Alterations of microRNA and microRNA-regulated messenger RNA expression in germinal center B-cell lymphomas determined by integrative sequencing analysis

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Supplementary Information

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Supplementary Materials and Methods

Cell culture

Cell lines (Namalwa, Raji, SU-DHL-4, and SU-DHL-6) were characterized and provided by Hans G. Drexler (DSMZ, Braunschweig, Germany). They were cultured with 5% CO2 in RPMI 1640 (Life Technologies) supplemented with 10% FBS at 37 °C.

RNA isolation from cell lines and Northern blotting

Total RNA was extracted from the above-mentioned cell lines using TRI Reagent (Sigma-Aldrich) according to the manufacturer's instructions. Thirty µg of total RNA was fractionated on a denaturing 12% polyacrylamide gel containing 8M Urea, transferred to a Hybond-N+ membrane (Amersham Biosciences) by semidry method and fixed by UV cross-linking (1200 j/cm^2 for 30 sec). Membranes were probed with ^{32}P-labelled sequences complementary to each putative novel miRNA. Twenty µmol of each oligonucleotide probe was end-labelled with [gamma-^{32}P] ATP (Hartmann Analytic) with T4 polynucleotide kinase (New England Biolabs). Prehybridization was carried out in 3 M NaCl, 1 M NaHPO4, 20%

SDS, 50X Denhardt's solution, and denatured salmon sperm DNA (Life Technologies). Hybridization was performed in the same solution at 55-60°C. Following hybridization, membranes were washed in 3 M NaCl, 1M NaHPO4, 20% SDS, 0.5 M EDTA for 10min. Membranes were exposed 3-5 h prior to signal detection on a FLA-7000 Phosphor Imager.

Overexpression and knockdown of novel miRNAs

To generate mimics of the novel miRNAs, the BLOCK-iTTM Pol II miR RNAi Expression Vector Kit (Life Technologies) was used according to the manufacturer's instructions. MiRCURY LNA™ probes for knockdown of miRNAs were purchased from Exiqon (Vedbaek, Denmark) (NB-miR-5-TCTCTCTGTGTCAGTGTG, NB-miR-19-TAGGGGCCTACAAC GTTG). For nucleofection (all experiments in triplicate), 2 x 106 cells were split the day before and were transfected with 2 µg of pcDNA6.2 containing pre-novel-miRNAs or 100 nM miRNA inhibitor using nucleofector V, solution V (Lonza, Basel, Switzerland), and programs M-013 (Raji) and M-13 (SU-DHL-4).

Expression of novel miRNAs in cell line and tissue panel

Expression of novel miRNAs was evaluated in a panel of published miRNA profiles of cell line and tissue datasets (ENCODE project(1); http://ftp.ebi.ac.uk/pub/databases/ensembl/encode/ integration_data_jan2011/byDataType/rna_signal/jan2011/hub/). These included A549 (adenocarcinoma of the lung), AG04450 (pulmonary fibroblasts), BJ (foreskin fibroblasts), GM12878 (B-lymphoblastoid cell line), H1 (human embryonic stem cells), Hela-S3 (cervical cancer), HepG2 (hepatocellular carcinoma), HMEC (mammary epithelial cells), HSMM (skeletal muscle myoblasts), HUVEC (human umbilical vein endothelial cells), K562 (chronic myelogenous leukemia), MCF-7 (mammary gland, adenocarcinoma), NHEK (epidermal keratinocytes), NHLF (lung fibroblasts), prostate (prostate tissue), and SK-N-SH_RA (neuroblastoma cell line, differentiated with retinoic acid).

Bioinformatic Methods

Genome and transcriptome analysis

RNA-seq reads (average of 11,320,300 / sample) were aligned with *TopHat* (2) (version 2.0.12). Differential gene expression was measured with *edgeR* (3) (version 3.8.6) using inter-sample normalized counts per millions (CPM) and applying multiple testing corrections using FDR. CPMs are normalizing the actual read counts mapping to a respective gene by the entire number of sequenced reads per sample times 1,000,000 (3). Thereby, CPMs are representing a measure of expression counts that are comparable across multiple samples.

Read pairs obtained by whole genome paired-end sequencing were mapped to the human reference genome (hg19) using BWA (4) version 0.5.9-r16 (maximum insert size of 1 kb). SAMtools (5) was used to generate a coordinate-sorted BAM file, and Picard (version 1.48) was used to merge BAM files from one sample and remove PCR duplicates. Detection of somatic SNVs from tumor and matched control whole genome sequencing data was performed as described previously (6). SNVs were functionally annotated using Annovar (7) and annotated for overlaps with SNPs (dbSNP build 135 and 1000 Genome project data) using BEDTools (8). Allele-specific copy-number alterations were detected as described in Richter et al (9).

MiRNA sequencing data processing and novel miRNA prediction

Adapter sequences were removed from raw reads using fastx_clipper (http://hannonlab.cshl.edu/fastx_toolkit/index.html). A total of 1,169,752,727 clipped reads were mapped onto the human genome (1000 genomes project, hs37d5100) using segemehl(10), with a minimum accuracy of 90% (average of 20,888,442 reads per sample, see Supplementary Table 2). Quantification of annotated microRNAs from miRBase version 19 was performed using ngsutils (11), partially counting multimapped reads. Read counts were inter-sample normalized leading to CPM values per annotated miRNA. Differential expression was achieved by applying edgeR and subsequent calculation of the FDR for multiple testing correction.

Novel miRNA prediction was performed using miRanalyzer (12) (version 0.3) using default parameters.

MiRNA target prediction

We used miRanda(13) (version August 2010) to predict potential interaction targets of miRNAs in the transcriptome. For narrowing down the list of miRNA-mRNA target correlations, we filtered for a miRsvr-score < -1.2 per correlation pair. We selected this score as it results in the 5% most significant miRNA-mRNA correlations(14).

Differential expression analysis on RNA-Seq data – novel miRNA overexpression/knockdown

In all sequencing reads, adapters and low quality ends were trimmed using *seqtk* (https://github.com/lh3/seqtk) and *cutadapt*(15). All reads shorter than 25 bases after trimming were discarded, leading to 11,320,300 reads on average per sample. Next, the preprocessed reads were aligned against the human genome sequence (hg19) with *TopHat*(2), which is capable of aligning RNA-Seq data because of the identification of splice junctions spanned by individual reads. On average, more than 80% of the preprocessed reads have been aligned against the reference sequence and were used for further analysis. To measure the transcript abundances representing an estimate of the gene expression levels in the samples, *HTSeq*(16) (version 0.5.4) was employed using gene annotations downloaded from Ensembl Genes 75(17). Differential gene expression was measured with *edgeR*(3) using inter-sample normalized counts per millions (CPM) and applying multiple testing corrections using FDR.

PAR-CLIP analysis

The preprocessing of PAR-CLIP reads was similar to that of RNA-Seq reads, however, because short reads align multiple times to the genome, we selected a cutoff of 17 bases per sequencing read after quality and adapter trimming using *cutadapt*. On average, this resulted in about 15,570,345 reads per sequencing sample. Next, reads were aligned with *BWA*(4) allowing for up to two mismatches between a single read sequence and the reference sequence of hg19. All reads that failed in this mapping (mapping quality <10) were aligned against the transcriptome database Ensembl Genes 75 using *BWA* allowing for up to two mismatches between both sequences(18). Next, the aligned reads were piled up into clusters by the PARA-suite (Kloetgen, Borkhardt et al., submitted) which applies a hierarchical clustering algorithm, where reads overlapping by at least 5 bases in their genomic mapping positions are stacked into a single cluster. To identify high confidence RNA-binding protein-bound regions, clusters having <5 reads and <25% T-C conversion frequency were excluded (for further details on analyzing PAR-CLIP datasets see(19)).

To equalize cluster lengths for subsequent mRNA-miRNA correlation analysis, crosslink-centered regions (CCRs) consisting of 20 nucleotides up- and downstream of the major T-C conversion site within a cluster (i.e. the T-C conversion site with the highest conversion frequency per cluster), were generated to calculate all possible 7-mers within the CCRs(20) (Figure 2C). The most significantly enriched (compared to random sequences of the same dinucleotide compositions) corresponded to the reverse complement of the miRNA seed region. The miRNA-mRNA correlation was achieved by matching miRNA seed positions 2-8 as well as miRNA seed positions 1-7 to the reverse complement of the enriched CCR 7-mers for each cluster. As we also had information on the expression levels of miRNAs and mRNAs, we kept only miRNA-mRNA pairs, which showed a differential expression between BL versus non-BL patient samples (differential expression FDR ≤0.05). All miRNAs meeting this cutoff (FDR ≤0.05) showed log2 fold expression changes of at least ± 0.6.

Enrichment analysis

We have performed enrichment analyses by applying a one-sided Fisher's exact test to the number of overlapping genes/miRNAs between two lists, thereby calculating a significance value for the respective enrichment between the two lists. On the one hand, this was applied to identify enrichments between our reported miRNA classifier and recently published miRNA classifiers for the respective lymphoma subtypes. Therefore, the total number of tested miRNAs was taken as a basis (667 in [28] and 602 in [10]). On the other hand, enriched genes of the negatively correlated miRNAs-mRNAs pairs were identified within KEGG pathways. The gene-basis was set to 22,525 genes, which were accessible for differential gene expression analysis based on RNA-Seq data after filtering lowly expressed genes (logCPM < 1 in all patients of all subgroups). Enrichment scores were calculated as follows: Enrichment = #overlap / (#DE genes * #pathway genes / #population genes).

Expressional correlation analysis

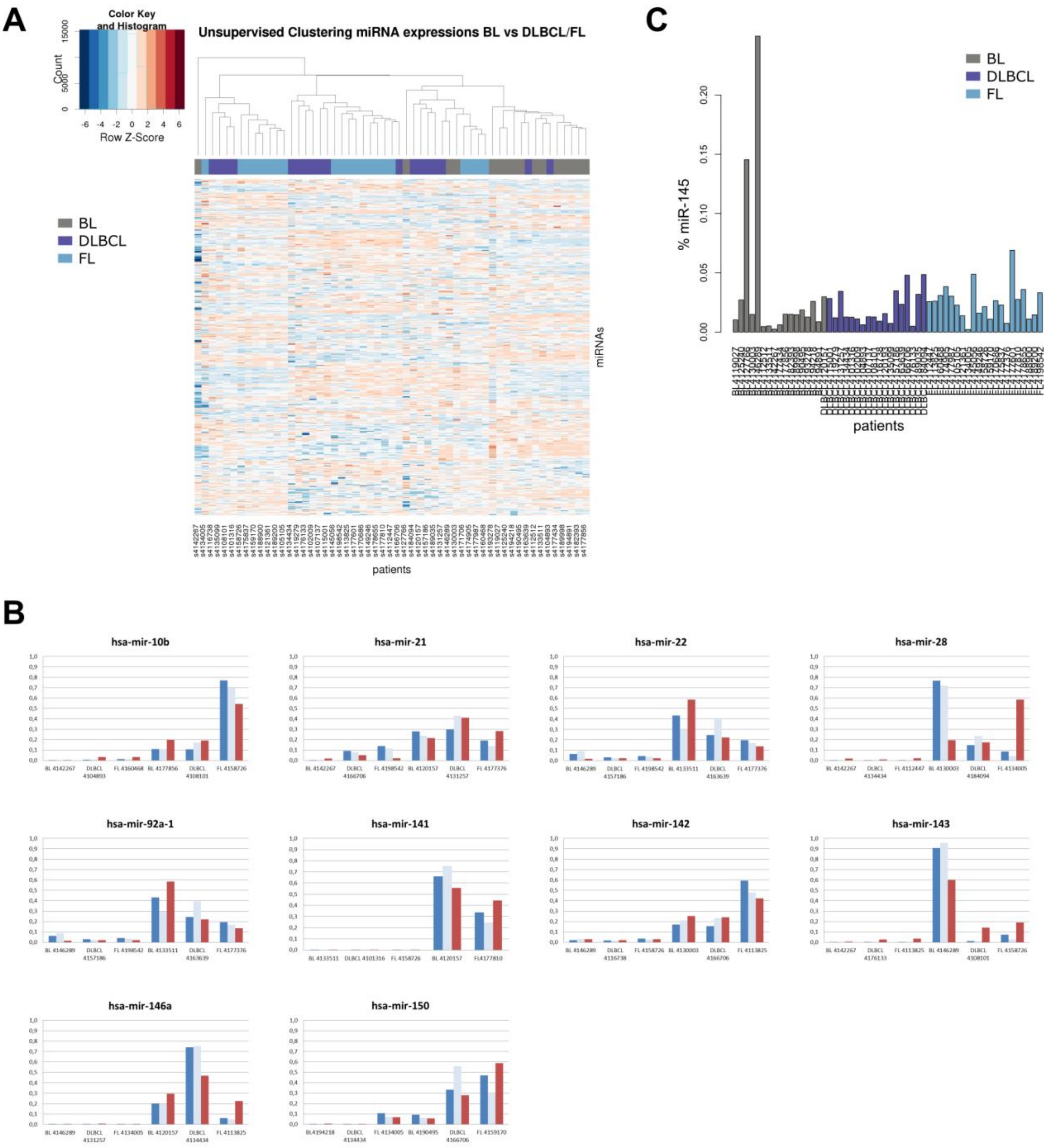
We have used the spearman's rank correlation to test for significant similarity between two expression patterns. This was applied to check for similar expressions of miRNAs between different platforms, i.e. between NGS derived expression values and qPCR derived expression values. We also used the spearman's rank correlation to check whether the expressional pattern of hsa-miR-143 and hsa-miR-145 were similar across all patient samples.

Leave-one-out cross-validation

To test the validity of our reported miRNA-classifiers, we have performed leave-one-out cross-validation (LOO-CV) on an independent dataset downloaded from NCBI GEO (Accession GSE22420) (21). Because these expression values were obtained from microarray experiments, we used LOO-CV to train our classifier on microarray expression values rather than on cpm values obtained from our RNA-Seq data. Additionally, we had to exclude miRNAs from the classifier which were not covered by the microarray (7 miRNAs each for the BL vs. DLBCL classifier and the BL vs. DLBCL/FL classifier). The class prediction for the left-out sample was performed using the K-nearest-neighbours algorithm with k=33 (half the size of the smaller BL group containing 64 samples). All cases showing less than 80% majority vote during the class prediction were excluded as not classified. Recall was calculated as the number of remaining predictions per classified cases and overall accuracy was calculated as the number of correct assignments after majority vote exclusion per all tested cases.

Supplementary Figures

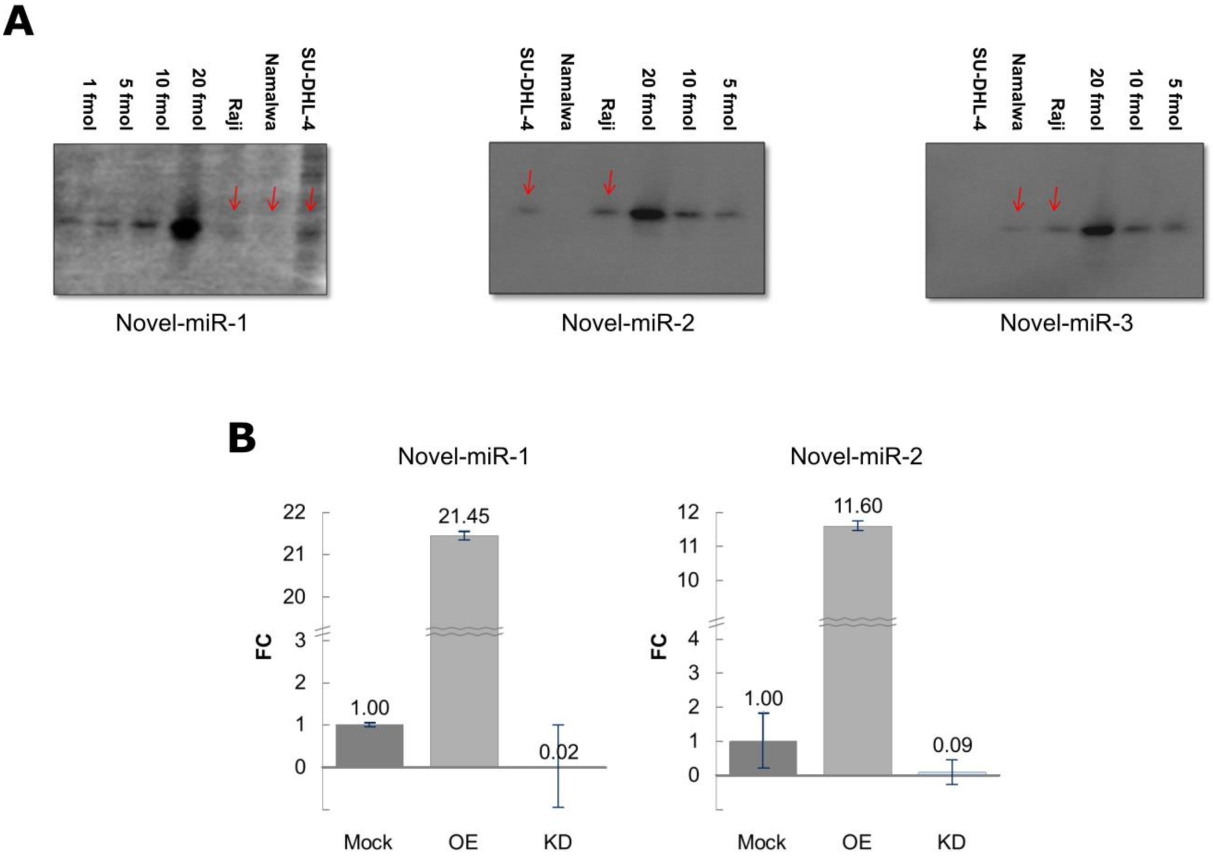
Supplementary Figure 1



Supplementary Figure 1. Validation of NGS data. A) For unsupervised clustering, miRNAs were discarded if less than 16 patients showed a base-line expression of > 0 log2 cpm after normalization. In total, 573 mature miRNAs were used for unsupervised clustering. FL (light blue), DLBCL (dark blue), and BL (grey). B) Validation of NGS miRNA expression by qRT-PCR. Light blue = qRT-PCR expression (normalized to *RNU48* as housekeeping gene), dark blue = qRT-PCR expression (normalized to *RNU24* as housekeeping gene), red:

expression according to NGS analysis. To allow for comparison across platforms, the expression levels were set to add up to 100 per experiment and are shown as % total expression. Also see Supplementary Table 3 for statistical analysis. C) Hsa-miR-145 expression across all patient samples. Color code as in A).

Supplementary Figure 2



Supplementary Figure 2. Validation of novel miRNAs. A) Northern blot results for all three validated novel miRNAs including RNA expression standards in the indicated concentrations. Red arrows point at the correctly processed mature novel miRNAs. Synthesized RNA oligonucleotides (sequences of the respective novel miRNAs) serve as size standards and were used in the indicated concentrations. B) Evaluation of knockdown and overexpression efficiencies of the respective novel miRNA prior to RNASeq. Experiments for novel-miR-1 were performed in SU-DHL-4, for novel-miR-2 in Raji. FC indicates fold change; OE, overexpression; KD, knockdown

Supplementary Tables

Supplementary Table 1: Patient information

PID	Diagnosis	Classification 2	Age at first diagnosis	Gender	MYC_STATUS	BCL2_BREAK	BCL6_BREAK	IGH_status
4112512	BL	NA	18	female	IG-MYC pos	negative	negative	IGH-MYC pos
4119027	BL	NA	12	male	IG-MYC pos	negative	negative	IGH-MYC pos
4125240	BL	NA	4	male	IG-MYC pos	negative	negative	IGH-MYC pos
4127766	BL	NA	8	male	IG-MYC pos	negative	negative	IGH-MYC pos
4130003	BL	NA	6	male	IG-MYC pos	negative	negative	IGH neg
4133511	BL	NA	5	male	IG-MYC pos	negative	negative	IGH-MYC pos
4142267	BL	NA	5	male	IG-MYC pos	negative	negative	IGH neg
4146289	BL	NA	14	male	IG-MYC pos	negative	negative	IGH-MYC pos
4177434	BL	NA	16	female	IG-MYC pos	negative	negative	IGH-MYC pos
4177856	BL	NA	10	male	IG-MYC pos	negative	negative	IGH-MYC pos
4182393	BL	NA	10	male	IG-MYC pos	negative	negative	IGH-MYC pos
4189998	BL	NA	13	male	IG-MYC pos	negative	negative	IGH-MYC pos
4190495	BL	NA	15	male	IG-MYC pos	negative	negative	IGH neg
4193278	BL	NA	17	male	IG-MYC pos	negative	negative	IGH neg
4194218	BL	NA	4	male	IG-MYC pos	negative	negative	IGH-MYC pos
4194891	BL	NA	4	male	IG-MYC pos	negative	negative	IGH-MYC pos
4101316	DLBCL	ABC	74	female	MYC neg	negative	negative	IGH neg
4102009	DLBCL	ABC	64	male	MYC neg	negative	negative	IGH neg
4104893	DLBCL	TypeIII	16	male	MYC neg	negative	negative	IGH-IRF4 pos
4107137	DLBCL	GCB	59	male	MYC neg	negative	positive	IGH pos
4108101	DLBCL	ABC	66	male	MYC neg	negative	negative	IGH neg
4115001	DLBCL	GCB	70	female	MYC neg	positive	negative	IGH-BCL2 pos
4116738	DLBCL	TypeIII	15	male	MYC neg	negative	positive	IGH neg
4119279	DLBCL	ABC	62	female	MYC neg	negative	negative	IGH neg
4120157	DLBCL	GCB	46	male	MYC neg	negative	negative	IGH pos
4120193	DLBCL	ABC	41	female	MYC neg	negative	negative	IGH neg
4131257	DLBCL	ABC	72	male	MYC neg	negative	positive	IGH pos
4134434	DLBCL	GCB	84	male	MYC neg	positive	positive	IGH pos
4135099	DLBCL	ABC	49	male	MYC neg	negative	positive	IGH pos
4157186	DLBCL	ABC	74	male	MYC neg	negative	negative	IGH neg
4163639	DLBCL	GCB	75	female	MYC neg	negative	negative	IGH neg
4166706	DLBCL	GCB	62	male	MYC neg	negative	positive	IGH pos
4176133	DLBCL	ABC	61	female	MYC neg	negative	positive	IGH pos
4184094	DLBCL	GCB	57	female	MYC neg	positive	negative	IGH-BCL2 pos
4189035	DLBCL	ABC	46	male	MYC neg	negative	negative	IGH neg
4105105	FL	grade 1/2	40	female	MYC neg	positive	negative	IGH-BCL2 pos
4112447	FL	grade 1/2	46	male	MYC neg	positive	positive	IGH-BCL2 pos
4113825	FL	grade 1/2	74	female	MYC neg	negative	negative	IGH neg
4121361	FL	grade 1/2	74	male	MYC neg	positive	negative	IGH-BCL2 pos
4134005	FL	grade 1/2	67	male	MYC neg	positive	negative	IGH-BCL2 pos
4145056	FL	grade 1/2	67	female	MYC neg	positive	negative	IGH-BCL2 pos
4149246	FL	grade 1/2	41	male	MYC neg	positive	positive	IGH-BCL2 pos
4158726	FL	grade 1/2	48	male	MYC neg	positive	negative	IGH-BCL2 pos
4159170	FL	grade 1/2	43	male	MYC neg	positive	negative	IGH-BCL2 pos
4160468	FL	grade 1/2	62	male	MYC neg	positive	negative	IGH-BCL2 pos
4170686	FL	grade 1/2	56	male	MYC neg	positive	negative	IGH-BCL2 pos
4174905	FL	grade 1/2	72	male	MYC neg	positive	negative	IGH-BCL2 pos
4175837	FL	grade 1/2	74	female	MYC neg	positive	positive	IGH-BCL2 pos
4177376	FL	grade 3A	73	female	MYC neg	positive	negative	IGH-BCL2 pos
4177601	FL	grade 2/3A	52	female	MYC neg	positive	negative	IGH-BCL2 pos
4177810	FL	grade 1/2	47	female	MYC neg	positive	negative	IGH-BCL2 pos
4177987	FL	grade 1/2	71	male	MYC neg	positive	negative	IGH-BCL2 pos
4178655	FL	grade 1/2	50	male	MYC neg	positive	negative	IGH-BCL2 pos
4188900	FL	grade 1/2	76	male	MYC neg	positive	negative	IGH neg
4189200	FL	grade 1/2	51	female	MYC neg	positive	negative	IGH-BCL2 pos
4198542	FL	grade 1/2/3A	68	female	MYC neg	negative	negative	IGH neg

PID indicates personal identifier; NA, not available

Supplementary Table 2: miRNA sequencing library statistics

Diagnosis	PID	raw reads	clipped reads	% clipped reads	mapped reads	% mapped reads	reads on primary miRs	% reads on primary miRs
BL	4112512	111,835,821	90,656,876	81.06%	83,739,794	92.37%	30,310,990	36.20%
BL	4119027	96,943,814	80,372,849	82.91%	74,224,275	92.35%	27,687,024	37.30%
BL	4125240	64,001,808	56,406,459	88.13%	53,503,949	94.85%	10,026,892	18.74%
BL	4127766	35,157,062	34,510,881	98.16%	33,693,807	97.63%	1,706,671	5.07%
BL	4130003	25,502,310	24,828,949	97.36%	23,122,148	93.13%	12,787,211	55.30%
BL	4133511	71,261,813	64,018,378	89.84%	59,083,671	92.29%	18,112,535	30.66%
BL	4142267	69,108,952	65,274,277	94.45%	56,674,054	86.82%	10,070,922	17.77%
BL	4146289	41,192,177	40,108,479	97.37%	37,541,386	93.60%	34,377,156	91.57%
BL	4177434	62,332,955	53,529,191	85.88%	46,581,276	87.02%	23,865,056	51.23%
BL	4177856	75,642,487	68,181,918	90.14%	61,370,463	90.01%	24,861,850	40.51%
BL	4182393	84,780,972	72,038,555	84.97%	66,059,591	91.70%	21,585,793	32.68%
BL	4189998	102,523,454	91,607,098	89.35%	83,325,274	90.96%	22,585,978	27.11%
BL	4190495	156,613,394	137,235,359	87.63%	130,397,032	95.02%	34,428,505	26.40%
BL	4193278	72,506,909	65,405,761	90.21%	57,367,702	87.71%	18,460,967	32.18%
BL	4194218	76,405,749	73,447,437	96.13%	67,907,053	92.46%	5,543,923	8.16%
BL	4194891	90,762,811	68,540,713	75.52%	63,179,485	92.18%	24,980,361	39.54%
DLBCL	4101316	67,519,903	64,199,209	95.08%	61,007,246	95.03%	28,775,304	47.17%
DLBCL	4102009	42,086,479	39,944,756	94.91%	36,818,259	92.17%	11,789,929	32.02%
DLBCL	4104893	95,311,645	85,124,518	89.31%	76,526,308	89.90%	21,888,192	28.60%
DLBCL	4107137	40,477,513	34,734,623	85.81%	31,436,185	90.50%	19,242,992	61.21%
DLBCL	4108101	57,832,471	55,071,105	95.23%	51,979,749	94.39%	27,543,402	52.99%
DLBCL	4115001	27,198,492	26,148,020	96.14%	25,497,799	97.51%	7,386,128	28.97%
DLBCL	4116738	78,232,596	68,884,140	88.05%	60,645,188	88.04%	31,000,823	51.12%
DLBCL	4119279	39,034,533	34,535,595	88.47%	32,847,597	95.11%	8,154,515	24.83%
DLBCL	4120157	45,688,615	41,860,450	91.62%	38,598,518	92.21%	8,676,661	22.48%
DLBCL	4120193	40,566,871	39,713,411	97.90%	37,901,161	95.44%	5,340,938	14.09%
DLBCL	4131257	31,446,420	30,697,771	97.62%	29,248,137	95.28%	10,648,290	36.41%
DLBCL	4134434	34,646,386	28,750,213	82.98%	25,728,439	89.49%	9,642,469	37.48%
DLBCL	4135099	82,046,323	75,673,959	92.23%	70,326,721	92.93%	42,315,069	60.17%
DLBCL	4157186	20,558,444	18,165,585	88.36%	17,261,128	95.02%	7,126,511	41.29%
DLBCL	4163639	82,468,882	76,639,372	92.93%	71,664,118	93.51%	22,990,794	32.08%
DLBCL	4166706	49,112,501	46,502,593	94.69%	43,144,375	92.78%	26,491,474	61.40%
DLBCL	4176133	27,241,860	26,650,486	97.83%	25,782,166	96.74%	4,973,146	19.29%
DLBCL	4184094	37,960,574	35,916,452	94.62%	33,999,067	94.66%	4,891,289	14.39%
DLBCL	4189035	39,456,122	33,743,677	85.52%	30,162,878	89.39%	18,823,323	62.41%
FL	4105105	66,137,979	64,339,942	97.28%	62,248,882	96.75%	33,016,425	53.04%
FL	4112447	45,773,088	42,548,261	92.95%	40,644,074	95.52%	10,268,194	25.26%
FL	4113825	41,550,848	31,506,429	75.83%	26,934,801	85.49%	15,915,215	59.09%
FL	4121361	73,759,960	67,969,941	92.15%	63,948,878	94.08%	49,654,552	77.65%
FL	4134005	67,942,851	61,098,231	89.93%	58,991,880	96.55%	12,599,478	21.36%
FL	4145056	26,282,929	23,842,066	90.71%	20,609,766	86.44%	9,084,189	44.08%
FL	4149246	20,825,007	15,932,481	76.51%	14,785,326	92.80%	12,274,678	83.02%
FL	4158726	80,798,657	77,575,725	96.01%	72,581,907	93.56%	56,127,947	77.33%
FL	4159170	90,316,042	87,915,910	97.34%	84,580,056	96.21%	48,098,750	56.87%
FL	4160468	66,934,137	64,234,781	95.97%	57,676,380	89.79%	45,480,635	78.85%
FL	4170686	28,225,201	28,047,528	99.37%	27,224,450	97.07%	6,080,646	22.34%
FL	4174905	40,688,848	39,370,043	96.76%	36,779,632	93.42%	17,879,064	48.61%
FL	4175837	145,487,505	142,602,072	98.02%	138,805,355	97.34%	47,162,234	33.98%
FL	4177376	59,033,653	57,041,478	96.63%	54,405,387	95.38%	29,629,182	54.46%
FL	4177601	39,845,682	39,113,638	98.16%	37,491,676	95.85%	5,775,674	15.41%
FL	4177810	23,339,328	22,495,874	96.39%	21,827,428	97.03%	9,958,437	45.62%
FL	4177987	38,144,137	34,176,587	89.60%	31,030,702	90.80%	21,971,916	70.81%
FL	4178655	33,166,391	29,713,962	89.59%	27,842,516	93.70%	21,914,993	78.71%
FL	4188900	87,727,261	78,502,242	89.48%	71,530,316	91.12%	40,556,165	56.70%
FL	4189200	62,264,380	29,431,654	47.27%	26,122,247	88.76%	23,250,761	89.01%
FL	4198542	41,391,420	38,304,878	92.54%	36,352,845	94.90%	13,960,509	38.40%

PID indicates personal identifier;

Supplementary Table 3: Validation of NGS expression via qRT-PCR of select miRNAs

miRNA	qRT-PCR RNU24 vs. NGS	qRT-PCR RNU48 vs. NGS
hsa-mir-10b	**0.003**	**0.017**
hsa-mir-21	**0.033**	**0.033**
hsa-mir-22	**0.017**	**0.017**
hsa-mir-28	0.058	0.058
hsa-mir-92a-1	0.103	0.136
hsa-mir-141	0.083	0.083
hsa-mir-142	**0.003**	**0.033**
hsa-mir-143	**0.003**	**0.003**
hsa-mir-146a	**0.003**	**0.003**
hsa-mir-150	**0.003**	**0.017**

P-values of the correlation analyses between qRT-PCRs with two housekeeping genes (RNU24 and RNu48) versus expression as determined by NGS are indicated. P-values ≤ 0.05 are highlighted.

