCH1, labeled with mCherry) expression vectors in combination with miR-128-3p expression vectors or empty vector controls (labeled with GFP). The transduced fetal liver cells were subsequently injected in the tail vein of lethally irradiated mouse recipients. The onset of leukemia in these mice was then monitored by analysis of lymphoblast counts in blood smears and physical appearance. At diagnosis, several tissues (spleen, lung, liver, kidney) were fixed for histological evaluation. Additional FACS analysis was performed to confirm that tumor cells are GFP-positive in the miR-128-3p overexpressing mice. Time-to-leukemia onset data were analyzed using the Kaplan-Meier method and the log-rank (Mantel-Cox) test for statistical significance.

**Histology and immunohistochemistry (IHC) of mouse tumor samples**

Dissected tissue samples were formalin fixed overnight at 4 °C, washed in PBS and paraffin-embedded according to standard procedures. Paraffin-embedded tissues were sectioned at 5 μm and stained with hematoxylin and eosin (H&E). Additional IHC staining was performed for Ki67. First, antigen retrieval was done in citrate buffer, pH 6 (Dako, Glostrup, Denmark) using an electric pressure cooker (PickCell Laboratories, The Netherlands). Colorimetric staining was performed using a rabbit polyclonal anti-Ki67 primary antibody (Cell Signaling, dilution 1/1000) and a biotinylated goat anti-rabbit secondary antibody (Dako, dilution 1/500) with Vectastain Elite ABC reagent (Vector Labs, Burlingame, CA, USA). Visualisation was done using DAB kit (Dako) and counterstained with hematoxylin. Stainings were analyzed with a BX51 Discussion microscope (Olympus, Shinjuku, Tokyo, Japan). Representative pictures were made with a cooled interline CCD camera.

**References for Methods section**

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**Supplementary Table 1**

Results PHF6 3'UTR-miRNA library screens: interaction scores are calculated based on 3 independent screens

23 miRNAs that are positive hits (interaction score < -1.94) are indicated in bold

* accession number in miRBase

** mature miRNA sequence of the mirs used in the library

*** miRNAs that are predicted by at least one of the following in silico prediction algorithms:

TargetScan, PicTar, miRanda, MirTarget2, Diana, microT --> indicated by "yes" (only indicated for the 23 positive hits)

| MicroRNA ID | accession number* | mature miRNA sequence** | interaction score | predicted ***(only for the 30 hits) |
|---|---|---|---|---|
| **hsa-miR-449b** | **MIMAT0003327** | **AGGCAGUGUAUUGUUAGCUGGC** | **-4,673835802** | **yes** |
| **hsa-miR-378** | **MIMAT0000731** | **CUCCUGACUCCAGGUCCUGUGU** | **-4,570671533** | |
| **hsa-miR-512-5p** | **MIMAT0002822** | **CACUCAGCCUUGAGGGCACUUUC** | **-3,999460203** | **yes** |
| **hsa-miR-192** | **MIMAT0000222** | **CUGACCUAUGAAUUGACAGCC** | **-3,78431907** | |
| **hsa-miR-802** | **MIMAT0004185** | **CAGUAACAAAGAUUCAUCCUUGU** | **-3,717571631** | |
| **hsa-miR-128b** | **MIMAT0000676** | **UCACAGUGAACCGGUCUCUUUC** | **-3,582263318** | **yes** |
| **hsa-miR-504** | **MIMAT0002875** | **AGACCCUGGUCUGCACUCUAU** | **-3,409181782** | |
| **hsa-miR-449** | **MIMAT0001541** | **UGGCAGUGUAUUGUUAGCUGGU** | **-3,235170215** | **yes** |
| **hsa-miR-574** | **MIMAT0003239** | **CACGCUCAUGCACACACCCAC** | **-3,038643434** | |
| **hsa-miR-215** | **MIMAT0000272** | **AUGACCUAUGAAUUGACAGAC** | **-2,932187703** | |
| **hsa-miR-640** | **MIMAT0003310** | **AUGAUCCAGGAACCUGCCUCU** | **-2,816121553** | |
| **hsa-miR-526b** | **MIMAT0002835** | **CUCUUGAGGGAAGCACUUUCUGUU** | **-2,744969052** | **yes** |
| **hsa-miR-527** | **MIMAT0002862** | **CUGCAAAGGGAAGCCCUUUCU** | **-2,666329312** | **yes** |
| **hsa-miR-328** | **MIMAT0000752** | **CUGGCCCUCUCUGCCCUUCCGU** | **-2,642174213** | **yes** |
| **hsa-miR-660** | **MIMAT0003338** | **UACCCAUUGCAUAUCGGAGUUG** | **-2,425200893** | |
| **hsa-miR-34c** | **MIMAT0000686** | **AGGCAGUGUAGUUAGCUGAUUGC** | **-2,27250551** | **yes** |
| **hsa-miR-217** | **MIMAT0000274** | **UACUGCAUCAGGAACUGAUUGGAU** | **-2,180790751** | **yes** |
| **hsa-miR-30a-5p** | **MIMAT0000087** | **UGUAAACAUCCUCGACUGGAAG** | **-2,114368585** | **yes** |
| **hsa-miR-634** | **MIMAT0003304** | **AACCAGCACCCCAACUUUGGAC** | **-2,044784935** | |
| **hsa-miR-485-3p** | **MIMAT0002176** | **GUCAUACACGGCUCUCCUCUCU** | **-2,044030707** | |
| **hsa-miR-329** | **MIMAT0001629** | **AACACACCUGGUUAACCUCUUU** | **-2,010051952** | |
| **hsa-miR-410** | **MIMAT0002171** | **AAUAUAACACAGAUGGCCUGU** | **-1,982362739** | **yes** |
| **hsa-miR-575** | **MIMAT0003240** | **GAGCCAGUUGGACAGGAGC** | **-1,972466815** | |
| hsa-miR-141 | MIMAT0000432 | UAACACUGUCUGGUAAAGAUGG | -1,934253753 | |
| hsa-miR-599 | MIMAT0003267 | GUUGUGUCAGUUUAUCAAAC | -1,906037771 | |
| hsa-miR-601 | MIMAT0003269 | UGGUCUAGGAUUGUUGGAGGAG | -1,900539339 | |
| hsa-miR-551a | MIMAT0003214 | GCGACCCACUCUUGGUUUCCA | -1,856609378 | |
| hsa-miR-193b | MIMAT0002819 | AACUGGCCCUCAAAGUCCCGCUUU | -1,813576398 | |
| hsa-miR-510 | MIMAT0002882 | UACUCAGGAGAGUGGCAAUCACA | -1,80431607 | **yes** |
| hsa-miR-580 | MIMAT0003245 | UUGAGAAUGAUGAAUCAUUAGG | -1,783405434 | |
| hsa-miR-448 | MIMAT0001532 | UUGCAUAUGUAGGAUGUCCCAU | -1,761799469 | |
| hsa-miR-551b | MIMAT0003233 | GCGACCCAUACUUGGUUUCAG | -1,737557416 | |
| hsa-miR-513 | MIMAT0002877 | UUCACAGGGAGGUGUCAUUUAU | -1,717715511 | |
| hsa-miR-302a* | MIMAT0000683 | UAAACGUGGAUGUACUUGCUUU | -1,707880901 | |
| hsa-miR-18b | MIMAT0001412 | UAAGGUGCAUCUAGUGCAGUUA | -1,707439585 | |
| hsa-miR-766 | MIMAT0003888 | ACUCCAGCCCCACAGCCUCAGC | -1,693683962 | |
| hsa-miR-30b | MIMAT0000420 | UGUAAACAUCCUACACUCAGCU | -1,631007737 | |
| hsa-miR-500 | MIMAT0002871 | AUGCACCUGGGCAAGGAUUCUG | -1,611606124 | |
| hsa-miR-502 | MIMAT0002873 | AUCCUUGCUAUCUGGGUGCUA | -1,608303796 | |
| hsa-miR-581 | MIMAT0003246 | UCUUGUGUUCUCUAGAUCAGU | -1,562473542 | |
| hsa-miR-339 | MIMAT0000764 | UCCCUGUCCUCCAGGAGCUCA | -1,539661414 | |
| hsa-miR-133b | MIMAT0000770 | UUGGUCCCCUUCAACCAGCUA | -1,45938836 | |
| hsa-miR-31 | MIMAT0000089 | GGCAAGAUGCUGGCAUAGCUG | -1,441584885 | |
| hsa-miR-495 | MIMAT0002817 | AAACAAACAUGGUGCACUUCUUU | -1,407065691 | |
| hsa-miR-521 | MIMAT0002854 | AACGCACUUCCCUUUAGAGUGU | -1,362362964 | |
| hsa-miR-493-3p | MIMAT0003161 | UGAAGGUCUACUGUGUGCCAG | -1,33266028 | |
| hsa-miR-137 | MIMAT0000429 | UAUUGCUUAAGAAUACGCGUAG | -1,322021493 | |
| hsa-miR-183 | MIMAT0000261 | UAUGGCACUGGUAGAAUUCACUG | -1,311562929 | |
| hsa-miR-189 | MIMAT0000079 | GUGCCUACUGAGCUGAUAUCAGU | -1,308321096 | |
| hsa-miR-124a | MIMAT0000422 | UUAAGGCACGCGGUGAAUGCCA | -1,28649303 | |
| hsa-miR-129 | MIMAT0000242 | CUUUUUGCGGUCUGGGCUUGC | -1,28534587 | |
| hsa-miR-586 | MIMAT0003252 | UAUGCAUUGUAUUUUUAGGUCC | -1,284855098 | |
| hsa-miR-548a | MIMAT0003251 | CAAAACUGGCAAUUACUUUUGC | -1,263967489 | |
| hsa-miR-614 | MIMAT0003282 | GAACGCCUGUUCUUGCCAGGUGG | -1,244338148 | |
| hsa-miR-25 | MIMAT0000081 | CAUUGCACUUGUCUCGGUCUGA | -1,236359545 | |
| hsa-miR-653 | MIMAT0003328 | UUGAAACAAUCUCUACUGAAC | -1,208209842 | |
| hsa-miR-630 | MIMAT0003299 | AGUAUUCUGUACCAGGGAAGGU | -1,20005136 | |

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| hsa-miR-193a | MIMAT0000459 | AACUGGCCUACAAAGUCCCAG | -1,180981651 |
| hsa-miR-139 | MIMAT0000250 | UCUACAGUGCACGUGUCU | -1,180719932 |
| hsa-miR-133a | MIMAT0000427 | UUGGUCCCCUUCAACCAGCUGU | -1,130973465 |
| hsa-miR-600 | MIMAT0003268 | ACUUACAGACAAGAGCCUUGCUC | -1,11326447 |
| hsa-miR-493-5p | MIMAT0002813 | UUGUACAUGGUAGGCUUUCAUU | -1,10998887 |
| hsa-miR-499 | MIMAT0002870 | UUAAGACUUGCAGUGAUGUUUAA | -1,09355389 |
| hsa-miR-642 | MIMAT0003312 | GUCCCUCUCCAAAUGUGUCUUG | -1,084799615 |
| hsa-miR-297 | MIMAT0004450 | AUGUAUGUGUGCAUGUGCAUG | -1,084071567 |
| hsa-miR-409-3p | MIMAT0001639 | CGAAUGUUGCUCGGUGAACCCCU | -1,072875728 |
| hsa-miR-421 | MIMAT0003339 | AUCAACAGACAUUAAUUGGGCGC | -1,062367959 |
| hsa-miR-576 | MIMAT0003241 | AUUCUAAUUUCUCCACGUCUUUG | -1,023727037 |
| hsa-miR-656 | MIMAT0003332 | AAUAUUAUACAGUCAACCUCU | -1,017121063 |
| hsa-miR-99a | MIMAT0000097 | AACCCGUAGAUCCGAUCUUGUG | -0,973017933 |
| hsa-miR-99b | MIMAT0000689 | CACCCGUAGAACCGACCUUGCG | -0,967033726 |
| hsa-miR-100 | MIMAT0000098 | AACCCGUAGAUCCGAACUUGUG | -0,9602037 |
| hsa-miR-324-5p | MIMAT0000761 | CGCAUCCCCUAGGGCAUUGGUGU | -0,955924053 |
| hsa-miR-18a | MIMAT0000072 | UAAGGUGCAUCUAGUGCAGAUA | -0,951171255 |
| hsa-miR-380-3p | MIMAT0000735 | UAUGUAAUAUGGUCCACAUCUU | -0,945036144 |
| hsa-miR-595 | MIMAT0003263 | GAAGUGUGCCGUGGUGUGUCU | -0,94180577 |
| hsa-miR-26b | MIMAT0000083 | UUCAAGUAAUUCAGGAUAGGUU | -0,93928048 |
| hsa-miR-490 | MIMAT0002806 | CAACCUGGAGGACUCCAUGCUG | -0,933681115 |
| hsa-miR-142-3p | MIMAT0000434 | UGUAGUGUUUCCUACUUUAUGGA | -0,930318338 |
| hsa-miR-548c | MIMAT0003285 | CAAAAAUCUCAAUUACUUUUGC | -0,915237927 |
| hsa-miR-486 | MIMAT0002177 | UCCUGUACUGAGCUGCCCCGAG | -0,909901749 |
| hsa-miR-506 | MIMAT0002878 | UAAGGCACCCUUCUGAGUAGA | -0,903043193 |
| hsa-miR-143 | MIMAT0000435 | UGAGAUGAAGCACUGUAGCUCA | -0,896381177 |
| hsa-miR-452* | MIMAT0001636 | UCAGUCUCAUCUGCAAAGAAG | -0,894998075 |
| hsa-miR-181a | MIMAT0000256 | AACAUUCAACGCUGUCGGUGAGU | -0,891029287 |
| hsa-miR-34a | MIMAT0000255 | UGGCAGUGUCUUAGCUGGUUGUU | -0,88880131 |
| hsa-miR-95 | MIMAT0000094 | UUCAACGGGUAUUUAUUGAGCA | -0,872030072 |
| hsa-miR-299-3p | MIMAT0000687 | UAUGUGGGAUGGUAAACCGCUU | -0,864323331 |
| hsa-miR-96 | MIMAT0000095 | UUUGGCACUAGCACAUUUUUGC | -0,863272272 |
| hsa-miR-618 | MIMAT0003287 | AAACUCUACUUGUCCUUCUGAGU | -0,862586808 |
| hsa-miR-196b | MIMAT0001080 | UAGGUAGUUUCCUGUUGUUGG | -0,854713247 |
| hsa-miR-566 | MIMAT0003230 | GGGCGCCUGUGAUCCCAAC | -0,830681032 |
| hsa-miR-620 | MIMAT0003289 | AUGGAGAUAGAUAUAGAAAU | -0,82096538 |
| hsa-miR-30e-5p | MIMAT0000692 | UGUAAACAUCCUUGACUGGA | -0,820646054 |
| hsa-miR-559 | MIMAT0003223 | UAAAGUAAAUAUGCACCAAAA | -0,813892692 |
| hsa-miR-770-5p | MIMAT0003948 | UCCAGUACCACGUGUCAGGGCCA | -0,804521567 |
| hsa-miR-552 | MIMAT0003215 | AACAGGUGACUGGUUAGACAA | -0,792212089 |
| hsa-miR-17-3p | MIMAT0000071 | ACUGCAGUGAAGGCACUUGU | -0,788976883 |
| hsa-miR-626 | MIMAT0003295 | AGCUGUCUGAAAAUGUCUU | -0,786431972 |
| hsa-miR-584 | MIMAT0003249 | UUAUGGUUUGCCUGGGACUGAG | -0,768975253 |
| hsa-miR-212 | MIMAT0000269 | UAACAGUCUCCAGUCACGGCC | -0,76650927 |
| hsa-miR-190 | MIMAT0000458 | UGAUAUGUUUGAUAUAUUAGGU | -0,754153571 |
| hsa-miR-597 | MIMAT0003265 | UGUGUCACUCGAUGACCACUGU | -0,744656527 |
| hsa-miR-548b | MIMAT0003254 | CAAGAACCUCAGUUGCUUUUGU | -0,740796818 |
| hsa-miR-655 | MIMAT0003331 | AUAAUACAUGGUUAACCUCUUU | -0,73678672 |
| hsa-miR-644 | MIMAT0003314 | AGUGUGGCUUUCUUAGAGC | -0,71476001 |
| hsa-miR-224 | MIMAT0000281 | CAAGUCACUAGUGGUUCCGUUUA | -0,710029532 |
| hsa-miR-514 | MIMAT0002883 | AUUGACACUUCUGUGAGUAG | -0,709150513 |
| hsa-miR-337 | MIMAT0000754 | UCCAGCUCCUAUAUGAUGCCUUU | -0,703988707 |
| hsa-miR-182 | MIMAT0000259 | UUUGGCAAUGGUAGAACUCACA | -0,696704024 |
| hsa-miR-30e-3p | MIMAT0000693 | CUUUCAGUCGGAUGUUUACAGC | -0,684906992 |
| hsa-miR-142-5p | MIMAT0000433 | CAUAAAGUAGAAAGCACUAC | -0,67286256 |
| hsa-miR-199a* | MIMAT0000232 | UACAGUAGUCUGCACAUUGGUU | -0,669129326 |
| hsa-miR-379 | MIMAT0000733 | UGGUAGACUAUGGAACGUA | -0,619038313 |
| hsa-miR-520g | MIMAT0002858 | ACAAAGUGCUUCCCUUUAGAGUGU | -0,6180495 |
| hsa-miR-556 | MIMAT0003220 | GAUGAGCUCAUUGUAAUAUG | -0,609025791 |
| hsa-miR-9* | MIMAT0000442 | UAAAGCUAGAUAACCGAAAGU | -0,608780142 |
| hsa-miR-657 | MIMAT0003335 | GGCAGGUUCUCACCCUCUCUAGG | -0,605950522 |
| hsa-miR-197 | MIMAT0000227 | UUCACCACCUUCUCCACCCAGC | -0,605119503 |
| hsa-miR-553 | MIMAT0003216 | AAAACGGUGAGAUUUUGUUUU | -0,604451426 |
| hsa-miR-651 | MIMAT0003321 | UUUAGGAUAAGCUUGACUUUUG | -0,596515119 |
| hsa-miR-149 | MIMAT0000450 | UCUGGCUCCGUGUCUUCACUCC | -0,566967862 |

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| hsa-miR-127 | MIMAT0000446 | UCGGAUCCGUCUGAGCUUGGCU | -0,555398121 |
| hsa-miR-222 | MIMAT0000279 | AGCUACAUCUGGCUACUGGGUCUC | -0,554877975 |
| hsa-miR-607 | MIMAT0003275 | GUUCAAAUCCAGAUCUAUAAC | -0,552970219 |
| hsa-miR-769-3p | MIMAT0003887 | CUGGGAUCUCCGGGGUCUUGGUU | -0,551826208 |
| hsa-miR-16 | MIMAT0000069 | UAGCAGCACGUAAAUAUUGGCG | -0,551070157 |
| hsa-miR-641 | MIMAT0003311 | AAAGACAUAGGAUAGAGUCACCUC | -0,548397528 |
| hsa-miR-569 | MIMAT0003234 | AGUUAAUGAAUCCUGGAAAGU | -0,5397311 |
| hsa-miR-520h | MIMAT0002867 | ACAAAGUGCUUCCCUUUAGAGU | -0,537370147 |
| hsa-miR-671 | MIMAT0003880 | AGGAAGCCCUGGAGGGGCUGGAGGU | -0,529230738 |
| hsa-miR-299-5p | MIMAT0002890 | UGGUUUACCGUCCCACAUACAU | -0,512400017 |
| hsa-miR-138 | MIMAT0000430 | AGCUGGUGUUGUGAAUC | -0,50764177 |
| hsa-miR-30a-3p | MIMAT0000088 | CUUUCAGUCGGAUGUUUGCAGC | -0,50217473 |
| hsa-miR-382 | MIMAT0000737 | GAAGUUGUUCGUGGUGGAUUCG | -0,491258841 |
| hsa-miR-654 | MIMAT0003330 | UGGUGGGCCGCAGAACAUGUGC | -0,487399278 |
| hsa-miR-28 | MIMAT0000085 | AAGGAGCUCACAGUCUAUUGAG | -0,477866322 |
| hsa-miR-492 | MIMAT0002812 | AGGACCUGCGGGACAAGAUUCUU | -0,4764092 |
| hsa-miR-645 | MIMAT0003315 | UCUAGGCUGGUACUGCUGA | -0,473435195 |
| hsa-miR-549 | MIMAT0003333 | UGACAACUAUGGAUGAGCUCU | -0,468767894 |
| hsa-miR-598 | MIMAT0003266 | UACGUCAUCGUUGUCAUCGUCA | -0,456958392 |
| hsa-miR-567 | MIMAT0003231 | AGUAUGUUCUUCCAGGACAGAAC | -0,447191327 |
| hsa-miR-613 | MIMAT0003281 | AGGAAUGUUCCUUCUUUGCC | -0,446365426 |
| hsa-miR-202* | MIMAT0002810 | UUUCCUAUGCAUAUACUUCUUU | -0,443786563 |
| hsa-miR-573 | MIMAT0003238 | CUGAAGUGAUGUGUAACUGAUCAG | -0,441589811 |
| hsa-miR-511 | MIMAT0002808 | GUGUCUUUUGCUCUGCAGUCA | -0,432741317 |
| hsa-miR-769-5p | MIMAT0003886 | UGAGACCUCUGGGUUCUGAGCU | -0,429095641 |
| hsa-miR-570 | MIMAT0003235 | GAAAACAGCAAUUACCUUUGCA | -0,427288003 |
| hsa-miR-578 | MIMAT0003243 | CUUCUUGUGCUCUAGGAUUGU | -0,418430807 |
| hsa-miR-621 | MIMAT0003290 | GGCUAGCAACAGCGCUUACCU | -0,414210611 |
| hsa-miR-154* | MIMAT0000453 | AAUCAUACACGGUUGACCUAUU | -0,399650207 |
| hsa-miR-555 | MIMAT0003219 | AGGGUAAGCUGAACCUCUGAU | -0,383855452 |
| hsa-miR-208 | MIMAT0000241 | AUAAGACGAGCAAAAAGCUUGU | -0,375022631 |
| hsa-miR-18a* | MIMAT0002891 | ACUGCCCUAAGUGCUCCUUCU | -0,374024591 |
| hsa-miR-587 | MIMAT0003253 | UUUCCAUAGGUGAUGAGUCAC | -0,367460875 |
| hsa-miR-10a | MIMAT0000253 | UACCCUGUAGAUCCGAAUUUGUG | -0,355638419 |
| hsa-miR-132 | MIMAT0000426 | UAACAGUCUACAGCCAUGGUCG | -0,35128735 |
| hsa-miR-568 | MIMAT0003232 | AUGUAUAAAUGUAUACACAC | -0,34800257 |
| hsa-miR-583 | MIMAT0003248 | CAAAGAGGAAGGUCCCAUUAC | -0,347787023 |
| hsa-miR-377 | MIMAT0000730 | AUCACACAAAGGCAACUUUUGU | -0,329531969 |
| hsa-miR-223 | MIMAT0000280 | UGUCAGUUUGUCAAAUACCCC | -0,326784202 |
| hsa-miR-624 | MIMAT0003293 | UAGUACCAGUACCUUGUGUUCA | -0,321762563 |
| hsa-miR-27a | MIMAT0000084 | UUCACAGUGGCUAAGUUCCGC | -0,316148753 |
| hsa-miR-519a | MIMAT0002869 | AAAGUGCAUCCUUUUAGAGUGUUAC | -0,314711316 |
| hsa-miR-221 | MIMAT0000278 | AGCUACAUUGUCUGCUGGGUUUC | -0,314138247 |
| hsa-miR-633 | MIMAT0003303 | CUAAUAGUAUCUACCACAAUAAA | -0,302636025 |
| hsa-miR-488 | MIMAT0002804 | CCCAGAUAAUGGCACUCUCAA | -0,296231146 |
| hsa-miR-542-3p | MIMAT0003389 | UGUGACAGAUUGAUAACUGAAA | -0,291113293 |
| hsa-miR-374 | MIMAT0000727 | UUAUAAUACAACCUGAUAAGUG | -0,285662874 |
| hsa-miR-668 | MIMAT0003881 | UGUCACUCGGCUCGGCCCACUAC | -0,284270801 |
| hsa-miR-29c | MIMAT0000681 | UAGCACCAUUUGAAAUCGGU | -0,281086639 |
| hsa-miR-196a | MIMAT0000226 | UAGGUAGUUUCAUGUUGUUGG | -0,280574093 |
| hsa-miR-33b | MIMAT0003301 | GUGCAUUGCUGUUGCAUUGCA | -0,270635178 |
| hsa-miR-186 | MIMAT0000456 | CAAAGAAUUCUCCUUUUGGGCUU | -0,267009259 |
| hsa-miR-487a | MIMAT0002178 | AAUCAUACAGGGACAUCCAGUU | -0,264772549 |
| hsa-miR-101 | MIMAT0000099 | UACAGUACUGUGAUAACUGAAG | -0,260971848 |
| hsa-miR-526a | MIMAT0002845 | CUCUAGAGGGAAGCACUUUCU | -0,252246052 |
| hsa-miR-611 | MIMAT0003279 | GCGAGGACCCCUCGGGGUCUGAC | -0,25060616 |
| hsa-miR-765 | MIMAT0003945 | UGGAGGAGAAGGAAGGUGAUG | -0,247552232 |
| hsa-miR-603 | MIMAT0003271 | CACACACUGCAAUUACUUUUGC | -0,24216463 |
| hsa-miR-577 | MIMAT0003242 | UAGAUAAAAUAUUGGUACCUG | -0,241768154 |
| hsa-miR-516-3p | MIMAT0002860 | UGCUUCCUUUCAGAGGGU | -0,231834652 |
| hsa-let-7e | MIMAT0000066 | UGAGGUAGGAGGUUGUAUAGU | -0,231717339 |
| hsa-miR-325 | MIMAT0000771 | CCUAGUAGGUGUCCAGUAAGUGU | -0,224397553 |
| hsa-miR-126* | MIMAT0000444 | CAUUAUUACUUUUGGUACGCG | -0,223396528 |
| hsa-let-7g | MIMAT0000414 | UGAGGUAGUAGUUUGUACAGU | -0,22082751 |
| hsa-miR-631 | MIMAT0003300 | AGACCUGGCCCAGACCUCAGC | -0,217537919 |