Supplementary Table 4: 25 miRNA classifiers separating B-cell lymphoma subtypes

miRNA	logFC	logCPM	p-value	FDR	cpm BL	cpm DLBCL
hsa-miR-20a-3p	-2.50	4.07	1.92E-12	9.71E-10	29.57	5.22
hsa-miR-221-3p	2.89	11.04	8.01E-12	2.02E-09	478.24	3539.57
hsa-miR-146a-5p	4.22	16.55	1.81E-11	3.05E-09	9293.79	172652.84
hsa-miR-141-3p	8.14	12.63	9.70E-11	1.02E-08	42.20	11905.84
hsa-miR-155-5p	3.87	13.27	1.03E-10	1.02E-08	1197.20	17531.21
hsa-miR-25-5p	-2.44	5.51	1.21E-10	1.02E-08	79.98	14.70
hsa-miR-196b-5p	3.76	5.16	7.07E-10	4.46E-08	4.64	63.07
hsa-miR-3681-5p	5.32	5.31	6.54E-10	4.46E-08	1.83	73.42
hsa-miR-200c-3p	4.70	7.67	1.33E-09	7.45E-08	14.33	370.91
hsa-miR-24-3p	2.66	8.88	2.58E-09	1.30E-07	123.21	780.97
hsa-miR-196a-5p	4.03	2.91	2.91E-09	1.34E-07	0.81	13.30
hsa-miR-664-3p	2.79	5.99	4.82E-09	2.03E-07	15.34	106.32
hsa-miR-130b-3p	-1.69	8.82	7.99E-09	3.04E-07	713.64	220.80
hsa-miR-664-5p	2.94	4.31	8.43E-09	3.04E-07	4.35	33.58
hsa-miR-10b-3p	2.93	2.79	1.18E-08	3.92E-07	1.49	11.62
hsa-miR-29b-2-5p	1.93	2.24	1.24E-08	3.92E-07	1.82	7.14
hsa-miR-23a-5p	2.24	2.76	1.62E-08	4.82E-07	2.24	10.60
hsa-miR-944	3.95	6.01	3.24E-08	9.08E-07	7.40	114.75
hsa-miR-193a-5p	2.09	6.56	3.87E-08	1.03E-06	34.58	147.85
hsa-miR-4677-3p	2.70	4.79	4.96E-08	1.25E-06	7.08	45.92
hsa-miR-339-5p	-2.26	5.89	5.64E-08	1.35E-06	101.54	21.14
hsa-miR-589-3p	-2.05	3.46	5.86E-08	1.35E-06	18.22	4.31
hsa-miR-98	2.09	11.99	6.24E-08	1.37E-06	1492.12	6346.58
hsa-miR-222-3p	2.12	9.93	7.27E-08	1.51E-06	351.22	1525.88
hsa-miR-374a-5p	2.50	8.15	7.47E-08	1.51E-06	81.97	464.14

miRNA	**logFC**	**logCPM**	**p-value**	**FDR**	**cpm BL**	**cpm FL**
hsa-miR-150-3p	3.75	4.97	4.45E-26	1.04E-23	3.85	52.05
hsa-miR-150-5p	4.12	12.86	6.01E-26	1.04E-23	722.73	12575.15
hsa-miR-20a-3p	-3.15	3.94	3.55E-26	1.04E-23	30.87	3.41
hsa-miR-19a-5p	-3.13	3.70	2.30E-23	2.97E-21	25.92	2.97
hsa-miR-18a-3p	-3.49	5.48	3.79E-22	3.92E-20	92.00	8.13
hsa-miR-335-3p	-3.58	8.20	7.95E-22	6.85E-20	614.46	51.34
hsa-miR-378a-3p	-2.43	10.47	1.01E-21	7.49E-20	2641.93	489.06
hsa-miR-184	4.86	3.88	8.06E-21	5.21E-19	0.85	25.05
hsa-miR-130b-3p	-2.79	8.61	1.25E-19	7.16E-18	760.44	110.29
hsa-miR-18a-5p	-3.01	7.05	9.84E-19	4.62E-17	263.04	32.68
hsa-miR-25-5p	-3.09	5.38	9.76E-19	4.62E-17	83.37	9.80
hsa-miR-19b-1-5p	-2.77	1.39	2.07E-18	8.94E-17	4.84	0.73
hsa-miR-151b	3.67	7.05	4.25E-17	1.69E-15	17.20	220.12
hsa-miR-17-5p	-2.32	9.52	1.91E-16	7.04E-15	1348.29	269.90
hsa-miR-92a-1-5p	-2.59	4.43	4.09E-16	1.41E-14	40.81	6.82
hsa-miR-221-3p	2.60	10.96	6.85E-16	2.21E-14	516.96	3123.54
hsa-miR-17-3p	-3.53	10.08	1.38E-15	4.20E-14	2252.58	194.47
hsa-miR-4517	-3.19	1.51	4.84E-15	1.39E-13	5.68	0.61
hsa-miR-29c-5p	2.32	5.53	1.32E-14	3.60E-13	14.05	70.51
hsa-miR-664-5p	2.55	4.12	1.62E-14	4.19E-13	4.61	26.97
hsa-miR-3622a-5p	3.63	1.02	4.44E-14	1.09E-12	0.27	3.20
hsa-miR-4420	-3.99	2.35	2.22E-13	5.22E-12	10.97	0.66
hsa-miR-377-5p	-3.44	1.75	1.75E-12	3.93E-11	6.65	0.58
hsa-miR-29b-3p	2.57	9.29	9.31E-12	2.01E-10	164.06	976.85
hsa-miR-19a-3p	-2.73	10.01	1.07E-11	2.20E-10	1987.69	300.17

Table is sorted by FDR. logFC indicates log fold change; logCPM, log counts per million, FDR, false discovery rate

miRNA	**logFC**	**logCPM**	**p-value**	**FDR**	**cpm FL**	**cpm DLBCL**
hsa-miR-200c-3p	-3.89	7.26	8.36E-11	4.16E-08	20.77	307.99
hsa-miR-424-3p	-2.12	3.98	2.60E-10	6.48E-08	6.16	26.89
hsa-miR-147b	-3.41	2.08	2.76E-09	4.58E-07	0.76	8.11
hsa-miR-3622a-5p	2.65	0.84	9.35E-09	7.76E-07	2.75	0.42
hsa-miR-4517	-2.34	0.64	7.56E-09	7.76E-07	0.52	2.64
hsa-miR-503	-1.81	1.81	8.73E-09	7.76E-07	1.60	5.53
hsa-miR-486-3p	2.64	5.25	1.34E-08	9.55E-07	62.03	9.95
hsa-miR-148a-5p	-2.64	9.30	3.26E-08	2.03E-06	184.70	1148.17
hsa-miR-378a-3p	-1.48	9.55	4.12E-08	2.28E-06	411.38	1146.34
hsa-miR-18a-3p	-1.80	3.84	5.79E-07	2.62E-05	6.62	23.09
hsa-miR-4449	-2.68	2.42	5.26E-07	2.62E-05	1.53	9.72
hsa-miR-92a-1-5p	-2.22	3.99	6.35E-07	2.64E-05	5.93	27.53
hsa-miR-129-2-3p	-4.30	3.72	9.54E-07	3.45E-05	1.34	26.66
hsa-miR-3653	2.93	4.98	9.69E-07	3.45E-05	52.34	6.81
hsa-miR-19a-5p	-2.09	2.71	1.97E-06	6.13E-05	2.59	11.04
hsa-miR-29b-3p	1.69	9.11	1.86E-06	6.13E-05	809.33	250.37
hsa-miR-4464	3.47	2.53	3.12E-06	9.13E-05	9.73	0.87
hsa-miR-450b-5p	-1.52	4.12	3.76E-06	1.04E-04	9.28	26.54
hsa-miR-18a-5p	-1.65	5.78	3.97E-06	1.04E-04	27.74	86.86
hsa-miR-29a-3p	1.62	13.09	4.69E-06	1.16E-04	12651.18	4113.90
hsa-miR-431-5p	-1.83	1.21	4.88E-06	1.16E-04	1.00	3.62
hsa-miR-944	-2.57	5.67	5.93E-06	1.34E-04	15.53	92.18
hsa-miR-150-5p	1.90	12.79	6.55E-06	1.39E-04	10730.09	2878.09
hsa-miR-20a-5p	-1.93	10.01	6.70E-06	1.39E-04	449.16	1706.57
hsa-miR-7-5p	-2.22	7.18	8.53E-06	1.70E-04	53.95	251.76

Table is sorted by FDR. logFC indicates log fold change; logCPM, log counts per million, FDR, false discovery rate

Supplementary Table 5: Differentially regulated genes targeted by hsa-miR-143

gene	p-value	pears. corr.	gene	p-value	pears. corr.	gene	p-value	pears. corr.
AMFR	0.0001	-0.56	USP22	0.0090	-0.38	DCUN1D1	0.0281	-0.32
FOXO1	0.0001	-0.54	PAG1	0.0094	-0.38	RBBP6	0.0294	-0.32
SMARCD2	0.0001	-0.54	FAM104A	0.0096	-0.38	GFER	0.0297	-0.32
IFT52	0.0001	-0.53	ZMYM2	0.0097	-0.38	PKN2	0.0300	-0.32
POLDIP3	0.0002	-0.53	CDK17	0.0098	-0.38	G2E3	0.0308	-0.32
CTDSPL2	0.0002	-0.53	PPM1A	0.0102	-0.37	PRKAB1	0.0318	-0.31
PEX5	0.0002	-0.52	LRBA	0.0102	-0.37	WDTC1	0.0320	-0.31
ASIC2	0.0002	-0.52	FOXJ3	0.0104	-0.37	SLU7	0.0321	-0.31
GGA2	0.0002	-0.52	UBXN1	0.0109	-0.37	RICTOR	0.0321	-0.31
GNA13	0.0003	-0.52	RNF8	0.0110	-0.37	POU2F1	0.0334	-0.31
KDM3B	0.0003	-0.51	PHF6	0.0112	-0.37	MGA	0.0336	-0.31
PSIP1	0.0003	-0.51	PRKD2	0.0113	-0.37	PCBP2	0.0339	-0.31
CAMK2D	0.0003	-0.51	WBP11	0.0114	-0.37	GPBP1	0.0341	-0.31
KDM3A	0.0004	-0.50	PHTF2	0.0119	-0.37	PAPOLB	0.0346	-0.31
CCDC94	0.0004	-0.50	GGNBP2	0.0123	-0.36	JARID2.AS1	0.0349	-0.31
CUL3	0.0004	-0.50	MARK2	0.0128	-0.36	MTPN	0.0360	-0.31
GCNT7	0.0005	-0.49	C12orf49	0.0137	-0.36	PUM2	0.0361	-0.31
RC3H2	0.0006	-0.48	UBE2E1	0.0137	-0.36	APC	0.0362	-0.31
CBFB	0.0006	-0.48	MIER3	0.0138	-0.36	TOE1	0.0371	-0.31
POLR2G	0.0010	-0.47	VCPIP1	0.0139	-0.36	RCOR1	0.0372	-0.31
KIAA1432	0.0010	-0.47	DHX40	0.0141	-0.36	KMT2E	0.0376	-0.30
NUDT16L1	0.0013	-0.46	MED1	0.0144	-0.36	DENND1B	0.0379	-0.30
AFF2	0.0015	-0.46	CRLF3	0.0148	-0.35	COMMD4	0.0386	-0.30
MED26	0.0015	-0.45	GCNT2	0.0148	-0.35	OXCT1.AS1	0.0392	-0.30
PSPC1	0.0018	-0.45	POM121C	0.0151	-0.35	MDC1	0.0396	-0.30
RAD17	0.0019	-0.45	RNF6	0.0151	-0.35	DMXL1	0.0405	-0.30
ACTR3	0.0020	-0.44	RBM22	0.0157	-0.35	MAPRE2	0.0407	-0.30
MYO1E	0.0020	-0.44	CHD6	0.0163	-0.35	CEP192	0.0409	-0.30
USP24	0.0021	-0.44	UBP1	0.0163	-0.35	POM121	0.0409	-0.30
PHF3	0.0021	-0.44	TXLNB	0.0168	-0.35	CLCN3	0.0414	-0.30
CALM3	0.0021	-0.44	SCAF8	0.0170	-0.35	NECAP1	0.0419	-0.30
CHMP1A	0.0022	-0.44	IRAK1BP1	0.0175	-0.35	MTMR4	0.0421	-0.30
STK16	0.0027	-0.43	RASGEF1B	0.0178	-0.35	DIAPH1	0.0422	-0.30
BARD1	0.0027	-0.43	WIPF1	0.0182	-0.34	KIAA1033	0.0429	-0.30
LANCL1	0.0027	-0.43	RRM2B	0.0188	-0.34	ZCCHC11	0.0432	-0.30
HELZ	0.0027	-0.43	MBOAT2	0.0191	-0.34	BCL10	0.0435	-0.30
TNKS2	0.0029	-0.43	SUPT4H1	0.0193	-0.34	HNRNPU	0.0438	-0.30
RBM27	0.0030	-0.43	SUZ12	0.0196	-0.34	JAKMIP2	0.0440	-0.30
MAP4K1	0.0033	-0.42	CDC27	0.0198	-0.34	KIF3A	0.0441	-0.30
DDX42	0.0033	-0.42	BRD2	0.0204	-0.34	GPCPD1	0.0444	-0.30
TSPAN13	0.0038	-0.42	HDAC7	0.0206	-0.34	INO80D	0.0455	-0.29
PRKCE	0.0042	-0.41	GMEB1	0.0208	-0.34	OSBPL9	0.0455	-0.29
URM1	0.0043	-0.41	NIN	0.0209	-0.34	UBE3C	0.0457	-0.29
LNPEP	0.0043	-0.41	ACAP2	0.0228	-0.33	HMGCR	0.0471	-0.29
CDK13	0.0044	-0.41	MLLT10	0.0236	-0.33	CIAPIN1	0.0472	-0.29
EIF2AK3	0.0045	-0.41	RNF169	0.0241	-0.33	RABEP1	0.0482	-0.29
C16orf80	0.0045	-0.41	YWHAZ	0.0247	-0.33	YPEL5	0.0490	-0.29
BPTF	0.0048	-0.41	ARFGEF2	0.0249	-0.33	OARD1	0.0015	-0.46
ZNF800	0.0052	-0.40	SLC15A4	0.0249	-0.33	PATZ1	0.0039	-0.42
VHL	0.0057	-0.40	KIAA0430	0.0250	-0.33	UBE2D3	0.0078	-0.39
PAN3	0.0059	-0.40	OPA1	0.0250	-0.33	PPM1D	0.0110	-0.37
LIMK1	0.0065	-0.39	OPA1.AS1	0.0254	-0.33	NEK6	0.0119	-0.37
C12orf76	0.0067	-0.39	ATG2B	0.0259	-0.33	SF1	0.0143	-0.36
KLF12	0.0070	-0.39	APAF1	0.0263	-0.32	FBXO46	0.0185	-0.34
ZNF318	0.0072	-0.39	SOX5	0.0263	-0.32	PACS1	0.0200	-0.34
PPP2R2A	0.0079	-0.38	DCP2	0.0264	-0.32	GOLGA4	0.0263	-0.33
UPF1	0.0079	-0.38	MUL1	0.0270	-0.32	JOSD1	0.0409	-0.30
GMFB	0.0084	-0.38	ZNF451	0.0273	-0.32	SF3B1	0.0427	-0.30
UBE2R2	0.0086	-0.38	CYFIP2	0.0277	-0.32	KCMF1	0.0448	-0.29
FAM134A	0.0088	-0.38	ZNF543	0.0278	-0.32	EBF1	0.0467	-0.29
GNB1	0.0089	-0.38	KAT7	0.0279	-0.32	NUDT17	0.0498	-0.29
SEPT9	0.0089	-0.38	TMPO.AS1	0.0280	-0.32	SSH2	0.0500	-0.29

Table is sorted by p-value. Pears. corr. indicates pearson correlation

Supplementary Table 6: Genes associated with the GO term “ubiquitin-protein transferase activity” targeted by hsa-miR-143

gene symbol	full name
AMFR	autocrine motility factor receptor
BARD1	brca1 associated ring domain 1
CUL3	cullin 3
G2E3	g2/m-phase specific e3 ubiquitin protein ligase
MUL1	mitochondrial e3 ubiquitin protein ligase 1
RBBP6	retinoblastoma binding protein 6
RC3H2	ring finger and ccch-type domains 2
RNF6	ring finger protein (c3h2c3 type) 6]
RNF8	ring finger protein 8
UBE2D3	ubiquitin-conjugating enzyme e2d 3
UBE2E1	ubiquitin-conjugating enzyme e2e 1
UBE2R2	ubiquitin-conjugating enzyme e2r 2
UBE3C	ubiquitin protein ligase e3c
VHL	von hippel-lindau tumor suppressor

Supplementary Table 7: Gene Ontology (GO) terms associated with the 186 predicted hsa-miR-143/mRNA target pairs

GO Term	Description	P-value	FDR q-value	Enrichment
GO:0005515	protein binding	1.34E-09	0.0000054	1.49
GO:0005488	binding	5.47E-08	0.00011	1.25
GO:1901363	heterocyclic compound binding	5.49E-08	0.0000739	1.62
GO:0097159	organic cyclic compound binding	0.000000103	0.000103	1.6
GO:0019899	enzyme binding	0.000000338	0.000273	2.6
GO:0004842	ubiquitin-protein transferase activity	0.00000042	0.000283	5.33
GO:0003676	nucleic acid binding	0.00000276	0.00159	1.71
GO:0008270	zinc ion binding	0.00000548	0.00276	2.47
GO:0016740	transferase activity	0.00000885	0.00397	2.03
GO:0003682	chromatin binding	0.00000913	0.00368	3.85
GO:0046914	transition metal ion binding	0.0000093	0.00341	2.27
GO:0003723	RNA binding	0.00000992	0.00334	2.23

Table is sorted by p-value. FDR indicates false discovery rate

Supplementary Table 8: List of all tested, bioinformatically predicted putative novel miRNAs

NB-probe #	**genomic location**	**mature miRNA sequence**
NB-miR-1	chr1:43914204-43914292	CCAGGGCAGAGGGCACAGGAATCT
NB-miR-2	chr20:43272717-43272813	GCAGGGCCGTCTACCTCCAAGGC
NB-miR-3	chr3:156878062-156878153	ACCTTGGGATCCTCAGAGGCTG
NB-miR-4	chr8:27290881-27290962	TTGGCTGGTCTCTGCTCCGCAGG
NB-miR-5	chr10:50035510-50035603	GCACACTGACACAGAGAGAGAGA
NB-miR-6	chr20:43272714-43272812	CAGGGCCGTCTACCTCCAAGGC
NB-miR-7	chr10:75936514-75936605	AAGCAGTTGCTGTGGTACCTGCT
NB-miR-8	chr5:72143946-72144041	AGACGCTGGCGGCCGGGCTGCCA
NB-miR-9	chr1:43914204-43914292	CAGGCCTGTGGCTCCTCCCTCA
NB-miR-10	chr1:32410164-32410309	CCTCCTCAGGCACTAGAGCTTCCC
NB-miR-11	chr20:43272714-43272812	CAAGGCAAACCTAGTCAGATTA
NB-miR-12	chr2:219206629-219206714	GTCCCCTGCTCCCTTGTTCCCCAGTC
NB-miR-13	chr17:73008757-73008842	CGCAAGACCTGAGCATGGCGGCCA
NB-miR-14	chr17:73008757-73008842	CTGCGCTGGGGCCTGAGCCGAGC
NB-miR-15	chrX:118533303-118533392	CCGGAGAGCCCCAGGCCCGAGCC
NB-miR-16	chr11:64863680-64863778	GCCGGGCCTAGCCCGGGGTCTGGAC
NB-miR-17	chr15:45003719-45003814	AGCATTCGGGCCGAGATGTCTCG
NB-miR-18	chrM:3363-3463	GTAGGCCCCTACGGGCTACTACAACCCT
NB-miR-19	chrM:3363-3463	CCAACGTTGTAGGCCCCTACGGGCTACT
NB-miR-20	chr12:52453530-52453613	TCACTGCAGGGCCCTAGCAATA

MiRNAs, which could be validated by Northern blotting (NB), are shaded in grey.

NB-probe indicates Northern blot probe number

Supplementary Table 9: Genes having both a novel-miR-1 seed sequence and being differentially expressed upon novel-miR-1 overexpression

Gene	logFC	logCPM	p-value	FDR	cpm control	cpm sample	miranda score	miranda mfe
ACAD9	-0.69	5.58	0.000	0.009	53.07	33.47	147	-17.42
ACO2	-0.33	7.52	0.000	0.027	198.07	157.34	161	-21.91
ADAM15	-0.48	6.60	0.000	0.010	106.53	76.07	283	-32.58
ATP13A2	-0.76	5.01	0.000	0.018	35.12	21.10	146	-22.28
CARD11	-0.37	7.72	0.000	0.010	231.27	180.22	148	-19.67
CBS	-0.50	6.09	0.000	0.020	74.65	52.48	151	-19.54
CD247	-0.82	4.49	0.001	0.029	24.92	13.78	140	-15.55
CDC45	-0.68	5.51	0.000	0.018	49.98	31.47	153	-18.18
CDCA7	-0.48	7.45	0.000	0.008	195.33	140.63	307	-39.83
CDK5	-1.00	4.31	0.000	0.014	21.59	10.70	140	-17.99
CENPM	-0.88	5.20	0.000	0.001	41.45	22.40	155	-21.74
CRELD2	-0.73	4.76	0.001	0.035	29.31	17.61	142	-16.61
CSRP1	-0.42	6.87	0.000	0.018	128.02	95.57	146	-19.12
DPP9	-0.38	6.87	0.001	0.032	126.46	97.44	144	-13.36
E2F1	-0.46	6.46	0.001	0.036	96.27	69.60	140	-14.74
ESYT1	-0.43	7.12	0.000	0.024	152.89	113.37	280	-28.46
FANCI	-0.41	7.03	0.001	0.045	143.14	107.43	145	-19.25
FLNA	-0.57	7.36	0.000	0.003	186.09	125.86	295	-32.3
FOXRED1	-0.63	5.17	0.001	0.041	39.02	25.26	157	-22.06
GPI	-0.26	8.75	0.000	0.016	462.17	386.51	296	-33.43
HARS	-0.43	6.75	0.001	0.048	117.46	87.61	437	-56.1
INTS9	-0.47	6.24	0.001	0.034	82.03	59.23	142	-17.5
L3MBTL2	-0.39	6.71	0.001	0.042	113.73	86.22	140	-11.98
LIG1	-0.87	5.87	0.000	0.000	66.88	36.50	144	-16.17
MAP4K2	-0.51	6.85	0.000	0.007	128.85	89.72	142	-20.71
MCM2	-0.44	7.65	0.000	0.003	223.62	164.75	148	-14.39
MCM5	-0.36	7.91	0.000	0.021	263.56	205.13	570	-71.59
MCM7	-0.33	9.03	0.000	0.010	576.37	458.35	154	-19.12
MFSD10	-0.57	5.65	0.001	0.032	55.28	37.16	143	-25.1
MTCH1	-0.37	6.90	0.001	0.041	129.75	99.97	142	-14.45
MTHFD1	-0.41	6.68	0.001	0.041	111.64	84.08	141	-17.47
MYBL2	-0.36	8.74	0.000	0.002	473.51	368.08	291	-34.06
NADSYN1	-0.65	5.81	0.000	0.007	62.86	39.31	286	-45.36
NOC4L	-0.61	5.24	0.001	0.047	40.71	26.52	145	-14.16
PITRM1	-0.46	6.42	0.001	0.032	93.34	68.13	291	-36.51
PRR12	-0.60	5.28	0.001	0.043	42.32	27.81	146	-13.65
RPL39	-1.77	4.34	0.000	0.000	24.71	7.10	140	-13.57
RPUSD1	-0.47	6.83	0.000	0.010	125.30	90.46	159	-19.81
RRP1	-0.43	6.68	0.000	0.016	112.01	82.57	301	-36.12
SAAL1	-0.74	5.59	0.000	0.003	53.88	32.58	146	-18.87
SAPCD2	-0.44	7.13	0.000	0.005	154.08	113.73	154	-20.51
SCRIB	-0.55	6.53	0.000	0.003	103.40	70.23	141	-16.73
SFI1	-0.65	5.17	0.000	0.029	39.59	25.02	445	-55.66
SLCO4A1	-0.64	5.07	0.001	0.044	36.08	23.03	302	-47.44
SNRNP25	-0.35	7.18	0.000	0.024	156.64	123.29	142	-16.19
SNRPE	-0.56	5.99	0.000	0.012	70.28	47.46	148	-22.87
SPRED2	-0.44	6.33	0.001	0.040	87.49	63.98	281	-33.66
SREBF1	-0.60	6.51	0.000	0.001	103.24	67.76	146	-14.89
SSBP4	-0.66	5.38	0.000	0.013	45.83	28.71	140	-14.51
TBC1D1	-0.35	7.69	0.000	0.007	226.41	176.95	432	-48.79
TBCD	-0.56	5.64	0.001	0.033	54.23	37.35	304	-44.06
THOP1	-0.39	7.46	0.000	0.029	192.49	147.18	300	-42.01
VARS2	-0.67	5.64	0.000	0.019	55.89	35.37	148	-31.45
WDHD1	-0.51	6.05	0.001	0.039	71.81	50.77	140	-12.31
ZC3H18	-0.49	6.74	0.000	0.020	117.70	84.36	142	-11.29