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| hsa-miR-151 | MIMAT0000757 | ACUAGACUGAAGCUCCUUGAGG | -0,21578116 |
| hsa-miR-425-5p | MIMAT0003393 | AAUGACACGAUCACUCCCGUUGA | -0,214106021 |
| hsa-miR-498 | MIMAT0002824 | UUUCAAGCCAGGGGGCGUUUUUC | -0,209050944 |
| hsa-miR-22 | MIMAT0000077 | AAGCUGCCAGUUGAAGAACUGU | -0,205814422 |
| hsa-miR-188 | MIMAT0000457 | CAUCCCUUGCAUGGUGGAGGGU | -0,202546219 |
| hsa-miR-487b | MIMAT0003180 | AAUCGUACAGGGUCAUCCACUU | -0,198668444 |
| hsa-miR-615 | MIMAT0003283 | UCCGAGCCUGGGUCUCCCUCU | -0,194073986 |
| hsa-miR-518f* | MIMAT0002841 | CUCUAGAGGGAAGCACUUUCUCU | -0,193216452 |
| hsa-miR-431 | MIMAT0001625 | UGUCUUGCAGGCCGUCAUGCA | -0,168829451 |
| hsa-miR-518f | MIMAT0002842 | AAAGCGCUUCUCUUUAGAGGA | -0,163838246 |
| hsa-miR-649 | MIMAT0003319 | AAACCUGUGUUGUUCAAGAGUC | -0,147960134 |
| hsa-miR-191 | MIMAT0000440 | CAACGGAAUCCCAAAAGCAGCU | -0,143440088 |
| hsa-miR-608 | MIMAT0003276 | AGGGGUGGUGUUGGGACAGCUCCGU | -0,136623537 |
| hsa-miR-453 | MIMAT0001630 | GAGGUUGUCCGUGGUGAGUUCG | -0,124671058 |
| hsa-miR-187 | MIMAT0000262 | UCGUGUCUUGUGUUGCAGCCG | -0,111615339 |
| hsa-miR-98 | MIMAT0000096 | UGAGGUAGUAAGUUGUAUUGUU | -0,107454546 |
| hsa-miR-185 | MIMAT0000455 | UGGAGAGAAAGGCAGUUC | -0,10442534 |
| hsa-miR-29a | MIMAT0000086 | UAGCACCAUCUGAAAUCGGUU | -0,091124489 |
| hsa-miR-509 | MIMAT0002881 | UGAUUGGUACGUCUGUGGGUAGA | -0,083624061 |
| hsa-miR-17-5p | MIMAT0000070 | CAAAGUGCUUACAGUGCAGGUAGU | -0,077175829 |
| hsa-miR-155 | MIMAT0000646 | UUAAUGCUAAUCGUGAUAGGGG | -0,075473226 |
| hsa-miR-526c | MIMAT0002831 | CUCUAGAGGGAAGCGCUUUCUGUU | -0,074501634 |
| hsa-miR-302b* | MIMAT0000714 | ACUUUAACAUGGAAGUGCUUUCU | -0,07120549 |
| hsa-miR-501 | MIMAT0002872 | AAUCCUUUGUCCCUGGGUGAGA | -0,071083076 |
| hsa-miR-554 | MIMAT0003217 | GCUAGUCCUGACUCAGCCAGU | -0,057865071 |
| hsa-miR-610 | MIMAT0003278 | UGAGCUAAAUGUGUGCUGGGA | -0,055063599 |
| hsa-miR-520d | MIMAT0002856 | AAAGUGCUUCUCUUUGGUGGGUU | -0,053350126 |
| hsa-miR-519b | MIMAT0002837 | AAAGUGCAUCCUUUUAGAGGUUU | -0,051575714 |
| hsa-miR-519e* | MIMAT0002828 | UUCUCCAAAAGGGAGCACUUUC | -0,04174857 |
| hsa-miR-376b | MIMAT0002172 | AUCAUAGAGGAAAAUCCAUGUU | -0,040664783 |
| hsa-miR-590 | MIMAT0003258 | GAGCUUAUUCAUAAAAGUGCAG | -0,038039384 |
| hsa-miR-26a | MIMAT0000082 | UUCAAGUAAUCCAGGAUAGGC | -0,032888911 |
| hsa-miR-452 | MIMAT0001635 | UGUUUGCAGAGGAAACUGAGAC | -0,032590708 |
| hsa-miR-623 | MIMAT0003292 | AUCCCUUGCAGGGGCUGUUGGGU | -0,028915645 |
| hsa-miR-153 | MIMAT0000439 | UUGCAUAGUCACAAAAGUGA | -0,027781916 |
| hsa-miR-24 | MIMAT0000080 | UGGCUCAGUUCAGCAGGAACAG | -0,026389395 |
| hsa-miR-519c | MIMAT0002832 | AAAGUGCAUCUUUUUAGAGGAU | -0,024904371 |
| hsa-miR-363* | MIMAT0003385 | CGGGUGGAUCACGAUGCAAUUU | -0,024110349 |
| hsa-miR-520e | MIMAT0002825 | AAAGUGCUUCCUUUUUGAGGG | -0,023108232 |
| hsa-miR-496 | MIMAT0002818 | AUUACAUGGCCAAUCUC | -0,022784592 |
| hsa-miR-33 | MIMAT0000091 | GUGCAUUGUAGUUGCAUUG | -0,019752176 |
| hsa-miR-302d | MIMAT0000718 | UAAGUGCUUCCAUGUUUGAGUGU | -0,018785312 |
| hsa-miR-596 | MIMAT0003264 | AAGCCUGCCCGGCUCCUCGGG | -0,010708219 |
| hsa-miR-526b* | MIMAT0002836 | AAAGUGCUUCCUUUUAGAGGC | -0,006930979 |
| hsa-miR-135b | MIMAT0000758 | UAUGGCUUUUCAUUCCUAUGUG | -0,004235799 |
| hsa-miR-562 | MIMAT0003226 | AAAGUAGCUGUACCAUUUGC | -0,002850401 |
| hsa-miR-520c | MIMAT0002846 | AAAGUGCUUCCUUUUAGAGGGUU | 0,00102835 |
| hsa-miR-801 | MIMAT0004209 | GAUUGCUCUGCGUGCGGAAUCGAC | 0,012341759 |
| hsa-miR-338 | MIMAT0000763 | UCCAGCAUCAGUGAUUUUGUUGA | 0,015262188 |
| hsa-miR-520d* | MIMAT0002855 | UCUACAAAGGGAAGCCCUUUCUG | 0,022480137 |
| hsa-miR-433 | MIMAT0001627 | AUCAUGAUGGGCUCCUCGGUGU | 0,029092462 |
| hsa-miR-652 | MIMAT0003322 | AAUGGCGCCACUAGGGUUGUGCA | 0,05232999 |
| hsa-miR-381 | MIMAT0000736 | UAUACAAGGGCAAGCUCUCUGU | 0,052518807 |
| hsa-miR-92 | MIMAT0000092 | UAUUGCACUUGUCCCGGCCUG | 0,060846062 |
| hsa-miR-484 | MIMAT0002174 | UCAGGCUCAGUCCCCUCCCGAU | 0,061317284 |
| hsa-miR-362 | MIMAT0000705 | AAUCCUUGGAACCUAGGUGUGAGU | 0,067122093 |
| hsa-miR-658 | MIMAT0003336 | GGCGGAGGGAAGUAGGUCCGUUGGU | 0,067930324 |
| hsa-miR-565 | MIMAT0003229 | GGCUGGCUCGCGAUGUCUGUUU | 0,068547685 |
| hsa-miR-182* | MIMAT0000260 | UGGUUCUAGACUUGCCAACUA | 0,079652033 |
| hsa-miR-523 | MIMAT0002840 | AACGCGCUUCCCUAUAGAGGG | 0,079759448 |
| hsa-miR-662 | MIMAT0003325 | UCCCACGUUGUGGCCCAGCAG | 0,079761213 |
| hsa-miR-361 | MIMAT0000703 | UUAUCAGAAUCUCCAGGGGUAC | 0,080007576 |
| hsa-miR-23b | MIMAT0000418 | AUCACAUUGCCAGGGAUUACC | 0,090695682 |
| hsa-miR-130a | MIMAT0000425 | CAGUGCAAUGUUAAAAGGGCAU | 0,091385276 |
| hsa-miR-320 | MIMAT0000510 | AAAAGCUGGGUUGAGAGGGCGAA | 0,092205778 |

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| hsa-miR-606 | MIMAT0003274 | AAACUACUGAAAAUCAAAGAU | 0,096835629 |
| hsa-miR-454-3p | MIMAT0003885 | UAGUGCAAUAUUGCUUAUAGGGUUU | 0,107947836 |
| hsa-miR-199a | MIMAT0000231 | CCCAGUGUUCAGACUACCUGUUC | 0,111584279 |
| hsa-miR-659 | MIMAT0003337 | CUUGGUUCAGGGAGGGUCCCCA | 0,111801375 |
| hsa-miR-323 | MIMAT0000755 | GCACAUUACACGGUCGACCUCU | 0,115700799 |
| hsa-miR-218 | MIMAT0000275 | UUGUGCUUGAUCUAACCAUGU | 0,116526199 |
| hsa-miR-518e | MIMAT0002861 | AAAGCGCUUCCCUUCAGAGUGU | 0,133893021 |
| hsa-miR-491 | MIMAT0002807 | AGUGGGGAACCCUUCCAUGAGGA | 0,139949247 |
| hsa-miR-519d | MIMAT0002853 | CAAAGUGCCUCCCUUUAGAGUGU | 0,150294189 |
| hsa-miR-181b | MIMAT0000257 | AACAUUCAUUGCUGUCGGUGGG | 0,15949443 |
| hsa-miR-643 | MIMAT0003313 | ACUUGUAUGCUAGCUCAGGUAG | 0,160369774 |
| hsa-miR-335 | MIMAT0000765 | UCAAGAGCAAUAACGAAAAAUGU | 0,161638867 |
| hsa-miR-150 | MIMAT0000451 | UCUCCCAACCCUUGUACCAGUG | 0,167831863 |
| hsa-miR-302c* | MIMAT0000716 | UUUAACAUGGGGGUACCUGCUG | 0,181549905 |
| hsa-miR-380-5p | MIMAT0000734 | UGGUUGACCAUAGAACAUGCGC | 0,184383889 |
| hsa-miR-520b | MIMAT0002843 | AAAGUGCUUCCUUUUAGAGGG | 0,188338911 |
| hsa-miR-525* | MIMAT0002839 | GAAGGCGCUUCCCUUUAGAGC | 0,189242841 |
| hsa-miR-342 | MIMAT0000753 | UCUCACACAGAAAUCGCACCCGUC | 0,19850904 |
| hsa-miR-483 | MIMAT0002173 | UCACUCCUCUCCUCCCGUCUUCU | 0,199014154 |
| hsa-miR-7 | MIMAT0000252 | UGGAAGACUAGUGAUUUUGUUG | 0,206737526 |
| hsa-miR-450 | MIMAT0001545 | UUUUUGCGAUGUGUUCCUAAUA | 0,210070866 |
| hsa-let-7i | MIMAT0000415 | UGAGGUAGUAGUUUGUGCUGU | 0,213388521 |
| hsa-miR-384 | MIMAT0001075 | AUUCCUAGAAAUUGUUCAUA | 0,215762491 |
| hsa-miR-181c | MIMAT0000258 | AACAUUCAACCUGUCGGUGAGU | 0,225510366 |
| hsa-miR-423 | MIMAT0001340 | AGCUCGGUCUGAGGCCCCUCAG | 0,22896848 |
| hsa-miR-572 | MIMAT0003237 | GUCCGCUCGGCGGUGGCCCA | 0,230169781 |
| hsa-miR-21 | MIMAT0000076 | UAGCUUAUCAGACUGAUGUUGA | 0,230999926 |
| hsa-miR-628 | MIMAT0003297 | UCUAGUAAGAGUGGCAGUCG | 0,232530224 |
| hsa-miR-563 | MIMAT0003227 | AGGUUGACAUACGUUUCCC | 0,251268547 |
| hsa-miR-370 | MIMAT0000722 | GCCUGCUGGGGUGGAACCUGG | 0,25361595 |
| hsa-miR-622 | MIMAT0003291 | ACAGUCUGCUGAGGUUGGAGC | 0,258530414 |
| hsa-miR-544 | MIMAT0003164 | AUUCUGCAUUUUUAGCAAGU | 0,262753665 |
| hsa-miR-548d | MIMAT0003323 | CAAAAACCACAGUUUCUUUUGC | 0,267844339 |
| hsa-miR-518d | MIMAT0002864 | CAAAGCGCUUCCCUUUGGAGC | 0,269991763 |
| hsa-miR-34b | MIMAT0000685 | UAGGCAGUGUCAUUAGCUGAUUG | 0,274475479 |
| hsa-miR-489 | MIMAT0002805 | AGUGACAUCACAUAUACGGCAGC | 0,279594639 |
| hsa-let-7f | MIMAT0000067 | UGAGGUAGUAGAUUGUAUAGUU | 0,282645196 |
| hsa-miR-564 | MIMAT0003228 | AGGCACGGUGUCAGCAGGC | 0,282756333 |
| hsa-miR-557 | MIMAT0003221 | GUUUGCACGGGUGGGCCUUGUCU | 0,289991154 |
| hsa-miR-19a | MIMAT0000073 | UGUGCAAAUCUAUGCAAAACUGA | 0,29890525 |
| hsa-miR-579 | MIMAT0003244 | AUUCAUUUGGUAUAAACCGCGAU | 0,306432428 |
| hsa-miR-200c | MIMAT0000617 | UAAUACUGCCGGGUAAUGAUGG | 0,321414296 |
| hsa-miR-632 | MIMAT0003302 | GUGUCUGCUUCCUGUGGGA | 0,325598509 |
| hsa-miR-561 | MIMAT0003225 | CAAAGUUUAAGAUCCUUGAAGU | 0,329846441 |
| hsa-miR-30d | MIMAT0000245 | UGUAAACAUCCCCGACUGGAAG | 0,330854559 |
| hsa-miR-10b | MIMAT0000254 | UACCCUGUAGAACCGAAUUUGU | 0,333163155 |
| hsa-miR-211 | MIMAT0000268 | UUCCCUUUGUCAUCCUUCGCCU | 0,344309741 |
| hsa-miR-451 | MIMAT0001631 | AAACCGUUACCAUUACUGAGUUU | 0,358317029 |
| hsa-miR-296 | MIMAT0000690 | AGGGCCCCCCCUCAAUCCUGU | 0,37786994 |
| hsa-miR-125b | MIMAT0000423 | UCCCUGAGACCCUAACUUGUGA | 0,38555003 |
| hsa-miR-198 | MIMAT0000228 | GGUCCAGAGGGGAGAUAGG | 0,389864609 |
| hsa-miR-23a | MIMAT0000078 | AUCACAUUGCCAGGGAUUUCC | 0,393553167 |
| hsa-miR-524 | MIMAT0002850 | GAAGGCGCUUCCCUUUGGAGU | 0,394503119 |
| hsa-miR-184 | MIMAT0000454 | UGGACGGAGAACUGAUAAGGGU | 0,398798168 |
| hsa-miR-768-3p | MIMAT0003947 | UCACAAUGCUGACACUCAAACUGCUGAC | 0,399242966 |
| hsa-miR-324-3p | MIMAT0000762 | CCACUGCCCCAGGUGCUGCUGG | 0,422054956 |
| hsa-miR-429 | MIMAT0001536 | UAAUACUGUCUGGUAAAACCGU | 0,422346487 |
| hsa-miR-376a | MIMAT0000729 | AUCAUAGAGGAAAAUCCACGU | 0,423918947 |
| hsa-miR-29b | MIMAT0000100 | UAGCACCAUUUGAAAUCAGUGUU | 0,424749451 |
| hsa-miR-148b | MIMAT0000759 | UCAGUGCAUCACAGAACUUUGU | 0,427693635 |
| hsa-miR-409-5p | MIMAT0001638 | AGGUUACCCGAGCAACUUUGCA | 0,436284304 |
| hsa-miR-517* | MIMAT0002851 | CCUCUAGAUGGAAGCACUGUCU | 0,439515798 |
| hsa-miR-106b | MIMAT0000680 | UAAAGUGCUGACAGUGCAGAU | 0,441526835 |
| hsa-miR-181d | MIMAT0002821 | AACAUUCAUUGUUGUCGGUGGGUU | 0,446025994 |
| hsa-miR-15b | MIMAT0000417 | UAGCAGCACAUCAUGGUUUACA | 0,45285634 |

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| hsa-miR-19b | MIMAT0000074 | UGUGCAAAUCCAUGCAAAACUGA | 0,456133968 |
| hsa-miR-199b | MIMAT0000263 | CCCAGUGUUUAGACUAUCUGUUC | 0,458288148 |
| hsa-miR-508 | MIMAT0002880 | UGAUUGUAGCCUUUUGGAGUAGA | 0,464874524 |
| hsa-miR-9 | MIMAT0000441 | UCUUUGGUUAUCUAGCUGUAUGA | 0,471413939 |
| hsa-miR-558 | MIMAT0003222 | UGAGCUGCUGUACCAAAAU | 0,475519554 |
| hsa-miR-422b | MIMAT0000732 | CUGGACUUGGAGUCAGAAGGCC | 0,48450102 |
| hsa-let-7c | MIMAT0000064 | UGAGGUAGUAGGUUGUAUGGUU | 0,486555783 |
| hsa-miR-302b | MIMAT0000715 | UAAGUGCUUCCAUGUUUUAGUAG | 0,486725838 |
| hsa-miR-220 | MIMAT0000277 | CCACACCGUAUCUGACACUUU | 0,504167189 |
| hsa-miR-648 | MIMAT0003318 | AAGUGUGCAGGGCACUGGU | 0,513193643 |
| hsa-miR-32 | MIMAT0000090 | UAUUGCACAUUACUAAGUUGC | 0,521161737 |
| hsa-miR-612 | MIMAT0003280 | GCUGGGCAGGGCUUCUGAGCUCCUU | 0,529699531 |
| hsa-miR-202 | MIMAT0002811 | AGAGGUAUAGGGCAUGGGAAAA | 0,541308073 |
| hsa-miR-505 | MIMAT0002876 | GUCAACACUUGCUGGUUUCCUC | 0,545170773 |
| hsa-miR-30c | MIMAT0000244 | UGUAAACAUCCUACACUCUCAGC | 0,545491372 |
| hsa-miR-302c | MIMAT0000717 | UAAGUGCUUCCAUGUUUCAGUGG | 0,569979612 |
| hsa-miR-768-5p | MIMAT0003946 | GUUGGAGGAUGAAAGUACGGAGUGAU | 0,570999048 |
| hsa-miR-522 | MIMAT0002868 | AAAAUGGUUCCCUUUAGAGUGUU | 0,573198909 |
| hsa-miR-593 | MIMAT0003261 | AGGCACCAGCCAGGCAUUGCUCAGC | 0,574402715 |
| hsa-miR-675 | MIMAT0004284 | UGGUGCGGAGAGGGCCCACAGUG | 0,57520902 |
| hsa-miR-412 | MIMAT0002170 | ACUUCACCUGGUCCACUAGCCGU | 0,575977545 |
| hsa-miR-216 | MIMAT0000273 | UAAUCUCAGCUGGCAACUGUG | 0,578614893 |
| hsa-miR-136 | MIMAT0000448 | ACUCCAUUUGUUUUGAUGAUGGA | 0,593948704 |
| hsa-miR-134 | MIMAT0000447 | UGUGACUGGUUGACCAGAGGG | 0,602261375 |
| hsa-miR-646 | MIMAT0003316 | AAGCAGCUGCCUCUGAGGC | 0,632135876 |
| hsa-miR-130b | MIMAT0000691 | CAGUGCAAUGAUGAAAGGGCAU | 0,643927619 |
| hsa-miR-20b | MIMAT0001413 | CAAAGUGCUCAUAGUGCAGGUAG | 0,650808502 |
| hsa-miR-146b | MIMAT0002809 | UGAGAACUGAAUUCCAUAGGCU | 0,667860885 |
| hsa-miR-93 | MIMAT0000093 | AAAGUGCUGUUCGUGCAGGUAG | 0,684185583 |
| hsa-miR-629 | MIMAT0003298 | GUUCUCCCAACGUAAGCCCAGC | 0,684983206 |
| hsa-miR-369-5p | MIMAT0001621 | AGAUCGACCGUGUUAUAUUCGC | 0,688641968 |
| hsa-miR-507 | MIMAT0002879 | UUUUGCACCUUUUGGAGUGAA | 0,70608634 |
| hsa-miR-455 | MIMAT0003150 | UAUGUGCCUUUGGACUACAUCG | 0,707359428 |
| hsa-miR-524* | MIMAT0002849 | CUACAAAGGGAAGCACUUUCUC | 0,715858262 |
| hsa-miR-210 | MIMAT0000267 | CUGUGCGUGUGACAGCGGCUGA | 0,721696949 |
| hsa-miR-92b | MIMAT0003218 | UAUUGCACUCGUCCCGGCCUC | 0,725863513 |
| hsa-miR-767-5p | MIMAT0003882 | UGCACCAUGGUUGUCUGAGCAUG | 0,726947455 |
| hsa-miR-302a | MIMAT0000684 | UAAGUGCUUCCAUGUUUUGGUGA | 0,732840127 |
| hsa-miR-27b | MIMAT0000419 | UUCACAGUGGCUAAGUUCUGC | 0,752023748 |
| hsa-miR-422a | MIMAT0001339 | CUGGACUUAGGGUCAGAAGGCC | 0,769855571 |
| hsa-miR-454-5p | MIMAT0003884 | ACCCUAUCAAUAUUGUCUCUGC | 0,779146056 |
| hsa-miR-661 | MIMAT0003324 | UGCCUGGGUCUCUGGCCUGCGCGU | 0,781734531 |
| hsa-miR-619 | MIMAT0003288 | GACCUGGACAUGUUUGUGCCCAGU | 0,791881332 |
| hsa-miR-148a | MIMAT0000243 | UCAGUGCACUACAGAACUUUGU | 0,791982084 |
| hsa-miR-191* | MIMAT0001618 | GCUGCGCUUGGAUUUCGUCCCC | 0,793585362 |
| hsa-miR-518a | MIMAT0002863 | AAAGCGCUUCCCUUUGCUGGA | 0,796969549 |
| hsa-miR-145 | MIMAT0000437 | GUCCAGUUUUCCCAGGAAUCCCUU | 0,802096876 |
| hsa-miR-373 | MIMAT0000726 | GAAGUGCUUCGAUUUUGGGGUGU | 0,807979193 |
| hsa-miR-758 | MIMAT0003879 | UUUGUGACCUGGUCCACUAACC | 0,815327289 |
| hsa-miR-411 | MIMAT0003329 | UAGUAGACCGUAUAGCGUACG | 0,820939728 |
| hsa-miR-503 | MIMAT0002874 | UAGCAGCGGGAACAGUUCUGCAG | 0,822411132 |
| hsa-miR-205 | MIMAT0000266 | UCCUUCAUUCCACCGGAGUCUG | 0,830121595 |
| hsa-miR-105 | MIMAT0000102 | UCAAAUGCUCAGACUCCUGU | 0,836568926 |
| hsa-miR-144 | MIMAT0000436 | UACAGUAUAGAUGAUGUACUAG | 0,844979261 |
| hsa-let-7b | MIMAT0000063 | UGAGGUAGUAGGUUGUGUGGUU | 0,852024474 |
| hsa-miR-376a* | MIMAT0003386 | GGUAGAUUCUCCUUCUAUGAG | 0,869890697 |
| hsa-miR-135a | MIMAT0000428 | UAUGGCUUUUUAUUCCUAUGUGA | 0,878704747 |
| hsa-miR-200a* | MIMAT0001620 | CAUCUUACCGGACAGUGCUGGA | 0,881220772 |
| hsa-miR-589 | MIMAT0003256 | UCAGAACAAAUGCCGGUUCCCAGA | 0,882340452 |
| hsa-miR-363 | MIMAT0000707 | AAUUGCACGGUAUCCAUCUGUA | 0,890943858 |
| hsa-miR-592 | MIMAT0003260 | UUGUGUCAAUAUGCGAUGAUGU | 0,900781054 |
| hsa-miR-512-3p | MIMAT0002823 | AAGUGCUGUCAUAGCUGAGGUC | 0,918485335 |
| hsa-miR-1 | MIMAT0000416 | UGGAAUGUAAAGAAGUAUGUA | 0,925305731 |
| hsa-miR-539 | MIMAT0003163 | GGAGAAAUUAUCCUUGGUGUGU | 0,937150608 |
| hsa-miR-627 | MIMAT0003296 | GUGAGUCUCUAAGAAAAGAGGA | 0,947293771 |

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| hsa-let-7d | MIMAT0000065 | AGAGGUAGUAGGUUGCAUAGU | 0,956128404 |
| hsa-miR-15a | MIMAT0000068 | UAGCAGCACAUAAUGGUUUGUG | 1,003523712 |
| hsa-miR-617 | MIMAT0003286 | AGACUUCCCAUUUGAAGGUGGC | 1,007206219 |
| hsa-miR-545 | MIMAT0003165 | AUCAGCAAACAUUUAUUGUGUG | 1,008023313 |
| hsa-miR-519e | MIMAT0002829 | AAAGUGCCUCCUUUUAGAGUGU | 1,020846592 |
| hsa-miR-525 | MIMAT0002838 | CUCCAGAGGGAUGCACUUUCU | 1,036933319 |
| hsa-miR-345 | MIMAT0000772 | UGCUGACUCCUAGUCCAGGGC | 1,061246749 |
| hsa-miR-520f | MIMAT0002830 | AAGUGCUUCCUUUUAGAGGGUU | 1,069342561 |
| hsa-miR-518c | MIMAT0002848 | CAAAGCGCUUCUCUUUAGAGUG | 1,070591141 |
| hsa-miR-203 | MIMAT0000264 | GUGAAAUGUUUAGGACCACUAG | 1,074174951 |
| hsa-miR-585 | MIMAT0003250 | UGGGCGUAUCUGUAUGCUA | 1,088793106 |
| hsa-miR-518b | MIMAT0002844 | CAAAGCGCUCCCCUUUAGAGGU | 1,120148083 |
| hsa-miR-497 | MIMAT0002820 | CAGCAGCACACUGUGGUUUGU | 1,128044361 |
| hsa-miR-432 | MIMAT0002814 | UCUUGGAGUAGGUCAUUGGGUGG | 1,132675075 |
| hsa-miR-605 | MIMAT0003273 | UAAAUCCCAUGGUGCCUUCUCCU | 1,140273001 |
| hsa-miR-369-3p | MIMAT0000721 | AAUAAUACAUGGUUGAUCUUU | 1,157699644 |
| hsa-miR-602 | MIMAT0003270 | GACACGGGCGACAGCUGCGGCCC | 1,161009119 |
| hsa-miR-219 | MIMAT0000276 | UGAUUGUCCAAACGCAAUUCU | 1,163436141 |
| hsa-miR-588 | MIMAT0003255 | UUGGCCACAAUGGGUUAGAAC | 1,1831254 |
| hsa-miR-516-5p | MIMAT0002859 | CAUCUGGAGGUAAGAAGCACUUU | 1,187294701 |
| hsa-miR-195 | MIMAT0000461 | UAGCAGCACAGAAAUAUUGGC | 1,222232304 |
| hsa-miR-154 | MIMAT0000452 | UAGGUUAUCCGUGUUGCCUUCG | 1,265003006 |
| hsa-miR-520a* | MIMAT0002833 | CUCCAGAGGGAAGUACUUUCU | 1,27039712 |
| hsa-miR-368 | MIMAT0000720 | ACAUAGAGGAAAUUCCACGUUU | 1,272434656 |
| hsa-miR-107 | MIMAT0000104 | AGCAGCAUUGUACAGGGCUAUCA | 1,304589067 |
| hsa-miR-609 | MIMAT0003277 | AGGGUGUUUCUCUCAUCUCU | 1,317421943 |
| hsa-miR-140 | MIMAT0000431 | AGUGGUUUUACCCUAUGGUAG | 1,320567017 |
| hsa-miR-520a | MIMAT0002834 | AAAGUGCUUCCCUUUGGACUGU | 1,35829185 |
| hsa-miR-650 | MIMAT0003320 | AGGAGGCAGCGCUCUCAGGAC | 1,361379687 |
| hsa-miR-214 | MIMAT0000271 | ACAGCAGGCACAGACAGGCAG | 1,374684582 |
| hsa-miR-635 | MIMAT0003305 | ACUUGGGCACUGAAACAAUGUCC | 1,392637109 |
| hsa-miR-636 | MIMAT0003306 | UGUGCUUGCUCGUCCCGCCCGCAG | 1,396311377 |
| hsa-miR-767-3p | MIMAT0003883 | UCUGCUCAUACCCCAUGGUUUCU | 1,396599227 |
| hsa-miR-663 | MIMAT0003326 | AGGCGGGGCGCCGCGGGACCGC | 1,417621221 |
| hsa-miR-383 | MIMAT0000738 | AGAUCAGAAGGUGAUUGUGGCU | 1,451598365 |
| hsa-miR-146a | MIMAT0000449 | UGAGAACUGAAUUCCAUGGGUU | 1,463308321 |
| hsa-miR-582 | MIMAT0003247 | UUACAGUUGUUCAACCAGUUACU | 1,471223722 |
| hsa-miR-616 | MIMAT0003284 | ACUCAAAACCCUUCAGUGACUU | 1,502393751 |
| hsa-miR-542-5p | MIMAT0003340 | UCGGGGAUCAUCAUGUCACGAG | 1,518601758 |
| hsa-miR-647 | MIMAT0003317 | GUGGCUGCACUCACUUCCUUC | 1,533921935 |
| hsa-miR-301 | MIMAT0000688 | CAGUGCAAUAGUAUUGUCAAAGC | 1,53990892 |
| hsa-miR-147 | MIMAT0000251 | GUGUGUGGAAAUGCUUCUGC | 1,543816351 |
| hsa-miR-425-3p | MIMAT0001343 | AUCGGGAAUGUCGUGUCCGCC | 1,546900248 |
| hsa-miR-346 | MIMAT0000773 | UGUCUGCCCGCAUGCCUGCCUCU | 1,547858661 |
| hsa-miR-106a | MIMAT0000103 | AAAAGUGCUUACAGUGCAGGUAGC | 1,558677746 |
| hsa-miR-372 | MIMAT0000724 | AAAGUGCUGCGACAUUUGAGCGU | 1,580645152 |
| hsa-miR-591 | MIMAT0003259 | AGACCAUGGGUUCUCAUUGU | 1,606566423 |
| hsa-miR-125a | MIMAT0000443 | UCCCUGAGACCCUUUAACCUGUG | 1,623331126 |
| hsa-miR-126 | MIMAT0000445 | UCGUACCGUGAGUAAUAAUGC | 1,633042409 |
| hsa-miR-330 | MIMAT0000751 | GCAAAGCACACGGCCUGCAGAGA | 1,654254363 |
| hsa-miR-375 | MIMAT0000728 | UUUGUUCGUUCGGCUCGCGUGA | 1,70460484 |
| hsa-miR-560 | MIMAT0003224 | GCGUGCGCCGGCCGGCCGCC | 1,714741715 |
| hsa-miR-152 | MIMAT0000438 | UCAGUGCAUGACAGAACUUGGG | 1,761252014 |
| hsa-miR-532 | MIMAT0002888 | CAUGCCUUGAGUGUAGGACCGU | 1,762168106 |
| hsa-miR-128a | MIMAT0000424 | UCACAGUGAACCGGUCUCUUUU | 1,785593805 |
| hsa-miR-371 | MIMAT0000723 | GUGCCGCCAUCUUUUGAGUGU | 1,802296884 |
| hsa-miR-200a | MIMAT0000682 | UAACACUGUCUGGUAACGAUGU | 1,804426494 |
| hsa-miR-181a* | MIMAT0000270 | ACCAUCGACCGUUGAUUGUACC | 1,811356407 |
| hsa-miR-625 | MIMAT0003294 | AGGGGGAAAGUUCUAUAGUCCU | 1,815423327 |
| hsa-miR-515-5p | MIMAT0002826 | UUCUCCAAAAGAAAGCACUUUCUG | 1,850944534 |
| hsa-miR-432* | MIMAT0002815 | CUGGAUGGCUCCUCCAUGUCU | 1,871851952 |
| hsa-miR-604 | MIMAT0003272 | AGGCUGCGGAAUUCAGGAC | 1,893475644 |
| hsa-miR-326 | MIMAT0000756 | CCUCUGGGCCCUUCCUCCAG | 1,896410081 |
| hsa-miR-518c* | MIMAT0002847 | UCUCUGGAGGGAAGCACUUUCUG | 1,923176059 |
| hsa-miR-194 | MIMAT0000460 | UGUAACAGCAACUCCAUGUGGA | 1,939080377 |

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| hsa-miR-20a | MIMAT0000075 | UAAAGUGCUUAUAGUGCAGGUAG | 1,962923142 |
| hsa-miR-517a | MIMAT0002852 | AUCGUGCAUCCCUUUAGAGUGUU | 1,973047455 |
| hsa-miR-200b | MIMAT0000318 | UAAUACUGCCUGGUAAUGAUGAC | 2,004069134 |
| hsa-miR-331 | MIMAT0000760 | GCCCCUGGGCCUAUCCUAGAA | 2,008183639 |
| hsa-miR-637 | MIMAT0003307 | ACUGGGGGCUUUCGGGCUCUGCGU | 2,0597728 |
| hsa-miR-373* | MIMAT0000725 | ACUCAAAAUGGGGGCGCUUUCC | 2,119372845 |
| hsa-miR-639 | MIMAT0003309 | AUCGCUGCGGUUGCGAGCGCUGU | 2,140857402 |
| hsa-let-7a | MIMAT0000062 | UGAGGUAGUAGGUUGUAUAGUU | 2,231606288 |
| hsa-miR-517c | MIMAT0002866 | AUCGUGCAUCCUUUUAGAGUGU | 2,236465977 |
| hsa-miR-517b | MIMAT0002857 | UCGUGCAUCCCUUUAGAGUGUU | 2,243843544 |
| hsa-miR-365 | MIMAT0000710 | UAAUGCCCCUAAAAAUCCUUAU | 2,311428083 |
| hsa-miR-485-5p | MIMAT0002175 | AGAGGCUGGCCGUGAUGAAUUC | 2,368282374 |
| hsa-miR-571 | MIMAT0003236 | UGAGUUGGCCAUCUGAGUGAG | 2,41784965 |
| hsa-miR-206 | MIMAT0000462 | UGGAAUGUAAGGAAGUGUGUGG | 2,426544671 |
| hsa-miR-638 | MIMAT0003308 | AGGGAUCGCGGGCGGGUGGCGGCCU | 2,464381148 |
| hsa-miR-340 | MIMAT0000750 | UCCGUCUCAGUUACUUUAUAGCC | 2,498663729 |
| hsa-miR-204 | MIMAT0000265 | UUCCCUUUGUCAUCCUAUGCCU | 2,546678716 |
| hsa-miR-550 | MIMAT0003257 | UGUCUUACUCCCUCAGGCACAU | 2,676488351 |
| hsa-miR-494 | MIMAT0002816 | UGAAACAUACACGGGAAACCUCUU | 2,676700499 |
| hsa-miR-424 | MIMAT0001341 | CAGCAGCAAUUCAUGUUUUGAA | 2,813540314 |
| hsa-miR-367 | MIMAT0000719 | AAUUGCACUUUAGCAAUGGUGA | 2,864888127 |
| hsa-miR-103 | MIMAT0000101 | AGCAGCAUUGUACAGGGCUAUGA | 2,875976696 |
| hsa-miR-515-3p | MIMAT0002827 | GAGUGCCUUCUUUUGGAGCGU | 2,959321616 |

**Supplementary Table 2**
Part 1: MicroRNAs that are amongst the top 50% expressed miRNAs in the dataset are indicated in bold

* mean expression (normalized, log2 value) in the T-ALL samples
** miRNAs that are in the top 50% expressed miRNAs and were positive hits from the PHF6 3'UTR screen are indicated by "yes"

| microRNA ID | mean expression* | hit in the 3'UTR screen** |
|---|---|---|
| **hsa-miR-223** | 11,410 | |
| **hsa-miR-20a** | 9,999 | |
| **hsa-miR-19b** | 9,640 | |
| **hsa-miR-92** | 9,501 | |
| **hsa-miR-93** | 9,357 | |
| **hsa-miR-150** | 8,794 | |
| **hsa-miR-26a** | 8,589 | |
| **hsa-miR-342** | 8,137 | |
| **hsa-miR-16** | 7,707 | |
| **hsa-miR-142-3p** | 7,643 | |
| **hsa-miR-222** | 7,485 | |
| **hsa-miR-191** | 7,398 | |
| **hsa-miR-146a** | 6,816 | |
| **hsa-miR-15b** | 6,582 | |
| **hsa-miR-376a** | 6,443 | |
| **hsa-miR-30c** | 6,271 | |
| **hsa-miR-30b** | 5,949 | |
| **hsa-miR-26b** | 5,922 | |
| **hsa-miR-146b** | 5,906 | |
| **hsa-miR-30a-5p** | 5,838 | yes |
| **hsa-miR-17-5p** | 5,807 | |
| **hsa-miR-181d** | 5,789 | |
| **hsa-miR-155** | 5,760 | |
| **hsa-miR-106b** | 5,709 | |
| **hsa-miR-140** | 5,643 | |
| **hsa-miR-662** | 5,614 | |
| **hsa-miR-181a** | 5,603 | |
| **hsa-let-7b** | 5,454 | |
| **hsa-miR-106a** | 5,380 | |
| **hsa-miR-331** | 5,229 | |
| **hsa-miR-594** | 5,147 | |
| **hsa-miR-19a** | 5,125 | |
| **hsa-miR-25** | 4,896 | |
| **hsa-miR-21** | 4,843 | |
| **hsa-miR-20b** | 4,758 | |
| **hsa-let-7a** | 4,689 | |
| **hsa-miR-29c** | 4,572 | |
| **hsa-miR-363** | 4,252 | |
| **hsa-miR-142-5p** | 4,125 | |
| **hsa-miR-126** | 3,726 | |
| **hsa-miR-186** | 3,719 | |
| **hsa-miR-130a** | 3,694 | |
| **hsa-miR-197** | 3,679 | |
| **hsa-miR-320** | 3,670 | |
| **hsa-miR-125a** | 3,618 | |
| **hsa-miR-423** | 3,434 | |
| **hsa-miR-374** | 3,385 | |
| **hsa-let-7g** | 3,353 | |
| **hsa-miR-30d** | 3,264 | |
| **hsa-miR-24** | 3,142 | |
| **hsa-miR-130b** | 3,124 | |
| **hsa-miR-15a** | 2,955 | |
| **hsa-miR-328** | 2,710 | yes |
| **hsa-miR-103** | 2,613 | |
| **hsa-let-7d** | 2,538 | |
| **hsa-miR-361** | 2,463 | |

| | | |
|---|---|---|
| **hsa-miR-196b** | 2,339 | |
| **hsa-miR-196a** | 2,326 | |
| **hsa-miR-324-5p** | 2,219 | |
| **hsa-miR-345** | 2,191 | |
| **hsa-miR-422a** | 2,110 | |
| **hsa-miR-28** | 2,109 | |
| **hsa-miR-18a** | 2,106 | |
| **hsa-miR-425-5p** | 2,076 | |
| **hsa-let-7i** | 2,049 | |
| **hsa-miR-200c** | 2,032 | |
| **hsa-miR-148a** | 2,001 | |
| **hsa-let-7c** | 1,858 | |
| **hsa-miR-451** | 1,803 | |
| **hsa-miR-18ahek** | 1,768 | |
| **hsa-miR-486** | 1,731 | |
| **hsa-let-7f** | 1,628 | |
| **hsa-miR-30e-5p** | 1,627 | |
| **hsa-miR-27a** | 1,591 | |
| **hsa-miR-194** | 1,408 | |
| **hsa-miR-181c** | 1,139 | |
| **hsa-miR-532** | 1,045 | |
| **hsa-miR-192** | 1,011 | yes |
| **hsa-miR-221** | 0,807 | |
| **hsa-miR-27b** | 0,673 | |
| **hsa-miR-149** | 0,383 | |
| **hsa-miR-365** | 0,375 | |
| **hsa-miR-301** | 0,201 | |
| **hsa-miR-660** | 0,193 | yes |
| **hsa-miR-340** | 0,097 | |
| **hsa-miR-132** | -0,064 | |
| **hsa-miR-378** | -0,118 | yes |
| **hsa-miR-565** | -0,258 | |
| **hsa-miR-125b** | -0,266 | |
| **hsa-miR-585** | -0,294 | |
| **hsa-miR-126hek** | -0,295 | |
| **hsa-miR-629** | -0,336 | |
| **hsa-miR-17-3p** | -0,352 | |
| **hsa-miR-145** | -0,355 | |
| **hsa-miR-324-3p** | -0,475 | |
| **hsa-miR-339** | -0,561 | |
| **hsa-miR-99b** | -0,631 | |
| **hsa-miR-199ahek** | -0,722 | |
| **hsa-miR-615** | -0,853 | |
| **hsa-miR-574** | -0,903 | yes |
| **hsa-miR-98** | -0,967 | |
| **hsa-miR-296** | -0,977 | |
| **hsa-miR-148b** | -1,116 | |
| **hsa-miR-213** | -1,192 | |
| **hsa-miR-459** | -1,281 | |
| **hsa-miR-32** | -1,428 | |
| **hsa-miR-101** | -1,459 | |
| **hsa-miR-10a** | -1,473 | |
| **hsa-miR-520c** | -1,596 | |
| **hsa-miR-30a-3p** | -1,604 | |
| **hsa-miR-335** | -1,633 | |
| **hsa-miR-29a** | -1,670 | |
| **hsa-miR-632** | -1,705 | |
| **hsa-miR-642** | -1,740 | |
| **hsa-miR-382** | -1,902 | |
| **hsa-miR-362** | -1,965 | |
| **hsa-miR-7** | -1,967 | |
| **hsa-miR-484** | -2,068 | |
| **hsa-miR-151** | -2,076 | |