Genes are listed in alphabetical order. logFC indicates log fold change; logCPM, log counts per million; FDR, false discovery rate; mfe, minimal free energy

Supplementary Table 10: Canonical miRNA-mRNA in BL and DLBCL/FL

Data from SU-DHL-4 / SU-DHL-6

CCR	miRNA	miRNA logFC	miRNA DE FDR	miRNA cpm BL	miRNA cpm nonBL	CCR Sequence	Seed Hit	Position Found in CCR	Read Count in Cluster	GeneID	Genes logFC	Genes DEG FDR	CPM control	CPM sample	FC corr.
cl_10083_chr4	hsa-miR-4446-3p	2.41	0.000000	0.69	3.74	GAAATCACACTCATATATAATCCAAGGCCAGCCCTGTGGTT	AGCCCTG	30	12	SORBS2	-1.13	0.00001	18.37	8.37	-2.74
cl_10803_chr5	hsa-miR-27a-3p	0.86	0.011903	616.77	1122.55	TCCATGTGTATTTTCTTATATACTGTGAATGTGAAAACCTA	CTGTGAA	23	14	TNPO1	-0.36	0.00399	102.67	80.04	-0.31
cl_1089_chr1	hsa-miR-3681-5p	5.07	0.000000	1.82	61.30	TTTAGGAGATAAGGTTCCACTAGAAGTAGGTAGTATACCCC	TCCACTA	16	19	SCMH1	-0.70	0.00002	48.40	29.74	-3.56
cl_11199_chr5	hsa-miR-455-3p	1.26	0.000225	16.17	38.86	ATTGCTCTCCAAGAGAAAGATGTGGATGGCCTGGACTGCAC	GGACTGC	33	14	CCDC112	-0.89	0.00000	17.86	9.64	-1.12
cl_11349_chr5	hsa-miR-3661	-1.44	0.000180	7.00	2.53	GGCAGCCAGCTATGTTCAGGTCACATCCAACTTCCTCTATG	CAGGTCA	17	6	AFF4	0.58	0.00021	52.36	78.41	-0.84
cl_11384_chr5	hsa-miR-33a-5p	-1.93	0.000079	145.43	38.10	CCCTTGTGGAATGCACCATCTGGAGAGAGAGAGGAATGTGG	AATGCAC	10	10	PHF15	1.05	0.00000	54.41	112.96	-2.03
cl_11384_chr5	hsa-miR-33b-5p	-1.74	0.000004	19.73	5.83	CCCTTGTGGAATGCACCATCTGGAGAGAGAGAGGAATGTGG	AATGCAC	10	10	PHF15	1.05	0.00000	54.41	112.96	-1.84
cl_11423_chr5	hsa-miR-2467-5p	1.46	0.003890	3.95	10.85	CAGCAGCTGCAGCCTCAAAATTTTTAACAATCAGGAGTTTG	AGCCTCA	11	10	SMAD5	-0.48	0.00249	51.53	36.95	-0.70
cl_11451_chr5	hsa-miR-214-5p	0.92	0.023829	10.48	19.83	ACAGGCATCCTTCTTCAACCTAACTGTGAAGGAGATGGTAA	ACAGGCA	1	14	KIF20A	-1.76	0.00000	82.14	24.21	-1.62
cl_11451_chr5	hsa-miR-27a-3p	0.86	0.011903	616.77	1122.55	ACAGGCATCCTTCTTCAACCTAACTGTGAAGGAGATGGTAA	CTGTGAA	24	14	KIF20A	-1.76	0.00000	82.14	24.21	-1.52
cl_11583_chr5	hsa-miR-130b-5p	-2.01	0.000006	211.10	52.39	AAAAGAAAAAGAGTAACACGTTGCAGGAATAAAAGCAGCCT	AAAGAGT	8	14	ARHGAP26	0.64	0.00096	16.21	25.32	-1.29
cl_1163_chr1	hsa-miR-4524a-3p	1.13	0.047890	0.62	1.40	TTGTCAGCAGCCACGACCCTTTGGTGTACCTGTCTCAGTTG	TGTCTCA	31	9	RNF220	-0.30	0.02242	86.03	70.02	-0.33
cl_11746_chr5	hsa-miR-99b-5p	1.08	0.019368	8109.71	17128.59	TCAAGGATGCTGAAACTGCTTTAAACGGGTGGGGTCCAGGG	ACGGGTG	25	81	KIF4B	-1.02	0.00139	22.36	11.04	-1.10
cl_11748_chr5	hsa-miR-24-3p	2.33	0.000001	117.91	594.79	TATTTTGAGCCAGATAATTCTTTGGGGGGTAGAGGTGACCT	TGAGCCA	6	8	KIF4B	-1.02	0.00139	22.36	11.04	-2.38
cl_11790_chr5	hsa-miR-29b-2-5p	1.86	0.000000	1.75	6.53	AATCCAAAATCAAACCTATCTAAACTCCCAAACCAGAAGCT	AAACCAG	30	12	PWWP2A	-0.27	0.03529	40.32	33.42	-0.50
cl_1196_chr1	hsa-miR-361-5p	0.91	0.009573	96.05	180.08	CTGATAAAACTCCTTTGACCTGACGATTGCTCTAAGTCCTA	CTGATAA	1	16	NASP	-1.68	0.00000	285.20	89.21	-1.52
cl_12055_chr5	hsa-miR-125a-3p	1.45	0.000079	1.91	5.30	GCAAATGATGATTACCTCTCTACCCTCCCACCTGTGCTGCC	CACCTGT	29	23	RMND5B	-0.60	0.00002	70.50	46.35	-0.88
cl_12055_chr5	hsa-let-7d-5p	0.97	0.003359	541.68	1061.17	GCAAATGATGATTACCTCTCTACCCTCCCACCTGTGCTGCC	TACCTCT	13	23	RMND5B	-0.60	0.00002	70.50	46.35	-0.59
cl_12127_chr5	hsa-miR-17-3p	-2.96	0.000000	2176.96	279.17	ATTTAAATGACATCACTGCTTCTGGGAACTGCAGTGGATGG	CTGCAGT	29	26	FLT4	1.78	0.00000	4.94	17.02	-5.28
cl_12324_chr6	hsa-miR-374b-5p	2.84	0.000010	34.89	250.55	CCTTCATACATAATTCATTATATGGGCCAGGAACCAACAGG	ATTATAT	17	7	NOL7	-0.56	0.00014	118.94	80.91	-1.58
cl_12335_chr6	hsa-miR-4517	-1.60	0.000287	5.06	1.68	GGAGTCTGTCACGGGCCAGCTGGGGGCATTCATATTTCCCA	CATATTT	31	18	CD83	2.00	0.00000	56.81	226.92	-3.20
cl_12388_chr6	hsa-miR-17-5p	-1.37	0.000088	1233.06	477.71	TCTCACTTTGTTGCCCACGCTGATGTTGAACTTGACGTGAG	CACTTTG	4	14	TPMT	0.56	0.00064	6.09	8.97	-0.77
cl_12388_chr6	hsa-miR-20b-5p	-1.12	0.042021	59.74	27.49	TCTCACTTTGTTGCCCACGCTGATGTTGAACTTGACGTGAG	CACTTTG	4	14	TPMT	0.56	0.00064	6.09	8.97	-0.63
cl_12388_chr6	hsa-miR-3609	-2.85	0.000000	596.50	83.01	TCTCACTTTGTTGCCCACGCTGATGTTGAACTTGACGTGAG	CACTTTG	4	14	TPMT	0.56	0.00064	6.09	8.97	-1.59
cl_12388_chr6	hsa-miR-93-5p	-1.06	0.001859	2255.60	1081.01	TCTCACTTTGTTGCCCACGCTGATGTTGAACTTGACGTGAG	CACTTTG	4	14	TPMT	0.56	0.00064	6.09	8.97	-0.59
cl_12642_chr6	hsa-miR-573	-2.99	0.000000	3.34	0.42	TGGGTGAAGTGACTTCAGTAATAACAATAATGTCAAATATC	ACTTCAG	12	43	NOTCH4	0.66	0.00658	7.87	12.42	-1.97
cl_12687_chr6	hsa-miR-139-3p	1.51	0.004679	2.42	6.94	GAGGGTCTCCAAGGTCTGGATGACGAGGCCCACGTTGTCCT	GTCTCCA	5	17	ITPR3	-0.46	0.00832	180.31	131.23	-0.69
cl_12723_chr6	hsa-miR-625-5p	-1.31	0.000026	20.75	8.38	GGCCCCGGCGGGGCGCCCCCTCCCCTCCCCCTCCTGCGAGC	TCCCCCT	26	10	SCUBE3	0.72	0.00203	1.97	3.26	-0.95
cl_12779_chr6	hsa-miR-625-5p	-1.31	0.000026	20.75	8.38	GCGCCCGCCCGCGCGCCCGCTCCTTCCCCCTCCCCCCGCCC	TCCCCCT	25	11	ZFAND3	0.78	0.00000	28.68	49.26	-1.02

cl_13184_chr6	hsa-miR-449a	-1.36	0.000063	5.99	2.35	AATCTAATTCTACAGTCCGATGATGTTACTGCCATCTCCTC	ACTGCCA	28	3145659	RWDD2A	0.81	0.00000	2.64	4.61	-1.10
cl_13407_chr6	hsa-miR-369-3p	-1.14	0.016758	3.61	1.65	TTATTATTTTAATATAGATCTGTAACTTCGGTTCCAAGTAC	TATTATT	2	8	FIG4	0.66	0.00006	22.55	35.61	-0.75
cl_13514_chr6	hsa-miR-148a-5p	1.68	0.005075	216.10	693.70	AGTACTCTCGTGAAGGAACTTTACAGGTGTCATTAAGGTTA	GAACTTT	16	12	HSF2	-0.77	0.00000	19.71	11.59	-1.29
cl_13514_chr6	hsa-miR-425-5p	1.28	0.007710	562.69	1362.90	AGTACTCTCGTGAAGGAACTTTACAGGTGTCATTAAGGTTA	TGTCATT	28	12	HSF2	-0.77	0.00000	19.71	11.59	-0.98
cl_13573_chr6	hsa-miR-19a-5p	-1.78	0.000041	24.62	7.20	GAACAAAACTCCAGGAAAATTGTTCGCTGGGTGAGCTGGTG	CAAAACT	4	5	ARHGAP18	0.89	0.00009	12.49	23.08	-1.58
cl_13573_chr6	hsa-miR-19b-1-5p	-1.98	0.000000	4.46	1.18	GAACAAAACTCCAGGAAAATTGTTCGCTGGGTGAGCTGGTG	CAAAACT	4	5	ARHGAP18	0.89	0.00009	12.49	23.08	-1.76
cl_13615_chr6	hsa-miR-9-5p	2.02	0.000177	22.16	90.19	ACCAAAGAGAGTAATAGCCTTTGCTATTGAAATATCTACAG	CCAAAGA	2	9	TBPL1	-0.61	0.00005	26.57	17.40	-1.23
cl_13725_chr6	hsa-miR-3613-3p	-0.59	0.049047	4.41	2.92	TTTTTCTTTTTTGTACAGTCTGACCATCTTTGCCTTTTAGT	TTTTTGT	8	31	STX11	1.23	0.00011	5.29	12.38	-0.73
cl_13739_chr6	hsa-miR-4797-3p	-2.18	0.000008	4.00	0.85	TGGTTGAAAAGCCGGAGGACTGAGATAAATTGGTGCCATGT	ACTGAGA	19	743	UTRN	1.37	0.00000	47.31	121.93	-2.98
cl_13766_chr6	hsa-miR-577	-1.72	0.000050	660.86	200.99	ATTTATACCCTATCTCAGTCTGGAACACTTATCTAAGACCA	TTATCTA	29	5	STXBP5	0.44	0.00895	17.73	24.09	-0.76
cl_13905_chr6	hsa-miR-181a-3p	-0.96	0.000287	612.96	314.69	CCGACCAGGTTACAGTCCGATGGTCATAATCCAGATGAGAG	CGATGGT	18	19	DYNLT1	0.39	0.00974	10.64	13.91	-0.37
cl_14112_chr7	hsa-miR-188-5p	0.79	0.036509	3.15	5.40	TTCACTATGTAGGTAAGGGATGCAAAATTTCACGGGAAATT	AGGGATG	16	5	PRKAR1B	-0.74	0.00014	51.78	31.08	-0.58
cl_14160_chr7	hsa-miR-199a-5p	1.59	0.000007	181.97	548.37	AGCGGAGGCTGTTCTGTTTCTTACACTGGGACTGAGACACG	CACTGGG	24	273	MAD1L1	-1.14	0.00000	95.37	43.34	-1.81
cl_14194_chr7	hsa-miR-181a-2-3p	-1.19	0.000679	227.17	99.88	CAGATATTTATGCCATCCAGTGGTTGCACTCAGATAAAAAT	CAGTGGT	18	7	SDK1	0.68	0.03704	10.53	16.82	-0.80
cl_1421_chr1	hsa-miR-4487	-1.24	0.005006	1.62	0.68	GTAATGGCTTCATTCAGCTCTGGATCTGTTCCTATGATTCC	CAGCTCT	15	16	CACHD1	0.92	0.00433	2.30	4.34	-1.14
cl_1421_chr1	hsa-miR-376a-3p	-2.14	0.000001	3.89	0.86	GTAATGGCTTCATTCAGCTCTGGATCTGTTCCTATGATTCC	CTATGAT	32	16	CACHD1	0.92	0.00433	2.30	4.34	-1.97
cl_14245_chr7	hsa-miR-92b-5p	0.98	0.008992	0.54	1.12	TCCTCAGAACCTCCACGCCTTCCTCATCTCCGTCCCTGGCA	CGTCCCT	31	23	FBXL18	-0.68	0.00001	16.68	10.39	-0.67
cl_14245_chr7	hsa-miR-5091	1.47	0.006360	2.44	6.77	TCCTCAGAACCTCCACGCCTTCCTCATCTCCGTCCCTGGCA	TCTCCGT	27	23	FBXL18	-0.68	0.00001	16.68	10.39	-1.00
cl_14298_chr7	hsa-miR-625-3p	-0.95	0.012667	40.61	21.02	AAACTATAGTCACAAATTAATAAGGTAGCAGTATCGAGTTT	TATAGTC	5	7	ICA1	2.57	0.00000	3.59	21.29	-2.43
cl_14315_chr7	hsa-miR-10b-3p	3.02	0.000000	1.45	11.98	AGAAATCCCCTGTGAATCTGTCAGGTCCTGGGCTTTTTTGG	AATCTGT	15	9	NDUFA4	-0.40	0.00520	42.52	32.28	-1.20
cl_14315_chr7	hsa-miR-659-5p	1.29	0.000787	2.67	6.44	AGAAATCCCCTGTGAATCTGTCAGGTCCTGGGCTTTTTTGG	AGGTCCT	23	9	NDUFA4	-0.40	0.00520	42.52	32.28	-0.51
cl_14315_chr7	hsa-miR-27a-3p	0.86	0.011903	616.77	1122.55	AGAAATCCCCTGTGAATCTGTCAGGTCCTGGGCTTTTTTGG	CTGTGAA	10	9	NDUFA4	-0.40	0.00520	42.52	32.28	-0.34
cl_14458_chr7	hsa-miR-484	-1.26	0.000040	1404.88	587.88	TTACCAAGATTCCTTCAGCCTGACGATCCTGTCTAGCTTTC	AGCCTGA	17	17	OSBPL3	0.62	0.01100	57.76	88.93	-0.78
cl_14708_chr7	hsa-miR-378a-3p	-1.54	0.000000	2405.55	827.87	ATCACTTGAGCCCAGAGGTTTGAGTCCAGTCTGGGCAACAC	GTCCAGT	24	11	CAMK2B	2.59	0.00185	1.99	11.97	-3.99
cl_14708_chr7	hsa-miR-378c	-1.27	0.000000	300.43	124.57	ATCACTTGAGCCCAGAGGTTTGAGTCCAGTCTGGGCAACAC	GTCCAGT	24	11	CAMK2B	2.59	0.00185	1.99	11.97	-3.29
cl_14708_chr7	hsa-miR-378d	-1.10	0.003182	14.73	6.83	ATCACTTGAGCCCAGAGGTTTGAGTCCAGTCTGGGCAACAC	GTCCAGT	24	11	CAMK2B	2.59	0.00185	1.99	11.97	-2.85
cl_14708_chr7	hsa-miR-378i	-2.12	0.000031	7.69	1.78	ATCACTTGAGCCCAGAGGTTTGAGTCCAGTCTGGGCAACAC	GTCCAGT	24	11	CAMK2B	2.59	0.00185	1.99	11.97	-5.50
cl_1475_chr1	hsa-miR-140-3p	0.74	0.009811	2206.05	3679.70	TGCTGTGTCATGCAGTCCGATGATCGGTCCTTGTGGTAAGG	TGTGGTA	32	9	LRRC7	-0.73	0.00000	26.92	16.18	-0.54
cl_15361_chr7	hsa-miR-130b-3p	-2.24	0.000000	701.16	148.59	GGGCACACTCCATTATGCACTGGATTGCAATTCTTAAATGG	TGCACTG	16	7	DOCK4	0.60	0.02029	12.21	18.50	-1.34
cl_15361_chr7	hsa-miR-301a-3p	-0.65	0.023052	241.53	153.73	GGGCACACTCCATTATGCACTGGATTGCAATTCTTAAATGG	TGCACTG	16	7	DOCK4	0.60	0.02029	12.21	18.50	-0.39
cl_15423_chr7	hsa-miR-449a	-1.36	0.000063	5.99	2.35	TCGCACTGCCAGTTTGATTTTTAAGTCAGAATCCTGGCTAT	ACTGCCA	5	24	CADPS2	0.59	0.00610	5.62	8.47	-0.80
cl_15423_chr7	hsa-miR-4755-3p	-1.99	0.000050	2.99	0.74	TCGCACTGCCAGTTTGATTTTTAAGTCAGAATCCTGGCTAT	CCTGGCT	33	24	CADPS2	0.59	0.00610	5.62	8.47	-1.18
cl_15553_chr7	hsa-miR-188-5p	0.79	0.036509	3.15	5.40	GTTTAATTGGCCTTTATCTCTGAGGGATGAGACTTTCCTAT	AGGGATG	23	7	CHCHD3	-0.63	0.00003	1483.24	956.50	-0.50
cl_155_chr1	hsa-miR-138-5p	1.70	0.013928	24.26	78.83	CCTGGAGGACCAGCTCCCGCTGGGGGAGTACGGCCTCAAGC	ACCAGCT	9	40	ISG15	-1.15	0.00040	29.93	13.50	-1.95
cl_155_chr1	hsa-miR-361-3p	1.24	0.003876	615.76	1454.95	CCTGGAGGACCAGCTCCCGCTGGGGGAGTACGGCCTCAAGC	TGGGGGA	21	40	ISG15	-1.15	0.00040	29.93	13.50	-1.42

cl_15608_chr7	hsa-miR-2110	1.05	0.000723	2.94	6.19	ATTCACTCCCCAAATGTCTGTAACTCGACTCCTTGATTTTC	TCCCCAA	7	26	DGKI	-0.68	0.00000	401.20	251.04	-0.71
cl_15639_chr7	hsa-miR-3661	-1.44	0.000180	7.00	2.53	AAGCTAGAGTATGGAAGGGGTAGGATTTGAACACAGGTCAT	CAGGTCA	34	18	TBXAS1	0.77	0.00032	11.42	19.48	-1.11
cl_15664_chr7	hsa-miR-3651	-2.34	0.000028	4.24	0.82	GGGCTATGAAGTGGAGCCTGTGGCTTCGGAAATCACCTTTC	GGCTATG	2	10	KIAA1147	0.90	0.00000	28.55	53.14	-2.10
cl_15708_chr7	hsa-miR-92a-1-5p	-1.14	0.012809	38.34	17.48	GTCCTAAGACCAACCTTTGATCATCTGTGGGCTCATGACTG	CCAACCT	10	6	TPK1	0.65	0.00069	6.02	9.43	-0.74
cl_1588_chr1	hsa-miR-589-3p	-1.73	0.000002	17.95	5.34	GTCCAGGCAAAGTTCTGAACTGGCCCCCCTCGCCCCTCACG	GTTCTGA	12	12	CYR61	0.85	0.03335	29.67	53.46	-1.47
cl_1603_chr1	hsa-miR-101-5p	1.15	0.002105	4.96	11.04	TACTGGCCAGGGTAGACTAATAACTGATGGCATTTATATGC	ATAACTG	20	19	HS2ST1	-0.60	0.00045	127.84	84.23	-0.69
cl_1603_chr1	hsa-miR-10b-5p	1.65	0.000237	64964.70	203496.95	TACTGGCCAGGGTAGACTAATAACTGATGGCATTTATATGC	CAGGGTA	8	19	HS2ST1	-0.60	0.00045	127.84	84.23	-0.99
cl_16404_chr8	hsa-miR-10b-5p	1.65	0.000237	64964.70	203496.95	ACTAGTTGGCAGGGTAAAGGTAATCCATTGTAGCAACTGGG	CAGGGTA	10	28	UNC5D	-0.52	0.00004	24.51	17.11	-0.85
cl_16404_chr8	hsa-miR-708-3p	0.98	0.026809	18.72	36.79	ACTAGTTGGCAGGGTAAAGGTAATCCATTGTAGCAACTGGG	CTAGTTG	2	28	UNC5D	-0.52	0.00004	24.51	17.11	-0.51
cl_16780_chr8	hsa-miR-589-3p	-1.73	0.000002	17.95	5.34	ATCGAGGTTCTGAACAGCGGTGCCAAGGAATCGAGTAATTT	GTTCTGA	7	8	TRAM1	0.47	0.00489	127.90	176.70	-0.81
cl_16903_chr8	hsa-miR-221-5p	1.18	0.015984	188.23	426.85	CTCCCCGCTCCTCCAAAACTTACCTGCCGAAGTGCCAGGTT	GCCAGGT	34	20	LRRCC1	-0.91	0.00000	30.25	16.08	-1.08
cl_17087_chr8	hsa-miR-155-5p	3.25	0.000000	1152.30	10989.11	TTTTGCATTAACAGGAAGATTGGAATGACTTGTGGCTGGAT	GCATTAA	5	37	ZNF706	-0.33	0.02365	66.99	53.22	-1.08
cl_17121_chr8	hsa-miR-127-5p	-1.65	0.000512	10.82	3.43	GTGAAGGTGACTGGCTTCAGTGAAGGTGTGGCAGGTGGTGT	GCTTCAG	14	24	ZFPM2	0.94	0.00126	2.86	5.50	-1.56
cl_17229_chr8	hsa-miR-543	-2.84	0.000000	7.68	1.04	CAAACAATGTTTGACTGGGCTGGTTGCCTAATCAGTGAAGC	AATGTTT	6	13	HAS2	0.93	0.00251	1.83	3.48	-2.63
cl_17378_chr8	hsa-miR-181a-2-3p	-1.19	0.000679	227.17	99.88	GCGGTATAAAGAAACCTCAGTGGTTGTATCAGTCAGCTTTC	CAGTGGT	18	72	ST3GAL1	1.01	0.00000	29.05	58.53	-1.20
cl_17581_chr8	hsa-miR-3194-5p	-1.19	0.004724	6.37	2.74	TGTCCCCCTGCGTGTCCCTCTGCAGCTGGCCCACAGTGGCT	GCTGGCC	25	10	MAPK15	3.94	0.00000	0.34	5.23	-4.70
cl_17581_chr8	hsa-miR-625-5p	-1.31	0.000026	20.75	8.38	TGTCCCCCTGCGTGTCCCTCTGCAGCTGGCCCACAGTGGCT	TCCCCCT	3	10	MAPK15	3.94	0.00000	0.34	5.23	-5.15
cl_17821_chr9	hsa-miR-379-3p	-2.39	0.000004	3.13	0.58	TGTGGAAAGGCACAGACAATTACATATCTGTTGAATGCCTT	TTACATA	20	9	ADAMTSL1	0.62	0.03078	3.02	4.63	-1.47
cl_17852_chr9	hsa-miR-3622a-5p	3.06	0.000010	0.23	1.89	GTGTCAACTGTGCCTGACTGTGTTAGAGAGCTTATTAAAAG	GTGCCTG	10	16	MTAP	-1.49	0.00000	65.56	23.28	-4.57
cl_18032_chr9	hsa-miR-3613-3p	-0.59	0.049047	4.41	2.92	GACTCGGGAGAAGGTCCACCTTTTTGTTCTATGCAGGCCTT	TTTTTGT	21	15	SHB	0.49	0.04647	3.43	4.81	-0.29
cl_18144_chr9	hsa-miR-103a-2-5p	-1.50	0.000002	5.75	2.00	GCAGGACGATCGTGAAAGTCTGATATTGGGAAAGAAGCTCA	AGAAGCT	33	16	PCSK5	0.68	0.04373	3.84	6.17	-1.02
cl_1818_chr1	hsa-miR-15b-3p	-0.95	0.002065	65.01	33.63	AGCAATGTTGTCATGGTTCCTCTATAGTGATTCGTATGAAG	TGATTCG	28	10	NTNG1	1.17	0.02029	2.38	5.34	-1.11
cl_1819_chr1	hsa-miR-296-5p	-1.00	0.001384	13.99	7.04	TATACACAGTGATTAAAGGTTTTGGGGCCCTAATAAATTTC	GGGCCCT	25	5290	NTNG1	1.17	0.02029	2.38	5.34	-1.16
cl_1830_chr1	hsa-miR-4687-5p	-0.90	0.006179	2.46	1.27	TGAGTCTTGAAGCCCAGGGCTGGGCCCGGGCAGAGCCGCCG	AGGGCTG	16	22929	VAV3	1.48	0.00000	12.77	35.63	-1.33
cl_18911_chr9	hsa-miR-130b-3p	-2.24	0.000000	701.16	148.59	GGCCCCTGGGCCTGCACTGATGCACTGGATCAGTGCCCCTC	TGCACTG	21	12	RAPGEF1	0.61	0.00010	179.93	274.39	-1.36
cl_18911_chr9	hsa-miR-301a-3p	-0.65	0.023052	241.53	153.73	GGCCCCTGGGCCTGCACTGATGCACTGGATCAGTGCCCCTC	TGCACTG	21	12	RAPGEF1	0.61	0.00010	179.93	274.39	-0.40
cl_18920_chr9	hsa-miR-1304-3p	-1.38	0.000040	25.27	9.67	GAGGCCCGGGGCCCAGGGAGTGAGACCCTTGCTTCTGACTT	AGTGAGA	19	33	NTNG2	1.18	0.00012	3.25	7.38	-1.64
cl_18923_chr9	hsa-miR-4677-3p	2.36	0.000008	6.84	35.21	AGTTGGTGATCACAGATTTTTCCTCAGGATATCTGTCCGTG	TCACAGA	10	10	TTF1	-0.35	0.01097	22.60	17.68	-0.84
cl_19201_chr10	hsa-miR-188-5p	0.79	0.036509	3.15	5.40	CCAGCCGTTCGCCTCGTTGCTTTTCCAGGGATGTTGTGAGT	AGGGATG	27	8	DIP2C	-2.09	0.00000	64.22	15.09	-1.65
cl_19276_chr10	hsa-miR-155-3p	1.63	0.003876	0.57	1.82	AGGCAGGCAGGACTCAGCGCTGATGGTAGGAGTCAGTGGAG	GTAGGAG	26	6	CALML3	-1.03	0.00496	2.45	1.20	-1.67
cl_19459_chr10	hsa-miR-27a-5p	0.94	0.010984	14.83	28.56	AGGTGTCCTCGCACGAACACTTTAGACCAAGCCCTTCTCTC	AAGCCCT	29	10	CACNB2	-0.93	0.00005	11.79	6.18	-0.88
cl_1958_chr1	hsa-miR-411-5p	-1.33	0.024549	47.59	18.90	AGGATTCCCTTACGCTCTACTATAGCTGTGTTACTGCTGCC	TCTACTA	16	7	IGSF3	2.54	0.00001	2.08	12.10	-3.38
cl_19610_chr10	hsa-miR-103a-2-5p	-1.50	0.000002	5.75	2.00	CACTGCTACTGGAGAAGCTTTGGGGAGCTGGCAAACTCTGA	AGAAGCT	13	33	ARHGAP12	0.65	0.00001	17.42	27.39	-0.98
cl_20300_chr10	hsa-miR-361-3p	1.24	0.003876	615.76	1454.95	GCATGGGGGAAACAGTCCCATGATCCAATCACCTCCCATCA	TGGGGGA	4	20	ALDH18A1	-0.70	0.00001	99.05	60.80	-0.87
cl_20364_chr10	hsa-miR-30a-3p	0.99	0.025009	59.24	117.52	TGGGTAACCACTGAAAGCATTTAAGCAAGAGAGTAACATGA	CTGAAAG	11	12	GOT1	-0.46	0.00157	30.97	22.49	-0.46