| | | |
|---|---|---|
| **hsa-miR-422b** | -2,110 | |
| **hsa-miR-425** | -2,214 | |
| **hsa-miR-30e-3p** | -2,279 | |
| **hsa-miR-375** | -2,334 | |
| **hsa-miR-182** | -2,495 | |
| **hsa-miR-188** | -2,533 | |
| **hsa-miR-597** | -2,548 | |
| **hsa-miR-99a** | -2,641 | |
| **hsa-miR-550** | -2,666 | |
| **hsa-miR-128a** | -2,671 | |
| **hsa-miR-100** | -2,902 | |
| **hsa-miR-31** | -2,929 | |
| **hsa-miR-128b** | -2,930 | yes |
| **hsa-miR-152** | -2,932 | |
| **hsa-miR-638** | -3,013 | |
| **hsa-miR-645** | -3,034 | |
| **hsa-miR-9** | -3,061 | |
| **hsa-miR-516-3p** | -3,068 | |
| **hsa-miR-510** | -3,230 | |
| **hsa-miR-610** | -3,311 | |
| **hsa-miR-548d** | -3,378 | |
| **hsa-miR-210** | -3,390 | |
| **hsa-miR-330** | -3,418 | |
| **hsa-miR-185** | -3,528 | |
| **hsa-miR-135a** | -3,580 | |
| **hsa-miR-193a** | -3,654 | |
| **hsa-miR-218** | -3,681 | |
| **hsa-miR-601** | -3,720 | |
| **hsa-miR-661** | -3,808 | |
| **hsa-miR-491** | -3,942 | |
| **hsa-miR-564** | -4,001 | |
| **hsa-miR-95** | -4,062 | |
| **hsa-miR-424** | -4,066 | |
| **hsa-miR-127** | -4,112 | |
| **hsa-miR-579** | -4,172 | |
| **hsa-miR-572** | -4,283 | |
| **hsa-miR-490** | -4,294 | |
| **hsa-miR-553** | -4,389 | |
| **hsa-miR-520d** | -4,469 | |
| **hsa-miR-135b** | -4,550 | |
| **hsa-miR-190** | -4,616 | |
| **hsa-miR-29b** | -4,721 | |
| **hsa-miR-23a** | -4,856 | |
| **hsa-miR-137** | -4,900 | |
| **hsa-miR-659** | -4,913 | |
| **hsa-miR-502** | -4,914 | |
| **hsa-miR-23b** | -4,957 | |
| **hsa-miR-576** | -5,031 | |
| hsa-mir-203 | -5,055 | |
| hsa-mir-507 | -5,200 | |
| hsa-mir-34a | -5,222 | |
| hsa-mir-22 | -5,294 | |
| hsa-mir-200b | -5,328 | |
| hsa-mir-501 | -5,427 | |
| hsa-mir-141 | -5,432 | |
| hsa-mir-505 | -5,454 | |
| hsa-mir-566 | -5,456 | |
| hsa-miR-545 | -5,487 | |
| hsa-miR-618 | -5,548 | |
| hsa-mir-542-3p | -5,586 | |
| hsa-mir-506 | -5,756 | |
| hsa-mir-206 | -5,817 | |
| hsa-mir-650 | -5,819 | |

| | |
|---|---|
| hsa-mir-525 | -5,846 |
| hsa-mir-616 | -5,848 |
| hsa-mir-624 | -5,873 |
| hsa-miR-105 | -5,876 |
| hsa-mir-181b | -5,914 |
| hsa-mir-34b | -5,921 |
| hsa-mir-199b | -5,928 |
| hsa-mir-371 | -5,988 |
| hsa-mir-381 | -6,003 |
| hsa-mir-346 | -6,051 |
| hsa-mir-195 | -6,055 |
| hsa-miR-589 | -6,058 |
| hsa-miR-649 | -6,080 |
| hsa-mir-215 | -6,089 |
| hsa-mir-18B | -6,118 |
| hsa-mir-520f | -6,126 |
| hsa-let-7e | -6,133 |
| hsa-mir-200a | -6,149 |
| hsa-mir-10b | -6,170 |
| hsa-mir-485-3p | -6,173 |
| hsa-miR-591 | -6,192 |
| hsa-mir-143 | -6,192 |
| hsa-miR-363hek | -6,210 |
| hsa-mir-370 | -6,270 |
| hsa-mir-133b | -6,328 |
| hsa-mir-500 | -6,400 |
| hsa-mir-107 | -6,407 |
| hsa-mir-432hek | -6,421 |
| hsa-mir-630 | -6,452 |
| hsa-mir-519a | -6,485 |
| hsa-mir-643 | -6,513 |
| hsa-mir-193b | -6,515 |
| hsa-miR-606 | -6,545 |
| hsa-mir-517c | -6,601 |
| hsa-mir-496 | -6,721 |
| hsa-mir-204 | -6,916 |
| hsa-mir-33 | -6,965 |
| hsa-mir-636 | -6,967 |
| hsa-mir-639 | -7,018 |
| hsa-mir-134 | -7,024 |
| hsa-mir-338 | -7,053 |
| hsa-mir-216 | -7,114 |
| hsa-mir-183 | -7,126 |
| hsa-mir-224 | -7,241 |
| hsa-mir-214 | -7,257 |
| hsa-mir-410 | -7,329 |
| hsa-mir-1 | -7,348 |
| hsa-miR-648 | -7,368 |
| hsa-miR-628 | -7,406 |
| hsa-mir-604 | -7,418 |
| hsa-mir-9hek | -7,437 |
| hsa-mir-514 | -7,439 |
| hsa-mir-515-3p | -7,461 |
| hsa-mir-153 | -7,463 |
| hsa-mir-508 | -7,485 |
| hsa-mir-96 | -7,539 |
| hsa-mir-433 | -7,540 |
| hsa-mir-518e | -7,564 |
| hsa-miR-504 | -7,572 |
| hsa-mir-503 | -7,621 |
| hsa-miR-592 | -7,621 |
| hsa-mir-182hek | -7,673 |
| hsa-mir-219 | -7,713 |

| | |
|---|---|
| hsa-miR-548a | -7,797 |
| hsa-mir-646 | -7,822 |
| hsa-mir-133a | -7,860 |
| hsa-mir-520dhek | -7,885 |
| hsa-mir-211 | -7,983 |
| hsa-miR-644 | -8,004 |
| hsa-miR-570 | -8,005 |
| hsa-mir-511 | -8,027 |
| hsa-miR-562 | -8,040 |
| hsa-mir-509 | -8,075 |
| hsa-mir-519e | -8,076 |
| hsa-mir-527 | -8,102 |
| hsa-mir-544 | -8,125 |
| hsa-miR-450 | -8,174 |
| hsa-mir-208 | -8,186 |
| hsa-mir-518b | -8,198 |
| hsa-miR-617 | -8,205 |
| hsa-mir-584 | -8,220 |
| hsa-miR-596 | -8,222 |
| hsa-mir-302d | -8,224 |
| hsa-mir-518d | -8,229 |
| hsa-mir-302b | -8,245 |
| hsa-mir-184 | -8,266 |
| hsa-mir-571 | -8,266 |
| hsa-mir-429 | -8,272 |
| hsa-mir-542-5p | -8,302 |
| hsa-mir-520h | -8,314 |
| hsa-mir-411 | -8,359 |
| hsa-mir-580 | -8,361 |
| hsa-mir-487b | -8,403 |
| hsa-mir-205 | -8,494 |
| hsa-mir-34c | -8,541 |
| hsa-mir-520g | -8,544 |
| hsa-mir-302a | -8,549 |
| hsa-mir-526a | -8,556 |
| hsa-mir-555 | -8,582 |
| hsa-mir-383 | -8,602 |
| hsa-mir-519ehek | -8,603 |
| hsa-mir-586 | -8,663 |
| hsa-miR-567 | -8,665 |
| hsa-mir-497 | -8,683 |
| hsa-mir-524 | -8,712 |
| hsa-mir-449b | -8,748 |
| hsa-mir-449 | -8,794 |
| hsa-mir-517hek | -8,825 |
| hsa-mir-139 | -8,827 |
| hsa-mir-367 | -8,842 |
| hsa-mir-369-5p | -8,856 |
| hsa-mir-452hek | -8,866 |
| hsa-mir-199a | -8,894 |
| hsa-mir-539 | -8,918 |
| hsa-miR-599 | -8,976 |
| hsa-mir-379 | -9,018 |
| hsa-mir-217 | -9,040 |
| hsa-mir-455 | -9,073 |
| hsa-mir-627 | -9,078 |
| hsa-mir-487a | -9,092 |
| hsa-mir-372 | -9,141 |
| hsa-mir-551b | -9,172 |
| hsa-mir-432 | -9,200 |
| hsa-mir-373 | -9,202 |
| hsa-miR-641 | -9,208 |
| hsa-mir-202 | -9,219 |

| | |
|---|---|
| hsa-mir-559 | -9,229 |
| hsa-mir-551a | -9,235 |
| hsa-miR-556 | -9,253 |
| hsa-miR-488 | -9,289 |
| hsa-miR-575 | -9,297 |
| hsa-mir-326 | -9,332 |
| hsa-mir-200ahek | -9,372 |
| hsa-mir-651 | -9,378 |
| hsa-mir-187 | -9,468 |
| hsa-mir-489 | -9,643 |
| hsa-mir-369-3p | -9,678 |
| hsa-mir-189 | -9,732 |
| hsa-mir-563 | -9,740 |
| hsa-mir-302ahek | -9,747 |
| hsa-mir-147 | -9,755 |
| hsa-mir-526bhek | -9,766 |
| hsa-mir-202hek | -9,771 |
| hsa-mir-573 | -9,803 |
| hsa-mir-302c | -9,825 |
| hsa-mir-656 | -9,846 |
| hsa-miR-548c | -9,938 |
| hsa-mir-329 | -10,013 |
| hsa-mir-655 | -10,159 |
| hsa-mir-368 | -10,407 |
| hsa-mir-520b | -10,827 |

**Supplementary Table 2**

Part 2: Complete miRNA custom library information

| mir name | chrom | position | Target sequence | mirname | Position1 | Position2 | Position3 | Position 4 | | |
|---|---|---|---|---|---|---|---|---|---|---|
| hsa-let-7a | | 9 | 95978060 UGAGGUAGUAGGUUGUAUAGUU | hsa-let-7a | 9:95978060-95978139+ | 11:121522440-121522511- | 22:44887293-44887366+ | NA | chr9 95978060 95978061 | q22.32 |
| hsa-let-7b | | 22 | 44888230 UGAGGUAGUAGGUUGUGUGGUU | hsa-let-7b | 22:44888230-44888312+ | NA | NA | NA | chr22 44888230 44888231 | q13.31 |
| hsa-let-7c | | 21 | 16834019 UGAGGUAGUAGGUUGUAUGGUU | hsa-let-7c | 21:16834019-16834102+ | NA | NA | NA | chr21 16834019 16834020 | q21.1 |
| hsa-let-7d | | 9 | 95980937 AGAGGUAGUAGGUUGCAUAGU | hsa-let-7d | 9:95980937-95981023+ | NA | NA | NA | chr9 95980937 95980938 | q22.32 |
| hsa-let-7e | | 19 | 56887851 UGAGGUAGGAGGUUGUAUAGU | hsa-let-7e | 19:56887851-56887929+ | NA | NA | NA | chr19 56887851 56887852 | q13.33 |
| hsa-let-7f | | 9 | 95978450 UGAGGUAGUAGAUUGUAUAGUU | hsa-let-7f | 9:95978450-95978536+ | 23:53600878-53600960- | NA | NA | chr9 95978450 95978451 | q22.32 |
| hsa-let-7g | | 3 | 52277334 UGAGGUAGUAGUUUGUACAGU | hsa-let-7g | 3:52277334-52277417- | NA | NA | NA | chr3 52277334 52277335 | p21.1 |
| hsa-let-7i | | 12 | 61283733 UGAGGUAGUAGUUUGUGCUGU | hsa-let-7i | 12:61283733-61283816+ | NA | NA | NA | chr12 61283733 61283734 | q14.1 |
| hsa-mir-1 | | 20 | 60561958 UGGAAUGUAAAGAAGUAUGUA | hsa-miR-1 | 20:60561958-60562028+ | NA | NA | NA | chr20 60561958 60561959 | q13.33 |
| hsa-mir-100 | | 11 | 1,22E+08 AACCCGUAGAUCCGAACUUGUG | hsa-miR-100 | 11:121528147-121528226- | NA | NA | NA | chr11 121528147 121528148 | q24.1 |
| hsa-mir-101 | | 1 | 65296705 UACAGUACUGUGAUAACUGAAG | hsa-miR-101 | 1:65296705-65296779- | 9:4840297-4840375+ | NA | NA | chr1 65296705 65296706 | p31.3 |
| hsa-mir-103 | | 5 | 1,68E+08 AGCAGCAUUGUACAGGGCUAUGA | hsa-miR-103 | 5:167920479-167920556- | 5:167920487-167920548+ | 20:3846141-3846218+ | 20:3846149-3846210- | chr5 167920479 167920480 | q35.1 |
| hsa-miR-105 | X | | 1,51E+08 UCAAAUGCUCAGACUCCUGU | hsa-miR-105 | 23:151311347-151311427- | 23:151313540-151313620- | NA | NA | chrX 151311347 151311348 | q28 |
| hsa-mir-106a | X | | 1,33E+08 AAAAGUGCUUACAGUGCAGGUAGC | hsa-miR-106a | 23:133131894-133131974- | NA | NA | NA | chrX 133131894 133131895 | q26.2 |
| hsa-mir-106b | | 7 | 99529552 UAAAGUGCUGACAGUGCAGAU | hsa-miR-106b | 7:99529552-99529633- | NA | NA | NA | chr7 99529552 99529553 | q22.1 |
| hsa-mir-107 | | 10 | 91342484 AGCAGCAUUGUACAGGGCUAUCA | hsa-miR-107 | 10:91342484-91342564- | NA | NA | NA | chr10 91342484 91342485 | q23.31 |
| hsa-mir-10a | | 17 | 44012199 UACCCUGUAGAUCCGAAUUUGUG | hsa-miR-10a | 17:44012199-44012308- | NA | NA | NA | chr17 44012199 44012200 | q21.32 |
| hsa-mir-10b | | 2 | 1,77E+08 UACCCUGUAGAACCGAAUUUGU | hsa-miR-10b | 2:176723277-176723386+ | NA | NA | NA | chr2 176723277 176723278 | q31.1 |
| hsa-mir-122a | | 18 | 54269286 UGGAGUGUGACAAUGGUGUUUGU | hsa-miR-122 | 18:54269286-54269370+ | NA | NA | NA | chr18 54269286 54269287 | q21.31 |
| hsa-mir-124a | | 8 | 9798308 UUAAGGCACGCGGUGAAUGCCA | hsa-miR-124 | 8:9798308-9798392- | 8:65454260-65454368+ | NA | NA | chr8 9798308 9798309 | p23.1 |
| hsa-mir-125a | | 19 | 56888319 UCCCUGAGACCCUUUAACCUGUG | hsa-miR-125a-5p | 19:56888319-56888404+ | NA | NA | NA | chr19 56888319 56888320 | q13.33 |
| hsa-mir-125b | | 11 | 1,21E+08 UCCCUGAGACCCUAACUUGUGA | hsa-miR-125b | 11:121475675-121475762- | 21:16884428-16884516+ | NA | NA | chr11 121475675 121475676 | q24.1 |
| hsa-miR-126 | | 9 | 1,39E+08 UCGUACCGUGAGUAAUAAUGC | hsa-miR-126 | 9:138684875-138684959+ | NA | NA | NA | chr9 138684875 138684876 | q34.3 |
| hsa-mir-126star | | 9 | 1,39E+08 CAUUAUUACUUUUGGUACGCG | hsa-miR-126* | 9:138684875-138684959+ | NA | NA | NA | chr9 138684875 138684876 | q34.3 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| hsa-mir-127 | 14 | 1E+08 | UCGGAUCCGUCUGAGCUUGGCU | hsa-miR-127-3p | 14:100419069-100419165+ | NA | NA | NA | chr14 100419069 10041907( | q32.31 |
| hsa-mir-128a | 2 | 1,36E+08 | UCACAGUGAACCGGUCUCUUUU | hsa-miR-128 | 2:136139437-136139518+ | NA | NA | NA | chr2 136139437 136139438 | q21.3 |
| hsa-mir-128b | 2 | 1,36E+08 | UCACAGUGAACCGGUCUCUUUC | hsa-miR-128 | 2:136139437-136139518+ | NA | NA | NA | chr2 136139437 136139438 | q21.3 |
| hsa-mir-129 | 7 | 1,28E+08 | CUUUUUGCGGUCUGGGCUUGC | hsa-miR-129-5p | 7:127635161-127635232+ | NA | NA | NA | chr7 127635161 127635162 | q32.1 |
| hsa-mir-130a | 11 | 57165247 | CAGUGCAAUGUUAAAAGGGCAU | hsa-miR-130a | 11:57165247-57165335+ | NA | NA | NA | chr11 57165247 57165248 | q12.1 |
| hsa-mir-130b | 22 | 20337593 | CAGUGCAAUGAUGAAAGGGCAU | hsa-miR-130b | 22:20337593-20337674+ | NA | NA | NA | chr22 20337593 20337594 | q11.21 |
| hsa-mir-132 | 17 | 1899952 | UAACAGUCUACAGCCAUGGUCG | hsa-miR-132 | 17:1899952-1900052- | NA | NA | NA | chr17 1899952 1899953 | p13.3 |
| hsa-mir-133a | 18 | 17659657 | UUGGUCCCCUUCAACCAGCUGU | hsa-miR-133a | 18:17659657-17659744- | 20:60572564-60572665+ | NA | NA | chr18 17659657 17659658 | q11.2 |
| hsa-mir-133b | 6 | 52121680 | UUGGUCCCCUUCAACCAGCUA | hsa-miR-133b | 6:52121680-52121798+ | NA | NA | NA | chr6 52121680 52121681 | p12.2 |
| hsa-mir-134 | 14 | 1,01E+08 | UGUGACUGGUUGACCAGAGGG | hsa-miR-134 | 14:100590777-100590849+ | NA | NA | NA | chr14 100590777 100590778 | q32.31 |
| hsa-mir-135a | 3 | 52303275 | UAUGGCUUUUUAUUCCUAUGUGA | hsa-miR-135a | 3:52303275-52303364- | 12:96481721-96481820+ | NA | NA | chr3 52303275 52303276 | p21.1 |
| hsa-mir-135b | 1 | 2,04E+08 | UAUGGCUUUUCAUUCCUAUGUG | hsa-miR-135b | 1:203684053-203684149- | NA | NA | NA | chr1 203684053 203684054 | q32.1 |
| hsa-mir-136 | 14 | 1E+08 | ACUCCAUUUGUUUUGAUGAUGGA | hsa-miR-136 | 14:100420792-100420873+ | NA | NA | NA | chr14 100420792 100420793 | q32.31 |
| hsa-mir-137 | 1 | 98284214 | UAUUGCUUAAGAAUACGCGUAG | hsa-miR-137 | 1:98284214-98284315- | NA | NA | NA | chr1 98284214 98284215 | p21.3 |
| hsa-mir-138 | 3 | 44130708 | AGCUGGUGUUGUGAAUC | hsa-miR-138 | 3:44130708-44130806+ | 16:55449931-55450014+ | NA | NA | chr3 44130708 44130709 | p21.33 |
| hsa-mir-139 | 11 | 72003755 | UCUACAGUGCACGUGUCU | hsa-miR-139-5p | 11:72003755-72003822- | NA | NA | NA | chr11 72003755 72003756 | q13.4 |
| hsa-mir-140 | 16 | 68524485 | AGUGGUUUUACCCUAUGGUAG | hsa-miR-140-5p | 16:68524485-68524584+ | NA | NA | NA | chr16 68524485 68524486 | q22.1 |
| hsa-mir-141 | 12 | 6943521 | UAACACUGUCUGGUAAAGAUGG | hsa-miR-141 | 12:6943521-6943615+ | NA | NA | NA | chr12 6943521 6943522 | p13.31 |
| hsa-mir-142-3p | 17 | 53763592 | UGUAGUGUUUCCUACUUUAUGGA | hsa-miR-142-3p | 17:53763592-53763678- | NA | NA | NA | chr17 53763592 53763593 | q22 |
| hsa-mir-142-5p | 17 | 53763592 | CAUAAAGUAGAAAGCACUAC | hsa-miR-142-5p | 17:53763592-53763678- | NA | NA | NA | chr17 53763592 53763593 | q22 |
| hsa-mir-143 | 5 | 1,49E+08 | UGAGAUGAAGCACUGUAGCUCA | hsa-miR-143 | 5:148788674-148788779+ | NA | NA | NA | chr5 148788674 148788675 | q33.1 |
| hsa-mir-145 | 5 | 1,49E+08 | GUCCAGUUUUCCCAGGAAUCCCUU | hsa-miR-145 | 5:148790402-148790489+ | NA | NA | NA | chr5 148790402 148790403 | q33.1 |
| hsa-mir-146a | 5 | 1,6E+08 | UGAGAACUGAAUUCCAUGGGUU | hsa-miR-146a | 5:159844937-159845035+ | NA | NA | NA | chr5 159844937 159844938 | q33.3 |
| hsa-miR-146b | 10 | 1,04E+08 | UGAGAACUGAAUUCCAUAGGCU | hsa-miR-146b-5p | 10:104186259-104186331+ | NA | NA | NA | chr10 104186259 10418626( | q24.32 |
| hsa-mir-147 | 9 | 1,22E+08 | GUGUGUGGAAAUGCUUCUGC | hsa-miR-147 | 9:122047078-122047149- | NA | NA | NA | chr9 122047078 122047079 | q33.2 |
| hsa-mir-148a | 7 | 25956064 | UCAGUGCACUACAGAACUUUGU | hsa-miR-148a | 7:25956064-25956131- | NA | NA | NA | chr7 25956064 25956065 | p15.2 |
| hsa-mir-148b | 12 | 53017267 | UCAGUGCAUCACAGAACUUUGU | hsa-miR-148b | 12:53017267-53017365+ | NA | NA | NA | chr12 53017267 53017268 | q13.13 |

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|---|---|---|---|---|---|---|---|---|---|---|
| hsa-mir-149 | 2 | 2,41E+08 | UCUGGCUCCGUGUCUUCACUCC | hsa-miR-149 | 2:241044091-241044179+ | NA | NA | NA | chr2 241044091 241044092 | q37.3 |
| hsa-mir-150 | 19 | 54695854 | UCUCCCAACCCUUGUACCAGUG | hsa-miR-150 | 19:54695854-54695937- | NA | NA | NA | chr19 54695854 54695855 | q13.33 |
| hsa-mir-151 | 8 | 1,42E+08 | ACUAGACUGAAGCUCCUUGAGG | hsa-miR-151-3p | 8:141811845-141811934- | NA | NA | NA | chr8 141811845 141811846 | q24.3 |
| hsa-mir-152 | 17 | 43469526 | UCAGUGCAUGACAGAACUUGGG | hsa-miR-152 | 17:43469526-43469612- | NA | NA | NA | chr17 43469526 43469527 | q21.32 |
| hsa-mir-153 | 2 | 2,2E+08 | UUGCAUAGUCACAAAAGUGA | hsa-miR-153 | 2:219867077-219867166- | 7:157059789-157059875- | NA | NA | chr2 219867077 219867078 | q35 |
| hsa-mir-154 | 14 | 1,01E+08 | UAGGUUAUCCGUGUUGCCUUCG | hsa-miR-154 | 14:100595845-100595928+ | NA | NA | NA | chr14 100595845 100595846 | q32.31 |
| hsa-mir-154star | 14 | 1,01E+08 | AAUCAUACACGGUUGACCUAUU | hsa-miR-154* | 14:100595845-100595928+ | NA | NA | NA | chr14 100595845 100595846 | q32.31 |
| hsa-mir-155 | 21 | 25868163 | UUAAUGCUAAUCGUGAUAGGGG | hsa-miR-155 | 21:25868163-25868227+ | NA | NA | NA | chr21 25868163 25868164 | q21.3 |
| hsa-mir-15a | 13 | 49521256 | UAGCAGCACAUAAUGGUUUGUG | hsa-miR-15a | 13:49521256-49521338- | NA | NA | NA | chr13 49521256 49521257 | q14.3 |
| hsa-mir-15b | 3 | 1,62E+08 | UAGCAGCACAUCAUGGUUUACA | hsa-miR-15b | 3:161605070-161605167+ | NA | NA | NA | chr3 161605070 161605071 | q26.1 |
| hsa-mir-16 | 13 | 49521110 | UAGCAGCACGUAAAUAUUGGCG | hsa-miR-16 | 13:49521110-49521198- | 3:161605227-161605307+ | NA | NA | chr13 49521110 49521111 | q14.3 |
| hsa-mir-17-3p | 13 | 90800860 | ACUGCAGUGAAGGCACUUGU | hsa-miR-17* | 13:90800860-90800943+ | NA | NA | NA | chr13 90800860 90800861 | q31.3 |
| hsa-mir-17-5p | 13 | 90800860 | CAAAGUGCUUACAGUGCAGGUAGU | hsa-miR-17 | 13:90800860-90800943+ | NA | NA | NA | chr13 90800860 90800861 | q31.3 |
| hsa-mir-181a | 1 | 1,97E+08 | AACAUUCAACGCUGUCGGUGAGU | hsa-miR-181a | 1:197094796-197094905- | 9:126494542-126494651+ | NA | NA | chr1 197094796 197094797 | q31.3 |
| hsa-mir-181b | 1 | 1,97E+08 | AACAUUCAUUGCUGUCGGUGGG | hsa-miR-181b | 1:197094625-197094734- | 9:126495810-126495898+ | NA | NA | chr1 197094625 197094626 | q31.3 |
| hsa-mir-181c | 19 | 13846513 | AACAUUCAACCUGUCGGUGAGU | hsa-miR-181c | 19:13846513-13846622+ | NA | NA | NA | chr19 13846513 13846514 | p13.12 |
| hsa-mir-181d | 19 | 13846689 | AACAUUCAUUGUUGUCGGUGGGUU | hsa-miR-181d | 19:13846689-13846825+ | NA | NA | NA | chr19 13846689 13846690 | p13.12 |
| hsa-mir-182 | 7 | 1,29E+08 | UUUGGCAAUGGUAGAACUCACA | hsa-miR-182 | 7:129197459-129197568- | NA | NA | NA | chr7 129197459 129197460 | q32.2 |
| hsa-mir-182star | 7 | 1,29E+08 | UGGUUCUAGACUUGCCAACUA | hsa-miR-182* | 7:129197459-129197568- | NA | NA | NA | chr7 129197459 129197460 | q32.2 |
| hsa-mir-183 | 7 | 1,29E+08 | UAUGGCACUGGUAGAAUUCACUG | hsa-miR-183 | 7:129201981-129202090- | NA | NA | NA | chr7 129201981 129201982 | q32.2 |
| hsa-mir-184 | 15 | 77289185 | UGGACGGAGAACUGAUAAGGGU | hsa-miR-184 | 15:77289185-77289268+ | NA | NA | NA | chr15 77289185 77289186 | q25.1 |
| hsa-miR-185 | 22 | 18400662 | UGGAGAGAAAGGCAGUUC | hsa-miR-185 | 22:18400662-18400743+ | NA | NA | NA | chr22 18400662 18400663 | q11.21 |
| hsa-mir-186 | 1 | 71305902 | CAAAGAAUUCUCCUUUUGGGCUU | hsa-miR-186 | 1:71305902-71305987- | NA | NA | NA | chr1 71305902 71305903 | p31.1 |
| hsa-mir-187 | 18 | 31738779 | UCGUGUCUUGUGUUGCAGCCG | hsa-miR-187 | 18:31738779-31738887- | NA | NA | NA | chr18 31738779 31738780 | q12.2 |
| hsa-mir-188 | X | 49654849 | CAUCCCUUGCAUGGUGGAGGGU | hsa-miR-188-5p | 23:49654849-49654934+ | NA | NA | NA | chrX 49654849 49654850 | p11.23 |
| hsa-mir-189 | 9 | 96888124 | GUGCCUACUGAGCUGAUAUCAGU | hsa-miR-24-1* | 9: 96888124-96888191+ | NA | NA | NA | chr9 96888124 96888125 | q22.32 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| hsa-mir-18a | 13 | 90801006 | UAAGGUGCAUCUAGUGCAGAUA | hsa-miR-18a | 13:90801006-90801076+ | NA | NA | NA | chr13 90801006 90801007 | q31.3 |
| hsa-mir-18astar | 13 | 90801006 | ACUGCCCUAAGUGCUCCUUCU | hsa-miR-18a* | 13:90801006-90801076+ | NA | NA | NA | chr13 90801006 90801007 | q31.3 |
| hsa-mir-18B | X | 1,33E+08 | UAAGGUGCAUCUAGUGCAGUUA | hsa-miR-18b | 23:133131737-133131807- | NA | NA | NA | chrX 133131737 133131738 | q26.2 |
| hsa-mir-190 | 15 | 60903209 | UGAUAUGUUUGAUAUAUUAGGU | hsa-miR-190 | 15:60903209-60903293+ | NA | NA | NA | chr15 60903209 60903210 | q22.2 |
| hsa-mir-191 | 3 | 49033055 | CAACGGAAUCCCAAAAGCAGCU | hsa-miR-191 | 3:49033055-49033146- | NA | NA | NA | chr3 49033055 49033056 | p21.31 |
| hsa-mir-192 | 11 | 64415185 | CUGACCUAUGAAUUGACAGCC | hsa-miR-192 | 11:64415185-64415294- | NA | NA | NA | chr11 64415185 64415186 | q13.1 |
| hsa-mir-193a | 17 | 26911128 | AACUGGCCUACAAAGUCCCAG | hsa-miR-193a-3p | 17:26911128-26911215+ | NA | NA | NA | chr17 26911128 26911129 | q11.2 |
| hsa-mir-193b | 16 | 14305325 | AACUGGCCCUCAAAGUCCCGCUUU | hsa-miR-193b | 16:14305325-14305407+ | NA | NA | NA | chr16 14305325 14305326 | p13.12 |
| hsa-mir-194 | 1 | 2,18E+08 | UGUAACAGCAACUCCAUGUGGA | hsa-miR-194 | 1:218358122-218358206- | 11:64415403-64415487- | NA | NA | chr1 218358122 218358123 | q41 |
| hsa-mir-195 | 17 | 6861658 | UAGCAGCACAGAAAUAUUGGC | hsa-miR-195 | 17:6861658-6861744- | NA | NA | NA | chr17 6861658 6861659 | p13.1 |
| hsa-mir-196a | 17 | 44064851 | UAGGUAGUUUCAUGUUGUUGG | hsa-miR-196a | 17:44064851-44064920- | 12:52671789-52671898+ | NA | NA | chr17 44064851 44064852 | q21.32 |
| hsa-mir-196b | 7 | 27175624 | UAGGUAGUUUCCUGUUGUUGG | hsa-miR-196b | 7:27175624-27175707- | NA | NA | NA | chr7 27175624 27175625 | p15.2 |
| hsa-mir-197 | 1 | 1,1E+08 | UUCACCACCUUCUCCACCCAGC | hsa-miR-197 | 1:109943038-109943112+ | NA | NA | NA | chr1 109943038 109943039 | p13.3 |
| hsa-mir-198 | 3 | 1,22E+08 | GGUCCAGAGGGGAGAUAGG | hsa-miR-198 | 3:121597205-121597266- | NA | NA | NA | chr3 121597205 121597206 | q13.33 |
| hsa-mir-199a | 19 | 10789102 | CCCAGUGUUCAGACUACCUGUUC | hsa-miR-199a-5p | 19:10789102-10789172- | 1:170380298-170380407- | NA | NA | chr19 10789102 10789103 | p13.2 |
| hsa-mir-199astar | 19 | 10789102 | UACAGUAGUCUGCACAUUGGUU | hsa-miR-199a-3p | 19:10789102-10789172- | 1:170380298-170380407- | NA | NA | chr19 10789102 10789103 | p13.2 |
| hsa-mir-199b | 9 | 1,3E+08 | CCCAGUGUUUAGACUAUCUGUUC | hsa-miR-199b-5p | 9:130046821-130046930- | NA | NA | NA | chr9 130046821 130046822 | q34.11 |
| hsa-mir-19a | 13 | 90801146 | UGUGCAAAUCUAUGCAAAACUGA | hsa-miR-19a | 13:90801146-90801227+ | NA | NA | NA | chr13 90801146 90801147 | q31.3 |
| hsa-mir-19b | 13 | 90801447 | UGUGCAAAUCCAUGCAAAACUGA | hsa-miR-19b | 13:90801447-90801533+ | 23:133131367-133131462- | NA | NA | chr13 90801447 90801448 | q31.3 |
| hsa-mir-200a | 1 | 1093106 | UAACACUGUCUGGUAACGAUGU | hsa-miR-200a | 1:1093106-1093195+ | NA | NA | NA | chr1 1093106 1093107 | p36.33 |
| hsa-mir-200astar | 1 | 1093106 | CAUCUUACCGGACAGUGCUGGA | hsa-miR-200a* | 1:1093106-1093195+ | NA | NA | NA | chr1 1093106 1093107 | p36.33 |
| hsa-mir-200b | 1 | 1092347 | UAAUACUGCCUGGUAAUGAUGAC | hsa-miR-200b | 1:1092347-1092441+ | NA | NA | NA | chr1 1092347 1092348 | p36.33 |
| hsa-mir-200c | 12 | 6943123 | UAAUACUGCCGGGUAAUGAUGG | hsa-miR-200c | 12:6943123-6943190+ | NA | NA | NA | chr12 6943123 6943124 | p13.31 |
| hsa-mir-202 | 10 | 1,35E+08 | AGAGGUAUAGGGCAUGGGAAAA | hsa-miR-202 | 10:134911006-134911115- | NA | NA | NA | chr10 134911006 134911007 | q26.3 |
| hsa-mir-202star | 10 | 1,35E+08 | UUUCCUAUGCAUAUACUUCUUU | hsa-miR-202* | 10:134911006-134911115- | NA | NA | NA | chr10 134911006 134911007 | q26.3 |
| hsa-mir-203 | 14 | 1,04E+08 | GUGAAAUGUUUAGGACCACUAG | hsa-miR-203 | 14:103653495-103653604+ | NA | NA | NA | chr14 103653495 103653496 | q32.33 |
| hsa-mir-204 | 9 | 72614711 | UUCCCUUUGUCAUCCUAUGCCU | hsa-miR-204 | 9:72614711-72614820- | NA | NA | NA | chr9 72614711 72614712 | q21.11 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| hsa-mir-205 | | 1 | 2,08E+08 | UCCUUCAUUCCACCGGAGUCUG | hsa-miR-205 | 1:207672101-207672210+ | NA | NA | NA | chr1 207672101 207672102 | q32.2 |
| hsa-mir-206 | | 6 | 52117106 | UGGAAUGUAAGGAAGUGUGUGG | hsa-miR-206 | 6:52117106-52117191+ | NA | NA | NA | chr6 52117106 52117107 | p12.2 |
| hsa-mir-208 | | 14 | 22927645 | AUAAGACGAGCAAAAAGCUUGU | hsa-miR-208a | 14:22927645-22927715- | NA | NA | NA | chr14 22927645 22927646 | q11.2 |
| hsa-mir-20a | | 13 | 90801320 | UAAAGUGCUUAUAGUGCAGGUAG | hsa-miR-20a | 13:90801320-90801390+ | NA | NA | NA | chr13 90801320 90801321 | q31.3 |
| hsa-mir-20b | X | | 1,33E+08 | CAAAGUGCUCAUAGUGCAGGUAG | hsa-miR-20b | 23:133131505-133131573- | NA | NA | NA | chrX 133131505 133131506 | q26.2 |
| hsa-mir-21 | | 17 | 55273409 | UAGCUUAUCAGACUGAUGUUGA | hsa-miR-21 | 17:55273409-55273480+ | NA | NA | NA | chr17 55273409 55273410 | q23.1 |
| hsa-mir-210 | | 11 | 558089 | CUGUGCGUGUGACAGCGGCUGA | hsa-miR-210 | 11:558089-558198- | NA | NA | NA | chr11 558089 558090 | p15.5 |
| hsa-mir-211 | | 15 | 29144527 | UUCCCUUUGUCAUCCUUCGCCU | hsa-miR-211 | 15:29144527-29144636- | NA | NA | NA | chr15 29144527 29144528 | q13.3 |
| hsa-mir-212 | | 17 | 1900315 | UAACAGUCUCCAGUCACGGCC | hsa-miR-212 | 17:1900315-1900424- | NA | NA | NA | chr17 1900315 1900316 | p13.3 |
| hsa-mir-213 | | 1 | 1,97E+08 | ACCAUCGACCGUUGAUUGUACC | hsa-miR-181a* | 1:197094796-197094905- | 9:126494542-126494651+ | NA | NA | chr1 197094796 197094797 | q31.3 |
| hsa-mir-214 | | 1 | 1,7E+08 | ACAGCAGGCACAGACAGGCAG | hsa-miR-214 | 1:170374561-170374670- | NA | NA | NA | chr1 170374561 170374562 | q24.3 |
| hsa-mir-215 | | 1 | 2,18E+08 | AUGACCUAUGAAUUGACAGAC | hsa-miR-215 | 1:218357818-218357927- | NA | NA | NA | chr1 218357818 218357819 | q41 |
| hsa-mir-216 | | 2 | 56069589 | UAAUCUCAGCUGGCAACUGUG | hsa-miR-216a | 2:56069589-56069698- | NA | NA | NA | chr2 56069589 56069590 | p16.1 |
| hsa-mir-217 | | 2 | 56063606 | UACUGCAUCAGGAACUGAUUGGAU | hsa-miR-217 | 2:56063606-56063715- | NA | NA | NA | chr2 56063606 56063607 | p16.1 |
| hsa-mir-218 | | 4 | 20138996 | UUGUGCUUGAUCUAACCAUGU | hsa-miR-218 | 4:20138996-20139105+ | 5:168127729-168127838- | NA | NA | chr4 20138996 20138997 | p15.31 |
| hsa-mir-219 | | 6 | 33283590 | UGAUUGUCCAAACGCAAUUCU | hsa-miR-219-5p | 6:33283590-33283699+ | 9:130194718-130194814- | NA | NA | chr6 33283590 33283591 | p21.32 |
| hsa-mir-22 | | 17 | 1563947 | AAGCUGCCAGUUGAAGAACUGU | hsa-miR-22 | 17:1563947-1564031- | NA | NA | NA | chr17 1563947 1563948 | p13.3 |
| hsa-mir-220 | X | | 1,23E+08 | CCACACCGUAUCUGACACUUU | hsa-miR-220a | 23:122523627-122523736- | NA | NA | NA | chrX 122523627 122523628 | q25 |
| hsa-mir-221 | X | | 45490529 | AGCUACAUUGUCUGCUGGGUUUC | hsa-miR-221 | 23:45490529-45490638- | NA | NA | NA | chrX 45490529 45490530 | p11.3 |
| hsa-mir-222 | X | | 45491365 | AGCUACAUCUGGCUACUGGGUCUC | hsa-miR-222 | 23:45491365-45491474- | NA | NA | NA | chrX 45491365 45491366 | p11.3 |
| hsa-mir-223 | X | | 65155437 | UGUCAGUUUGUCAAAUACCCC | hsa-miR-223 | 23:65155437-65155546+ | NA | NA | NA | chrX 65155437 65155438 | q12 |
| hsa-mir-224 | X | | 1,51E+08 | CAAGUCACUAGUGGUUCCGUUUA | hsa-miR-224 | 23:150877706-150877786- | NA | NA | NA | chrX 150877706 150877707 | q28 |
| hsa-mir-23a | | 19 | 13808401 | AUCACAUUGCCAGGGAUUUCC | hsa-miR-23a | 19:13808401-13808473- | NA | NA | NA | chr19 13808401 13808402 | p13.12 |
| hsa-mir-23b | | 9 | 96887311 | AUCACAUUGCCAGGGAUUACC | hsa-miR-23b | 9:96887311-96887407+ | NA | NA | NA | chr9 96887311 96887312 | q22.32 |
| hsa-mir-24 | | 9 | 96888124 | UGGCUCAGUUCAGCAGGAACAG | hsa-miR-24 | 9:96888124-96888191+ | 19:13808101-13808173- | NA | NA | chr9 96888124 96888125 | q22.32 |
| hsa-mir-25 | | 7 | 99529119 | CAUUGCACUUGUCUCGGUCUGA | hsa-miR-25 | 7:99529119-99529202- | NA | NA | NA | chr7 99529119 99529120 | q22.1 |