cl_20484_chr10	hsa-miR-4687-5p	-0.90	0.006179	2.46	1.27	AAACTTGAGAAGGGCTGTCCTTATCCCCTCATTTCACGCCT	AGGGCTG	11	78	SORCS1	1.58	0.00001	1.61	4.81	-1.42
cl_20541_chr10	hsa-miR-449a	-1.36	0.000063	5.99	2.35	CTTTGTTGGGAAGGTTCCCTTTGCACTGCCATGGAAGGCTG	ACTGCCA	25	15	TCF7L2	0.59	0.00878	6.18	9.27	-0.80
cl_20541_chr10	hsa-miR-3667-3p	-1.36	0.008075	1.56	0.64	CTTTGTTGGGAAGGTTCCCTTTGCACTGCCATGGAAGGCTG	GGAAGGT	9	15	TCF7L2	0.59	0.00878	6.18	9.27	-0.79
cl_20541_chr10	hsa-miR-130b-3p	-2.24	0.000000	701.16	148.59	CTTTGTTGGGAAGGTTCCCTTTGCACTGCCATGGAAGGCTG	TGCACTG	22	15	TCF7L2	0.59	0.00878	6.18	9.27	-1.31
cl_20541_chr10	hsa-miR-301a-3p	-0.65	0.023052	241.53	153.73	CTTTGTTGGGAAGGTTCCCTTTGCACTGCCATGGAAGGCTG	TGCACTG	22	15	TCF7L2	0.59	0.00878	6.18	9.27	-0.38
cl_20754_chr10	hsa-miR-27a-5p	0.94	0.010984	14.83	28.56	AAGCCCTTGCATAACCACTCTGCCCGCTGCCTCCGCTCATC	AAGCCCT	1	5	UROS	-0.35	0.00715	47.26	37.13	-0.33
cl_2096_chr1	hsa-miR-16-5p	1.05	0.011450	5367.05	11108.90	GGTCTCTTGATTCCAGATGCTGCTAGGGGGGAAAAAAAAAC	GCTGCTA	19	14	PIP5K1A	-0.30	0.03879	48.23	39.29	-0.31
cl_2096_chr1	hsa-miR-195-5p	0.98	0.008752	364.88	722.27	GGTCTCTTGATTCCAGATGCTGCTAGGGGGGAAAAAAAAAC	GCTGCTA	19	14	PIP5K1A	-0.30	0.03879	48.23	39.29	-0.29
cl_21098_chr11	hsa-miR-424-5p	-1.81	0.000003	177.32	50.51	TCAGCACCTGCTGATACAACTGAAGCTGCTGATGTGCCCCC	GCTGCTG	25	8	FAM160A2	0.47	0.00159	22.39	31.01	-0.85
cl_21169_chr11	hsa-miR-17-5p	-1.37	0.000088	1233.06	477.71	TCTCCACACTTTGATGTGAATGGAGGTAGGAACCCACAATA	CACTTTG	7	16	SBF2	0.44	0.00246	34.30	46.62	-0.61
cl_21169_chr11	hsa-miR-20b-5p	-1.12	0.042021	59.74	27.49	TCTCCACACTTTGATGTGAATGGAGGTAGGAACCCACAATA	CACTTTG	7	16	SBF2	0.44	0.00246	34.30	46.62	-0.49
cl_21169_chr11	hsa-miR-3609	-2.85	0.000000	596.50	83.01	TCTCCACACTTTGATGTGAATGGAGGTAGGAACCCACAATA	CACTTTG	7	16	SBF2	0.44	0.00246	34.30	46.62	-1.26
cl_21169_chr11	hsa-miR-93-5p	-1.06	0.001859	2255.60	1081.01	TCTCCACACTTTGATGTGAATGGAGGTAGGAACCCACAATA	CACTTTG	7	16	SBF2	0.44	0.00246	34.30	46.62	-0.47
cl_21249_chr11	hsa-miR-3922-3p	1.24	0.017898	0.75	1.82	ATCTCCCAATAAAATTGAGATGGGCCAGACCTGAAACACTT	GGCCAGA	23	5	SOX6	-0.74	0.00000	32.59	19.46	-0.92
cl_22132_chr11	hsa-miR-4755-3p	-1.99	0.000050	2.99	0.74	CAAGGCTGGGGTCGTGGGTTTGAATCCTGGCTTTGAGCTTC	CCTGGCT	26	23	LRRC32	2.50	0.00003	7.58	42.88	-4.97
cl_2246_chr1	hsa-miR-708-5p	1.88	0.000003	14.78	54.47	TGCTGAGGGTAAAGCTCCTTTGACCAGGGGGCAAAAAAAAA	GCTCCTT	14	5	MEF2D	-0.60	0.00036	100.65	66.27	-1.13
cl_22502_chr11	hsa-miR-3648	-1.65	0.002386	7.08	2.27	GGGGCGGGGGAGGTCGCGGCTCGGGTGGTGCCGCCGCACGG	CGCGGCT	15	18	NCAM1	1.32	0.01354	2.60	6.52	-2.18
cl_22662_chr11	hsa-miR-149-5p	-1.00	0.003123	13.82	6.89	TTGAGCCAGAATCTCACTCTTGTCACCCAGGCTGGAGTACA	AGCCAGA	4	12	THY1	0.80	0.01446	45.69	79.40	-0.80
cl_22662_chr11	hsa-miR-1254	-1.46	0.000090	5.06	1.83	TTGAGCCAGAATCTCACTCTTGTCACCCAGGCTGGAGTACA	CCAGGCT	27	12	THY1	0.80	0.01446	45.69	79.40	-1.16
cl_22742_chr11	hsa-miR-181a-2-3p	-1.19	0.000679	227.17	99.88	CAATTATATTTTCTCCTGGGTCTGTAGGTCAGTGGTAATGT	CAGTGGT	30	11	SIAE	0.57	0.00183	14.21	21.07	-0.67
cl_22762_chr11	hsa-miR-204-5p	-1.38	0.014138	67.02	25.73	GGAATTCCCTCCTTGACATCTAATGTAGGTAAGGGAATAAT	AAGGGAA	31	42	FEZ1	2.70	0.00000	3.26	21.14	-3.72
cl_22884_chr11	hsa-miR-4645-3p	0.66	0.038686	3.63	5.68	TGTTCCCCAGTTCTACTGTCTGATGTTCAAATAGCTCAGAA	ACTGTCT	15	5	NCAPD3	-0.62	0.00291	114.08	74.19	-0.41
cl_22884_chr11	hsa-miR-199a-3p	0.65	0.033491	809.01	1268.66	TGTTCCCCAGTTCTACTGTCTGATGTTCAAATAGCTCAGAA	CTACTGT	13	5	NCAPD3	-0.62	0.00291	114.08	74.19	-0.40
cl_22884_chr11	hsa-miR-199b-3p	0.65	0.033410	807.77	1267.49	TGTTCCCCAGTTCTACTGTCTGATGTTCAAATAGCTCAGAA	CTACTGT	13	5	NCAPD3	-0.62	0.00291	114.08	74.19	-0.40
cl_22970_chr12	hsa-let-7d-5p	0.97	0.003359	541.68	1061.17	TCCAGGAATCTCTTAGCAACTACCTCTTAATTAGCAAAAGC	TACCTCT	21	23	EFCAB4B	-0.41	0.00478	38.12	28.59	-0.40
cl_23139_chr12	hsa-miR-296-3p	-1.98	0.000000	6.56	1.66	GAATTGTTTTAACCCTCTGATGCTGAGGCAAGAAGGCTGAG	AACCCTC	11	10	GRIN2B	0.80	0.01029	1.19	2.07	-1.59
cl_23302_chr12	hsa-miR-200c-3p	3.71	0.000013	13.86	181.49	TATCTGCCTAGTACCAGTATTAGTGAGACTGTGGATTTTAT	AGTATTA	16	20	FGD4	-1.20	0.00002	15.56	6.79	-4.44
cl_23302_chr12	hsa-miR-150-3p	3.38	0.000000	3.49	36.47	TATCTGCCTAGTACCAGTATTAGTGAGACTGTGGATTTTAT	GTACCAG	11	20	FGD4	-1.20	0.00002	15.56	6.79	-4.04
cl_23361_chr12	hsa-miR-17-5p	-1.37	0.000088	1233.06	477.71	GTCTTCAAAAAGAATCACACTTTGTAGGGTAAGTTCCGAAC	CACTTTG	18	28	CNTN1	1.42	0.00009	1.68	4.48	-1.94
cl_23361_chr12	hsa-miR-20b-5p	-1.12	0.042021	59.74	27.49	GTCTTCAAAAAGAATCACACTTTGTAGGGTAAGTTCCGAAC	CACTTTG	18	28	CNTN1	1.42	0.00009	1.68	4.48	-1.58
cl_23361_chr12	hsa-miR-3609	-2.85	0.000000	596.50	83.01	GTCTTCAAAAAGAATCACACTTTGTAGGGTAAGTTCCGAAC	CACTTTG	18	28	CNTN1	1.42	0.00009	1.68	4.48	-4.03
cl_23361_chr12	hsa-miR-93-5p	-1.06	0.001859	2255.60	1081.01	GTCTTCAAAAAGAATCACACTTTGTAGGGTAAGTTCCGAAC	CACTTTG	18	28	CNTN1	1.42	0.00009	1.68	4.48	-1.50
cl_23587_chr12	hsa-miR-432-5p	-1.20	0.006297	9.90	4.31	AGTTGAGGTCCAAGAATGCATTGGTACCACGCTTCCAGGGA	TCCAAGA	9	56	SMUG1	0.42	0.00418	17.07	22.84	-0.50
cl_23643_chr12	hsa-miR-766-3p	0.67	0.048792	39.23	62.52	AGCCTGTTTGGGTGCTGGAGTAGCTGGACCCTCTTTGGGGA	CTGGAGT	15	10	NACA	-0.82	0.00000	404.16	229.62	-0.55
cl_23682_chr12	hsa-miR-4420	-2.03	0.000161	9.58	2.34	CAGTGACATGGGCAACCGTTTCTCGAAATTGACACAGCACT	CAGTGAC	1	12	LRIG3	1.17	0.00027	2.88	6.49	-2.38

cl_2370_chr1	hsa-miR-204-5p	-1.38	0.014138	67.02	25.73	ATAATGTACGTAAGGGAAGTTTTTATTAAAATGTCTCTAGA	AAGGGAA	12	5	ATF6	0.35	0.01572	36.99	47.22	-0.49
cl_23786_chr12	hsa-miR-708-3p	0.98	0.026809	18.72	36.79	TGACCAATCGTACTGTCAATTGATGTCCACTAGTTGTTAAT	CTAGTTG	30	126	CCT2	-1.17	0.00000	389.18	172.41	-1.15
cl_23786_chr12	hsa-miR-3681-5p	5.07	0.000000	1.82	61.30	TGACCAATCGTACTGTCAATTGATGTCCACTAGTTGTTAAT	TCCACTA	26	126	CCT2	-1.17	0.00000	389.18	172.41	-5.96
cl_23879_chr12	hsa-miR-3667-3p	-1.36	0.008075	1.56	0.64	CAAGAAATGATCTCCATACGTAGGAAGGTAGTCCTACTGGA	GGAAGGT	23	11	PPFIA2	0.91	0.00697	1.11	2.08	-1.23
cl_24133_chr12	hsa-miR-3691-5p	-1.17	0.000276	7.92	3.54	ATAGTAGATCCACTTGATCATTCCCATTACTCTGAGCTTTT	ATCCACT	8	24	CMKLR1	0.83	0.00790	21.60	38.45	-0.97
cl_24138_chr12	hsa-miR-4999-5p	1.47	0.000026	0.45	1.31	CTCTGTCTTCCTTCTTCCTATAGGTGTTCAGGTACAGCACT	TACAGCA	33	22	SART3	-0.30	0.02347	107.01	86.97	-0.44
cl_24245_chr12	hsa-miR-222-5p	2.42	0.000036	0.56	3.04	ATAGAGGCTGCTTGGAGAGCTGTACTGAGGACTCTGCTAAG	TACTGAG	23	9	DTX1	-1.04	0.00004	254.75	124.22	-2.51
cl_24290_chr12	hsa-miR-204-5p	-1.38	0.014138	67.02	25.73	TATCATTGGTCAAACCCAACTGAAAGCCGGGGTAAGGGAAC	AAGGGAA	34	7	TBX3	1.03	0.00123	1.62	3.31	-1.42
cl_24447_chr12	hsa-miR-431-5p	-1.83	0.000093	8.66	2.42	CCGGGAGGAAGTCTAACCTTTGGGAGACTCCAAGACAGCAG	CAAGACA	31	17	RILPL2	0.84	0.00033	19.01	34.08	-1.54
cl_24447_chr12	hsa-miR-432-5p	-1.20	0.006297	9.90	4.31	CCGGGAGGAAGTCTAACCTTTGGGAGACTCCAAGACAGCAG	TCCAAGA	29	17	RILPL2	0.84	0.00033	19.01	34.08	-1.01
cl_2446_chr1	hsa-miR-27b-5p	-0.99	0.003393	21.19	10.62	GAATGAAGCTCTGTCTCAAAAACAAAAAAAAAGTGTTAATA	AAGCTCT	6	64	GPR161	1.35	0.00762	1.58	4.01	-1.33
cl_24652_chr12	hsa-miR-221-5p	1.18	0.015984	188.23	426.85	ATCAGCCGGCACCTGCCAGGTGAGTGCTGCGCGCGGGGCCT	GCCAGGT	15	21	PGAM5	-1.13	0.00000	66.85	30.46	-1.34
cl_24996_chr13	hsa-miR-548s	1.29	0.011693	0.70	1.77	AGAAATCCACATGTGTGGACTGGCCATTCTTACAGAGGAGA	TGGCCAT	21	14	SUCLA2	-0.62	0.00000	32.98	21.47	-0.80
cl_25135_chr13	hsa-let-7d-5p	0.97	0.003359	541.68	1061.17	TGATTCAGGAAGTCTACCTCTGACGATCTTAGAAACCTGAA	TACCTCT	15	9	PCDH9	-1.94	0.00004	56.58	14.70	-1.89
cl_25977_chr14	hsa-miR-4524a-3p	1.13	0.047890	0.62	1.40	ATTTATACCTCCTTCTAAAGAAGTGTTGTCTCAATATGTTC	TGTCTCA	27	72	SLC35F4	-0.71	0.00000	8.24	5.03	-0.80
cl_26537_chr14	hsa-miR-181a-2-3p	-1.19	0.000679	227.17	99.88	CCGCCCTGACCAGCGCCAAGTGGCCAGCGGGGGCAGTGGTG	CAGTGGT	34	7	BEGAIN	0.82	0.03473	1.68	2.97	-0.97
cl_26537_chr14	hsa-miR-18a-3p	-2.46	0.000000	88.89	16.14	CCGCCCTGACCAGCGCCAAGTGGCCAGCGGGGGCAGTGGTG	GGGCAGT	31	7	BEGAIN	0.82	0.03473	1.68	2.97	-2.02
cl_27023_chr15	hsa-miR-106b-5p	-1.55	0.000000	617.66	211.04	TTTTAATATTGATATGCTTATACACTTACACTTTATGCACA	CACTTTA	29	10	B2M	1.21	0.00000	2723.06	6284.85	-1.87
cl_27540_chr15	hsa-miR-628-5p	1.10	0.000433	4.00	8.61	TTGACAGGGCCTTGACAAACTGGGTCACTGACGTCAGCATG	TCAGCAT	34	13	CHRNB4	-0.60	0.00027	7.68	5.06	-0.66
cl_27846_chr15	hsa-let-7d-5p	0.97	0.003359	541.68	1061.17	CCTGTGAGGAGGGTTACCTCTGTGGAGCCGGTGAAGGCGAT	TACCTCT	15	11	ALDH1A3	-0.69	0.02338	22.21	13.74	-0.67
cl_27858_chr15	hsa-miR-33a-5p	-1.93	0.000079	145.43	38.10	ACAGTGAATGCACTCTTCTCTGCCTGGCCCTGAGAGACACA	AATGCAC	7	26	PCSK6	0.73	0.01602	4.60	7.62	-1.41
cl_27858_chr15	hsa-miR-33b-5p	-1.74	0.000004	19.73	5.83	ACAGTGAATGCACTCTTCTCTGCCTGGCCCTGAGAGACACA	AATGCAC	7	26	PCSK6	0.73	0.01602	4.60	7.62	-1.27
cl_2798_chr1	hsa-miR-103a-2-5p	-1.50	0.000002	5.75	2.00	CAACAGCAGAAGCTTTGATCTGCGGATGAATTGGAGTCCTG	AGAAGCT	8	11	CHI3L1	2.27	0.00065	21.30	102.42	-3.40
cl_2798_chr1	hsa-miR-5695	-1.35	0.003064	1.44	0.54	CAACAGCAGAAGCTTTGATCTGCGGATGAATTGGAGTCCTG	TTGGAGT	31	11	CHI3L1	2.27	0.00065	21.30	102.42	-3.05
cl_27993_chr16	hsa-miR-155-3p	1.63	0.003876	0.57	1.82	GCATAGTCGCTGGCAGGAGATGGGGTGTCGGTAGGAGGGCT	GTAGGAG	31	50	ZNF598	-0.78	0.00000	70.94	41.29	-1.27
cl_2802_chr1	hsa-miR-4487	-1.24	0.005006	1.62	0.68	TCCTGCCAGCTCTGCCTCCTTTTCAACTCTCCACATTTTGT	CAGCTCT	7	19	BTG2	0.75	0.00006	115.17	193.59	-0.93
cl_28215_chr16	hsa-miR-17-3p	-2.96	0.000000	2176.96	279.17	GGCTGCCGCTGAACCCGCCCTGGAGTTCTGCAGTCCGATCA	CTGCAGT	28	6	SNN	0.45	0.04468	32.10	43.77	-1.32
cl_2852_chr1	hsa-miR-361-3p	1.24	0.003876	615.76	1454.95	GCAGCTGGAACATGAAAATCTGGGGGAGGGGGAAGAGAAAT	TGGGGGA	21	8	CDK18	-0.70	0.00226	13.33	8.22	-0.86
cl_28569_chr16	hsa-miR-369-3p	-1.14	0.016758	3.61	1.65	TTCTTAATGTAGAACTTTATTATTATAAACTTCTGTACTAG	TATTATT	18	10	ZNF720	0.28	0.03286	21.81	26.48	-0.32
cl_28989_chr16	hsa-miR-92a-3p	-1.64	0.000068	115704.25	37245.94	GAGGGATAAGCCTGCAATATTGACTTCACCCTACCCTTCCG	TGCAATA	13	16	DPEP2	1.81	0.00000	4.06	14.23	-2.96
cl_29294_chr16	hsa-miR-4746-5p	-0.99	0.005796	10.48	5.29	GAGCCCAGATTTTGAGGAAGTGACGGACCGGTCCCAACTGG	GGACCGG	25	10	IRF8	0.78	0.00037	316.32	542.76	-0.77
cl_2937_chr1	hsa-miR-376a-3p	-2.14	0.000001	3.89	0.86	GAAAGTGTCCTACAGTCCTATGATTAGGTCTCGGTCTTTGG	CTATGAT	18	14	LPGAT1	0.62	0.00033	29.67	45.69	-1.34
cl_2937_chr1	hsa-miR-4523	-1.05	0.028608	2.00	0.93	GAAAGTGTCCTACAGTCCTATGATTAGGTCTCGGTCTTTGG	CTCGGTC	30	14	LPGAT1	0.62	0.00033	29.67	45.69	-0.66
cl_2937_chr1	hsa-miR-3667-5p	-1.09	0.016230	1.50	0.71	GAAAGTGTCCTACAGTCCTATGATTAGGTCTCGGTCTTTGG	GGTCTTT	33	14	LPGAT1	0.62	0.00033	29.67	45.69	-0.68
cl_29449_chr16	hsa-miR-150-3p	3.38	0.000000	3.49	36.47	CAGCCGATTCAAGGCTGATGTACCAGCACCGCAGGGACCCT	GTACCAG	20	9	CPNE7	-1.66	0.00041	11.98	3.79	-5.62

cl_29520_chr17	hsa-miR-4687-5p	-0.90	0.006179	2.46	1.27	CCCCTGCCCCCGCCGCCCCTTCTCCTCCCGGAAGGGCTGGG	AGGGCTG	33	8	WDR81	0.44	0.00288	42.11	57.31	-0.40
cl_29614_chr17	hsa-miR-3940-3p	-0.81	0.023652	4.97	2.86	CTCTGAGGTGGGCTCTGGGGTGGTCGGGCTGGGGGCGGGCT	CGGGCTG	25	384	GP1BA	2.62	0.00000	1.96	12.06	-2.12
cl_29857_chr17	hsa-miR-18a-5p	-1.95	0.000000	240.54	62.15	ATACGTGCACCACCTTACCCTATACGACCTGGAGGCCCGTG	CACCTTA	11	8	SMCR8	0.69	0.00220	10.17	16.39	-1.34
cl_29857_chr17	hsa-miR-18b-5p	-1.77	0.000287	7.70	2.25	ATACGTGCACCACCTTACCCTATACGACCTGGAGGCCCGTG	CACCTTA	11	8	SMCR8	0.69	0.00220	10.17	16.39	-1.22
cl_30161_chr17	hsa-miR-1260a	1.07	0.037052	1.66	3.50	ACATAGCTCTTCGGACCTTGTGGGATGTGCAGGCCAGGAAA	GTGGGAT	20	7	DDX52	-0.33	0.01578	39.68	31.61	-0.35
cl_30192_chr17	hsa-miR-641	-0.72	0.009573	7.16	4.36	AGCCCTCTAGCCACCCGACTTGTCTTTAATGCCTATAAAAT	TGTCTTT	21	77	PLXDC1	1.03	0.00012	7.64	15.58	-0.75
cl_30342_chr17	hsa-miR-378a-3p	-1.54	0.000000	2405.55	827.87	ATTTCACCAGGGTGACAGTCTGACGATCAGTCCAGTTCTCC	GTCCAGT	30	6	RUNDC3A	1.70	0.00207	0.82	2.67	-2.62
cl_30342_chr17	hsa-miR-378c	-1.27	0.000000	300.43	124.57	ATTTCACCAGGGTGACAGTCTGACGATCAGTCCAGTTCTCC	GTCCAGT	30	6	RUNDC3A	1.70	0.00207	0.82	2.67	-2.16
cl_30342_chr17	hsa-miR-378d	-1.10	0.003182	14.73	6.83	ATTTCACCAGGGTGACAGTCTGACGATCAGTCCAGTTCTCC	GTCCAGT	30	6	RUNDC3A	1.70	0.00207	0.82	2.67	-1.87
cl_30342_chr17	hsa-miR-378i	-2.12	0.000031	7.69	1.78	ATTTCACCAGGGTGACAGTCTGACGATCAGTCCAGTTCTCC	GTCCAGT	30	6	RUNDC3A	1.70	0.00207	0.82	2.67	-3.61
cl_30362_chr17	hsa-miR-211-5p	4.32	0.000000	0.08	1.66	TGCAATTTTTCCAGATTCCCTCTGGAAGGGAAAAAGAAAAG	AAGGGAA	26	8	GJC1	-2.18	0.00000	29.30	6.47	-9.42
cl_30539_chr17	hsa-miR-3200-3p	1.32	0.046718	6.16	15.43	TGTAAAATCAAACTCAGTGGTGAGCTTTACGAGCAAGGTGA	CAAGGTG	34	18	UTP18	-0.71	0.00000	39.62	24.26	-0.94
cl_3082_chr1	hsa-miR-4424	3.24	0.000289	2.58	24.40	GCTTTGAAGTTAACTCTGGGTTTGACTCTAGTTTGACATTT	TAACTCT	11	9	ENAH	-0.92	0.00244	22.95	12.12	-2.98
cl_31050_chr17	hsa-miR-4797-3p	-2.18	0.000008	4.00	0.85	CGTGGACACTCACTGGAGGGTCGAACACTGAGAGCTGCGGG	ACTGAGA	27	17	CCDC40	0.70	0.01066	1.36	2.20	-1.53
cl_31333_chr18	hsa-miR-101-5p	1.15	0.002105	4.96	11.04	GTCATCCTTCGTGTGATAACTGGCAGGTGTTGCAACTGTGT	ATAACTG	16	15	VAPA	-0.38	0.00902	94.19	72.30	-0.44
cl_31333_chr18	hsa-miR-21-3p	2.80	0.000301	738.25	5152.52	GTCATCCTTCGTGTGATAACTGGCAGGTGTTGCAACTGTGT	GGTGTTG	26	15	VAPA	-0.38	0.00902	94.19	72.30	-1.07
cl_3134_chr1	hsa-miR-485-5p	-1.88	0.001384	12.78	3.45	GAGACTGAGGCACCTGGGGATTTTCTGTAGCCTCTTTAGGG	AGCCTCT	29	11	TRIM17	1.17	0.00000	1.00	2.24	-2.19
cl_31353_chr18	hsa-miR-29b-2-5p	1.86	0.000000	1.75	6.53	GGGAAGATAAAACCAGCACGTGTAATGTAATACATGACAAT	AAACCAG	10	48	IMPA2	-1.29	0.00000	27.80	11.37	-2.41
cl_31353_chr18	hsa-miR-29b-1-5p	1.62	0.000155	2.19	6.84	GGGAAGATAAAACCAGCACGTGTAATGTAATACATGACAAT	AACCAGC	11	48	IMPA2	-1.29	0.00000	27.80	11.37	-2.09
cl_31446_chr18	hsa-miR-144-5p	-1.28	0.017651	225.06	92.61	CTGTTGGTTCTACCTTCCGATGATATCCACAGTCTGTCCAC	GATATCC	22	13	LAMA3	2.00	0.00000	4.08	16.29	-2.56
cl_31446_chr18	hsa-miR-3074-3p	-1.17	0.003837	2.43	1.05	CTGTTGGTTCTACCTTCCGATGATATCCACAGTCTGTCCAC	TGATATC	21	13	LAMA3	2.00	0.00000	4.08	16.29	-2.33
cl_31955_chr18	hsa-miR-211-5p	4.32	0.000000	0.08	1.66	CCTTTTTCTCTGAAGTCTCTTAAGGGAAGAATATATATTTT	AAGGGAA	22	5	CYB5A	-0.82	0.00219	39.78	22.60	-3.53
cl_32135_chr19	hsa-miR-424-5p	-1.81	0.000003	177.32	50.51	CGAGCTGGACAGCACGCTGCTGCCCCAGGGCTCCCCAAACG	GCTGCTG	16	9	SBNO2	1.34	0.00000	49.31	124.72	-2.42
cl_32173_chr19	hsa-miR-3648	-1.65	0.002386	7.08	2.27	CCCCAACAGGCCACCCTGTGTGCGCGCCGCGGCTGCATGGA	CGCGGCT	28	17	APC2	0.62	0.00028	6.56	10.04	-1.01
cl_32173_chr19	hsa-miR-663b	-1.67	0.001109	4.93	1.56	CCCCAACAGGCCACCCTGTGTGCGCGCCGCGGCTGCATGGA	GGCCACC	9	17	APC2	0.62	0.00028	6.56	10.04	-1.02
cl_32186_chr19	hsa-miR-184	7.17	0.000000	0.85	123.55	CGACCCCCCGTCACCGTCCATCCCTCCCACGGCCCGAGCGC	CCGTCCA	14	55	TCF3	-1.95	0.00000	817.43	212.00	-13.96
cl_32575_chr19	hsa-miR-4446-3p	2.41	0.000000	0.69	3.74	CCCGCACCGACGATTTCCGATGAGCCCTGGCCTCCAGGAGC	AGCCCTG	23	15	CARM1	-0.67	0.00000	104.83	65.93	-1.62
cl_32576_chr19	hsa-miR-34b-3p	0.97	0.012352	0.77	1.59	GTGATTGACAATCCCCGTGTTGGCTGCGCAGCGAGAGGGAG	GTGATTG	1	15	CARM1	-0.67	0.00000	104.83	65.93	-0.65
cl_32607_chr19	hsa-miR-3605-3p	0.78	0.043923	3.22	5.54	CCATGGCTACGGGGAGCTGGTAAAAACTGCCACGGAGGCAA	ACGGAGG	32	36	ECSIT	-1.00	0.00000	62.21	31.13	-0.78
cl_32607_chr19	hsa-miR-34a-5p	1.22	0.000260	144.34	336.94	CCATGGCTACGGGGAGCTGGTAAAAACTGCCACGGAGGCAA	ACTGCCA	26	36	ECSIT	-1.00	0.00000	62.21	31.13	-1.22
cl_32721_chr19	hsa-miR-766-3p	0.67	0.048792	39.23	62.52	CAGATGCTGAGGTGAGGCACTGGAGTTGGGAGACTTGCTGC	CTGGAGT	20	23	ILVBL	-0.35	0.01802	34.39	27.06	-0.23
cl_32721_chr19	hsa-miR-150-5p	3.62	0.000000	649.65	7980.39	CAGATGCTGAGGTGAGGCACTGGAGTTGGGAGACTTGCTGC	TGGGAGA	27	23	ILVBL	-0.35	0.01802	34.39	27.06	-1.25
cl_33164_chr19	hsa-miR-4446-3p	2.41	0.000000	0.69	3.74	CTGCCCTCCCCCTGCAGCCCTGATCGTGGTGGGCAGTAGCC	AGCCCTG	16	17	ARHGAP33	-0.70	0.00017	32.54	20.10	-1.68
cl_33482_chr19	hsa-miR-191-3p	-0.97	0.012382	8.66	4.37	CCGGGAGTGCATTTCCACCTTGGCGCAGCCGGATCTCCCTC	GCGCAGC	23	15	PNMAL2	1.11	0.00093	0.53	1.15	-1.08
cl_33678_chr19	hsa-miR-130b-5p	-2.01	0.000006	211.10	52.39	GGGCAAAGAGTAGGGTCCTGTGGTTGGAGCAGGAGCTTGGA	AAAGAGT	5	19	SIGLEC10	1.37	0.00023	35.80	92.33	-2.75