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|---|---|---|---|---|---|---|---|---|---|---|
| hsa-mir-26a | 3 | 37985899 | UUCAAGUAAUCCAGGAUAGGC | hsa-miR-26a | 3:37985899-37985975+ | 12:56504659-56504742- | NA | NA | chr3 37985899 37985900 | p22.2 |
| hsa-mir-26b | 2 | 2,19E+08 | UUCAAGUAAUUCAGGAUAGGUU | hsa-miR-26b | 2:218975613-218975689+ | NA | NA | NA | chr2 218975613 218975614 | q35 |
| hsa-mir-27a | 19 | 13808254 | UUCACAGUGGCUAAGUUCCGC | hsa-miR-27a | 19:13808254-13808331- | NA | NA | NA | chr19 13808254 13808255 | p13.12 |
| hsa-mir-27b | 9 | 96887548 | UUCACAGUGGCUAAGUUCUGC | hsa-miR-27b | 9:96887548-96887644+ | NA | NA | NA | chr9 96887548 96887549 | q22.32 |
| hsa-mir-28 | 3 | 1,9E+08 | AAGGAGCUCACAGUCUAUUGAG | hsa-miR-28-5p | 3:189889263-189889348+ | NA | NA | NA | chr3 189889263 189889264 | q28 |
| hsa-mir-296 | 20 | 56826065 | AGGGCCCCCCCUCAAUCCUGU | hsa-miR-296-5p | 20:56826065-56826144- | NA | NA | NA | chr20 56826065 56826066 | q13.32 |
| hsa-miR-299-3p | 14 | 1,01E+08 | UAUGUGGGAUGGUAAACCGCUU | hsa-miR-299-3p | 14:100559884-100559946+ | NA | NA | NA | chr14 100559884 100559885 | q32.31 |
| hsa-mir-299-5p | 14 | 1,01E+08 | UGGUUUACCGUCCCACAUACAU | hsa-miR-299-5p | 14:100559884-100559946+ | NA | NA | NA | chr14 100559884 100559885 | q32.31 |
| hsa-mir-29a | 7 | 1,3E+08 | UAGCACCAUCUGAAAUCGGUU | hsa-miR-29a | 7:130212046-130212109- | NA | NA | NA | chr7 130212046 130212047 | q32.3 |
| hsa-mir-29b | 7 | 1,3E+08 | UAGCACCAUUUGAAAUCAGUGUU | hsa-miR-29b | 7:130212758-130212838- | 1:206042411-206042491- | NA | NA | chr7 130212758 130212759 | q32.3 |
| hsa-mir-29c | 1 | 2,06E+08 | UAGCACCAUUUGAAAUCGGU | hsa-miR-29c | 1:206041820-206041907- | NA | NA | NA | chr1 206041820 206041821 | q32.2 |
| hsa-mir-301 | 17 | 54583279 | CAGUGCAAUAGUAUUGUCAAAGC | hsa-miR-301a | 17:54583279-54583364- | NA | NA | NA | chr17 54583279 54583280 | q22 |
| hsa-mir-302a | 4 | 1,14E+08 | UAAGUGCUUCCAUGUUUUGGUGA | hsa-miR-302a | 4:113788788-113788856- | NA | NA | NA | chr4 113788788 113788789 | q25 |
| hsa-mir-302astar | 4 | 1,14E+08 | UAAACGUGGAUGUACUUGCUUU | hsa-miR-302a* | 4:113788788-113788856- | NA | NA | NA | chr4 113788788 113788789 | q25 |
| hsa-mir-302b | 4 | 1,14E+08 | UAAGUGCUUCCAUGUUUUAGUAG | hsa-miR-302b | 4:113789090-113789162- | NA | NA | NA | chr4 113789090 113789091 | q25 |
| hsa-mir-302bstar | 4 | 1,14E+08 | ACUUUAACAUGGAAGUGCUUUCU | hsa-miR-302b* | 4:113789090-113789162- | NA | NA | NA | chr4 113789090 113789091 | q25 |
| hsa-mir-302c | 4 | 1,14E+08 | UAAGUGCUUCCAUGUUUCAGUGG | hsa-miR-302c | 4:113788968-113789035- | NA | NA | NA | chr4 113788968 113788969 | q25 |
| hsa-mir-302cstar | 4 | 1,14E+08 | UUUAACAUGGGGGUACCUGCUG | hsa-miR-302c* | 4:113788968-113789035- | NA | NA | NA | chr4 113788968 113788969 | q25 |
| hsa-mir-302d | 4 | 1,14E+08 | UAAGUGCUUCCAUGUUUGAGUGU | hsa-miR-302d | 4:113788609-113788676- | NA | NA | NA | chr4 113788609 113788610 | q25 |
| hsa-mir-30a-3p | 6 | 72169975 | CUUUCAGUCGGAUGUUUGCAGC | hsa-miR-30a* | 6:72169975-72170045- | NA | NA | NA | chr6 72169975 72169976 | q13 |
| hsa-mir-30a-5p | 6 | 72169975 | UGUAAACAUCCUCGACUGGAAG | hsa-miR-30a | 6:72169975-72170045- | NA | NA | NA | chr6 72169975 72169976 | q13 |
| hsa-mir-30b | 8 | 1,36E+08 | UGUAAACAUCCUACACUCAGCU | hsa-miR-30b | 8:135881945-135882032- | NA | NA | NA | chr8 135881945 135881946 | q24.22 |
| hsa-mir-30c | 1 | 40995543 | UGUAAACAUCCUACACUCUCAGC | hsa-miR-30c | 1:40995543-40995631+ | 6:72143384-72143455- | NA | NA | chr1 40995543 40995544 | p34.2 |
| hsa-mir-30d | 8 | 1,36E+08 | UGUAAACAUCCCCGACUGGAAG | hsa-miR-30d | 8:135886301-135886370- | NA | NA | NA | chr8 135886301 135886302 | q24.22 |
| hsa-mir-30e-3p | 1 | 40992614 | CUUUCAGUCGGAUGUUUACAGC | hsa-miR-30e* | 1:40992614-40992705+ | NA | NA | NA | chr1 40992614 40992615 | p34.2 |
| hsa-mir-30e-5p | 1 | 40992614 | UGUAAACAUCCUUGACUGGA | hsa-miR-30e | 1:40992614-40992705+ | NA | NA | NA | chr1 40992614 40992615 | p34.2 |
| hsa-mir-31 | 9 | 21502114 | GGCAAGAUGCUGGCAUAGCUG | hsa-miR-31 | 9:21502114-21502184- | NA | NA | NA | chr9 21502114 21502115 | p21.3 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| hsa-mir-32 | | 9 | 1,11E+08 | UAUUGCACAUUACUAAGUUGC | hsa-miR-32 | 9:110848330-110848399- | NA | NA | NA | chr9 110848330 110848331 | q31.3 |
| hsa-mir-320 | | 8 | 22158420 | AAAAGCUGGGUUGAGAGGGCGAA | hsa-miR-320a | 8:22158420-22158501- | NA | NA | NA | chr8 22158420 22158421 | p21.3 |
| hsa-mir-323 | | 14 | 1,01E+08 | GCACAUUACACGGUCGACCUCU | hsa-miR-323-3p | 14:100561822-100561907+ | NA | NA | NA | chr14 100561822 100561823 | q32.31 |
| hsa-mir-324-3p | | 17 | 7067340 | CCACUGCCCCAGGUGCUGCUGG | hsa-miR-324-3p | 17:7067340-7067422- | NA | NA | NA | chr17 7067340 7067341 | p13.1 |
| hsa-mir-324-5p | | 17 | 7067340 | CGCAUCCCCUAGGGCAUUGGUGU | hsa-miR-324-5p | 17:7067340-7067422- | NA | NA | NA | chr17 7067340 7067341 | p13.1 |
| hsa-mir-325 | X | | 76142220 | CCUAGUAGGUGUCCAGUAAGUGU | hsa-miR-325 | 23:76142220-76142317- | NA | NA | NA | chrX 76142220 76142221 | q21.1 |
| hsa-mir-326 | | 11 | 74723784 | CCUCUGGGCCCUUCCUCCAG | hsa-miR-326 | 11:74723784-74723878- | NA | NA | NA | chr11 74723784 74723785 | q13.4 |
| hsa-mir-328 | | 16 | 65793725 | CUGGCCCUCUCUGCCCUUCCGU | hsa-miR-328 | 16:65793725-65793799- | NA | NA | NA | chr16 65793725 65793726 | q22.1 |
| hsa-mir-329 | | 14 | 1,01E+08 | AACACACCUGGUUAACCUCUUU | hsa-miR-329 | 14:100562875-100562954+ | 14:100563190-100563273+ | NA | NA | chr14 100562875 100562876 | q32.31 |
| hsa-mir-33 | | 22 | 40626894 | GUGCAUUGUAGUUGCAUUG | hsa-miR-33a | 22:40626894-40626962+ | NA | NA | NA | chr22 40626894 40626895 | q13.2 |
| hsa-mir-330 | | 19 | 50834092 | GCAAAGCACACGGCCUGCAGAGA | hsa-miR-330-3p | 19:50834092-50834185- | NA | NA | NA | chr19 50834092 50834093 | q13.32 |
| hsa-mir-331 | | 12 | 94226327 | GCCCCUGGGCCUAUCCUAGAA | hsa-miR-331-3p | 12:94226327-94226420+ | NA | NA | NA | chr12 94226327 94226328 | q22 |
| hsa-mir-335 | | 7 | 1,3E+08 | UCAAGAGCAAUAACGAAAAAUGU | hsa-miR-335 | 7:129923188-129923281+ | NA | NA | NA | chr7 129923188 129923189 | q32.2 |
| hsa-mir-337 | | 14 | 1E+08 | UCCAGCUCCUAUAUGAUGCCUUU | hsa-miR-337-3p | 14:100410583-100410675+ | NA | NA | NA | chr14 100410583 100410584 | q32.31 |
| hsa-mir-338 | | 17 | 76714278 | UCCAGCAUCAGUGAUUUUGUUGA | hsa-miR-338-3p | 17:76714278-76714344- | NA | NA | NA | chr17 76714278 76714279 | q25.3 |
| hsa-mir-339 | | 7 | 1029095 | UCCCUGUCCUCCAGGAGCUCA | hsa-miR-339-5p | 7:1029095-1029188- | NA | NA | NA | chr7 1029095 1029096 | p22.3 |
| hsa-mir-340 | | 5 | 1,79E+08 | UCCGUCUCAGUUACUUUAUAGCC | hsa-miR-340* | 5:179374909-179375003- | NA | NA | NA | chr5 179374909 179374910 | q35.3 |
| hsa-mir-342 | | 14 | 99645745 | UCUCACACAGAAAUCGCACCCGUC | hsa-miR-342-3p | 14:99645745-99645843+ | NA | NA | NA | chr14 99645745 99645746 | q32.2 |
| hsa-mir-345 | | 14 | 99843949 | UGCUGACUCCUAGUCCAGGGC | hsa-miR-345 | 14:99843949-99844046+ | NA | NA | NA | chr14 99843949 99843950 | q32.2 |
| hsa-mir-346 | | 10 | 88014431 | UGUCUGCCCGCAUGCCUGCCUCU | hsa-miR-346 | 10:88014431-88014525- | NA | NA | NA | chr10 88014431 88014432 | q23.2 |
| hsa-mir-34a | | 1 | 9134314 | UGGCAGUGUCUUAGCUGGUUGUU | hsa-miR-34a | 1:9134314-9134423- | NA | NA | NA | chr1 9134314 9134315 | p36.23 |
| hsa-mir-34b | | 11 | 1,11E+08 | UAGGCAGUGUCAUUAGCUGAUUG | hsa-miR-34b* | 11:110888873-110888956+ | NA | NA | NA | chr11 110888873 110888874 | q23.1 |
| hsa-mir-34c | | 11 | 1,11E+08 | AGGCAGUGUAGUUAGCUGAUUGC | hsa-miR-34c-5p | 11:110889374-110889450+ | NA | NA | NA | chr11 110889374 110889375 | q23.1 |
| hsa-mir-361 | X | | 85045297 | UUAUCAGAAUCUCCAGGGGUAC | hsa-miR-361-5p | 23:85045297-85045368- | NA | NA | NA | chrX 85045297 85045298 | q21.2 |
| hsa-mir-362 | X | | 49660312 | AAUCCUUGGAACCUAGGUGUGAGU | hsa-miR-362-5p | 23:49660312-49660376+ | NA | NA | NA | chrX 49660312 49660313 | p11.23 |
| hsa-mir-363 | X | | 1,33E+08 | AAUUGCACGGUAUCCAUCUGUA | hsa-miR-363 | 23:133131074-133131148- | NA | NA | NA | chrX 133131074 133131075 | q26.2 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| hsa-miR-363star | X | 1,33E+08 | CGGGUGGAUCACGAUGCAAUUU | hsa-miR-363* | 23:133131074-133131148- | NA | NA | NA | chrX 133131074 133131075 | q26.2 | |
| hsa-mir-365 | 16 | 14310643 | UAAUGCCCCUAAAAAUCCUUAU | hsa-miR-365 | 16:14310643-14310729+ | 17:26926543-26926653+ | NA | NA | chr16 14310643 14310644 | p13.12 | |
| hsa-mir-367 | 4 | 1,14E+08 | AAUUGCACUUUAGCAAUGGUGA | hsa-miR-367 | 4:113788479-113788546- | NA | NA | NA | chr4 113788479 113788480 | q25 | |
| hsa-mir-368 | 14 | 1,01E+08 | ACAUAGAGGAAAUUCCACGUUU | hsa-miR-376c | 14:100575780-100575845+ | NA | NA | NA | chr14 100575780 100575781 | q32.31 | |
| hsa-mir-369-3p | 14 | 1,01E+08 | AAUAAUACAUGGUUGAUCUUU | hsa-miR-369-3p | 14:100601688-100601757+ | NA | NA | NA | chr14 100601688 100601689 | q32.31 | |
| hsa-mir-369-5p | 14 | 1,01E+08 | AGAUCGACCGUGUUAUAUUCGC | hsa-miR-369-5p | 14:100601688-100601757+ | NA | NA | NA | chr14 100601688 100601689 | q32.31 | |
| hsa-mir-370 | 14 | 1E+08 | GCCUGCUGGGGUGGAACCUGG | hsa-miR-370 | 14:100447229-100447303+ | NA | NA | NA | chr14 100447229 100447230 | q32.31 | |
| hsa-mir-371 | 19 | 58982741 | GUGCCGCCAUCUUUUGAGUGU | hsa-miR-371-3p | 19:58982741-58982807+ | NA | NA | NA | chr19 58982741 58982742 | q13.41 | |
| hsa-mir-372 | 19 | 58982956 | AAAGUGCUGCGACAUUUGAGCGU | hsa-miR-372 | 19:58982956-58983022+ | NA | NA | NA | chr19 58982956 58982957 | q13.41 | |
| hsa-mir-373 | 19 | 58983771 | GAAGUGCUUCGAUUUUGGGGUGU | hsa-miR-373 | 19:58983771-58983839+ | NA | NA | NA | chr19 58983771 58983772 | q13.41 | |
| hsa-mir-373star | 19 | 58983771 | ACUCAAAAUGGGGGCGCUUUCC | hsa-miR-373* | 19:58983771-58983839+ | NA | NA | NA | chr19 58983771 58983772 | q13.41 | |
| hsa-mir-374 | X | 73423846 | UUAUAAUACAACCUGAUAAGUG | hsa-miR-374a | 23:73423846-73423917- | NA | NA | NA | chrX 73423846 73423847 | q13.2 | |
| hsa-mir-375 | 2 | 2,2E+08 | UUUGUUCGUUCGGCUCGCGUGA | hsa-miR-375 | 2:219574611-219574674- | NA | NA | NA | chr2 219574611 219574612 | q35 | |
| hsa-mir-376a | 14 | 1,01E+08 | AUCAUAGAGGAAAAUCCACGU | hsa-miR-376a | 14:100576872-100576939+ | 14:100576159-100576238+ | NA | NA | chr14 100576872 100576873 | q32.31 | |
| hsa-miR-376astar | 14 | 1,01E+08 | GGUAGAUUCUCCUUCUAUGAG | hsa-miR-376a* | 14:100576872-100576939+ | 14:100576159-100576238+ | NA | NA | chr14 100576872 100576873 | q32.31 | |
| hsa-mir-376b | 14 | 1,01E+08 | AUCAUAGAGGAAAAUCCAUGUU | hsa-miR-376b | 14:100576526-100576625+ | NA | NA | NA | chr14 100576526 100576527 | q32.31 | |
| hsa-mir-377 | 14 | 1,01E+08 | AUCACACAAAGGCAACUUUUGU | hsa-miR-377 | 14:100598140-100598208+ | NA | NA | NA | chr14 100598140 100598141 | q32.31 | |
| hsa-mir-378 | 5 | 1,49E+08 | CUCCUGACUCCAGGUCCUGUGU | hsa-miR-378* | 5:149092581-149092646+ | NA | NA | NA | chr5 149092581 149092582 | q33.1 | |
| hsa-mir-379 | 14 | 1,01E+08 | UGGUAGACUAUGGAACGUA | hsa-miR-379 | 14:100558156-100558222+ | NA | NA | NA | chr14 100558156 100558157 | q32.31 | |
| hsa-mir-380-3p | 14 | 1,01E+08 | UAUGUAAUAUGGUCCACAUCUU | hsa-miR-380 | 14:100561107-100561167+ | NA | NA | NA | chr14 100561107 100561108 | q32.31 | |
| hsa-miR-380-5p | 14 | 1,01E+08 | UGGUUGACCAUAGAACAUGCGC | hsa-miR-380* | 14:100561107-100561167+ | NA | NA | NA | chr14 100561107 100561108 | q32.31 | |
| hsa-mir-381 | 14 | 1,01E+08 | UAUACAAGGGCAAGCUCUCUGU | hsa-miR-381 | 14:100582010-100582084+ | NA | NA | NA | chr14 100582010 100582011 | q32.31 | |
| hsa-mir-382 | 14 | 1,01E+08 | GAAGUUGUUCGUGGUGGAUUCG | hsa-miR-382 | 14:100590396-100590471+ | NA | NA | NA | chr14 100590396 100590397 | q32.31 | |
| hsa-mir-383 | 8 | 14755318 | AGAUCAGAAGGUGAUUGUGGCU | hsa-miR-383 | 8:14755318-14755390- | NA | NA | NA | chr8 14755318 14755319 | p22 | |
| hsa-mir-384 | X | 76056092 | AUUCCUAGAAAUUGUUCAUA | hsa-miR-384 | 23:76056092-76056179- | NA | NA | NA | chrX 76056092 76056093 | q21.1 | |
| hsa-mir-409-5p | 14 | 1,01E+08 | AGGUUACCCGAGCAACUUUGCA | hsa-miR-409-5p | 14:100601390-100601468+ | NA | NA | NA | chr14 100601390 100601391 | q32.31 | |
| hsa-mir-410 | 14 | 1,01E+08 | AAUAUAACACAGAUGGCCUGU | hsa-miR-410 | 14:100602002-100602081+ | NA | NA | NA | chr14 100602002 100602003 | q32.31 | |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| hsa-mir-411 | | 14 | 1,01E+08 | UAGUAGACCGUAUAGCGUACG | hsa-miR-411 | 14:100559415-100559510+ | NA | NA | NA | chr14 100559415 100559416 | q32.31 |
| hsa-mir-412 | | 14 | 1,01E+08 | ACUUCACCUGGUCCACUAGCCGU | hsa-miR-412 | 14:100601537-100601627+ | NA | NA | NA | chr14 100601537 100601538 | q32.31 |
| hsa-mir-422a | | 15 | 61950182 | CUGGACUUAGGGUCAGAAGGCC | hsa-miR-422a | 15:61950182-61950271- | NA | NA | NA | chr15 61950182 61950183 | q22.31 |
| hsa-mir-422b | | 5 | 1,49E+08 | CUGGACUUGGAGUCAGAAGGCC | hsa-miR-378 | 5:149092581-149092646+ | NA | NA | NA | chr5 149092581 149092582 | q33.1 |
| hsa-mir-423 | | 17 | 25468223 | AGCUCGGUCUGAGGCCCCUCAG | hsa-miR-423-3p | 17:25468223-25468316+ | NA | NA | NA | chr17 25468223 25468224 | q11.2 |
| hsa-mir-424 | X | | 1,34E+08 | CAGCAGCAAUUCAUGUUUUGAA | hsa-miR-424 | 23:133508310-133508407- | NA | NA | NA | chrX 133508310 133508311 | q26.3 |
| hsa-mir-425 | | 3 | 49032585 | AUCGGGAAUGUCGUGUCCGCC | hsa-miR-425* | 3:49032585-49032671- | NA | NA | NA | chr3 49032585 49032586 | p21.31 |
| hsa-miR-425-5p | | 3 | 49032585 | AAUGACACGAUCACUCCCGUUGA | hsa-miR-425 | 3:49032585-49032671- | NA | NA | NA | chr3 49032585 49032586 | p21.31 |
| hsa-mir-429 | | 1 | 1094248 | UAAUACUGUCUGGUAAAACCGU | hsa-miR-429 | 1:1094248-1094330+ | NA | NA | NA | chr1 1094248 1094249 | p36.33 |
| hsa-mir-432 | | 14 | 1E+08 | UCUUGGAGUAGGUCAUUGGGUGG | hsa-miR-432 | 14:100420573-100420666+ | NA | NA | NA | chr14 100420573 100420574 | q32.31 |
| hsa-mir-432star | | 14 | 1E+08 | CUGGAUGGCUCCUCCAUGUCU | hsa-miR-432* | 14:100420573-100420666+ | NA | NA | NA | chr14 100420573 100420574 | q32.31 |
| hsa-mir-433 | | 14 | 1E+08 | AUCAUGAUGGGCUCCUCGGUGU | hsa-miR-433 | 14:100417976-100418068+ | NA | NA | NA | chr14 100417976 100417977 | q32.31 |
| hsa-miR-448 | X | | 1,14E+08 | UUGCAUAUGUAGGAUGUCCCAU | hsa-miR-448 | 23:113964273-113964383+ | NA | NA | NA | chrX 113964273 113964274 | q23 |
| hsa-mir-449 | | 5 | 54502117 | UGGCAGUGUAUUGUUAGCUGGU | hsa-miR-449a | 5:54502117-54502207- | NA | NA | NA | chr5 54502117 54502118 | q11.2 |
| hsa-mir-449b | | 5 | 54502231 | AGGCAGUGUAUUGUUAGCUGGC | hsa-miR-449b | 5:54502231-54502327- | NA | NA | NA | chr5 54502231 54502232 | q11.2 |
| hsa-miR-450 | X | | 1,34E+08 | UUUUUGCGAUGUGUUCCUAAUA | hsa-miR-450a | 23:133502037-133502127- | 23:133502204-133502303- | NA | NA | chrX 133502037 133502038 | q26.3 |
| hsa-mir-451 | | 17 | 24212513 | AAACCGUUACCAUUACUGAGUUU | hsa-miR-451 | 17:24212513-24212584- | NA | NA | NA | chr17 24212513 24212514 | q11.2 |
| hsa-mir-452 | X | | 1,51E+08 | UGUUUGCAGAGGAAACUGAGAC | hsa-miR-452 | 23:150878756-150878840- | NA | NA | NA | chrX 150878756 150878757 | q28 |
| hsa-mir-452star | NA | NA | | UCAGUCUCAUCUGCAAAGAAG | NO | NA | NA | NA | NA | #VALUE! | |
| hsa-mir-453 | | 14 | 1,01E+08 | GAGGUUGUCCGUGGUGAGUUCG | hsa-miR-453 | 14:100592280-100592359+ | NA | NA | NA | chr14 100592280 100592281 | q32.31 |
| hsa-mir-455 | | 9 | 1,16E+08 | UAUGUGCCUUUGGACUACAUCG | hsa-miR-455-5p | 9:116011535-116011630+ | NA | NA | NA | chr9 116011535 116011536 | q32 |
| hsa-mir-459 | NA | NA | | NA | NO | NA | NA | NA | NA | #VALUE! | |
| hsa-mir-483 | | 11 | 2111940 | UCACUCCUCUCCUCCCGUCUUCU | hsa-miR-483-3p | 11:2111940-2112015- | NA | NA | NA | chr11 2111940 2111941 | p15.5 |
| hsa-miR-484 | | 16 | 15644652 | UCAGGCUCAGUCCCCUCCCGAU | hsa-miR-484 | 16:15644652-15644730+ | NA | NA | NA | chr16 15644652 15644653 | p13.11 |
| hsa-mir-485-3p | | 14 | 1,01E+08 | GUCAUACACGGCUCUCCUCUCU | hsa-miR-485-3p | 14:100591509-100591581+ | NA | NA | NA | chr14 100591509 100591510 | q32.31 |
| hsa-mir-485-5p | | 14 | 1,01E+08 | AGAGGCUGGCCGUGAUGAAUUC | hsa-miR-485-5p | 14:100591509-100591581+ | NA | NA | NA | chr14 100591509 100591510 | q32.31 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| hsa-mir-486 | | 8 | 41637116 | UCCUGUACUGAGCUGCCCCGAG | hsa-miR-486-5p | 8:41637116-41637183- | NA | NA | NA | chr8 41637116 41637117 | p11.21 |
| hsa-mir-487a | | 14 | 1,01E+08 | AAUCAUACAGGGACAUCCAGUU | hsa-miR-487a | 14:100588536-100588615+ | NA | NA | NA | chr14 100588536 100588537 | q32.31 |
| hsa-mir-487b | | 14 | 1,01E+08 | AAUCGUACAGGGUCAUCCACUU | hsa-miR-487b | 14:100582545-100582628+ | NA | NA | NA | chr14 100582545 100582546 | q32.31 |
| hsa-miR-488 | | 1 | 1,75E+08 | CCCAGAUAAUGGCACUCUCAA | hsa-miR-488* | 1:175265122-175265204- | NA | NA | NA | chr1 175265122 175265123 | q25.2 |
| hsa-mir-489 | | 7 | 92951184 | AGUGACAUCACAUAUACGGCAGC | hsa-miR-489 | 7:92951184-92951267- | NA | NA | NA | chr7 92951184 92951185 | q21.3 |
| hsa-mir-490 | | 7 | 1,36E+08 | CAACCUGGAGGACUCCAUGCUG | hsa-miR-490-3p | 7:136238454-136238581+ | NA | NA | NA | chr7 136238454 136238455 | q33 |
| hsa-mir-491 | | 9 | 20706104 | AGUGGGGAACCCUUCCAUGAGGA | hsa-miR-491-5p | 9:20706104-20706187+ | NA | NA | NA | chr9 20706104 20706105 | p21.3 |
| hsa-mir-492 | | 12 | 93752305 | AGGACCUGCGGGACAAGAUUCUU | hsa-miR-492 | 12:93752305-93752420+ | NA | NA | NA | chr12 93752305 93752306 | q22 |
| hsa-mir-493 | | 14 | 1E+08 | UUGUACAUGGUAGGCUUUCAUU | hsa-miR-493* | 14:100405150-100405238+ | NA | NA | NA | chr14 100405150 100405151 | q32.31 |
| hsa-mir-493-3p | | 14 | 1E+08 | UGAAGGUCUACUGUGUGCCAG | hsa-miR-493 | 14:100405150-100405238+ | NA | NA | NA | chr14 100405150 100405151 | q32.31 |
| hsa-mir-494 | | 14 | 1,01E+08 | UGAAACAUACACGGGAAACCUCUU | hsa-miR-494 | 14:100565724-100565804+ | NA | NA | NA | chr14 100565724 100565725 | q32.31 |
| hsa-mir-495 | | 14 | 1,01E+08 | AAACAAACAUGGUGCACUUCUUU | hsa-miR-495 | 14:100569845-100569926+ | NA | NA | NA | chr14 100569845 100569846 | q32.31 |
| hsa-mir-496 | | 14 | 1,01E+08 | AUUACAUGGCCAAUCUC | hsa-miR-496 | 14:100596663-100596764+ | NA | NA | NA | chr14 100596663 100596664 | q32.31 |
| hsa-mir-497 | | 17 | 6861954 | CAGCAGCACACUGUGGUUUGU | hsa-miR-497 | 17:6861954-6862065- | NA | NA | NA | chr17 6861954 6861955 | p13.1 |
| hsa-miR-498 | | 19 | 58869263 | UUUCAAGCCAGGGGGCGUUUUUC | hsa-miR-498 | 19:58869263-58869386+ | NA | NA | NA | chr19 58869263 58869264 | q13.41 |
| hsa-mir-499 | | 20 | 33041840 | UUAAGACUUGCAGUGAUGUUUAA | hsa-miR-499-5p | 20:33041840-33041961+ | NA | NA | NA | chr20 33041840 33041841 | q11.22 |
| hsa-mir-500 | X | | 49659779 | AUGCACCUGGGCAAGGAUUCUG | hsa-miR-500* | 23:49659779-49659862+ | NA | NA | NA | chrX 49659779 49659780 | p11.23 |
| hsa-mir-501 | X | | 49661070 | AAUCCUUUGUCCCUGGGUGAGA | hsa-miR-501-5p | 23:49661070-49661153+ | NA | NA | NA | chrX 49661070 49661071 | p11.23 |
| hsa-mir-502 | X | | 49665946 | AUCCUUGCUAUCUGGGUGCUA | hsa-miR-502-5p | 23:49665946-49666031+ | NA | NA | NA | chrX 49665946 49665947 | p11.23 |
| hsa-mir-503 | X | | 1,34E+08 | UAGCAGCGGGAACAGUUCUGCAG | hsa-miR-503 | 23:133508024-133508094- | NA | NA | NA | chrX 133508024 133508025 | q26.3 |
| hsa-miR-504 | X | | 1,38E+08 | AGACCCUGGUCUGCACUCUAU | hsa-miR-504 | 23:137577538-137577620- | NA | NA | NA | chrX 137577538 137577539 | q26.3 |
| hsa-mir-505 | X | | 1,39E+08 | GUCAACACUUGCUGGUUUCCUC | hsa-miR-505 | 23:138833973-138834056- | NA | NA | NA | chrX 138833973 138833974 | q27.1 |
| hsa-mir-506 | X | | 1,46E+08 | UAAGGCACCCUUCUGAGUAGA | hsa-miR-506 | 23:146119930-146120053- | NA | NA | NA | chrX 146119930 146119931 | q27.3 |
| hsa-mir-507 | X | | 1,46E+08 | UUUUGCACCUUUUGGAGUGAA | hsa-miR-507 | 23:146120194-146120287- | NA | NA | NA | chrX 146120194 146120195 | q27.3 |
| hsa-mir-508 | X | | 1,46E+08 | UGAUUGUAGCCUUUUGGAGUAGA | hsa-miR-508-3p | 23:146126123-146126237- | NA | NA | NA | chrX 146126123 146126124 | q27.3 |
| hsa-mir-509 | X | | 1,46E+08 | UGAUUGGUACGUCUGUGGGUAGA | hsa-miR-509-3p | 23:146149742-146149835- | 23:146147970-146148060- | 23:146148862-146148936- | NA | chrX 146149742 146149743 | q27.3 |
| hsa-mir-510 | X | | 1,46E+08 | UACUCAGGAGAGUGGCAAUCACA | hsa-miR-510 | 23:146161545-146161618- | NA | NA | NA | chrX 146161545 146161546 | q27.3 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| hsa-mir-511 | | 10 | 17927113 | GUGUCUUUUGCUCUGCAGUCA | hsa-miR-511 | 10:17927113-17927199+ | 10:18174042-18174128+ | NA | NA | chr10 17927113 17927114 | p12.33 | |
| hsa-miR-512-3p | | 19 | 58861745 | AAGUGCUGUCAUAGCUGAGGUC | hsa-miR-512-3p | 19:58861745-58861828+ | 19:58864223-58864320+ | NA | NA | chr19 58861745 58861746 | q13.41 | |
| hsa-mir-512-5p | | 19 | 58861745 | CACUCAGCCUUGAGGGCACUUUC | hsa-miR-512-5p | 19:58861745-58861828+ | 19:58864223-58864320+ | NA | NA | chr19 58861745 58861746 | q13.41 | |
| hsa-mir-513 | X | | 1,46E+08 | UUCACAGGGAGGUGUCAUUUAU | hsa-miR-513b | 23:146088254-146088337- | NA | NA | NA | chrX 146088254 146088255 | q27.3 | |
| hsa-mir-514 | X | | 1,46E+08 | AUUGACACUUCUGUGAGUAG | hsa-miR-514 | 23:146168457-146168554- | 23:146171153-146171240- | 23:146173851-146173938- | NA | chrX 146168457 146168458 | q27.3 | |
| hsa-mir-515-3p | | 19 | 58874069 | GAGUGCCUUCUUUUGGAGCGU | hsa-miR-515-3p | 19:58874069-58874151+ | 19:58880075-58880157+ | NA | NA | chr19 58874069 58874070 | q13.41 | |
| hsa-mir-515-5p | | 19 | 58874069 | UUCUCCAAAAGAAAGCACUUUCUG | hsa-miR-515-5p | 19:58874069-58874151+ | 19:58880075-58880157+ | NA | NA | chr19 58874069 58874070 | q13.41 | |
| hsa-mir-516-3p | NA | NA | NA | UGCUUCCUUUCAGAGGGU | hsa-miR-516a-3p hsa | NA | NA | NA | NA | #VALUE! | | |
| hsa-mir-516-5p | | 19 | 58931911 | CAUCUGGAGGUAAGAAGCACUUU | hsa-miR-516b | 19:58931911-58932000+ | 19:58920508-58920592+ | NA | NA | chr19 58931911 58931912 | q13.41 | |
| hsa-mir-517a | NA | NA | NA | AUCGUGCAUCCCUUUAGAGUGUU | hsa-miR-517a hsa-m | NA | NA | NA | NA | #VALUE! | | |
| hsa-mir-517b | | 19 | 58916142 | UCGUGCAUCCCUUUAGAGUGUU | hsa-miR-517b | 19:58916142-58916208+ | NA | NA | NA | chr19 58916142 58916143 | q13.41 | |
| hsa-mir-517c | | 19 | 58936379 | AUCGUGCAUCCUUUUAGAGUGU | hsa-miR-517c | 19:58936379-58936473+ | NA | NA | NA | chr19 58936379 58936380 | q13.41 | |
| hsa-mir-517star | | 19 | 58907334 | CCUCUAGAUGGAAGCACUGUCU | hsa-miR-517* | 19: 58907334-58907420+ | NA | NA | NA | chr19 58907334 58907335 | q13.41 | |
| hsa-mir-518a | | 19 | 58926072 | AAAGCGCUUCCCUUUGCUGGA | hsa-miR-518a-3p | 19:58926072-58926156+ | 19:58934399-58934485+ | NA | NA | chr19 58926072 58926073 | q13.41 | |
| hsa-mir-518b | | 19 | 58897803 | CAAAGCGCUCCCCUUUAGAGGU | hsa-miR-518b | 19:58897803-58897885+ | NA | NA | NA | chr19 58897803 58897804 | q13.41 | |
| hsa-mir-518c | | 19 | 58903801 | CAAAGCGCUUCUCUUUAGAGUG | hsa-miR-518c | 19:58903801-58903901+ | NA | NA | NA | chr19 58903801 58903802 | q13.41 | |
| hsa-mir-518cstar | | 19 | 58903801 | UCUCUGGAGGGAAGCACUUUCUG | hsa-miR-518c* | 19:58903801-58903901+ | NA | NA | NA | chr19 58903801 58903802 | q13.41 | |
| hsa-mir-518d | | 19 | 58929943 | CAAAGCGCUUCCCUUUGGAGC | hsa-miR-518d-3p | 19:58929943-58930029+ | NA | NA | NA | chr19 58929943 58929944 | q13.41 | |
| hsa-mir-518e | | 19 | 58924904 | AAAGCGCUUCCCUUCAGAGUGU | hsa-miR-518e | 19:58924904-58924991+ | NA | NA | NA | chr19 58924904 58924905 | q13.41 | |
| hsa-mir-518f | | 19 | 58895081 | AAAGCGCUUCUCUUUAGAGGA | hsa-miR-518f | 19:58895081-58895167+ | NA | NA | NA | chr19 58895081 58895082 | q13.41 | |
| hsa-mir-519a | | 19 | 58947463 | AAAGUGCAUCCUUUUAGAGUGUUAC | hsa-miR-519a | 19:58947463-58947547+ | 19:58957410-58957496+ | NA | NA | chr19 58947463 58947464 | q13.41 | |
| hsa-mir-519b | | 19 | 58890279 | AAAGUGCAUCCUUUUAGAGGUUU | hsa-miR-519b-3p | 19:58890279-58890359+ | NA | NA | NA | chr19 58890279 58890280 | q13.41 | |
| hsa-mir-519c | | 19 | 58881535 | AAAGUGCAUCUUUUUAGAGGAU | hsa-miR-519c-3p | 19:58881535-58881621+ | NA | NA | NA | chr19 58881535 58881536 | q13.41 | |
| hsa-mir-519d | | 19 | 58908413 | CAAAGUGCCUCCCUUUAGAGUGU | hsa-miR-519d | 19:58908413-58908500+ | NA | NA | NA | chr19 58908413 58908414 | q13.41 | |
| hsa-mir-519e | | 19 | 58875006 | AAAGUGCCUCCUUUUAGAGUGU | hsa-miR-519e | 19:58875006-58875089+ | NA | NA | NA | chr19 58875006 58875007 | q13.41 | |
| hsa-mir-519estar | | 19 | 58875006 | UUCUCCAAAAGGGAGCACUUUC | hsa-miR-519e* | 19:58875006-58875089+ | NA | NA | NA | chr19 58875006 58875007 | q13.41 | |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| hsa-mir-520a | | 19 | 58885947 | AAAGUGCUUCCCUUUGGACUGU | hsa-miR-520a-3p | 19:58885947-58886031+ | NA | NA | NA | chr19 58885947 58885948 | q13.41 |
| hsa-mir-520astar | | 19 | 58885947 | CUCCAGAGGGAAGUACUUUCU | hsa-miR-520a-5p | 19:58885947-58886031+ | NA | NA | NA | chr19 58885947 58885948 | q13.41 |
| hsa-mir-520b | | 19 | 58902519 | AAAGUGCUUCCUUUUAGAGGG | hsa-miR-520c-3p | 19:58902519-58902605+ | NA | NA | NA | chr19 58902519 58902520 | q13.41 |
| hsa-mir-520c | NA | NA | | AAAGUGCUUCCUUUUAGAGGGUU | hsa-miR-520f hsa-m | NA | NA | NA | NA | #VALUE! | |
| hsa-mir-520d | | 19 | 58915162 | AAAGUGCUUCUCUUUGGUGGGUU | hsa-miR-520d-3p | 19:58915162-58915248+ | NA | NA | NA | chr19 58915162 58915163 | q13.41 |
| hsa-mir-520dstar | | 19 | 58915162 | UCUACAAAGGGAAGCCCUUUCUG | hsa-miR-520d-5p | 19:58915162-58915248+ | NA | NA | NA | chr19 58915162 58915163 | q13.41 |
| hsa-mir-520e | | 19 | 58870777 | AAAGUGCUUCCUUUUUGAGGG | hsa-miR-520e | 19:58870777-58870863+ | NA | NA | NA | chr19 58870777 58870778 | q13.41 |
| hsa-mir-520f | | 19 | 58877225 | AAGUGCUUCCUUUUAGAGGGUU | hsa-miR-520f | 19:58877225-58877311+ | NA | NA | NA | chr19 58877225 58877226 | q13.41 |
| hsa-mir-520g | | 19 | 58917232 | ACAAAGUGCUUCCCUUUAGAGUGU | hsa-miR-520g | 19:58917232-58917321+ | NA | NA | NA | chr19 58917232 58917233 | q13.41 |
| hsa-mir-520h | | 19 | 58917232 | ACAAAGUGCUUCCCUUUAGAGU | hsa-miR-520g | 19:58917232-58917321+ | NA | NA | NA | chr19 58917232 58917233 | q13.41 |
| hsa-mir-521 | | 19 | 58943702 | AACGCACUUCCCUUUAGAGUGU | hsa-miR-521 | 19:58943702-58943788+ | 19:58911660-58911746+ | NA | NA | chr19 58943702 58943703 | q13.41 |
| hsa-mir-522 | | 19 | 58946277 | AAAAUGGUUCCCUUUAGAGUGUU | hsa-miR-522 | 19:58946277-58946363+ | NA | NA | NA | chr19 58946277 58946278 | q13.41 |
| hsa-mir-523 | | 19 | 58893451 | AACGCGCUUCCCUAUAGAGGG | hsa-miR-523 | 19:58893451-58893537+ | NA | NA | NA | chr19 58893451 58893452 | q13.41 |
| hsa-mir-524 | | 19 | 58906068 | GAAGGCGCUUCCCUUUGGAGU | hsa-miR-524-3p | 19:58906068-58906154+ | NA | NA | NA | chr19 58906068 58906069 | q13.41 |
| hsa-mir-525 | | 19 | 58892599 | CUCCAGAGGGAUGCACUUUCU | hsa-miR-525-5p | 19:58892599-58892683+ | NA | NA | NA | chr19 58892599 58892600 | q13.41 |
| hsa-miR-525star | | 19 | 58892599 | GAAGGCGCUUCCCUUUAGAGC | hsa-miR-525-3p | 19:58892599-58892683+ | NA | NA | NA | chr19 58892599 58892600 | q13.41 |
| hsa-mir-526a | NA | NA | | CUCUAGAGGGAAGCACUUUCU | hsa-miR-526a hsa-m | NA | NA | NA | NA | #VALUE! | |
| hsa-mir-526b | | 19 | 58889459 | CUCUUGAGGGAAGCACUUUCUGUU | hsa-miR-526b | 19:58889459-58889541+ | NA | NA | NA | chr19 58889459 58889460 | q13.41 |
| hsa-mir-526bstar | | 19 | 58889459 | AAAGUGCUUCCUUUUAGAGGC | hsa-miR-526b* | 19:58889459-58889541+ | NA | NA | NA | chr19 58889459 58889460 | q13.41 |
| hsa-mir-526c | NA | NA | | CUCUAGAGGGAAGCGCUUUCUGUU | hsa-miR-519c-5p hsa | NA | NA | NA | NA | #VALUE! | |
| hsa-mir-527 | NA | NA | | CUGCAAAGGGAAGCCCUUUCU | hsa-miR-518a-5p hsa | NA | NA | NA | NA | #VALUE! | |
| hsa-miR-532 | X | | 49654494 | CAUGCCUUGAGUGUAGGACCGU | hsa-miR-532-5p | 23:49654494-49654584+ | NA | NA | NA | chrX 49654494 49654495 | p11.23 |
| hsa-mir-539 | | 14 | 1,01E+08 | GGAGAAAUUAUCCUUGGUGUGU | hsa-miR-539 | 14:100583411-100583488+ | NA | NA | NA | chr14 100583411 100583412 | q32.31 |
| hsa-mir-542-3p | X | | 1,34E+08 | UGUGACAGAUUGAUAACUGAAA | hsa-miR-542-3p | 23:133503037-133503133- | NA | NA | NA | chrX 133503037 133503038 | q26.3 |
| hsa-mir-542-5p | X | | 1,34E+08 | UCGGGGAUCAUCAUGUCACGAG | hsa-miR-542-5p | 23:133503037-133503133- | NA | NA | NA | chrX 133503037 133503038 | q26.3 |
| hsa-mir-544 | | 14 | 1,01E+08 | AUUCUGCAUUUUUAGCAAGU | hsa-miR-544 | 14:100584748-100584838+ | NA | NA | NA | chr14 100584748 100584749 | q32.31 |
| hsa-miR-545 | X | | 73423664 | AUCAGCAAACAUUUAUUGUGUG | hsa-miR-545 | 23:73423664-73423769- | NA | NA | NA | chrX 73423664 73423665 | q13.2 |

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|---|---|---|---|---|---|---|---|---|---|---|
| hsa-miR-548a | 6 | 18679994 | CAAAACUGGCAAUUACUUUUGC | hsa-miR-548a-3p | 6:18679994-18680090+ | 6:135601991-135602087+ | 8:105565773-105565869- | NA | chr6 18679994 18679995 | p22.3 |
| hsa-mir-548b | 6 | 1,19E+08 | CAAGAACCUCAGUUGCUUUUGU | hsa-miR-548b-3p | 6:119431911-119432007- | NA | NA | NA | chr6 119431911 119431912 | q22.31 |
| hsa-miR-548c | 12 | 63302556 | CAAAAAUCUCAAUUACUUUUGC | hsa-miR-548c-3p | 12:63302556-63302652+ | NA | NA | NA | chr12 63302556 63302557 | q14.2 |
| hsa-mir-548d | 8 | 1,24E+08 | CAAAAACCACAGUUUCUUUUGC | hsa-miR-548d-3p | 8:124429455-124429551- | 17:62898067-62898163- | NA | NA | chr8 124429455 124429456 | q24.13 |
| hsa-mir-549 | 15 | 78921374 | UGACAACUAUGGAUGAGCUCU | hsa-miR-549 | 15:78921374-78921469- | NA | NA | NA | chr15 78921374 78921375 | q25.1 |
| hsa-mir-550 | 7 | 30295935 | UGUCUUACUCCCUCAGGCACAU | hsa-miR-550* | 7:30295935-30296031+ | 7:32739118-32739214+ | NA | NA | chr7 30295935 30295936 | p15.1 |
| hsa-mir-551a | 1 | 3467119 | GCGACCCACUCUUGGUUUCCA | hsa-miR-551a | 1:3467119-3467214- | NA | NA | NA | chr1 3467119 3467120 | p36.32 |
| hsa-mir-551b | 3 | 1,7E+08 | GCGACCCAUACUUGGUUUCAG | hsa-miR-551b | 3:169752336-169752431+ | NA | NA | NA | chr3 169752336 169752337 | q26.2 |
| hsa-mir-552 | 1 | 34907787 | AACAGGUGACUGGUUAGACAA | hsa-miR-552 | 1:34907787-34907882- | NA | NA | NA | chr1 34907787 34907788 | p34.3 |
| hsa-mir-553 | 1 | 1,01E+08 | AAAACGGUGAGAUUUUGUUUU | hsa-miR-553 | 1:100519385-100519452+ | NA | NA | NA | chr1 100519385 100519386 | p21.2 |
| hsa-mir-554 | 1 | 1,5E+08 | GCUAGUCCUGACUCAGCCAGU | hsa-miR-554 | 1:149784896-149784991+ | NA | NA | NA | chr1 149784896 149784897 | q21.3 |
| hsa-mir-555 | 1 | 1,54E+08 | AGGGUAAGCUGAACCUCUGAU | hsa-miR-555 | 1:153582765-153582860- | NA | NA | NA | chr1 153582765 153582766 | q22 |
| hsa-miR-556 | 1 | 1,61E+08 | GAUGAGCUCAUUGUAAUAUG | hsa-miR-556-5p | 1:160578960-160579054+ | NA | NA | NA | chr1 160578960 160578961 | q23.3 |
| hsa-miR-557 | 1 | 1,67E+08 | GUUUGCACGGGUGGGCCUUGUCU | hsa-miR-557 | 1:166611386-166611483+ | NA | NA | NA | chr1 166611386 166611387 | q24.2 |
| hsa-mir-558 | 2 | 32610724 | UGAGCUGCUGUACCAAAAU | hsa-miR-558 | 2:32610724-32610817+ | NA | NA | NA | chr2 32610724 32610725 | p22.3 |
| hsa-mir-559 | 2 | 47458318 | UAAAGUAAAUAUGCACCAAAA | hsa-miR-559 | 2:47458318-47458413+ | NA | NA | NA | chr2 47458318 47458319 | p21 |
| hsa-miR-561 | 2 | 1,89E+08 | CAAAGUUUAAGAUCCUUGAAGU | hsa-miR-561 | 2:188870464-188870560+ | NA | NA | NA | chr2 188870464 188870465 | q32.1 |
| hsa-miR-562 | 2 | 2,33E+08 | AAAGUAGCUGUACCAUUUGC | hsa-miR-562 | 2:232745607-232745701+ | NA | NA | NA | chr2 232745607 232745608 | q37.1 |
| hsa-mir-563 | 3 | 15890282 | AGGUUGACAUACGUUUCCC | hsa-miR-563 | 3:15890282-15890360+ | NA | NA | NA | chr3 15890282 15890283 | p24.3 |
| hsa-mir-564 | 3 | 44878384 | AGGCACGGUGUCAGCAGGC | hsa-miR-564 | 3:44878384-44878477+ | NA | NA | NA | chr3 44878384 44878385 | p21.31 |
| hsa-mir-565 | NA | NA | GGCUGGCUCGCGAUGUCUGUUU | NO | NA | NA | NA | NA | #VALUE! | |
| hsa-mir-566 | 3 | 50185763 | GGGCGCCUGUGAUCCCAAC | hsa-miR-566 | 3:50185763-50185856+ | NA | NA | NA | chr3 50185763 50185764 | p21.31 |
| hsa-miR-567 | 3 | 1,13E+08 | AGUAUGUUCUUCCAGGACAGAAC | hsa-miR-567 | 3:113314338-113314435+ | NA | NA | NA | chr3 113314338 113314339 | q13.2 |
| hsa-miR-569 | 3 | 1,72E+08 | AGUUAAUGAAUCCUGGAAAGU | hsa-miR-569 | 3:172307147-172307242- | NA | NA | NA | chr3 172307147 172307148 | q26.2 |
| hsa-miR-570 | 3 | 1,97E+08 | GAAAACAGCAAUUACCUUUGCA | hsa-miR-570 | 3:196911452-196911548+ | NA | NA | NA | chr3 196911452 196911453 | q29 |
| hsa-mir-571 | 4 | 333946 | UGAGUUGGCCAUCUGAGUGAG | hsa-miR-571 | 4:333946-334041+ | NA | NA | NA | chr4 333946 333947 | p16.3 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| hsa-mir-572 | 4 | 10979549 | GUCCGCUCGGCGGUGGCCCA | hsa-miR-572 | 4:10979549-10979643+ | NA | NA | NA | chr4 10979549 10979550 | p15.33 | |
| hsa-mir-573 | 4 | 24130913 | CUGAAGUGAUGUGUAACUGAUCAG | hsa-miR-573 | 4:24130913-24131011- | NA | NA | NA | chr4 24130913 24130914 | p15.2 | |
| hsa-mir-574 | 4 | 38546048 | CACGCUCAUGCACACACCCAC | hsa-miR-574-3p | 4:38546048-38546143+ | NA | NA | NA | chr4 38546048 38546049 | p14 | |
| hsa-miR-575 | 4 | 83893514 | GAGCCAGUUGGACAGGAGC | hsa-miR-575 | 4:83893514-83893607- | NA | NA | NA | chr4 83893514 83893515 | q21.22 | |
| hsa-miR-576 | 4 | 1,11E+08 | AUUCUAAUUUCUCCACGUCUUUG | hsa-miR-576-5p | 4:110629303-110629400+ | NA | NA | NA | chr4 110629303 110629304 | q25 | |
| hsa-miR-578 | 4 | 1,67E+08 | CUUCUUGUGCUCUAGGAUUGU | hsa-miR-578 | 4:166526844-166526939+ | NA | NA | NA | chr4 166526844 166526845 | q32.3 | |
| hsa-miR-579 | 5 | 32430241 | AUUCAUUUGGUAUAAACCGCGAU | hsa-miR-579 | 5:32430241-32430338- | NA | NA | NA | chr5 32430241 32430242 | p13.3 | |
| hsa-mir-580 | 5 | 36183751 | UUGAGAAUGAUGAAUCAUUAGG | hsa-miR-580 | 5:36183751-36183847- | NA | NA | NA | chr5 36183751 36183752 | p13.2 | |
| hsa-miR-583 | 5 | 95440598 | CAAAGAGGAAGGUCCCAUUAC | hsa-miR-583 | 5:95440598-95440672+ | NA | NA | NA | chr5 95440598 95440599 | q15 | |
| hsa-mir-584 | 5 | 1,48E+08 | UUAUGGUUUGCCUGGGACUGAG | hsa-miR-584 | 5:148422069-148422165- | NA | NA | NA | chr5 148422069 148422070 | q33.1 | |
| hsa-miR-585 | 5 | 1,69E+08 | UGGGCGUAUCUGUAUGCUA | hsa-miR-585 | 5:168623183-168623276- | NA | NA | NA | chr5 168623183 168623184 | q35.1 | |
| hsa-mir-586 | 6 | 45273389 | UAUGCAUUGUAUUUUUAGGUCC | hsa-miR-586 | 6:45273389-45273485- | NA | NA | NA | chr6 45273389 45273390 | p12.3 | |
| hsa-miR-587 | 6 | 1,07E+08 | UUUCCAUAGGUGAUGAGUCAC | hsa-miR-587 | 6:107338693-107338788+ | NA | NA | NA | chr6 107338693 107338694 | q21 | |
| hsa-miR-588 | 6 | 1,27E+08 | UUGGCCACAAUGGGUUAGAAC | hsa-miR-588 | 6:126847470-126847552+ | NA | NA | NA | chr6 126847470 126847471 | q22.32 | |
| hsa-miR-589 | 7 | 5501976 | UCAGAACAAAUGCCGGUUCCCAGA | hsa-miR-589* | 7:5501976-5502074- | NA | NA | NA | chr7 5501976 5501977 | p22.1 | |
| hsa-miR-591 | 7 | 95686910 | AGACCAUGGGUUCUCAUUGU | hsa-miR-591 | 7:95686910-95687004- | NA | NA | NA | chr7 95686910 95686911 | q21.3 | |
| hsa-miR-592 | 7 | 1,26E+08 | UUGUGUCAAUAUGCGAUGAUGU | hsa-miR-592 | 7:126485378-126485474- | NA | NA | NA | chr7 126485378 126485379 | q31.33 | |
| hsa-mir-593 | 7 | 1,28E+08 | AGGCACCAGCCAGGCAUUGCUCAGC | hsa-miR-593* | 7:127509149-127509248+ | NA | NA | NA | chr7 127509149 127509150 | q32.1 | |
| hsa-miR-594 | NA | NA | CCCAUCUGGGGUGGCCUGUGACUUU | NO | NA | NA | NA | NA | #VALUE! | | |
| hsa-miR-596 | 8 | 1752804 | AAGCCUGCCCGGCUCCUCGGG | hsa-miR-596 | 8:1752804-1752880+ | NA | NA | NA | chr8 1752804 1752805 | p23.3 | |
| hsa-miR-597 | 8 | 9636592 | UGUGUCACUCGAUGACCACUGU | hsa-miR-597 | 8:9636592-9636688+ | NA | NA | NA | chr8 9636592 9636593 | p23.1 | |
| hsa-miR-599 | 8 | 1,01E+08 | GUUGUGUCAGUUUAUCAAAC | hsa-miR-599 | 8:100618040-100618134- | NA | NA | NA | chr8 100618040 100618041 | q22.2 | |
| hsa-mir-600 | 9 | 1,25E+08 | ACUUACAGACAAGAGCCUUGCUC | hsa-miR-600 | 9:124913646-124913743- | NA | NA | NA | chr9 124913646 124913647 | q33.2 | |
| hsa-mir-601 | 9 | 1,25E+08 | UGGUCUAGGAUUGUUGGAGGAG | hsa-miR-601 | 9:125204625-125204703- | NA | NA | NA | chr9 125204625 125204626 | q33.2 | |
| hsa-miR-603 | 10 | 24604620 | CACACACUGCAAUUACUUUUGC | hsa-miR-603 | 10:24604620-24604716+ | NA | NA | NA | chr10 24604620 24604621 | p12.1 | |
| hsa-mir-604 | 10 | 29873939 | AGGCUGCGGAAUUCAGGAC | hsa-miR-604 | 10:29873939-29874032- | NA | NA | NA | chr10 29873939 29873940 | p11.23 | |
| hsa-miR-606 | 10 | 76982222 | AAACUACUGAAAAUCAAAGAU | hsa-miR-606 | 10:76982222-76982317+ | NA | NA | NA | chr10 76982222 76982223 | q22.2 | |