cl_34014_chr20	hsa-miR-106b-3p	-1.41	0.000000	1010.79	381.55	GAGCCGACAGTGACCTGACCTGGAAAGTGCGGAGGAAAGGA	AGTGCGG	26	11	SLC23A2	0.57	0.00844	44.55	66.02	-0.80
cl_34014_chr20	hsa-miR-4420	-2.03	0.000161	9.58	2.34	GAGCCGACAGTGACCTGACCTGGAAAGTGCGGAGGAAAGGA	CAGTGAC	8	11	SLC23A2	0.57	0.00844	44.55	66.02	-1.15
cl_34100_chr20	hsa-miR-3667-3p	-1.36	0.008075	1.56	0.64	CTTATCTTAGTGACGGATAGTGCAGGAAGGTGCTGTCCTCA	GGAAGGT	25	9	MACROD2	1.25	0.00036	18.21	43.26	-1.69
cl_34672_chr20	hsa-miR-335-3p	-2.49	0.000000	566.47	100.76	ATGAAAAAAAAAAAAAGAACTTTTCTGCTAGGAAGATTATAC	TGAAAAA	2	47	TSHZ2	1.88	0.00000	4.94	18.12	-4.67
cl_3469_chr2	hsa-miR-125a-3p	1.45	0.000079	1.91	5.30	GCCAGCATCCTGGTTCCCTCTGAAGGCACCTGTGGGGCCTA	CACCTGT	27	46	TSSC1	-0.30	0.03658	44.10	35.74	-0.44
cl_35180_chr21	hsa-miR-4746-5p	-0.99	0.005796	10.48	5.29	GGACCGGAGCCGGGGCCTTTTTCTTTAAGACTCGCAGCACT	GGACCGG	1	25	CBR3	1.62	0.00000	0.93	2.85	-1.61
cl_35269_chr21	hsa-miR-485-5p	-1.88	0.001384	12.78	3.45	ATTTCCCGTGCCTGTGTGCATGTTAGCCTCTGACTATTCCT	AGCCTCT	25	16	MX2	0.66	0.00908	39.51	62.36	-1.24
cl_35578_chr22	hsa-miR-766-3p	0.67	0.048792	39.23	62.52	TTGATACAGAGTTCTCACTCTGACGCCCAGGCTGGAGTGCA	CTGGAGT	32	12	YPEL1	-0.74	0.00021	21.93	13.15	-0.50
cl_35578_chr22	hsa-miR-146a-5p	3.62	0.000000	9075.99	111335.84	TTGATACAGAGTTCTCACTCTGACGCCCAGGCTGGAGTGCA	GTTCTCA	11	12	YPEL1	-0.74	0.00021	21.93	13.15	-2.67
cl_35578_chr22	hsa-miR-146b-5p	1.74	0.002333	17080.92	57155.72	TTGATACAGAGTTCTCACTCTGACGCCCAGGCTGGAGTGCA	GTTCTCA	11	12	YPEL1	-0.74	0.00021	21.93	13.15	-1.29
cl_35578_chr22	hsa-miR-589-5p	1.66	0.001088	53.45	169.52	TTGATACAGAGTTCTCACTCTGACGCCCAGGCTGGAGTGCA	GTTCTCA	11	12	YPEL1	-0.74	0.00021	21.93	13.15	-1.23
cl_35668_chr22	hsa-miR-191-3p	-0.97	0.012382	8.66	4.37	ACTCCCTCCGGCGCAGCCGATTTAGTGAGTCCGAGAGCAGA	GCGCAGC	11	21	KIAA1671	1.27	0.00000	6.46	15.56	-1.24
cl_35692_chr22	hsa-miR-125a-3p	1.45	0.000079	1.91	5.30	TGAGTGTGCACCTGTACTTGTGGAAGTGTACTCTTGGGGAT	CACCTGT	9	13	TPST2	-0.37	0.00366	56.90	43.95	-0.54
cl_35775_chr22	hsa-miR-485-5p	-1.88	0.001384	12.78	3.45	GGAAGCCTCAAGCCTCTGGGTTTTGGGAGAACGCTAGGAAA	AGCCTCT	11	5	TBC1D10A	1.03	0.00000	13.06	26.65	-1.93
cl_36217_chr22	hsa-miR-125a-3p	1.45	0.000079	1.91	5.30	CAGAGGTGGTGGCATGCACCTGTAGCTCAGCTGTTCGGGAG	CACCTGT	17	7	FAM19A5	-0.83	0.02620	5.28	2.97	-1.20
cl_36217_chr22	hsa-miR-221-3p	2.71	0.000000	461.69	3018.51	CAGAGGTGGTGGCATGCACCTGTAGCTCAGCTGTTCGGGAG	TGTAGCT	21	7	FAM19A5	-0.83	0.02620	5.28	2.97	-2.25
cl_36217_chr22	hsa-miR-222-3p	2.13	0.000000	339.42	1483.20	CAGAGGTGGTGGCATGCACCTGTAGCTCAGCTGTTCGGGAG	TGTAGCT	21	7	FAM19A5	-0.83	0.02620	5.28	2.97	-1.76
cl_36473_chrX	hsa-miR-3648	-1.65	0.002386	7.08	2.27	GGCGCGCGGCTTTCGGGCGGTCGGCGTCGGCGTCGAGCCCT	CGCGGCT	5	8	RPS6KA3	0.60	0.00014	62.71	95.17	-0.99
cl_36477_chrX	hsa-miR-654-5p	-1.68	0.000699	4.43	1.38	TCTGGCCTCCAGAATCTCTCTGCTCCCACCAGTTAATGCAC	CCCACCA	25	7	RPS6KA3	0.60	0.00014	62.71	95.17	-1.01
cl_36508_chrX	hsa-miR-374a-5p	2.74	0.000000	79.70	534.11	AAAAGTGAGGATGGAATCGCTGTAATGACCATTATAACAAA	ATTATAA	31	17	KLHL15	-0.79	0.00000	20.29	11.74	-2.17
cl_37500_chrX	hsa-miR-3661	-1.44	0.000180	7.00	2.53	GCCAAATCTCCAAGGCCTCTTCGGGCGGAAGACAGGTCAGG	CAGGTCA	33	22	PDZD4	0.92	0.01544	1.58	3.00	-1.33
cl_37633_chrY	hsa-miR-345-5p	1.22	0.000700	68.98	161.32	CCTATGTTCACTCAAGGCCCTAGAGTTCTACAGTCAGCAGA	AGTCAGC	32	36	TMSB4Y	-1.02	0.03634	1.59	0.78	-1.25
cl_37633_chrY	hsa-miR-3136-5p	1.49	0.009911	0.81	2.26	CCTATGTTCACTCAAGGCCCTAGAGTTCTACAGTCAGCAGA	CAGTCAG	31	36	TMSB4Y	-1.02	0.03634	1.59	0.78	-1.52
cl_3781_chr2	hsa-miR-3648	-1.65	0.002386	7.08	2.27	GGCCTGGCGGGCGTCGCGGCTGCCCCTCGCCCCCTCCTGCA	CGCGGCT	15	6	ZNF513	0.95	0.00000	9.49	18.27	-1.56
cl_414_chr1	hsa-miR-188-3p	1.50	0.002747	0.97	2.82	CAAGAATGTGGGAGTATGTCTGCCGGTTTCAACACACACAG	GTGGGAG	8	27	UBE4B	-0.39	0.00291	58.61	44.70	-0.59
cl_429_chr1	hsa-miR-27b-5p	-0.99	0.003393	21.19	10.62	CCCCAAGCTCTCTCGAGTCCTGTCCCTTCCGCCATTCCTCT	AAGCTCT	5	71	CASZ1	0.55	0.02186	7.31	10.72	-0.55
cl_475_chr1	hsa-miR-181b-3p	-0.88	0.018103	19.40	10.56	AGCACTGGCCTGGCTCACCCTTCAGTGAGCACAGAGAAGCA	CAGTGAG	23	20	VPS13D	0.67	0.00063	47.50	75.72	-0.59
cl_475_chr1	hsa-miR-4755-3p	-1.99	0.000050	2.99	0.74	AGCACTGGCCTGGCTCACCCTTCAGTGAGCACAGAGAAGCA	CCTGGCT	9	20	VPS13D	0.67	0.00063	47.50	75.72	-1.34
cl_5154_chr2	hsa-miR-3613-3p	-0.59	0.049047	4.41	2.92	GTTTTTTTTGTCTTCGAAAGTGGCTTGGCTTTTCTTGTTGG	TTTTTGT	5	34	RND3	1.60	0.00000	3.91	11.87	-0.95
cl_5205_chr2	hsa-miR-4755-3p	-1.99	0.000050	2.99	0.74	ACAGAACTTTAACCTGGCTTTGCCAGTCCGACGCTCTCAAC	CCTGGCT	13	8	GPD2	0.50	0.02392	19.89	28.05	-0.99
cl_5338_chr2	hsa-miR-374b-5p	2.84	0.000010	34.89	250.55	TTACTACTACACTGAAAATTTTGATTATATTCTAGTATTTT	ATTATAT	24	10	PPIG	-0.26	0.03304	90.94	75.69	-0.75
cl_5431_chr2	hsa-miR-369-3p	-1.14	0.016758	3.61	1.65	ACAGAAAAGCGTTCTAAGTCTGACAATTTATTATTCAATGC	TATTATT	29	6	CHN1	1.88	0.00000	6.18	22.83	-2.15
cl_5659_chr2	hsa-let-7d-5p	0.97	0.003359	541.68	1061.17	GAAAATGTGCCTTTCATTCATTACCTCTCTGGAGACTTCTT	TACCTCT	22	8	NIF3L1	-0.79	0.00000	49.01	28.34	-0.77
cl_5847_chr2	hsa-miR-25-3p	-1.36	0.000000	10846.28	4235.46	TGGCTCAGCTGGGAGGGCGTTGCAATGGCAGGTGGCATGCG	TGCAATG	21	23	RUFY4	1.84	0.00001	4.22	15.08	-2.49
cl_5955_chr2	hsa-miR-155-3p	1.63	0.003876	0.57	1.82	AATGAGTAGTAGGAGAGGACTGGCTTGTGCTGGGGGTCCTC	GTAGGAG	9	6	IRS1	-0.70	0.00273	25.28	15.51	-1.15

cl_6263_chr3	hsa-miR-3136-5p	1.49	0.009911	0.81	2.26	ATGCAAGGTCTACAGTCAGATGAGCATCTAACACAATTTGG	CAGTCAG	13	11	SETMAR	-1.03	0.00000	14.48	7.08	-1.54
cl_6299_chr3	hsa-miR-138-1-3p	2.08	0.003225	3.50	14.83	ATAAAAGAAAGTAGCAATTATTCAAATGAGAAACACTTCTG	AAGTAGC	9	5	RAD18	-0.97	0.00000	45.04	22.95	-2.02
cl_6596_chr3	hsa-miR-19a-5p	-1.78	0.000041	24.62	7.20	GTGATACCTCATCAGACAGCTGTTGACAAAACTGCTATGTG	CAAAACT	27	5	STAC	1.03	0.00348	1.11	2.28	-1.84
cl_6596_chr3	hsa-miR-19b-1-5p	-1.98	0.000000	4.46	1.18	GTGATACCTCATCAGACAGCTGTTGACAAAACTGCTATGTG	CAAAACT	27	5	STAC	1.03	0.00348	1.11	2.28	-2.05
cl_6620_chr3	hsa-miR-17-3p	-2.96	0.000000	2176.96	279.17	GGAGCTGCAGTGAAGCGAACTGGGGGAACTATTCAGAGGCT	CTGCAGT	5	38	PLCD1	1.96	0.00000	4.93	19.17	-5.80
cl_6655_chr3	hsa-miR-17-3p	-2.96	0.000000	2176.96	279.17	AACAGGTGATCTTATGGATATTTGGGAGCTGCAGTGGATAC	CTGCAGT	29	20	CX3CR1	1.95	0.00000	0.81	3.14	-5.78
cl_6674_chr3	hsa-miR-296-5p	-1.00	0.001384	13.99	7.04	TAGAGCTGGTACCAAATAAATGGGTGGGGGTGGGGCCCTGC	GGGCCCT	33	19	ULK4	0.69	0.00000	17.81	28.71	-0.69
cl_6676_chr3	hsa-miR-369-3p	-1.14	0.016758	3.61	1.65	AAATTCAATTCCGGGTTGGATTTACTTTCGTGTATTATTAC	TATTATT	33	20	ULK4	0.69	0.00000	17.81	28.71	-0.78
cl_6939_chr3	hsa-miR-17-5p	-1.37	0.000088	1233.06	477.71	TTTGTTTAAGGTTGGAGGTCTGCTGTAGCACTTTGGTACCA	CACTTTG	29	12	CACNA1D	3.16	0.00000	1.64	14.70	-4.33
cl_6939_chr3	hsa-miR-20b-5p	-1.12	0.042021	59.74	27.49	TTTGTTTAAGGTTGGAGGTCTGCTGTAGCACTTTGGTACCA	CACTTTG	29	12	CACNA1D	3.16	0.00000	1.64	14.70	-3.54
cl_6939_chr3	hsa-miR-3609	-2.85	0.000000	596.50	83.01	TTTGTTTAAGGTTGGAGGTCTGCTGTAGCACTTTGGTACCA	CACTTTG	29	12	CACNA1D	3.16	0.00000	1.64	14.70	-9.00
cl_6939_chr3	hsa-miR-93-5p	-1.06	0.001859	2255.60	1081.01	TTTGTTTAAGGTTGGAGGTCTGCTGTAGCACTTTGGTACCA	CACTTTG	29	12	CACNA1D	3.16	0.00000	1.64	14.70	-3.36
cl_6952_chr3	hsa-miR-3667-3p	-1.36	0.008075	1.56	0.64	CAGGTCCACGCCACGGTAGGTGAACCTGCGGAAGGTCTGCT	GGAAGGT	30	38	CACNA2D3	0.81	0.00262	6.09	10.65	-1.09
cl_6990_chr3	hsa-miR-1254	-1.46	0.000090	5.06	1.83	AGCAAGAGAGAGTAGGGAGTTGCCAGGCTCTTTTTATATAC	CCAGGCT	23	24	ABHD6	0.49	0.00351	6.95	9.77	-0.72
cl_7040_chr3	hsa-miR-27a-5p	0.94	0.010984	14.83	28.56	TGGAGAAGCCCTCATCTCTCTGGCACCAAAGACAGTGACAT	AAGCCCT	6	13	CADPS	-4.03	0.00000	74.14	4.55	-3.80
cl_7040_chr3	hsa-miR-9-5p	2.02	0.000177	22.16	90.19	TGGAGAAGCCCTCATCTCTCTGGCACCAAAGACAGTGACAT	CCAAAGA	26	13	CADPS	-4.03	0.00000	74.14	4.55	-8.15
cl_7113_chr3	hsa-miR-19a-3p	-2.41	0.000000	1852.64	349.18	CCGTGACTGCCCTCTAGGGGTGAAAGACTAACTTTGCACAC	TTGCACA	34	5	FRMD4B	1.09	0.00000	10.94	23.34	-2.63
cl_7113_chr3	hsa-miR-19b-3p	-1.82	0.000000	1655.38	468.75	CCGTGACTGCCCTCTAGGGGTGAAAGACTAACTTTGCACAC	TTGCACA	34	5	FRMD4B	1.09	0.00000	10.94	23.34	-1.99
cl_712_chr1	hsa-miR-4424	3.24	0.000289	2.58	24.40	CCTCGCGTAACTCTTCCCTCTTTTCCTCTAATCAGACAGCC	TAACTCT	8	5	ID3	-1.54	0.00000	106.48	36.60	-4.99
cl_7144_chr3	hsa-miR-17-3p	-2.96	0.000000	2176.96	279.17	AATAGGCCCTGCAGTCTTTTTGTAGCGGTACTGACGTCTTT	CTGCAGT	9	6	EIF4E3	1.37	0.00000	6.45	16.64	-4.05
cl_7144_chr3	hsa-miR-3613-3p	-0.59	0.049047	4.41	2.92	AATAGGCCCTGCAGTCTTTTTGTAGCGGTACTGACGTCTTT	TTTTTGT	17	6	EIF4E3	1.37	0.00000	6.45	16.64	-0.81
cl_7200_chr3	hsa-miR-3942-5p	-0.98	0.015065	2.95	1.47	ATTGCTTAGAAGCAGCCACATTTTAAAATTTGCTTTGTACC	ATTGCTT	1	11	ROBO1	1.69	0.00000	12.93	41.66	-1.66
cl_7297_chr3	hsa-miR-4446-3p	2.41	0.000000	0.69	3.74	TAAGCTAAAAAGAGCCCTGTTTGTTCTCTAGGTCAGATCAA	AGCCCTG	13	49	DCBLD2	-0.50	0.01879	14.59	10.28	-1.22
cl_7297_chr3	hsa-miR-21-5p	0.77	0.013126	41871.47	71633.34	TAAGCTAAAAAGAGCCCTGTTTGTTCTCTAGGTCAGATCAA	TAAGCTA	1	49	DCBLD2	-0.50	0.01879	14.59	10.28	-0.39
cl_742_chr1	hsa-miR-20a-3p	-2.86	0.000000	28.86	3.93	GTTTGGGGGAGTCGGGAGGATGCAGTCTCTTTGCAGCAGTG	ATGCAGT	20	179	RUNX3	0.43	0.02380	59.56	80.13	-1.23
cl_742_chr1	hsa-miR-93-3p	-2.56	0.000000	153.44	25.99	GTTTGGGGGAGTCGGGAGGATGCAGTCTCTTTGCAGCAGTG	CAGCAGT	34	179	RUNX3	0.43	0.02380	59.56	80.13	-1.10
cl_7488_chr3	hsa-miR-641	-0.72	0.009573	7.16	4.36	TCTTGTCTTTGGTTTCAGAGTGGGGTATGTAAGCGAGGTAT	TGTCTTT	4	25	ILDR1	1.82	0.00000	2.27	8.00	-1.32
cl_7700_chr3	hsa-miR-4662a-5p	1.64	0.000301	0.82	2.46	AATGTTAAAGACTCTTTTTCTGCTCCAGCACACTGGCTAAA	TGGCTAA	34	6	TOPBP1	-0.83	0.00000	202.23	113.47	-1.37
cl_7739_chr3	hsa-miR-1304-3p	-1.38	0.000040	25.27	9.67	GGTCTCTGTTCTACATCAGCTGATCTGCTTCCAGTGAGACT	AGTGAGA	33	42	MRAS	0.66	0.01123	6.48	10.25	-0.92
cl_7739_chr3	hsa-miR-181b-3p	-0.88	0.018103	19.40	10.56	GGTCTCTGTTCTACATCAGCTGATCTGCTTCCAGTGAGACT	CAGTGAG	32	42	MRAS	0.66	0.01123	6.48	10.25	-0.58
cl_7765_chr3	hsa-miR-500a-5p	-0.95	0.004910	11.56	5.93	ATGCCAGGATTAAAAGCAGCTGGTGGCTCGCTGGGTACCTC	AGGATTA	6	6	CLSTN2	1.87	0.00001	2.00	7.32	-1.78
cl_788_chr1	hsa-miR-145-5p	-1.46	0.002408	414.75	150.53	CTTTGTCCTGAATGTGCTATTGCTACATGACTGGACTAGGC	ACTGGAC	30	11	PIGV	0.47	0.00257	7.90	10.94	-0.69
cl_8050_chr3	hsa-miR-4781-3p	1.58	0.000108	0.49	1.50	AGTGAGGTAGTAGTTAGTCGTCTTTCCTACAACATTTTAGC	CAACATT	30	14	EIF5A2	-0.80	0.00019	7.19	4.14	-1.26
cl_8218_chr3	hsa-miR-432-5p	-1.20	0.006297	9.90	4.31	GTGGCTTCCAAGATAGTACCTGTAGTAATTCTGGAGCTTGT	TCCAAGA	7	27	DGKG	3.10	0.00000	3.01	25.90	-3.71
cl_8369_chr3	hsa-miR-2467-5p	1.46	0.003890	3.95	10.85	TTAATGGCACCCACCGGGCCTGGGTGGAGCCTCAGCACCAC	AGCCTCA	28	8	DLG1	-0.38	0.00692	94.72	72.84	-0.55

cl_8530_chr4	hsa-miR-181a-3p	-0.96	0.000287	612.96	314.69	GATGGTAATAACGGTGGTCGTGACGATGGTGGTGGTGATGA	CGATGGT	24	8	MSX1	1.39	0.00001	0.58	1.51	-1.33
cl_8732_chr4	hsa-miR-10b-3p	3.02	0.000000	1.45	11.98	CATTATTAAAAGTAAGAATCTGTGCCAGAAACAAAAACATT	AATCTGT	17	5	LCORL	-1.45	0.00000	53.91	19.78	-4.37
cl_8754_chr4	hsa-miR-221-3p	2.71	0.000000	461.69	3018.51	TCTGTCATACCTCCCCTCGGTTAGATGTGACCCTGTAGCTC	TGTAGCT	34	9	GPR125	-1.08	0.00444	8.24	3.89	-2.93
cl_8754_chr4	hsa-miR-222-3p	2.13	0.000000	339.42	1483.20	TCTGTCATACCTCCCCTCGGTTAGATGTGACCCTGTAGCTC	TGTAGCT	34	9	GPR125	-1.08	0.00444	8.24	3.89	-2.30
cl_8900_chr4	hsa-miR-23a-5p	1.60	0.000302	2.14	6.53	TGCATCTTGCATCTGAATTCTTCCTCAGGAACCCCAATAAA	GAACCCC	29	21	PDS5A	-0.56	0.00001	278.84	189.36	-0.89
cl_9235_chr4	hsa-miR-766-3p	0.67	0.048792	39.23	62.52	CGATTTTCCCTCTGTCGTCCTGGAGTAATGATTAATATCCC	CTGGAGT	20	6	COPS4	-0.60	0.00000	58.60	38.59	-0.40
cl_9291_chr4	hsa-miR-641	-0.72	0.009573	7.16	4.36	GGAAGAGTTCTACAGCCCCATGATTAGGTCTGTCTTTTAGT	TGTCTTT	31	26	FAM13A	0.62	0.01100	9.41	14.43	-0.45
cl_9425_chr4	hsa-miR-1295a	-1.77	0.001363	16.54	4.85	GTGAGCACAATGCTAGGGCCTAAAAGATGGTGAACTATGCC	GGCCTAA	17	1137	DKK2	0.66	0.00754	1.00	1.58	-1.17
cl_9693_chr4	hsa-miR-335-3p	-2.49	0.000000	566.47	100.76	AAACTAAATTCAGCAGCGTGTGAAAAACCTTACCTACCACA	TGAAAAA	21	10	IL15	1.42	0.00000	2.55	6.85	-3.55
cl_9800_chr4	hsa-miR-378a-3p	-1.54	0.000000	2405.55	827.87	TCCCCCCATGCCCACCCACCTGACCCCTCTTGTCCAGTCCA	GTCCAGT	32	67	TRIM2	0.84	0.00027	6.23	11.13	-1.29
cl_9800_chr4	hsa-miR-378c	-1.27	0.000000	300.43	124.57	TCCCCCCATGCCCACCCACCTGACCCCTCTTGTCCAGTCCA	GTCCAGT	32	67	TRIM2	0.84	0.00027	6.23	11.13	-1.06
cl_9800_chr4	hsa-miR-378d	-1.10	0.003182	14.73	6.83	TCCCCCCATGCCCACCCACCTGACCCCTCTTGTCCAGTCCA	GTCCAGT	32	67	TRIM2	0.84	0.00027	6.23	11.13	-0.92
cl_9800_chr4	hsa-miR-378i	-2.12	0.000031	7.69	1.78	TCCCCCCATGCCCACCCACCTGACCCCTCTTGTCCAGTCCA	GTCCAGT	32	67	TRIM2	0.84	0.00027	6.23	11.13	-1.78
cl_10083_chr4	hsa-miR-3922-3p	1.24	0.017898	0.75	1.82	GAAATCACACTCATATATAATCCAAGGCCAGCCCTGTGGTT	AGGCCAG	25	12	SORBS2	-1.13	0.00001	18.37	8.37	-1.41
cl_10083_chr4	hsa-miR-140-3p	0.74	0.009811	2206.05	3679.70	GAAATCACACTCATATATAATCCAAGGCCAGCCCTGTGGTT	CTGTGGT	34	12	SORBS2	-1.13	0.00001	18.37	8.37	-0.84
cl_10440_chr5	hsa-miR-4662a-5p	1.64	0.000301	0.82	2.46	CTTGTGGAGACTTCTGGTATTGGCTAGGGGGTCATCCTGTT	TTGGCTA	20	11	CDH12	-1.47	0.00000	194.46	70.14	-2.42
cl_10644_chr5	hsa-miR-4999-5p	1.47	0.000026	0.45	1.31	TTATAAAGAGCTGATACAGCTCAAGAGTGGAAAAACAAATA	ATACAGC	14	53	NDUFS4	-0.38	0.01006	37.97	29.17	-0.56
cl_10803_chr5	hsa-miR-23a-3p	0.83	0.001283	640.05	1134.81	TCCATGTGTATTTTCTTATATACTGTGAATGTGAAAACCTA	AATGTGA	28	14	TNPO1	-0.36	0.00399	102.67	80.04	-0.30
cl_10803_chr5	hsa-miR-181a-5p	1.32	0.014841	7336.45	18322.20	TCCATGTGTATTTTCTTATATACTGTGAATGTGAAAACCTA	TGAATGT	26	14	TNPO1	-0.36	0.00399	102.67	80.04	-0.47
cl_10803_chr5	hsa-miR-181c-5p	2.83	0.000011	218.96	1560.77	TCCATGTGTATTTTCTTATATACTGTGAATGTGAAAACCTA	TGAATGT	26	14	TNPO1	-0.36	0.00399	102.67	80.04	-1.02
cl_1089_chr1	hsa-miR-138-1-3p	2.08	0.003225	3.50	14.83	TTTAGGAGATAAGGTTCCACTAGAAGTAGGTAGTATACCCC	GAAGTAG	23	19	SCMH1	-0.70	0.00002	48.40	29.74	-1.46
cl_11223_chr5	hsa-miR-296-3p	-1.98	0.000000	6.56	1.66	CACCTGCCCGCAACCCTTGTTTTTAGTGGAAAAGATCTGTA	CAACCCT	11	8	TNFAIP8	0.44	0.02745	94.44	128.24	-0.87
cl_1156_chr1	hsa-miR-3065-3p	-1.21	0.004663	1.20	0.49	GGTGCTGGGCTCAAACCTCCTGTGGAGCAGCCCCCACCCCA	GGTGCTG	1	251	CCDC24	1.02	0.00303	4.96	10.08	-1.24
cl_1163_chr1	hsa-miR-628-5p	1.10	0.000433	4.00	8.61	TTGTCAGCAGCCACGACCCTTTGGTGTACCTGTCTCAGTTG	GTCAGCA	3	9	RNF220	-0.30	0.02242	86.03	70.02	-0.33
cl_1164_chr1	hsa-miR-151a-5p	1.39	0.000409	359.84	940.64	ACCGCAGCCGTCCTCCCTCCTCGCCCCGCGCCCTCCCTCCC	CTCCTCG	17	18	RNF220	-0.30	0.02242	86.03	70.02	-0.41
cl_1164_chr1	hsa-miR-151b	3.24	0.000000	15.47	146.00	ACCGCAGCCGTCCTCCCTCCTCGCCCCGCGCCCTCCCTCCC	CTCCTCG	17	18	RNF220	-0.30	0.02242	86.03	70.02	-0.96
cl_11692_chr5	hsa-miR-154-5p	-1.78	0.000287	2.46	0.71	CAGGCTAACCTGGAGTGCCATATCCAGGAAATAACCTGAAC	ATAACCT	31	6	ANXA6	0.83	0.00050	190.05	337.97	-1.48
cl_11790_chr5	hsa-miR-29b-1-5p	1.62	0.000155	2.19	6.84	AATCCAAAATCAAACCTATCTAAACTCCCAAACCAGAAGCT	AAACCAG	30	12	PWWP2A	-0.27	0.03529	40.32	33.42	-0.44
cl_11899_chr5	hsa-miR-15b-3p	-0.95	0.002065	65.01	33.63	ATTGAATATTAGTGATAGCATGATTCATAATGATACTGTAT	ATGATTC	20	7	RANBP17	0.36	0.03485	4.25	5.44	-0.34
cl_11906_chr5	hsa-miR-154-5p	-1.78	0.000287	2.46	0.71	GCATAACCTTAGAAACATACTGAAGCTGTGGATAAATTCAG	ATAACCT	3	19	RANBP17	0.36	0.03485	4.25	5.44	-0.63
cl_11953_chr5	hsa-miR-4745-5p	-1.56	0.000679	4.57	1.52	TTCCTGAGAACAAGTAGCCATTTGGTCCCACTCCTGCTTAT	CCCACTC	27	14	STC2	0.86	0.03234	1.41	2.55	-1.34
cl_12055_chr5	hsa-miR-30b-3p	1.06	0.009573	2.25	4.76	GCAAATGATGATTACCTCTCTACCCTCCCACCTGTGCTGCC	CCTCCCA	24	23	RMND5B	-0.60	0.00002	70.50	46.35	-0.64
cl_1208_chr1	hsa-miR-149-5p	-1.00	0.003123	13.82	6.89	CCATTGTTGGTTTCTAGAGATGGAGCCAGGCCCAGGGACCC	GAGCCAG	23	8	POMGNT1	0.40	0.00199	28.52	37.71	-0.40
cl_12176_chr6	hsa-miR-5695	-1.35	0.003064	1.44	0.54	CCTCAGCTTCCTTCCGGGCCTTGGAGCGTGTGCAAGTGCGT	CTTGGAG	20	19	FOXC1	2.38	0.00000	0.95	4.98	-3.21
cl_13131_chr6	hsa-miR-188-3p	1.50	0.002747	0.97	2.82	TTAGAAGCTTAGGTTGTGTATTTTTAATGTGGGAAAACAAG	TGTGGGA	28	37	IRAK1BP1	-0.45	0.00274	71.93	52.58	-0.68

cl_13195_chr6	hsa-miR-299-3p	-1.46	0.003877	4.09	1.48	TGCCCACATCGTTCTACAGATCGACAATGCCCGTCTTGCTG	CCCACAT	3	83	NT5E	0.92	0.00981	4.87	9.18	-1.34
cl_13223_chr6	hsa-let-7b-3p	1.17	0.001317	16.34	36.79	TATTTGTATACTTCTAGGGGTCTGGTGGTTCTAGCGACTGA	TTGTATA	4	86	PM20D2	-1.10	0.00000	57.20	26.62	-1.29
cl_14194_chr7	hsa-miR-130b-3p	-2.24	0.000000	701.16	148.59	CAGATATTTATGCCATCCAGTGGTTGCACTCAGATAAAAAT	TTGCACT	24	7	SDK1	0.68	0.03704	10.53	16.82	-1.51
cl_14194_chr7	hsa-miR-301a-3p	-0.65	0.023052	241.53	153.73	CAGATATTTATGCCATCCAGTGGTTGCACTCAGATAAAAAT	TTGCACT	24	7	SDK1	0.68	0.03704	10.53	16.82	-0.44
cl_1421_chr1	hsa-miR-15b-3p	-0.95	0.002065	65.01	33.63	GTAATGGCTTCATTCAGCTCTGGATCTGTTCCTATGATTCC	ATGATTC	34	16	CACHD1	0.92	0.00433	2.30	4.34	-0.88
cl_14245_chr7	hsa-miR-184	7.17	0.000000	0.85	123.55	TCCTCAGAACCTCCACGCCTTCCTCATCTCCGTCCCTGGCA	TCCGTCC	29	23	FBXL18	-0.68	0.00001	16.68	10.39	-4.90
cl_14254_chr7	hsa-miR-589-3p	-1.73	0.000002	17.95	5.34	GACCCATCTCGCGGCGGGGGTTTTGTTCTGTTGCCGCCTAA	TGTTCTG	24	5	RNF216	0.66	0.00001	42.08	66.54	-1.14
cl_1472_chr1	hsa-miR-582-5p	1.76	0.002936	4.61	15.62	CATGGCCTTGGGGAAAACACTGAACTGTAGAGGATCGAAAG	AACTGTA	23	18	DEPDC1	-1.95	0.00000	33.25	8.59	-3.44
cl_1475_chr1	hsa-miR-29c-5p	2.01	0.000000	12.60	50.98	TGCTGTGTCATGCAGTCCGATGATCGGTCCTTGTGGTAAGG	ATCGGTC	23	9	LRRC7	-0.73	0.00000	26.92	16.18	-1.48
cl_1475_chr1	hsa-miR-425-5p	1.28	0.007710	562.69	1362.90	TGCTGTGTCATGCAGTCCGATGATCGGTCCTTGTGGTAAGG	GTGTCAT	5	9	LRRC7	-0.73	0.00000	26.92	16.18	-0.94
cl_14791_chr7	hsa-miR-154-5p	-1.78	0.000287	2.46	0.71	CCTCTTCCCATCATAACCTTTGACGAGTCGACCTGTTCTCC	ATAACCT	13	11	GRB10	0.55	0.01905	6.77	9.91	-0.98
cl_15068_chr7	hsa-miR-181a-2-3p	-1.19	0.000679	227.17	99.88	TCTCGGGTGGACTTAATCAGTGGGTCATAGGTTTTGCTTGG	TCAGTGG	17	25	SEMA3D	1.52	0.00001	1.87	5.36	-1.80
cl_15071_chr7	hsa-miR-3074-3p	-1.17	0.003837	2.43	1.05	AAACATTGAGCTAACTGATATTAATTTCTATAGCTAATTTT	CTGATAT	15	6	SEMA3D	1.52	0.00001	1.87	5.36	-1.77
cl_15138_chr7	hsa-miR-148b-5p	1.23	0.012750	26.06	60.93	TAGAAGCAGAACTGTCAGCTTGTGCCTTGAGGCTTCCAGAA	CAGAACT	7	8	CDK6	-0.78	0.00077	81.25	47.26	-0.96
cl_15186_chr7	hsa-miR-155-3p	1.63	0.003876	0.57	1.82	CAAATTTTCCTTTCATATTCTGATCTTTGTAGGATAGGTGT	TGTAGGA	28	24	LMTK2	-0.37	0.03896	25.62	19.78	-0.61
cl_15664_chr7	hsa-miR-484	-1.26	0.000040	1404.88	587.88	GGGCTATGAAGTGGAGCCTGTGGCTTCGGAAATCACCTTTC	GAGCCTG	14	10	KIAA1147	0.90	0.00000	28.55	53.14	-1.13
cl_15777_chr7	hsa-miR-3194-5p	-1.19	0.004724	6.37	2.74	GGGCAGCGGCACCATCCGGGTGCTCGGCTGGCAAGGCCTGA	GGCTGGC	26	12	SSPO	1.65	0.00000	0.77	2.42	-1.97
cl_1577_chr1	hsa-miR-4767	1.69	0.000000	1.09	3.49	CCTCCGCGCGCGCCCGCCCCTTGCCGGCGCCCACCCCCGCC	CGCCCGC	11	8	SSX2IP	-1.82	0.00000	44.04	12.47	-3.07
cl_15803_chr7	hsa-miR-211-5p	4.32	0.000000	0.08	1.66	CCACAAAGGGAGTGAGAAATTCGGGCTCAGGCACCCCACCC	AAAGGGA	5	9	CDK5	-0.71	0.00004	4.55	2.78	-3.07
cl_15803_chr7	hsa-miR-342-5p	0.77	0.020518	31.43	53.35	CCACAAAGGGAGTGAGAAATTCGGGCTCAGGCACCCCACCC	GCACCCC	31	9	CDK5	-0.71	0.00004	4.55	2.78	-0.54
cl_1588_chr1	hsa-miR-1254	-1.46	0.000090	5.06	1.83	GTCCAGGCAAAGTTCTGAACTGGCCCCCCTCGCCCCTCACG	TCCAGGC	2	12	CYR61	0.85	0.03335	29.67	53.46	-1.24
cl_16066_chr8	hsa-miR-577	-1.72	0.000050	660.86	200.99	GTATATGTTTATCTTTATTTTTATAATATGCAAATACATTT	TTTATCT	8	6	MFHAS1	1.16	0.00014	37.05	82.57	-1.99
cl_16068_chr8	hsa-miR-19a-3p	-2.41	0.000000	1852.64	349.18	CTTTCCTTTTACTTTTCCACTTGGGTTGTTTGCACGCTACA	TTTGCAC	29	16	MFHAS1	1.16	0.00014	37.05	82.57	-2.78
cl_16068_chr8	hsa-miR-19b-3p	-1.82	0.000000	1655.38	468.75	CTTTCCTTTTACTTTTCCACTTGGGTTGTTTGCACGCTACA	TTTGCAC	29	16	MFHAS1	1.16	0.00014	37.05	82.57	-2.10
cl_16118_chr8	hsa-miR-4677-3p	2.36	0.000008	6.84	35.21	ATGTTCCACTGTCCGACGATTTGGGAATGAGACTCACAGTT	CTCACAG	33	319	FAM167A	-3.14	0.00000	88.76	10.07	-7.42
cl_16255_chr8	hsa-miR-130b-3p	-2.24	0.000000	701.16	148.59	CTGTATAAAGACGTAAAGAATTTGCCTTGCACTTAACATGG	TTGCACT	27	6	NKX3-1	1.30	0.00018	0.69	1.70	-2.90
cl_16255_chr8	hsa-miR-301a-3p	-0.65	0.023052	241.53	153.73	CTGTATAAAGACGTAAAGAATTTGCCTTGCACTTAACATGG	TTGCACT	27	6	NKX3-1	1.30	0.00018	0.69	1.70	-0.84
cl_1636_chr1	hsa-miR-21-3p	2.80	0.000301	738.25	5152.52	ATTGACATGATATAGTTATCTGGTGTTTTCCTAAAATAACG	TGGTGTT	21	16	ZNF326	-0.57	0.00001	44.07	29.74	-1.59
cl_16674_chr8	hsa-miR-361-3p	1.24	0.003876	615.76	1454.95	CTCTGGGGGGAGTATGGTTGTGCTGACACATTAATTTTGGC	CTGGGGG	3	11	CLVS1	-1.24	0.00000	112.18	47.60	-1.53
cl_1692_chr1	hsa-miR-136-5p	-1.04	0.012262	12.69	6.18	CAGGAGAATGGAGAGTTGTCTGGGTCTGGCATCTCCAAACA	AATGGAG	7	11	BCAR3	1.33	0.00000	10.91	27.41	-1.38
cl_17087_chr8	hsa-miR-141-5p	2.49	0.037052	0.93	5.06	TTTTGCATTAACAGGAAGATTGGAATGACTTGTGGCTGGAT	GGAAGAT	14	37	ZNF706	-0.33	0.02365	66.99	53.22	-0.83
cl_17121_chr8	hsa-miR-181b-3p	-0.88	0.018103	19.40	10.56	GTGAAGGTGACTGGCTTCAGTGAAGGTGTGGCAGGTGGTGT	TCAGTGA	17	24	ZFPM2	0.94	0.00126	2.86	5.50	-0.83
cl_17121_chr8	hsa-miR-4420	-2.03	0.000161	9.58	2.34	GTGAAGGTGACTGGCTTCAGTGAAGGTGTGGCAGGTGGTGT	TCAGTGA	17	24	ZFPM2	0.94	0.00126	2.86	5.50	-1.91
cl_17188_chr8	hsa-miR-3613-3p	-0.59	0.049047	4.41	2.92	TTCCAAAAGTTTAGATTTTTTGCCCTAAACAATGTCAACTA	TTTTTTG	16	17	TRPS1	0.74	0.00456	10.91	18.23	-0.44
cl_17229_chr8	hsa-miR-181b-3p	-0.88	0.018103	19.40	10.56	CAAACAATGTTTGACTGGGCTGGTTGCCTAATCAGTGAAGC	TCAGTGA	32	13	HAS2	0.93	0.00251	1.83	3.48	-0.82

cl_17229_chr8	hsa-miR-4420	-2.03	0.000161	9.58	2.34	CAAACAATGTTTGACTGGGCTGGTTGCCTAATCAGTGAAGC	TCAGTGA	32	13	HAS2	0.93	0.00251	1.83	3.48	-1.88
cl_18089_chr9	hsa-miR-766-3p	0.67	0.048792	39.23	62.52	AAACCAAACATGTATCGGGCTGGAGACCACACTACAGGCTT	GCTGGAG	19	12	MAMDC2	-0.61	0.00086	194.33	127.62	-0.41
cl_18144_chr9	hsa-miR-3074-3p	-1.17	0.003837	2.43	1.05	GCAGGACGATCGTGAAAGTCTGATATTGGGAAAGAAGCTCA	CTGATAT	20	16	PCSK5	0.68	0.04373	3.84	6.17	-0.80
cl_1818_chr1	hsa-miR-625-3p	-0.95	0.012667	40.61	21.02	AGCAATGTTGTCATGGTTCCTCTATAGTGATTCGTATGAAG	CTATAGT	22	10	NTNG1	1.17	0.02029	2.38	5.34	-1.11
cl_18339_chr9	hsa-miR-708-5p	1.88	0.000003	14.78	54.47	AGTACTCTTCTTTGTCAGTATATCAACCTACAGCTCCTGAA	AGCTCCT	32	7	IARS	-0.91	0.00000	254.38	135.56	-1.71
cl_1833_chr1	hsa-miR-3074-3p	-1.17	0.003837	2.43	1.05	GGCCTCAGTTTGTTCAACTCTGATATTCTCCTGATTCTAAA	CTGATAT	20	7	VAV3	1.48	0.00000	12.77	35.63	-1.73
cl_18920_chr9	hsa-miR-296-5p	-1.00	0.001384	13.99	7.04	GAGGCCCGGGGCCCAGGGAGTGAGACCCTTGCTTCTGACTT	GGGGCCC	8	33	NTNG2	1.18	0.00012	3.25	7.38	-1.18
cl_18921_chr9	hsa-miR-625-5p	-1.31	0.000026	20.75	8.38	TCCAGGGCTTCCCCCGGCCTTACCTGCCGATGACCTCGATG	TTCCCCC	9	11	NTNG2	1.18	0.00012	3.25	7.38	-1.55
cl_19276_chr10	hsa-miR-345-5p	1.22	0.000700	68.98	161.32	AGGCAGGCAGGACTCAGCGCTGATGGTAGGAGTCAGTGGAG	GAGTCAG	30	6	CALML3	-1.03	0.00496	2.45	1.20	-1.26
cl_19462_chr10	hsa-miR-26a-5p	2.23	0.000003	6330.25	29697.53	GTTGAGGGAAAGGTGAAAAGTACATATTACTTGATTACTAT	TACTTGA	28	18	CACNB2	-0.93	0.00005	11.79	6.18	-2.08
cl_19462_chr10	hsa-miR-26b-5p	0.84	0.010386	2601.75	4666.53	GTTGAGGGAAAGGTGAAAAGTACATATTACTTGATTACTAT	TACTTGA	28	18	CACNB2	-0.93	0.00005	11.79	6.18	-0.78
cl_20298_chr10	hsa-miR-125a-5p	1.58	0.000340	2323.77	6956.82	ACTACACTTACCGTAGAGGGTTTAGCTCAGGGGTAGAGCAT	CTCAGGG	26	8	SORBS1	-2.10	0.00005	30.66	7.16	-3.32
cl_20300_chr10	hsa-miR-30b-3p	1.06	0.009573	2.25	4.76	GCATGGGGGAAACAGTCCCATGATCCAATCACCTCCCATCA	CCTCCCA	32	20	ALDH18A1	-0.70	0.00001	99.05	60.80	-0.75
cl_20331_chr10	hsa-miR-32-5p	1.83	0.000017	26.26	93.07	GGAGTGCAGCAGTGCAATCATAACTTAGCGGGGCTCAAGCA	GTGCAAT	12	10	PGAM1	-0.50	0.00440	112.17	79.32	-0.91
cl_20331_chr10	hsa-miR-92b-3p	1.32	0.000295	726.65	1808.99	GGAGTGCAGCAGTGCAATCATAACTTAGCGGGGCTCAAGCA	GTGCAAT	12	10	PGAM1	-0.50	0.00440	112.17	79.32	-0.66
cl_20541_chr10	hsa-miR-19a-3p	-2.41	0.000000	1852.64	349.18	CTTTGTTGGGAAGGTTCCCTTTGCACTGCCATGGAAGGCTG	TTTGCAC	20	15	TCF7L2	0.59	0.00878	6.18	9.27	-1.41
cl_20541_chr10	hsa-miR-19b-3p	-1.82	0.000000	1655.38	468.75	CTTTGTTGGGAAGGTTCCCTTTGCACTGCCATGGAAGGCTG	TTTGCAC	20	15	TCF7L2	0.59	0.00878	6.18	9.27	-1.07
cl_20582_chr10	hsa-miR-146a-5p	3.62	0.000000	9075.99	111335.84	AGTTCTCCAGGTCCAACGATTACCCTTCTGTTCCGGTCCTG	AGTTCTC	1	32	TRUB1	-0.29	0.02493	23.71	19.40	-1.05
cl_20582_chr10	hsa-miR-146b-5p	1.74	0.002333	17080.92	57155.72	AGTTCTCCAGGTCCAACGATTACCCTTCTGTTCCGGTCCTG	AGTTCTC	1	32	TRUB1	-0.29	0.02493	23.71	19.40	-0.50
cl_20659_chr10	hsa-miR-573	-2.99	0.000000	3.34	0.42	GCCCGTGAGCAGTCACTTCATGTTCTCTCGCGGTTCTAGCA	CACTTCA	14	5	WDR11	0.71	0.00004	78.17	128.17	-2.13
cl_2098_chr1	hsa-miR-339-5p	-2.28	0.000000	98.79	20.26	GGGGCTGGACAGGGCCAGGTTGGGAGAGGTGAGTGAAACGA	GACAGGG	8	38	PI4KB	0.43	0.00064	61.74	83.13	-0.98
cl_21060_chr11	hsa-miR-149-5p	-1.00	0.003123	13.82	6.89	CGCAGCCCCGGCGGACCCACTGTTGGACCTGAGGAGCCAGC	GAGCCAG	34	50	MIR4687	0.90	0.00003	0.52	0.98	-0.90
cl_2107_chr1	hsa-miR-24-3p	2.33	0.000001	117.91	594.79	TGAGAAGACCTCTGGAGGACTGAGCCGACTTCAGGATGAGG	CTGAGCC	20	11	CGN	-1.42	0.00007	2.41	0.90	-3.32
cl_21169_chr11	hsa-miR-136-5p	-1.04	0.012262	12.69	6.18	TCTCCACACTTTGATGTGAATGGAGGTAGGAACCCACAATA	AATGGAG	19	16	SBF2	0.44	0.00246	34.30	46.62	-0.46
cl_21249_chr11	hsa-miR-30c-2-3p	0.84	0.035995	5.28	9.42	ATCTCCCAATAAAATTGAGATGGGCCAGACCTGAAACACTT	TCTCCCA	2	5	SOX6	-0.74	0.00000	32.59	19.46	-0.63
cl_21406_chr11	hsa-miR-339-5p	-2.28	0.000000	98.79	20.26	GTCAGGATTGTTTACACCCTTGACAGGGGGTGGCATGGCTG	GACAGGG	22	7	FBXO3	0.69	0.00002	24.20	38.94	-1.57
cl_21409_chr11	hsa-miR-5695	-1.35	0.003064	1.44	0.54	CTTGGAGAGAGGACGTGGTATGCAGCTAACACAGGACCTGA	CTTGGAG	1	13	ABTB2	0.61	0.00971	30.00	45.67	-0.82
cl_21638_chr11	hsa-miR-500a-5p	-0.95	0.004910	11.56	5.93	TTTCCTATAAACTGTGAGACTCAACTAACAAGGATTCCCTC	AAGGATT	30	521	MPEG1	1.34	0.00009	50.74	128.09	-1.27
cl_21772_chr11	hsa-miR-4518	-1.83	0.000964	8.95	2.49	TCCCAGCTTCCTCTACACCCTGAGAACCGCTGCCGAGAGAC	CCCTGAG	18	35	GPR137	0.32	0.01822	35.18	43.96	-0.59
cl_22479_chr11	hsa-miR-140-3p	0.74	0.009811	2206.05	3679.70	GAAGGGGAGGCGGGGAATGCTCCGCGAGGGGCTGTGGTGAC	CTGTGGT	32	9	PPP2R1B	-0.49	0.00153	59.54	42.38	-0.36
cl_22480_chr11	hsa-miR-4424	3.24	0.000289	2.58	24.40	CCACAGTACTGTTTTCGATATTAACTCAAGCTTAAGAGAGC	TTAACTC	21	22	PPP2R1B	-0.49	0.00153	59.54	42.38	-1.59
cl_22884_chr11	hsa-miR-2110	1.05	0.000723	2.94	6.19	TGTTCCCCAGTTCTACTGTCTGATGTTCAAATAGCTCAGAA	TTCCCCA	3	5	NCAPD3	-0.62	0.00291	114.08	74.19	-0.65
cl_22896_chr11	hsa-miR-145-5p	-1.46	0.002408	414.75	150.53	TTAGCAACTGGAGGTTACCATAGGGCTCTGCGAAGATGAAG	AACTGGA	6	18	B3GAT1	2.36	0.00000	1.14	5.82	-3.45
cl_22969_chr12	hsa-miR-125a-5p	1.58	0.000340	2323.77	6956.82	CCCTGCTTAGCTGAGTGTCATGCGGGGAGACTCAGGGGTCC	CTCAGGG	31	30	EFCAB4B	-0.41	0.00478	38.12	28.59	-0.66
cl_22969_chr12	hsa-miR-425-5p	1.28	0.007710	562.69	1362.90	CCCTGCTTAGCTGAGTGTCATGCGGGGAGACTCAGGGGTCC	GTGTCAT	15	30	EFCAB4B	-0.41	0.00478	38.12	28.59	-0.53