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|---|---|---|---|---|---|---|---|---|---|---|
| hsa-miR-607 | 10 | 98578416 | GUUCAAAUCCAGAUCUAUAAC | hsa-miR-607 | 10:98578416-98578511- | NA | NA | NA | chr10 98578416 98578417 | q24.1 |
| hsa-miR-608 | 10 | 1,03E+08 | AGGGGUGGUGUUGGGACAGCUCCGU | hsa-miR-608 | 10:102724732-102724831+ | NA | NA | NA | chr10 102724732 102724733 | q24.31 |
| hsa-mir-609 | 10 | 1,06E+08 | AGGGUGUUUCUCUCAUCUCU | hsa-miR-609 | 10:105968537-105968631- | NA | NA | NA | chr10 105968537 105968538 | q25.1 |
| hsa-mir-610 | 11 | 28034938 | UGAGCUAAAUGUGUGCUGGGA | hsa-miR-610 | 11:28034938-28035033+ | NA | NA | NA | chr11 28034938 28034939 | p14.1 |
| hsa-mir-612 | 11 | 64968505 | GCUGGGCAGGGCUUCUGAGCUCCUU | hsa-miR-612 | 11:64968505-64968604+ | NA | NA | NA | chr11 64968505 64968506 | q13.1 |
| hsa-mir-613 | 12 | 12808850 | AGGAAUGUUCCUUCUUUGCC | hsa-miR-613 | 12:12808850-12808944+ | NA | NA | NA | chr12 12808850 12808851 | p13.1 |
| hsa-mir-614 | 12 | 12960030 | GAACGCCUGUUCUUGCCAGGUGG | hsa-miR-614 | 12:12960030-12960119+ | NA | NA | NA | chr12 12960030 12960031 | p13.1 |
| hsa-mir-615 | 12 | 52714001 | UCCGAGCCUGGGUCUCCCUCU | hsa-miR-615-3p | 12:52714001-52714096+ | NA | NA | NA | chr12 52714001 52714002 | q13.13 |
| hsa-mir-616 | 12 | 56199213 | ACUCAAAACCCUUCAGUGACUU | hsa-miR-616* | 12:56199213-56199309- | NA | NA | NA | chr12 56199213 56199214 | q13.3 |
| hsa-miR-617 | 12 | 79750443 | AGACUUCCCAUUUGAAGGUGGC | hsa-miR-617 | 12:79750443-79750539- | NA | NA | NA | chr12 79750443 79750444 | q21.31 |
| hsa-miR-618 | 12 | 79853646 | AAACUCUACUUGUCCUUCUGAGU | hsa-miR-618 | 12:79853646-79853743- | NA | NA | NA | chr12 79853646 79853647 | q21.31 |
| hsa-miR-619 | 12 | 1,08E+08 | GACCUGGACAUGUUUGUGCCCAGU | hsa-miR-619 | 12:107754813-107754911- | NA | NA | NA | chr12 107754813 107754814 | q24.11 |
| hsa-miR-621 | 13 | 40282902 | GGCUAGCAACAGCGCUUACCU | hsa-miR-621 | 13:40282902-40282997+ | NA | NA | NA | chr13 40282902 40282903 | q14.11 |
| hsa-mir-622 | 13 | 89681437 | ACAGUCUGCUGAGGUUGGAGC | hsa-miR-622 | 13:89681437-89681532+ | NA | NA | NA | chr13 89681437 89681438 | q31.3 |
| hsa-mir-624 | 14 | 30553603 | UAGUACCAGUACCUUGUGUUCA | hsa-miR-624* | 14:30553603-30553699- | NA | NA | NA | chr14 30553603 30553604 | q12 |
| hsa-mir-626 | 15 | 39771075 | AGCUGUCUGAAAAUGUCUU | hsa-miR-626 | 15:39771075-39771168+ | NA | NA | NA | chr15 39771075 39771076 | q15.1 |
| hsa-mir-627 | 15 | 40279060 | GUGAGUCUCUAAGAAAAGAGGA | hsa-miR-627 | 15:40279060-40279156- | NA | NA | NA | chr15 40279060 40279061 | q15.1 |
| hsa-miR-628 | 15 | 53452430 | UCUAGUAAGAGUGGCAGUCG | hsa-miR-628-3p | 15:53452430-53452524- | NA | NA | NA | chr15 53452430 53452431 | q21.3 |
| hsa-miR-629 | 15 | 68158765 | GUUCUCCCAACGUAAGCCCAGC | hsa-miR-629* | 15:68158765-68158861- | NA | NA | NA | chr15 68158765 68158766 | q23 |
| hsa-mir-630 | 15 | 70666612 | AGUAUUCUGUACCAGGGAAGGU | hsa-miR-630 | 15:70666612-70666708+ | NA | NA | NA | chr15 70666612 70666613 | q24.1 |
| hsa-miR-631 | 15 | 73433005 | AGACCUGGCCCAGACCUCAGC | hsa-miR-631 | 15:73433005-73433079- | NA | NA | NA | chr15 73433005 73433006 | q24.2 |
| hsa-mir-632 | 17 | 27701241 | GUGUCUGCUUCCUGUGGGA | hsa-miR-632 | 17:27701241-27701334+ | NA | NA | NA | chr17 27701241 27701242 | q11.2 |
| hsa-mir-633 | 17 | 58375308 | CUAAUAGUAUCUACCACAAUAAA | hsa-miR-633 | 17:58375308-58375405+ | NA | NA | NA | chr17 58375308 58375309 | q23.2 |
| hsa-mir-634 | 17 | 62213652 | AACCAGCACCCCAACUUUGGAC | hsa-miR-634 | 17:62213652-62213748+ | NA | NA | NA | chr17 62213652 62213653 | q24.2 |
| hsa-mir-635 | 17 | 63932187 | ACUUGGGCACUGAAACAAUGUCC | hsa-miR-635 | 17:63932187-63932284- | NA | NA | NA | chr17 63932187 63932188 | q24.2 |
| hsa-mir-636 | 17 | 72244127 | UGUGCUUGCUCGUCCCGCCCGCAG | hsa-miR-636 | 17:72244127-72244225- | NA | NA | NA | chr17 72244127 72244128 | q25.2 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| hsa-mir-637 | | 19 | 3912412 | ACUGGGGGCUUUCGGGCUCUGCGU | hsa-miR-637 | 19:3912412-3912510- | NA | NA | NA | chr19 3912412 3912413 | p13.3 |
| hsa-miR-638 | | 19 | 10690080 | AGGGAUCGCGGGCGGGUGGCGGCCU | hsa-miR-638 | 19:10690080-10690179+ | NA | NA | NA | chr19 10690080 10690081 | p13.2 |
| hsa-mir-639 | | 19 | 14501355 | AUCGCUGCGGUUGCGAGCGCUGU | hsa-miR-639 | 19:14501355-14501452+ | NA | NA | NA | chr19 14501355 14501356 | p13.12 |
| hsa-miR-641 | | 19 | 45480290 | AAAGACAUAGGAUAGAGUCACCUC | hsa-miR-641 | 19:45480290-45480388- | NA | NA | NA | chr19 45480290 45480291 | q13.2 |
| hsa-miR-642 | | 19 | 50870026 | GUCCCUCUCCAAAUGUGUCUUG | hsa-miR-642 | 19:50870026-50870122+ | NA | NA | NA | chr19 50870026 50870027 | q13.32 |
| hsa-mir-643 | | 19 | 57476862 | ACUUGUAUGCUAGCUCAGGUAG | hsa-miR-643 | 19:57476862-57476958+ | NA | NA | NA | chr19 57476862 57476863 | q13.33 |
| hsa-miR-644 | | 20 | 32517791 | AGUGUGGCUUUCUUAGAGC | hsa-miR-644 | 20:32517791-32517884+ | NA | NA | NA | chr20 32517791 32517792 | q11.22 |
| hsa-miR-645 | | 20 | 48635730 | UCUAGGCUGGUACUGCUGA | hsa-miR-645 | 20:48635730-48635823+ | NA | NA | NA | chr20 48635730 48635731 | q13.13 |
| hsa-mir-646 | | 20 | 58316927 | AAGCAGCUGCCUCUGAGGC | hsa-miR-646 | 20:58316927-58317020+ | NA | NA | NA | chr20 58316927 58316928 | q13.33 |
| hsa-miR-647 | | 20 | 62044428 | GUGGCUGCACUCACUUCCUUC | hsa-miR-647 | 20:62044428-62044523- | NA | NA | NA | chr20 62044428 62044429 | q13.33 |
| hsa-miR-648 | | 22 | 16843634 | AAGUGUGCAGGGCACUGGU | hsa-miR-648 | 22:16843634-16843727- | NA | NA | NA | chr22 16843634 16843635 | q11.21 |
| hsa-miR-649 | | 22 | 19718465 | AAACCUGUGUUGUUCAAGAGUC | hsa-miR-649 | 22:19718465-19718561- | NA | NA | NA | chr22 19718465 19718466 | q11.21 |
| hsa-mir-650 | | 22 | 21495270 | AGGAGGCAGCGCUCUCAGGAC | hsa-miR-650 | 22:21495270-21495365+ | NA | NA | NA | chr22 21495270 21495271 | q11.22 |
| hsa-mir-651 | X | | 8055006 | UUUAGGAUAAGCUUGACUUUUG | hsa-miR-651 | 23:8055006-8055102+ | NA | NA | NA | chrX 8055006 8055007 | p22.31 |
| hsa-mir-652 | X | | 1,09E+08 | AAUGGCGCCACUAGGGUUGUGCA | hsa-miR-652 | 23:109185213-109185310+ | NA | NA | NA | chrX 109185213 109185214 | q22.3 |
| hsa-miR-653 | | 7 | 92950008 | UUGAAACAAUCUCUACUGAAC | hsa-miR-653 | 7:92950008-92950103- | NA | NA | NA | chr7 92950008 92950009 | q21.3 |
| hsa-mir-654 | | 14 | 1,01E+08 | UGGUGGGCCGCAGAACAUGUGC | hsa-miR-654-5p | 14:100576309-100576389+ | NA | NA | NA | chr14 100576309 100576310 | q32.31 |
| hsa-mir-655 | | 14 | 1,01E+08 | AUAAUACAUGGUUAACCUCUUU | hsa-miR-655 | 14:100585640-100585736+ | NA | NA | NA | chr14 100585640 100585641 | q32.31 |
| hsa-mir-656 | | 14 | 1,01E+08 | AAUAUUAUACAGUCAACCUCU | hsa-miR-656 | 14:100602814-100602891+ | NA | NA | NA | chr14 100602814 100602815 | q32.31 |
| hsa-mir-657 | | 17 | 76713671 | GGCAGGUUCUCACCCUCUCUAGG | hsa-miR-657 | 17:76713671-76713768- | NA | NA | NA | chr17 76713671 76713672 | q25.3 |
| hsa-mir-658 | | 22 | 36570225 | GGCGGAGGGAAGUAGGUCCGUUGGU | hsa-miR-658 | 22:36570225-36570324- | NA | NA | NA | chr22 36570225 36570226 | q13.1 |
| hsa-mir-659 | | 22 | 36573631 | CUUGGUUCAGGGAGGGUCCCCA | hsa-miR-659 | 22:36573631-36573727- | NA | NA | NA | chr22 36573631 36573632 | q13.1 |
| hsa-mir-660 | X | | 49664589 | UACCCAUUGCAUAUCGGAGUUG | hsa-miR-660 | 23:49664589-49664685+ | NA | NA | NA | chrX 49664589 49664590 | p11.23 |
| hsa-miR-661 | | 8 | 1,45E+08 | UGCCUGGGUCUCUGGCCUGCGCGU | hsa-miR-661 | 8:145091347-145091435- | NA | NA | NA | chr8 145091347 145091348 | q24.3 |
| hsa-mir-662 | | 16 | 760184 | UCCCACGUUGUGGCCCAGCAG | hsa-miR-662 | 16:760184-760278+ | NA | NA | NA | chr16 760184 760185 | p13.3 |
| hsa-mir-7 | | 9 | 85774483 | UGGAAGACUAGUGAUUUUGUUG | hsa-miR-7 | 9:85774483-85774592- | 15:86956060-86956169+ | NA | NA | chr9 85774483 85774484 | q21.32 |
| hsa-mir-9 | | 1 | 1,55E+08 | UCUUUGGUUAUCUAGCUGUAUGA | hsa-miR-9 | 1:154656757-154656845- | 5:87998427-87998513- | NA | NA | chr1 154656757 154656758 | q22 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| hsa-mir-92 | | 13 | 90801569 | UAUUGCACUUGUCCCGGCCUG | hsa-miR-92a | 13:90801569-90801646+ | 23:133131234-133131308- | NA | NA | chr13 90801569 90801570 | q31.3 |
| hsa-mir-93 | | 7 | 99529327 | AAAGUGCUGUUCGUGCAGGUAG | hsa-miR-93 | 7:99529327-99529406- | NA | NA | NA | chr7 99529327 99529328 | q22.1 |
| hsa-mir-95 | | 4 | 8057928 | UUCAACGGGUAUUUAUUGAGCA | hsa-miR-95 | 4:8057928-8058008- | NA | NA | NA | chr4 8057928 8057929 | p16.1 |
| hsa-mir-96 | | 7 | 1,29E+08 | UUUGGCACUAGCACAUUUUUGC | hsa-miR-96 | 7:129201768-129201845- | NA | NA | NA | chr7 129201768 129201769 | q32.2 |
| hsa-mir-98 | X | | 53599909 | UGAGGUAGUAAGUUGUAUUGUU | hsa-miR-98 | 23:53599909-53600027- | NA | NA | NA | chrX 53599909 53599910 | p11.22 |
| hsa-mir-99a | | 21 | 16833280 | AACCCGUAGAUCCGAUCUUGUG | hsa-miR-99a | 21:16833280-16833360+ | NA | NA | NA | chr21 16833280 16833281 | q21.1 |
| hsa-mir-99b | | 19 | 56887677 | CACCCGUAGAACCGACCUUGCG | hsa-miR-99b | 19:56887677-56887746+ | NA | NA | NA | chr19 56887677 56887678 | q13.33 |
| hsa-mir-9star | | 1 | 1,55E+08 | UAAAGCUAGAUAACCGAAAGU | hsa-miR-9* | 1:154656757-154656845- | 5:87998427-87998513- | NA | NA | chr1 154656757 154656758 | q22 |

**Supplementary Table 3**

MicroRNAs significantly (pfp-value <0.05) higher expressed in the T-ALL samples compared to normal thymocyte subsets (calculated by Rank Product analysis)

| MicroRNA ID | RP/Rsum | FC (T-ALL/thymocytes) | pfp-value | p-value |
|---|---|---|---|---|
| hsa-miR-376a | 1,4539 | 11991,795 | 0 | 0 |
| hsa-miR-662 | 2,1197 | 4540,9549 | 0 | 0 |
| hsa-miR-520c | 7,5683 | 183,5463 | 0 | 0 |
| hsa-miR-223 | 10,9664 | 50,3626 | 0 | 0 |
| hsa-miR-137 | 19,0798 | 18,1339 | 0 | 0 |
| hsa-miR-451 | 20,1175 | 19,923 | 0 | 0 |
| hsa-miR-520d | 20,2122 | 12,9944 | 0 | 0 |
| hsa-miR-486 | 25,5761 | 12,5769 | 0 | 0 |
| hsa-miR-645 | 27,8354 | 7,4237 | 0 | 0 |
| hsa-miR-30e-5p | 29,7833 | 7,8211 | 0 | 0 |
| hsa-miR-574 | 30,3813 | 7,3025 | 0 | 0 |
| hsa-miR-606 | 30,6922 | 6,9002 | 0 | 0 |
| hsa-miR-145 | 32,2768 | 6,4396 | 0 | 0 |
| hsa-miR-496 | 34,9681 | 5,7975 | 0 | 0 |
| hsa-miR-126 | 35,3136 | 5,9416 | 0 | 0 |
| hsa-miR-182 | 40,5373 | 4,6662 | 0 | 0 |
| hsa-miR-23a | 42,202 | 8,9298 | 0 | 0 |
| hsa-miR-224 | 44,2166 | 4,8375 | 0 | 0 |
| hsa-miR-410 | 44,8108 | 4,9999 | 0 | 0 |
| hsa-miR-10a | 45,4867 | 4,0832 | 0 | 0 |
| hsa-miR-199b | 46,9037 | 4,4184 | 0 | 0 |
| hsa-miR-604 | 49,6007 | 2,8057 | 0 | 0 |
| hsa-miR-381 | 52,77 | 2,9465 | 0 | 0 |
| hsa-miR-363 | 53,3555 | 2,5076 | 0 | 0 |
| hsa-miR-126hek | 54,0412 | 2,7739 | 0 | 0 |
| hsa-miR-135a | 55,9135 | 2,5253 | 0,0012 | 1,00E-04 |
| hsa-miR-128b | 59,0607 | 2,6388 | 0,0041 | 3,00E-04 |
| hsa-miR-638 | 61,0699 | 2,0785 | 0,0082 | 7,00E-04 |
| hsa-miR-199ahek | 61,8263 | 2,5361 | 0,0083 | 7,00E-04 |
| hsa-let-7b | 63,0563 | 2,1762 | 0,0123 | 0,0011 |
| hsa-miR-105 | 65,1596 | 2,2959 | 0,0174 | 0,0016 |
| hsa-miR-487b | 65,3755 | 2,62 | 0,0172 | 0,0017 |
| hsa-miR-382 | 65,9299 | 4,2746 | 0,0197 | 0,002 |
| hsa-miR-206 | 66,1476 | 1,648 | 0,02 | 0,002 |
| hsa-miR-520f | 68,6075 | 2,1155 | 0,0286 | 0,003 |
| hsa-miR-572 | 70,1251 | 1,8817 | 0,0372 | 0,004 |
| hsa-miR-153 | 71,0743 | 2,0137 | 0,0438 | 0,0049 |

**Supplementary Table 4: Overview of studies describing miR-128(-3p) in cancer**

**Studies describing miR-128(-3p) as a tumor suppressive miRNA**

| cancer type | Target gene(s) | phenotype/affected pathway | reference (PMID) |
|---|---|---|---|
| overian cancer | | miR-128 down regulation | Woo et al. (22909061) |
| neuroblastoma | | miR-128 down regulation | Evangelisti et al. (19713529) |
| prostate cancer | | miR-128 down regulation | Khan et al. (19955085) |
| glioblastoma | *E2F3a* | miR-128 down regulation | Zhang et al. (18810376) |
| lung cancer | *EGFR* | deletion of miR-128 releases represion on EGFR expression, and impacts on clinical response and survival following gefitinib treatment | Weiss et al. (18304967) |
| pituitary cancer | *BMI1* | miR-128(-3p) down regulation results in higher expression of its target BMI1, which in turn leads to PTEN repression and increased tumorigenicity | Palumbo et al. (22614013) |
| glioma | *BMI1* | miR-128 down regulation | Peruzzi et al. (23733246) |
| | p70S6K1 (protein) | miR-128 down regulation affects cell proliferation, tumor growth and angiogenesis | Shi et al. (22442669) |
| breast cancer | *BMI1, CSF1, KLF4, LIN28A, NANOG, SNAIL* | miR-128 down regulation results in higher expression of its target genes, thereby impacting on PI3K/AKT and STAT3 signaling pathways | Qian et al. (23019226) |

**Studies describing miR-128(-3p) as an oncogenic miRNA**

| cancer type | Target gene(s) | phenotype/affected pathway | reference (PMID) |
|---|---|---|---|
| breast cancer | *BAX* | higher expression of miR-128 in drug-resistant breast cancers | Ji et al. (23526655) |
| breast cancer | | miR-128 upregulation | Zhu et al. (21953503)<br>Picker and Jackson (21745011) |
| breast cancer | | miR-128 upregulation was linked to ER+/LNN- breast cancer agressiveness | Foekens et al. (18755890) |
| non-small-cell lung cancer | *E2F5* | miR-128 expression targets *E2F5,* inhibits apoptosis and confers resitance to cisplatin, doxorubicin and 5-fluorouracyl treatments | Donzelli et al. (22193543) |
| acute leukemia | | miR-128 is higher expressed in ALL than in AML | Mi et al. (18056805)<br>Zhu et al. (22209839) |