cl_22970_chr12	hsa-miR-196a-5p	3.97	0.000000	0.79	12.42	TCCAGGAATCTCTTAGCAACTACCTCTTAATTAGCAAAAGC	ACTACCT	19	23	EFCAB4B	-0.41	0.00478	38.12	28.59	-1.65
cl_22970_chr12	hsa-miR-196b-5p	3.59	0.000000	4.45	53.68	TCCAGGAATCTCTTAGCAACTACCTCTTAATTAGCAAAAGC	ACTACCT	19	23	EFCAB4B	-0.41	0.00478	38.12	28.59	-1.49
cl_22970_chr12	hsa-let-7a-5p	1.81	0.000004	5051.85	17753.96	TCCAGGAATCTCTTAGCAACTACCTCTTAATTAGCAAAAGC	CTACCTC	20	23	EFCAB4B	-0.41	0.00478	38.12	28.59	-0.75
cl_22970_chr12	hsa-let-7b-5p	1.71	0.000000	786.57	2572.37	TCCAGGAATCTCTTAGCAACTACCTCTTAATTAGCAAAAGC	CTACCTC	20	23	EFCAB4B	-0.41	0.00478	38.12	28.59	-0.71
cl_22970_chr12	hsa-let-7e-5p	1.57	0.000051	350.23	1042.74	TCCAGGAATCTCTTAGCAACTACCTCTTAATTAGCAAAAGC	CTACCTC	20	23	EFCAB4B	-0.41	0.00478	38.12	28.59	-0.65
cl_22970_chr12	hsa-let-7f-5p	1.13	0.000287	8944.06	19581.46	TCCAGGAATCTCTTAGCAACTACCTCTTAATTAGCAAAAGC	CTACCTC	20	23	EFCAB4B	-0.41	0.00478	38.12	28.59	-0.47
cl_22970_chr12	hsa-let-7g-5p	1.85	0.000001	5123.47	18520.87	TCCAGGAATCTCTTAGCAACTACCTCTTAATTAGCAAAAGC	CTACCTC	20	23	EFCAB4B	-0.41	0.00478	38.12	28.59	-0.77
cl_22970_chr12	hsa-let-7i-5p	1.16	0.000505	4537.30	10130.51	TCCAGGAATCTCTTAGCAACTACCTCTTAATTAGCAAAAGC	CTACCTC	20	23	EFCAB4B	-0.41	0.00478	38.12	28.59	-0.48
cl_2335_chr1	hsa-miR-145-5p	-1.46	0.002408	414.75	150.53	GTTCTAATATTAGACTGTGGTGATGGTTGTCCAACTGGATA	AACTGGA	33	22	VANGL2	0.75	0.02619	8.00	13.45	-1.09
cl_23621_chr12	hsa-miR-17-3p	-2.96	0.000000	2176.96	279.17	GCAGTGGCCTGATCTTGATCTTGGCTCACTGCAGACTTAGC	ACTGCAG	28	5	SUOX	1.26	0.00000	4.16	9.98	-3.74
cl_23668_chr12	hsa-miR-432-5p	-1.20	0.006297	9.90	4.31	TAAACGTGGCTCCAAGGTCCTGGGGAGGTGGATCACGACGA	CTCCAAG	10	20	OS9	0.50	0.00014	180.32	255.15	-0.60
cl_23684_chr12	hsa-miR-3074-3p	-1.17	0.003837	2.43	1.05	TTTGTCTATTCCCTGATGACTGATATTTCAACTCAGTGTGT	CTGATAT	20	19	LRIG3	1.17	0.00027	2.88	6.49	-1.37
cl_23780_chr12	hsa-miR-361-3p	1.24	0.003876	615.76	1454.95	CGTGGCAACCGGCTCCGGGATGGCTGGCTGGGGGGCCTAGT	CTGGGGG	28	10805	MDM2	-1.40	0.00000	216.24	82.20	-1.73
cl_23786_chr12	hsa-miR-4645-3p	0.66	0.038686	3.63	5.68	TGACCAATCGTACTGTCAATTGATGTCCACTAGTTGTTAAT	TACTGTC	11	126	CCT2	-1.17	0.00000	389.18	172.41	-0.77
cl_24053_chr12	hsa-miR-424-5p	-1.81	0.000003	177.32	50.51	GACACTCTTTCTATCCCCATTTGCTGCTTTACTTTCTCCAC	TGCTGCT	22	14	GNPTAB	0.54	0.00388	46.50	67.40	-0.97
cl_24055_chr12	hsa-miR-4517	-1.60	0.000287	5.06	1.68	TTTAAATATTTGTAGATATTTGGAAACATATCTCATATTAA	TCATATT	33	9	CCDC53	0.75	0.00000	17.46	29.42	-1.20
cl_24210_chr12	hsa-miR-103a-2-5p	-1.50	0.000002	5.75	2.00	TGATAAGAAGCACTGGCCCTTCATGGTGGTGAGTGATGCTG	AAGAAGC	5	22	FAM109A	0.46	0.04725	2.17	2.99	-0.69
cl_24245_chr12	hsa-miR-374b-3p	0.94	0.035995	6.48	12.41	ATAGAGGCTGCTTGGAGAGCTGTACTGAGGACTCTGCTAAG	CTGCTAA	34	9	DTX1	-1.04	0.00004	254.75	124.22	-0.97
cl_2463_chr1	hsa-miR-130b-5p	-2.01	0.000006	211.10	52.39	AAGAGTCAGCCTGGGACATATGAGAAAGAGATGCCGGTCTC	GAAAGAG	24	7	SELE	2.01	0.00004	1.80	7.29	-4.05
cl_24646_chr12	hsa-miR-32-5p	1.83	0.000017	26.26	93.07	TGCCTTGGTGTCCTCTGTTGTGCAATGGGCACCTTTCATCA	GTGCAAT	20	7	POLE	-1.38	0.00000	195.30	75.17	-2.52
cl_24646_chr12	hsa-miR-92b-3p	1.32	0.000295	726.65	1808.99	TGCCTTGGTGTCCTCTGTTGTGCAATGGGCACCTTTCATCA	GTGCAAT	20	7	POLE	-1.38	0.00000	195.30	75.17	-1.81
cl_24755_chr13	hsa-miR-132-3p	-0.85	0.002610	123.76	68.55	TTTGAGACTGTTCTACAGTCTGACGGCATGAACATCAACGC	GACTGTT	6	67	ATP8A2	0.66	0.00865	2.60	4.12	-0.56
cl_24759_chr13	hsa-miR-543	-2.84	0.000000	7.68	1.04	GCTTCACACAGCAGGGGTTATATACAAGAATGTTCACAAAG	GAATGTT	28	6	ATP8A2	0.66	0.00865	2.60	4.12	-1.88
cl_24771_chr13	hsa-miR-361-3p	1.24	0.003876	615.76	1454.95	CGAGGGACGAGGGCTGGGGGTGGGGAGCGGTGTCTCTGCCC	CTGGGGG	14	164	CDK8	-0.53	0.00034	17.74	12.31	-0.65
cl_24948_chr13	hsa-miR-485-5p	-1.88	0.001384	12.78	3.45	AGCTGGTGCCAGACCCAGCCTCCTGAAGGAACCATGTCCTG	CAGCCTC	16	13	EPSTI1	0.90	0.00154	27.57	51.35	-1.68
cl_24969_chr13	hsa-miR-188-3p	1.50	0.002747	0.97	2.82	GGCCCGGGTTCGACTCCCGGTGTGGGAACGCCGAAATTTTA	TGTGGGA	21	14	NUFIP1	-1.22	0.00000	8.37	3.59	-1.84
cl_24996_chr13	hsa-miR-455-3p	1.26	0.000225	16.17	38.86	AGAAATCCACATGTGTGGACTGGCCATTCTTACAGAGGAGA	TGGACTG	16	14	SUCLA2	-0.62	0.00000	32.98	21.47	-0.78
cl_25135_chr13	hsa-let-7a-5p	1.81	0.000004	5051.85	17753.96	TGATTCAGGAAGTCTACCTCTGACGATCTTAGAAACCTGAA	CTACCTC	14	9	PCDH9	-1.94	0.00004	56.58	14.70	-3.52
cl_25135_chr13	hsa-let-7b-5p	1.71	0.000000	786.57	2572.37	TGATTCAGGAAGTCTACCTCTGACGATCTTAGAAACCTGAA	CTACCTC	14	9	PCDH9	-1.94	0.00004	56.58	14.70	-3.32
cl_25135_chr13	hsa-let-7e-5p	1.57	0.000051	350.23	1042.74	TGATTCAGGAAGTCTACCTCTGACGATCTTAGAAACCTGAA	CTACCTC	14	9	PCDH9	-1.94	0.00004	56.58	14.70	-3.06
cl_25135_chr13	hsa-let-7f-5p	1.13	0.000287	8944.06	19581.46	TGATTCAGGAAGTCTACCTCTGACGATCTTAGAAACCTGAA	CTACCTC	14	9	PCDH9	-1.94	0.00004	56.58	14.70	-2.20
cl_25135_chr13	hsa-let-7g-5p	1.85	0.000001	5123.47	18520.87	TGATTCAGGAAGTCTACCTCTGACGATCTTAGAAACCTGAA	CTACCTC	14	9	PCDH9	-1.94	0.00004	56.58	14.70	-3.60
cl_25135_chr13	hsa-let-7i-5p	1.16	0.000505	4537.30	10130.51	TGATTCAGGAAGTCTACCTCTGACGATCTTAGAAACCTGAA	CTACCTC	14	9	PCDH9	-1.94	0.00004	56.58	14.70	-2.25
cl_25164_chr13	hsa-miR-3136-5p	1.49	0.009911	0.81	2.26	TTCTTCACAATCAAATTCAGTCAATAGCCCAAGACTGATAG	TCAGTCA	17	31	DACH1	-0.85	0.00000	15.77	8.78	-1.26
cl_25188_chr13	hsa-miR-140-3p	0.74	0.009811	2206.05	3679.70	AATCAAGTTCTAGAGTCCAATGATCTTAATCACTGTGGTGT	CTGTGGT	33	19	UCHL3	-0.93	0.00000	41.29	21.64	-0.69

cl_25372_chr13	hsa-miR-106a-5p	-1.48	0.000168	35.65	12.76	TCATTGGGCACTTTCCCATCTCCAACTCGGAAGTAAGCCCA	GCACTTT	8	17	GPR183	1.96	0.00000	8.88	34.59	-2.90
cl_25372_chr13	hsa-miR-106b-5p	-1.55	0.000000	617.66	211.04	TCATTGGGCACTTTCCCATCTCCAACTCGGAAGTAAGCCCA	GCACTTT	8	17	GPR183	1.96	0.00000	8.88	34.59	-3.04
cl_25372_chr13	hsa-miR-17-5p	-1.37	0.000088	1233.06	477.71	TCATTGGGCACTTTCCCATCTCCAACTCGGAAGTAAGCCCA	GCACTTT	8	17	GPR183	1.96	0.00000	8.88	34.59	-2.68
cl_25372_chr13	hsa-miR-20b-5p	-1.12	0.042021	59.74	27.49	TCATTGGGCACTTTCCCATCTCCAACTCGGAAGTAAGCCCA	GCACTTT	8	17	GPR183	1.96	0.00000	8.88	34.59	-2.19
cl_25372_chr13	hsa-miR-93-5p	-1.06	0.001859	2255.60	1081.01	TCATTGGGCACTTTCCCATCTCCAACTCGGAAGTAAGCCCA	GCACTTT	8	17	GPR183	1.96	0.00000	8.88	34.59	-2.08
cl_25522_chr13	hsa-miR-221-5p	1.18	0.015984	188.23	426.85	AGAGATGCCCACTCAACCCCTTACTACTATGCCAGGCCTCA	TGCCAGG	30	11	TUBGCP3	-0.56	0.00001	60.04	40.60	-0.67
cl_25995_chr14	hsa-miR-193b-5p	-1.17	0.019368	21.00	9.29	TTTTAAACCCCTATTAGCTATAGGCCCACGATCCAGAGTTC	AAACCCC	5	33	RTN1	1.10	0.00002	4.16	8.93	-1.29
cl_2620_chr1	hsa-miR-500a-5p	-0.95	0.004910	11.56	5.93	TTAAACCAAGGATTCTAACATGTGCTTCTCTTCTCCAAACT	AAGGATT	8	5	RGL1	1.19	0.00001	21.15	48.33	-1.14
cl_26797_chr15	hsa-miR-2467-5p	1.46	0.003890	3.95	10.85	GGCGGGCCAGCGCCGCGGAGTTTCGGGTCCGAGGAGCCTCG	GAGCCTC	34	6	TJP1	-1.07	0.00000	136.54	64.81	-1.57
cl_26985_chr15	hsa-miR-146a-5p	3.62	0.000000	9075.99	111335.84	CTCAGTTCTCCAGTACGACGTTTCCTGTCTTGAGCAGGAGC	AGTTCTC	4	8	STARD9	-0.49	0.00438	20.47	14.60	-1.76
cl_26985_chr15	hsa-miR-146b-5p	1.74	0.002333	17080.92	57155.72	CTCAGTTCTCCAGTACGACGTTTCCTGTCTTGAGCAGGAGC	AGTTCTC	4	8	STARD9	-0.49	0.00438	20.47	14.60	-0.85
cl_27858_chr15	hsa-miR-4518	-1.83	0.000964	8.95	2.49	ACAGTGAATGCACTCTTCTCTGCCTGGCCCTGAGAGACACA	CCCTGAG	28	26	PCSK6	0.73	0.01602	4.60	7.62	-1.33
cl_27858_chr15	hsa-miR-4755-3p	-1.99	0.000050	2.99	0.74	ACAGTGAATGCACTCTTCTCTGCCTGGCCCTGAGAGACACA	GCCTGGC	22	26	PCSK6	0.73	0.01602	4.60	7.62	-1.45
cl_2788_chr1	hsa-miR-641	-0.72	0.009573	7.16	4.36	ATGTCTTGATAAGATACAACTGACACCGAGTACTGACCCAG	ATGTCTT	1	5	CYB5R1	0.68	0.00000	17.17	27.48	-0.49
cl_28500_chr16	hsa-miR-3681-5p	5.07	0.000000	1.82	61.30	CGTTCTCTCCTTGAATCCACTCGCCAGCCCGCCGCCCTCTG	ATCCACT	15	7	ALDOA	-0.42	0.02659	639.84	477.09	-2.15
cl_28675_chr16	hsa-miR-17-3p	-2.96	0.000000	2176.96	279.17	GTGTTCAGAGCTCAGTCCGATGCTCCCTCCACTGCAGCACC	ACTGCAG	31	31	N4BP1	0.30	0.03307	36.42	44.74	-0.88
cl_28808_chr16	hsa-miR-3065-3p	-1.21	0.004663	1.20	0.49	TGCAGCGGGAGGACACAGTGTACCGGGTGCTGGGTGCCCAC	GGTGCTG	26	19	MT2A	1.57	0.00206	5.01	14.92	-1.91
cl_28898_chr16	hsa-miR-193b-5p	-1.17	0.019368	21.00	9.29	GATATGTATTAAACCCCCCCTGTGTTACAGGTACTGGCATG	AAACCCC	11	6	CDH11	1.01	0.00147	18.33	37.01	-1.19
cl_29152_chr16	hsa-miR-378a-3p	-1.54	0.000000	2405.55	827.87	CTTTCAGTCCAGCATCTGAGTGTTGGCAACCAGCCCAGAGA	AGTCCAG	6	7	MAF	2.02	0.00000	13.35	54.02	-3.10
cl_29152_chr16	hsa-miR-378c	-1.27	0.000000	300.43	124.57	CTTTCAGTCCAGCATCTGAGTGTTGGCAACCAGCCCAGAGA	AGTCCAG	6	7	MAF	2.02	0.00000	13.35	54.02	-2.56
cl_29152_chr16	hsa-miR-378d	-1.10	0.003182	14.73	6.83	CTTTCAGTCCAGCATCTGAGTGTTGGCAACCAGCCCAGAGA	AGTCCAG	6	7	MAF	2.02	0.00000	13.35	54.02	-2.22
cl_29152_chr16	hsa-miR-378i	-2.12	0.000031	7.69	1.78	CTTTCAGTCCAGCATCTGAGTGTTGGCAACCAGCCCAGAGA	AGTCCAG	6	7	MAF	2.02	0.00000	13.35	54.02	-4.28
cl_29630_chr17	hsa-miR-150-3p	3.38	0.000000	3.49	36.47	GCGGGCATGAGGAGTGACTGTGTACCATTTCAGCTGTTTCT	TGTACCA	21	59	DHX33	-1.13	0.00000	43.83	20.04	-3.82
cl_30152_chr17	hsa-miR-125a-5p	1.58	0.000340	2323.77	6956.82	TGATCTCAGGGTCGGAATCCTGCTGTCTCGTCTGCTACTAA	CTCAGGG	5	18	DUSP14	-0.76	0.00001	8.12	4.81	-1.20
cl_30152_chr17	hsa-miR-4524a-3p	1.13	0.047890	0.62	1.40	TGATCTCAGGGTCGGAATCCTGCTGTCTCGTCTGCTACTAA	CTGTCTC	23	18	DUSP14	-0.76	0.00001	8.12	4.81	-0.85
cl_30161_chr17	hsa-miR-3922-3p	1.24	0.017898	0.75	1.82	ACATAGCTCTTCGGACCTTGTGGGATGTGCAGGCCAGGAAA	AGGCCAG	31	7	DDX52	-0.33	0.01578	39.68	31.61	-0.41
cl_30161_chr17	hsa-miR-188-3p	1.50	0.002747	0.97	2.82	ACATAGCTCTTCGGACCTTGTGGGATGTGCAGGCCAGGAAA	TGTGGGA	19	7	DDX52	-0.33	0.01578	39.68	31.61	-0.49
cl_30345_chr17	hsa-miR-221-5p	1.18	0.015984	188.23	426.85	GTCCCTGCTTTAGAGGTCATTGCCAGGGTTGTTGAGGCAAC	TGCCAGG	21	141	SLC25A39	-0.73	0.00001	178.71	107.89	-0.86
cl_30539_chr17	hsa-miR-9-3p	2.32	0.000225	2.29	11.53	TGTAAAATCAAACTCAGTGGTGAGCTTTACGAGCAAGGTGA	AGCTTTA	23	18	UTP18	-0.71	0.00000	39.62	24.26	-1.64
cl_30574_chr17	hsa-miR-339-5p	-2.28	0.000000	98.79	20.26	CCTGCGCTAGCTCCAGAGCTTGAGACAGGGTCCGGGCGGAG	GACAGGG	24	12	PCTP	0.83	0.00003	7.20	12.81	-1.90
cl_30576_chr17	hsa-miR-369-3p	-1.14	0.016758	3.61	1.65	TAAACTAATAGCTCACTAGTTGAGTGTATTATGCCTTTCAC	GTATTAT	26	19	PCTP	0.83	0.00003	7.20	12.81	-0.95
cl_3082_chr1	hsa-miR-708-3p	0.98	0.026809	18.72	36.79	GCTTTGAAGTTAACTCTGGGTTTGACTCTAGTTTGACATTT	TCTAGTT	27	9	ENAH	-0.92	0.00244	22.95	12.12	-0.90
cl_31019_chr17	hsa-miR-654-5p	-1.68	0.000699	4.43	1.38	CCGGCCCACCGTGGCACCCCTGACGATCGCGGGGTGGGGTA	GCCCACC	4	28	CANT1	0.35	0.00595	29.56	37.64	-0.58
cl_31353_chr18	hsa-miR-141-5p	2.49	0.037052	0.93	5.06	GGGAAGATAAAACCAGCACGTGTAATGTAATACATGACAAT	GGAAGAT	2	48	IMPA2	-1.29	0.00000	27.80	11.37	-3.21
cl_31452_chr18	hsa-miR-331-3p	-0.86	0.033410	175.92	96.56	TCTTCATTTCACAGCTTGGTTGGCTCATCTCATCCAGGGGC	CCAGGGG	34	20	TTC39C	0.63	0.02164	15.98	24.73	-0.55

cl_31497_chr18	hsa-miR-132-3p	-0.85	0.002610	123.76	68.55	ATCCGACTGTTTATTTAAATTTTCTTAGTGTTCTGTTTTAT	GACTGTT	5	86	CDH2	1.90	0.00001	1.68	6.29	-1.62
cl_31497_chr18	hsa-miR-589-3p	-1.73	0.000002	17.95	5.34	ATCCGACTGTTTATTTAAATTTTCTTAGTGTTCTGTTTTAT	TGTTCTG	29	86	CDH2	1.90	0.00001	1.68	6.29	-3.29
cl_31909_chr18	hsa-miR-136-5p	-1.04	0.012262	12.69	6.18	CAATGGAGAAGGTAACTGGCTGATCTCTTTTTTTTACACCG	AATGGAG	2	30	TMX3	0.69	0.00002	56.28	90.99	-0.72
cl_32186_chr19	hsa-miR-30b-3p	1.06	0.009573	2.25	4.76	CGACCCCCCGTCACCGTCCATCCCTCCCACGGCCCGAGCGC	CCTCCCA	23	55	TCF3	-1.95	0.00000	817.43	212.00	-2.06
cl_32221_chr19	hsa-miR-3194-5p	-1.19	0.004724	6.37	2.74	TGGGCTGGCTGGCGGGCATGTCTGTTCCAGGAGGCACGCCC	GGCTGGC	7	9	MKNK2	0.75	0.00009	166.70	280.11	-0.89
cl_32453_chr19	hsa-miR-2355-5p	0.92	0.009772	10.03	18.95	AGAAGACGTTCTCGCTCCATTTCCTGGGGAAAGAGCCGTAA	CTGGGGA	24	23	ARHGEF18	-0.53	0.00697	136.44	94.54	-0.48
cl_32503_chr19	hsa-miR-15b-3p	-0.95	0.002065	65.01	33.63	TTCTGATGATTCTGCCAGGATGGGGGAAGTAGGGAACTTAA	ATGATTC	6	6	MUC16	4.94	0.00000	1.27	39.08	-4.71
cl_32567_chr19	hsa-miR-615-3p	2.51	0.000000	2.50	14.25	CTGTGGAGCTTGACTCTGGCTCGGTGAAGAGACATGGGTGA	GGCTCGG	18	5	ILF3	-1.17	0.00000	878.29	389.71	-2.94
cl_32696_chr19	hsa-miR-2110	1.05	0.000723	2.94	6.19	GAGGTTCCCCACGCGGGAAATGGGGCTTGGAGGGGGTTAAT	TTCCCCA	5	13	ASF1B	-1.54	0.00000	79.93	27.42	-1.63
cl_32878_chr19	hsa-miR-3648	-1.65	0.002386	7.08	2.27	AGGCCACGCCCGCGAAGAGGTCAGCCGCGGCCAGATTGCCG	CCGCGGC	25	8	LPAR2	0.71	0.00100	11.55	18.85	-1.17
cl_33115_chr19	hsa-miR-138-5p	1.70	0.013928	24.26	78.83	CCTCCAGCTGAGACCGGCGGTGTTATTCCCACACCAGCATA	CACCAGC	32	16	UBA2	-1.08	0.00000	124.66	58.78	-1.84
cl_33453_chr19	hsa-miR-1260a	1.07	0.037052	1.66	3.50	ACAAAGGGGGTCGATCCGGGTGGGAAGAGCTTCGAGTCATA	GGTGGGA	19	11	QPCTL	-0.58	0.00098	16.77	11.21	-0.62
cl_34052_chr20	hsa-miR-125a-5p	1.58	0.000340	2323.77	6956.82	GGTACAGCTCAGGGGTAGAGTATTTGACTTCAGAAAATGTC	CTCAGGG	8	32	PLCB1	-1.77	0.00000	20.06	5.88	-2.80
cl_34100_chr20	hsa-miR-3065-3p	-1.21	0.004663	1.20	0.49	CTTATCTTAGTGACGGATAGTGCAGGAAGGTGCTGTCCTCA	GGTGCTG	29	9	MACROD2	1.25	0.00036	18.21	43.26	-1.51
cl_3470_chr2	hsa-miR-196a-5p	3.97	0.000000	0.79	12.42	TAATGCTGATTTTTAAAAACTACCTCCTAAAGTGCTGTGTG	ACTACCT	19	10	TSSC1	-0.30	0.03658	44.10	35.74	-1.20
cl_3470_chr2	hsa-miR-196b-5p	3.59	0.000000	4.45	53.68	TAATGCTGATTTTTAAAAACTACCTCCTAAAGTGCTGTGTG	ACTACCT	19	10	TSSC1	-0.30	0.03658	44.10	35.74	-1.09
cl_3470_chr2	hsa-let-7a-5p	1.81	0.000004	5051.85	17753.96	TAATGCTGATTTTTAAAAACTACCTCCTAAAGTGCTGTGTG	CTACCTC	20	10	TSSC1	-0.30	0.03658	44.10	35.74	-0.55
cl_3470_chr2	hsa-let-7b-5p	1.71	0.000000	786.57	2572.37	TAATGCTGATTTTTAAAAACTACCTCCTAAAGTGCTGTGTG	CTACCTC	20	10	TSSC1	-0.30	0.03658	44.10	35.74	-0.52
cl_3470_chr2	hsa-let-7d-5p	0.97	0.003359	541.68	1061.17	TAATGCTGATTTTTAAAAACTACCTCCTAAAGTGCTGTGTG	CTACCTC	20	10	TSSC1	-0.30	0.03658	44.10	35.74	-0.29
cl_3470_chr2	hsa-let-7e-5p	1.57	0.000051	350.23	1042.74	TAATGCTGATTTTTAAAAACTACCTCCTAAAGTGCTGTGTG	CTACCTC	20	10	TSSC1	-0.30	0.03658	44.10	35.74	-0.48
cl_3470_chr2	hsa-let-7f-5p	1.13	0.000287	8944.06	19581.46	TAATGCTGATTTTTAAAAACTACCTCCTAAAGTGCTGTGTG	CTACCTC	20	10	TSSC1	-0.30	0.03658	44.10	35.74	-0.34
cl_3470_chr2	hsa-let-7g-5p	1.85	0.000001	5123.47	18520.87	TAATGCTGATTTTTAAAAACTACCTCCTAAAGTGCTGTGTG	CTACCTC	20	10	TSSC1	-0.30	0.03658	44.10	35.74	-0.56
cl_3470_chr2	hsa-let-7i-5p	1.16	0.000505	4537.30	10130.51	TAATGCTGATTTTTAAAAACTACCTCCTAAAGTGCTGTGTG	CTACCTC	20	10	TSSC1	-0.30	0.03658	44.10	35.74	-0.35
cl_3470_chr2	hsa-miR-34a-3p	0.99	0.002408	1.08	2.19	TAATGCTGATTTTTAAAAACTACCTCCTAAAGTGCTGTGTG	GCTGATT	5	10	TSSC1	-0.30	0.03658	44.10	35.74	-0.30
cl_35051_chr21	hsa-miR-132-3p	-0.85	0.002610	123.76	68.55	TGATCATTTAGGGTGGAATCTGACTGTTTAATTTTCCTTGC	GACTGTT	22	12	APP	0.88	0.00037	82.49	151.67	-0.75
cl_35265_chr21	hsa-miR-106b-3p	-1.41	0.000000	1010.79	381.55	GAAACACTCGCGCACACCCCTCAGTGCGCCCCGGGCGGGGG	CAGTGCG	22	313	BACE2	1.88	0.00000	11.14	40.86	-2.64
cl_35311_chr21	hsa-miR-148b-5p	1.23	0.012750	26.06	60.93	GACACTCCTCAGAACTGCTGTCTTACACATGCAGGTCGGTG	CAGAACT	10	51	CBS	-2.61	0.00000	39.36	6.46	-3.20
cl_35663_chr22	hsa-miR-296-5p	-1.00	0.001384	13.99	7.04	GGACAGGCCCTCTCGGATGTTGGCAGGGGGCCCCTTCTCTG	GGGGCCC	27	5	KIAA1671	1.27	0.00000	6.46	15.56	-1.26
cl_35668_chr22	hsa-miR-3917	-1.74	0.000012	6.53	1.93	ACTCCCTCCGGCGCAGCCGATTTAGTGAGTCCGAGAGCAGA	GTCCGAG	29	21	KIAA1671	1.27	0.00000	6.46	15.56	-2.20
cl_35917_chr22	hsa-miR-154-5p	-1.78	0.000287	2.46	0.71	TGGTGGGTAACGGAGGAGCTTGAATTCAATAACCTTCATTT	ATAACCT	29	10	CYTH4	1.29	0.00000	27.44	66.95	-2.29
cl_36460_chrX	hsa-miR-92b-5p	0.98	0.008992	0.54	1.12	ACCTGCGTACAGCCGTCCCCTTTATCCACGGTTTTGCTTTC	CCGTCCC	13	25	PDHA1	-0.71	0.00000	95.03	58.14	-0.69
cl_37162_chrX	hsa-miR-4523	-1.05	0.028608	2.00	0.93	TTCTCTCGGTGTCCACAGCTTACTGCCCGCTTTCCAGTAGG	TCTCGGT	4	81	AMOT	1.81	0.00001	1.20	4.22	-1.91
cl_37500_chrX	hsa-miR-432-5p	-1.20	0.006297	9.90	4.31	GCCAAATCTCCAAGGCCTCTTCGGGCGGAAGACAGGTCAGG	CTCCAAG	8	22	PDZD4	0.92	0.01544	1.58	3.00	-1.10
cl_37633_chrY	hsa-miR-628-5p	1.10	0.000433	4.00	8.61	CCTATGTTCACTCAAGGCCCTAGAGTTCTACAGTCAGCAGA	GTCAGCA	33	36	TMSB4Y	-1.02	0.03634	1.59	0.78	-1.12
cl_37635_chrY	hsa-miR-181a-2-3p	-1.19	0.000679	227.17	99.88	AGTAGAGATGTGGAGGAATCTTGAGTATGACTCAGTGGAAC	TCAGTGG	32	15	NLGN4Y	0.87	0.03142	3.39	6.19	-1.03

cl_3781_chr2	hsa-miR-4755-3p	-1.99	0.000050	2.99	0.74	GGCCTGGCGGGCGTCGCGGCTGCCCCTCGCCCCCTCCTGCA	GCCTGGC	2	6	ZNF513	0.95	0.00000	9.49	18.27	-1.88
cl_4372_chr2	hsa-miR-449a	-1.36	0.000063	5.99	2.35	GCGGCTGACTTTGTACACACTGCCCTGGGTCTGGAGATACC	CACTGCC	18	11	TACR1	0.81	0.00261	2.29	4.01	-1.10
cl_4477_chr2	hsa-miR-103a-2-5p	-1.50	0.000002	5.75	2.00	ACAGAAAATGAAAGAAGCATTAAGCCATGGGAGAGTAGAAA	AAGAAGC	12	22	CD8B	1.39	0.00089	6.03	15.82	-2.09
cl_4680_chr2	hsa-miR-3940-3p	-0.81	0.023652	4.97	2.86	TCTCACTGTGTTGCTTAGGCTGGTGTGAAATTCCCGGGCTC	CCGGGCT	34	22	SH3RF3	1.56	0.00012	3.44	10.15	-1.26
cl_475_chr1	hsa-miR-1304-3p	-1.38	0.000040	25.27	9.67	AGCACTGGCCTGGCTCACCCTTCAGTGAGCACAGAGAAGCA	CAGTGAG	23	20	VPS13D	0.67	0.00063	47.50	75.72	-0.93
cl_475_chr1	hsa-miR-4420	-2.03	0.000161	9.58	2.34	AGCACTGGCCTGGCTCACCCTTCAGTGAGCACAGAGAAGCA	TCAGTGA	22	20	VPS13D	0.67	0.00063	47.50	75.72	-1.36
cl_5187_chr2	hsa-miR-3667-3p	-1.36	0.008075	1.56	0.64	AAAGTCAAAAGAGGAAGGAATACCAGTGGCAAAAATCATTT	AGGAAGG	12	26	GALNT1	0.44	0.00945	59.79	81.18	-0.60
cl_5338_chr2	hsa-miR-30a-3p	0.99	0.025009	59.24	117.52	TTACTACTACACTGAAAATTTTGATTATATTCTAGTATTTT	ACTGAAA	11	10	PPIG	-0.26	0.03304	90.94	75.69	-0.26
cl_5425_chr2	hsa-miR-3648	-1.65	0.002386	7.08	2.27	TGGAAACCGCGGCACTGCTTTGGGAGGAGGCTCAATACGTC	CCGCGGC	7	11	WIPF1	0.64	0.00019	210.18	328.48	-1.06
cl_5484_chr2	hsa-miR-21-5p	0.77	0.013126	41871.47	71633.34	GGGTAGGTTATATAATAAGCTGATATTTTGATGAGTTACTA	ATAAGCT	15	10	DFNB59	-0.84	0.00000	28.40	15.91	-0.65
cl_5545_chr2	hsa-miR-151a-5p	1.39	0.000409	359.84	940.64	AGCCGCTCCTCGCTACCCACTATGCTCTGCGACATCGACCT	CTCCTCG	6	19	ZC3H15	-0.44	0.00163	135.44	99.88	-0.61
cl_5545_chr2	hsa-miR-151b	3.24	0.000000	15.47	146.00	AGCCGCTCCTCGCTACCCACTATGCTCTGCGACATCGACCT	CTCCTCG	6	19	ZC3H15	-0.44	0.00163	135.44	99.88	-1.42
cl_5606_chr2	hsa-miR-4518	-1.83	0.000964	8.95	2.49	GGATCCCTGAGTGGGATTCCTGTGTGAAAGGCATTTTCACC	CCCTGAG	5	10	SLC39A10	0.62	0.00277	30.06	46.25	-1.14
cl_5905_chr2	hsa-miR-3940-3p	-0.81	0.023652	4.97	2.86	TCATGCCAGTTTGTGAAGGTTGACCCGGGCTCTGCTTTGAG	CCGGGCT	25	28	EPHA4	1.61	0.00144	4.16	12.72	-1.31
cl_5955_chr2	hsa-miR-361-3p	1.24	0.003876	615.76	1454.95	AATGAGTAGTAGGAGAGGACTGGCTTGTGCTGGGGGTCCTC	CTGGGGG	30	6	IRS1	-0.70	0.00273	25.28	15.51	-0.87
cl_6263_chr3	hsa-miR-3200-3p	1.32	0.046718	6.16	15.43	ATGCAAGGTCTACAGTCAGATGAGCATCTAACACAATTTGG	GCAAGGT	3	11	SETMAR	-1.03	0.00000	14.48	7.08	-1.37
cl_6387_chr3	hsa-miR-221-5p	1.18	0.015984	188.23	426.85	TTGGAGCCATCTAACACGTGTGCCAGGCCTGGTCCTGCACC	TGCCAGG	21	28	NUP210	-0.42	0.00506	379.21	283.01	-0.50
cl_6447_chr3	hsa-let-7a-5p	1.81	0.000004	5051.85	17753.96	TTCAGCTACCTCCTAAACTCTCTTCTCCCTGTTTTCAGCTG	CTACCTC	6	7	PLCL2	-0.72	0.00007	60.11	36.52	-1.30
cl_6447_chr3	hsa-let-7b-5p	1.71	0.000000	786.57	2572.37	TTCAGCTACCTCCTAAACTCTCTTCTCCCTGTTTTCAGCTG	CTACCTC	6	7	PLCL2	-0.72	0.00007	60.11	36.52	-1.23
cl_6447_chr3	hsa-let-7d-5p	0.97	0.003359	541.68	1061.17	TTCAGCTACCTCCTAAACTCTCTTCTCCCTGTTTTCAGCTG	CTACCTC	6	7	PLCL2	-0.72	0.00007	60.11	36.52	-0.70
cl_6447_chr3	hsa-let-7e-5p	1.57	0.000051	350.23	1042.74	TTCAGCTACCTCCTAAACTCTCTTCTCCCTGTTTTCAGCTG	CTACCTC	6	7	PLCL2	-0.72	0.00007	60.11	36.52	-1.13
cl_6447_chr3	hsa-let-7f-5p	1.13	0.000287	8944.06	19581.46	TTCAGCTACCTCCTAAACTCTCTTCTCCCTGTTTTCAGCTG	CTACCTC	6	7	PLCL2	-0.72	0.00007	60.11	36.52	-0.81
cl_6447_chr3	hsa-let-7g-5p	1.85	0.000001	5123.47	18520.87	TTCAGCTACCTCCTAAACTCTCTTCTCCCTGTTTTCAGCTG	CTACCTC	6	7	PLCL2	-0.72	0.00007	60.11	36.52	-1.33
cl_6447_chr3	hsa-let-7i-5p	1.16	0.000505	4537.30	10130.51	TTCAGCTACCTCCTAAACTCTCTTCTCCCTGTTTTCAGCTG	CTACCTC	6	7	PLCL2	-0.72	0.00007	60.11	36.52	-0.83
cl_691_chr1	hsa-miR-335-5p	-1.09	0.000328	118.94	55.71	CTTTTCCGTCCTGGGAACTGTCAGTCTGGGAGAGCTCTTGA	GCTCTTG	34	12	ZBTB40	0.51	0.01022	37.87	53.87	-0.56
cl_6939_chr3	hsa-miR-106a-5p	-1.48	0.000168	35.65	12.76	TTTGTTTAAGGTTGGAGGTCTGCTGTAGCACTTTGGTACCA	GCACTTT	28	12	CACNA1D	3.16	0.00000	1.64	14.70	-4.68
cl_6939_chr3	hsa-miR-106b-5p	-1.55	0.000000	617.66	211.04	TTTGTTTAAGGTTGGAGGTCTGCTGTAGCACTTTGGTACCA	GCACTTT	28	12	CACNA1D	3.16	0.00000	1.64	14.70	-4.90
cl_7355_chr3	hsa-miR-378a-3p	-1.54	0.000000	2405.55	827.87	GACCCTGAAAGTCCAGGAATTGGGTTAAAATTCCTAAACCT	AGTCCAG	10	20	CBLB	0.68	0.00710	44.53	71.48	-1.05
cl_7355_chr3	hsa-miR-378c	-1.27	0.000000	300.43	124.57	GACCCTGAAAGTCCAGGAATTGGGTTAAAATTCCTAAACCT	AGTCCAG	10	20	CBLB	0.68	0.00710	44.53	71.48	-0.87
cl_7355_chr3	hsa-miR-378d	-1.10	0.003182	14.73	6.83	GACCCTGAAAGTCCAGGAATTGGGTTAAAATTCCTAAACCT	AGTCCAG	10	20	CBLB	0.68	0.00710	44.53	71.48	-0.75
cl_7355_chr3	hsa-miR-378i	-2.12	0.000031	7.69	1.78	GACCCTGAAAGTCCAGGAATTGGGTTAAAATTCCTAAACCT	AGTCCAG	10	20	CBLB	0.68	0.00710	44.53	71.48	-1.45
cl_7419_chr3	hsa-miR-4521	-2.95	0.000000	35.56	4.58	GCATAAATTCTGTTTGTCCTTAGGCGATCTCATAGTGACTA	TCCTTAG	17	7	ATP6V1A	0.49	0.01833	49.42	69.31	-1.44
cl_7491_chr3	hsa-miR-4797-3p	-2.18	0.000008	4.00	0.85	CTTGGTGGGTTTTACTCACTTTCTACTGAGCATTGTACAAG	TACTGAG	24	12	CD86	1.36	0.00000	32.55	83.35	-2.96
cl_7491_chr3	hsa-miR-3609	-2.85	0.000000	596.50	83.01	CTTGGTGGGTTTTACTCACTTTCTACTGAGCATTGTACAAG	TCACTTT	16	12	CD86	1.36	0.00000	32.55	83.35	-3.86
cl_7700_chr3	hsa-miR-199a-5p	1.59	0.000007	181.97	548.37	AATGTTAAAGACTCTTTTTCTGCTCCAGCACACTGGCTAAA	ACACTGG	30	6	TOPBP1	-0.83	0.00000	202.23	113.47	-1.33

cl_788_chr1	hsa-miR-3942-5p	-0.98	0.015065	2.95	1.47	CTTTGTCCTGAATGTGCTATTGCTACATGACTGGACTAGGC	TATTGCT	18	11	PIGV	0.47	0.00257	7.90	10.94	-0.46
cl_7937_chr3	hsa-miR-130a-3p	0.76	0.008363	223.96	380.59	TAGGTTTTTCCGTGTTGCACTATGTACCCGTATACCATTTC	TTGCACT	15	7	KCNAB1	-0.45	0.00020	41.67	30.49	-0.34
cl_7949_chr3	hsa-miR-589-3p	-1.73	0.000002	17.95	5.34	ACATTTAAACTTTGTTCTGTTGGCAGCAGGGAACCATGACC	TGTTCTG	13	10	SHOX2	2.60	0.00000	0.61	3.67	-4.49
cl_797_chr1	hsa-miR-10b-3p	3.02	0.000000	1.45	11.98	CTAGGTCACATGGCAGAATCTGGGCTAGAAGCCAAACTCCC	GAATCTG	16	102	NUDC	-0.97	0.00000	48.28	24.63	-2.93
cl_8018_chr3	hsa-miR-155-5p	3.25	0.000000	1152.30	10989.11	CAGCATTAGTTCATCTTGACTGATGCCCTTGACTTCAGAGT	AGCATTA	2	11	GOLIM4	-0.58	0.00180	39.99	26.79	-1.88
cl_8067_chr3	hsa-miR-3136-5p	1.49	0.009911	0.81	2.26	CTCTCTAATAATGCCTGTACTCTCTAAGCTTCAGTCATACC	TCAGTCA	31	26	ECT2	-1.10	0.00002	71.79	33.43	-1.64
cl_8370_chr3	hsa-miR-148b-5p	1.23	0.012750	26.06	60.93	AAAGAGTAAGCACTCACCTTTGGGGGCAGAGCAGAACTGGC	CAGAACT	32	27	DLG1	-0.38	0.00692	94.72	72.84	-0.46
cl_8670_chr4	hsa-miR-145-5p	-1.46	0.002408	414.75	150.53	TTCTCCAGCCATAACAGAACTGGATAAAAGCTACTCTAGGT	AACTGGA	18	11	HS3ST1	1.95	0.00000	1.48	5.73	-2.85
cl_8886_chr4	hsa-miR-485-5p	-1.88	0.001384	12.78	3.45	AAGCAGCCTCCTTGTTTCTGTGGGTTGAGTCTCCCTAGCCT	CAGCCTC	4	12	FAM114A1	0.75	0.00566	8.53	14.38	-1.41
cl_9210_chr4	hsa-miR-4662a-5p	1.64	0.000301	0.82	2.46	TCACTTTTCTTCCTTCTCCATGAGTCGAGTTGTTTGGCTAA	TTGGCTA	34	17	C4orf22	-0.81	0.00073	4.35	2.48	-1.33
cl_9271_chr4	hsa-miR-421	1.18	0.004426	77.75	176.19	CTCACTTTGACTGTTGACAATGTCCAGCCTCTCTTATATGC	CTGTTGA	11	13	KLHL8	-0.84	0.00000	83.48	46.64	-0.99
cl_9498_chr4	hsa-miR-181b-3p	-0.88	0.018103	19.40	10.56	TCAGTGAAACTATATTTAGTTGCTAGAGGTTGTCTGGTGTA	TCAGTGA	1	13	TRAM1L1	0.63	0.00031	3.61	5.60	-0.56
cl_9498_chr4	hsa-miR-4420	-2.03	0.000161	9.58	2.34	TCAGTGAAACTATATTTAGTTGCTAGAGGTTGTCTGGTGTA	TCAGTGA	1	13	TRAM1L1	0.63	0.00031	3.61	5.60	-1.28
cl_9500_chr4	hsa-miR-409-5p	-1.67	0.004657	47.31	14.84	GAGTGTAAAGGGTGTGTAGGTGGTTCTGGTAACCAGAGCCA	GGTAACC	28	22	TRAM1L1	0.63	0.00031	3.61	5.60	-1.06
cl_9693_chr4	hsa-miR-93-3p	-2.56	0.000000	153.44	25.99	AAACTAAATTCAGCAGCGTGTGAAAAACCTTACCTACCACA	TCAGCAG	10	10	IL15	1.42	0.00000	2.55	6.85	-3.65
cl_9696_chr4	hsa-miR-204-5p	-1.38	0.014138	67.02	25.73	CAGGCCAGAACACATGCCTCTGTCGTGAAAAGGGAGGAAAA	AAAGGGA	29	21	INPP4B	2.00	0.00000	7.16	28.60	-2.76
cl_9800_chr4	hsa-miR-654-5p	-1.68	0.000699	4.43	1.38	TCCCCCCATGCCCACCCACCTGACCCCTCTTGTCCAGTCCA	GCCCACC	10	67	TRIM2	0.84	0.00027	6.23	11.13	-1.40
cl_9833_chr4	hsa-miR-130b-3p	-2.24	0.000000	701.16	148.59	TTCAATGTTCTACAGTATGGTGATCATTTTGCACTCAGTGT	TTGCACT	29	6	CTSO	1.88	0.00000	7.57	27.91	-4.21
cl_9833_chr4	hsa-miR-301a-3p	-0.65	0.023052	241.53	153.73	TTCAATGTTCTACAGTATGGTGATCATTTTGCACTCAGTGT	TTGCACT	29	6	CTSO	1.88	0.00000	7.57	27.91	-1.23
cl_9833_chr4	hsa-miR-19a-3p	-2.41	0.000000	1852.64	349.18	TTCAATGTTCTACAGTATGGTGATCATTTTGCACTCAGTGT	TTTGCAC	28	6	CTSO	1.88	0.00000	7.57	27.91	-4.53
cl_9833_chr4	hsa-miR-19b-3p	-1.82	0.000000	1655.38	468.75	TTCAATGTTCTACAGTATGGTGATCATTTTGCACTCAGTGT	TTTGCAC	28	6	CTSO	1.88	0.00000	7.57	27.91	-3.43

Data from Raji/Namalwa

CCR	miRNA	miRNA logFC	miRNA DE FDR	miRNA cpm BL	miRNA cpm nonBL	CCR Sequence	Seed Hit	Position in CCR	Read Count in Cluster	GeneID	Genes logFC	Genes DEG FDR	CPM control	CPM sample	FC Correlation
cl_10406_chr5	hsa-miR-17-3p	-2.96	0.000000	2176.96	279.17	ATTTAAATGACATCACTGCTTCTGGGAACTGCAGTGGATGG	CTGCAGT	29	41	FLT4	1.78	0.00000	4.94	17.02	-5.28
cl_10536_chr6	hsa-miR-577	-1.72	0.000050	660.86	200.99	GTCAGGTTATCTATCCATGGTCACTTGGGTGGCAATCAGCA	TTATCTA	7	13	DSP	1.88	0.00006	2.68	9.88	-3.23
cl_10546_chr6	hsa-miR-543	-2.84	0.000000	7.68	1.04	CCAGCCTCGTGTCTGACCTTTGGGGCAATGTTTACTTTGGC	AATGTTT	27	35	SLC35B3	0.36	0.00855	26.59	34.13	-1.02
cl_10612_chr6	hsa-miR-4517	-1.60	0.000287	5.06	1.68	GGAGTCTGTCACGGGCCAGCTGGGGGCATTCATATTTCCCA	CATATTT	31	10	CD83	2.00	0.00000	56.81	226.92	-3.20
cl_10649_chr6	hsa-miR-199a-3p	0.65	0.033491	809.01	1268.66	AGCAGCTTCGGAGAGACGGCTGTTTCAGGCTACTGTGCCTT	CTACTGT	30	21	KDM1B	-0.38	0.04632	53.23	40.98	-0.24

cl_10649_chr6	hsa-miR-199b-3p	0.65	0.033410	807.77	1267.49	AGCAGCTTCGGAGAGACGGCTGTTTCAGGCTACTGTGCCTT	CTACTGT	30	21	KDM1B	-0.38	0.04632	53.23	40.98	-0.25
cl_10662_chr6	hsa-miR-141-5p	2.49	0.037052	0.93	5.06	AATTAGCGCTGTGGCACCACTGTGGAAGATGAGTTGGAGGA	GAAGATG	25	27	E2F3	-0.71	0.00000	35.58	21.68	-1.78
cl_10848_chr6	hsa-miR-573	-2.99	0.000000	3.34	0.42	TGGGTGAAGTGACTTCAGTAATAACAATAATGTCAAATATC	ACTTCAG	12	40	NOTCH4	0.66	0.00658	7.87	12.42	-1.97
cl_10913_chr6	hsa-miR-625-5p	-1.31	0.000026	20.75	8.38	GGCCCCGGCGGGGCGCCCCCTCCCCTCCCCCTCCTGCGAGC	TCCCCCT	26	12	SCUBE3	0.72	0.00203	1.97	3.26	-0.95
cl_10996_chr6	hsa-miR-193b-5p	-1.17	0.019368	21.00	9.29	CTGGCCTCGGACTAATCCTATGGGGCGCTTGCAAACCCCGG	AACCCCG	34	14	FOXP4	0.54	0.00390	25.77	37.50	-0.63
cl_1120_chr1	hsa-miR-3622a-5p	3.06	0.000010	0.23	1.89	GTCCAGGACAGGTGCCTGCCTGTCGTGCGGGACCCCTATTG	GTGCCTG	12	8	DOCK7	-0.54	0.00180	28.73	19.78	-1.65
cl_11317_chr6	hsa-miR-449a	-1.36	0.000063	5.99	2.35	AATCTAATTCTACAGTCCGATGATGTTACTGCCATCTCCTC	ACTGCCA	28	1107853	RWDD2A	0.81	0.00000	2.64	4.61	-1.10
cl_11448_chr6	hsa-miR-342-5p	0.77	0.020518	31.43	53.35	CTCTCTCCCACCCCTCCCCCTCACAGATCCTTCCCTCCCCG	CACCCCT	9	26	CCNC	-0.37	0.02256	87.35	67.57	-0.28
cl_11448_chr6	hsa-miR-4677-3p	2.36	0.000008	6.84	35.21	CTCTCTCCCACCCCTCCCCCTCACAGATCCTTCCCTCCCCG	TCACAGA	21	26	CCNC	-0.37	0.02256	87.35	67.57	-0.87
cl_114_chr1	hsa-miR-138-5p	1.70	0.013928	24.26	78.83	CCTGGAGGACCAGCTCCCGCTGGGGGAGTACGGCCTCAAGC	ACCAGCT	9	22	ISG15	-1.15	0.00040	29.93	13.50	-1.95
cl_114_chr1	hsa-miR-361-3p	1.24	0.003876	615.76	1454.95	CCTGGAGGACCAGCTCCCGCTGGGGGAGTACGGCCTCAAGC	TGGGGGA	21	22	ISG15	-1.15	0.00040	29.93	13.50	-1.42
cl_11522_chr6	hsa-miR-369-3p	-1.14	0.016758	3.61	1.65	TTATTATTTTAATATAGATCTGTAACTTCGGTTCCAAGTAC	TATTATT	2	34	FIG4	0.66	0.00006	22.55	35.61	-0.75
cl_11645_chr6	hsa-miR-365a-5p	-0.99	0.047890	4.19	2.08	TTATGGCATTCGATGCAAAGTGAAGATATAAAGTCCCTTGT	AGTCCCT	32	20	RSPO3	1.14	0.00024	2.47	5.44	-1.13
cl_11799_chr6	hsa-miR-3613-3p	-0.59	0.049047	4.41	2.92	TTTTTCTTTTTTGTACAGTCTGACCATCTTTGCCTTTTAGT	TTTTTGT	8	19	STX11	1.23	0.00011	5.29	12.38	-0.73
cl_11805_chr6	hsa-miR-18a-3p	-2.46	0.000000	88.89	16.14	GGGGAGTTTGACTGGGGCAGTACACCTGTCAAACAGTAATG	GGGCAGT	15	5	UTRN	1.37	0.00000	47.31	121.93	-3.36
cl_11836_chr6	hsa-miR-577	-1.72	0.000050	660.86	200.99	ATTTATACCCTATCTCAGTCTGGAACACTTATCTAAGACCA	TTATCTA	29	49	STXBP5	0.44	0.00895	17.73	24.09	-0.76
cl_12122_chr7	hsa-miR-4420	-2.03	0.000161	9.58	2.34	GCTGTGGAGGGGGTTGGAACTGGCTGGGAGAGTCAGTGACG	CAGTGAC	34	25	PDGFA	1.26	0.00026	2.97	7.09	-2.55
cl_12131_chr7	hsa-miR-188-5p	0.79	0.036509	3.15	5.40	TTCACTATGTAGGTAAGGGATGCAAAATTTCACGGGAAATT	AGGGATG	16	5	PRKAR1B	-0.74	0.00014	51.78	31.08	-0.58
cl_1297_chr1	hsa-miR-101-5p	1.15	0.002105	4.96	11.04	TACTGGCCAGGGTAGACTAATAACTGATGGCATTTATATGC	ATAACTG	20	55	HS2ST1	-0.60	0.00045	127.84	84.23	-0.69
cl_1297_chr1	hsa-miR-10b-5p	1.65	0.000237	64964.70	203496.95	TACTGGCCAGGGTAGACTAATAACTGATGGCATTTATATGC	CAGGGTA	8	55	HS2ST1	-0.60	0.00045	127.84	84.23	-0.99
cl_1319_chr1	hsa-miR-26a-5p	2.23	0.000003	6330.25	29697.53	AATCCTGACTTGAATGCAGATGTTTGATGAAGCTTTCTGGA	ACTTGAA	8	19	ZNF326	-0.57	0.00001	44.07	29.74	-1.27
cl_1319_chr1	hsa-miR-26b-5p	0.84	0.010386	2601.75	4666.53	AATCCTGACTTGAATGCAGATGTTTGATGAAGCTTTCTGGA	ACTTGAA	8	19	ZNF326	-0.57	0.00001	44.07	29.74	-0.48
cl_1339_chr1	hsa-miR-125a-5p	1.58	0.000340	2323.77	6956.82	CCTAAGAACTGTCGAAGATCTGGAAAGTCAGGGAGAGTATC	TCAGGGA	28	22	CDC7	-1.42	0.00000	59.97	22.36	-2.25
cl_13535_chr7	hsa-miR-92a-1-5p	-1.14	0.012809	38.34	17.48	GTCCTAAGACCAACCTTTGATCATCTGTGGGCTCATGACTG	CCAACCT	10	8	TPK1	0.65	0.00069	6.02	9.43	-0.74
cl_1360_chr1	hsa-miR-944	3.11	0.000048	7.33	63.31	TTTACTTGTATTTTTATAATTTACAGTCCTAAGATCGAGGC	ATAATTT	16	21	DR1	-0.43	0.00077	91.00	67.63	-1.33
cl_13640_chr7	hsa-miR-149-5p	-1.00	0.003123	13.82	6.89	CAGCTGAGCCAGATGACTCCTAAATCCATGAAAGATGATTT	AGCCAGA	7	7	PRKAG2	0.92	0.00002	9.78	18.45	-0.91
cl_13870_chr8	hsa-miR-3648	-1.65	0.002386	7.08	2.27	AAGGAGGCGCCGCCGCCCCCTCCCCGCGGCTGCGCCCCAGC	CGCGGCT	25	11	MFHAS1	1.16	0.00014	37.05	82.57	-1.91
cl_1396_chr1	hsa-miR-3922-3p	1.24	0.017898	0.75	1.82	CCTTTCCTTATGACCAAGGTTGATTGGGCCAGAAGTGGTAT	GGCCAGA	27	13	PTBP2	-1.28	0.00000	53.86	22.22	-1.59
cl_13972_chr8	hsa-miR-379-3p	-2.39	0.000004	3.13	0.58	ATTTCTATTTGGTATTGAGTTGCTAGAGTTCTTTACATAAT	TTACATA	33	18	ASAH1	0.42	0.04097	132.15	176.21	-0.99
cl_14183_chr8	hsa-miR-485-5p	-1.88	0.001384	12.78	3.45	TTTCCCTTTGGTGGATTGGCTGAGAGGCAGCCTCTGGGGCT	AGCCTCT	29	21	KCNU1	1.70	0.00941	1.09	3.55	-3.20
cl_1462_chr1	hsa-miR-15b-3p	-0.95	0.002065	65.01	33.63	AGCAATGTTGTCATGGTTCCTCTATAGTGATTCGTATGAAG	TGATTCG	28	23	NTNG1	1.17	0.02029	2.38	5.34	-1.11

cl_1465_chr1	hsa-miR-296-5p	-1.00	0.001384	13.99	7.04	TATACACAGTGATTAAAGGTTTTGGGGCCCTAATAAATTTC	GGGCCCT	25	2847	NTNG1	1.17	0.02029	2.38	5.34	-1.16
cl_1474_chr1	hsa-miR-4687-5p	-0.90	0.006179	2.46	1.27	TGAGTCTTGAAGCCCAGGGCTGGGCCCGGGCAGAGCCGCCG	AGGGCTG	16	19825	VAV3	1.48	0.00000	12.77	35.63	-1.33
cl_14854_chr8	hsa-miR-127-5p	-1.65	0.000512	10.82	3.43	GTGAAGGTGACTGGCTTCAGTGAAGGTGTGGCAGGTGGTGT	GCTTCAG	14	6	ZFPM2	0.94	0.00126	2.86	5.50	-1.56
cl_15072_chr8	hsa-miR-181a-2-3p	-1.19	0.000679	227.17	99.88	GCGGTATAAAGAAACCTCAGTGGTTGTATCAGTCAGCTTTC	CAGTGGT	18	105	ST3GAL1	1.01	0.00000	29.05	58.53	-1.20
cl_15609_chr9	hsa-miR-3613-3p	-0.59	0.049047	4.41	2.92	GACTCGGGAGAAGGTCCACCTTTTTGTTCTATGCAGGCCTT	TTTTTGT	21	13	SHB	0.49	0.04647	3.43	4.81	-0.29
cl_1577_chr1	hsa-miR-142-5p	1.61	0.000008	14066.72	42815.44	ATGTCTTTATGGCTCTTCGAATTTAACTTTAAGAAGGAGTT	CTTTATG	5	675	BCAS2	-0.52	0.00029	19.61	13.68	-0.83
cl_15932_chr9	hsa-miR-708-5p	1.88	0.000003	14.78	54.47	TGGGCAGTCCCGAAAGCTCATTGGCCAAGCGCTCCTTCAGG	GCTCCTT	31	32	GALNT12	-0.54	0.02726	9.95	6.87	-1.01
cl_16342_chr9	hsa-miR-1304-3p	-1.38	0.000040	25.27	9.67	GAGGCCCGGGGCCCAGGGAGTGAGACCCTTGCTTCTGACTT	AGTGAGA	19	16	NTNG2	1.18	0.00012	3.25	7.38	-1.64
cl_16346_chr9	hsa-miR-4677-3p	2.36	0.000008	6.84	35.21	AGTTGGTGATCACAGATTTTTCCTCAGGATATCTGTCCGTG	TCACAGA	10	7	TTF1	-0.35	0.01097	22.60	17.68	-0.84
cl_16893_chr10	hsa-miR-3667-5p	-1.09	0.016230	1.50	0.71	GTTGACCTTAAACCGGACACTTTCTTCTTTGCGGTCTTTCC	GGTCTTT	33	6	ARHGAP12	0.65	0.00001	17.42	27.39	-0.71
cl_16894_chr10	hsa-miR-103a-2-5p	-1.50	0.000002	5.75	2.00	CACTGCTACTGGAGAAGCTTTGGGGAGCTGGCAAACTCTGA	AGAAGCT	13	42	ARHGAP12	0.65	0.00001	17.42	27.39	-0.98
cl_17530_chr10	hsa-miR-30a-3p	0.99	0.025009	59.24	117.52	TGGGTAACCACTGAAAGCATTTAAGCAAGAGAGTAACATGA	CTGAAAG	11	18	GOT1	-0.46	0.00157	30.97	22.49	-0.46
cl_17654_chr10	hsa-let-7a-5p	1.81	0.000004	5051.85	17753.96	TTTGAAAGCTTTGTCAAATCTGGGATTGTACCTCAGTTTGC	TACCTCA	29	12	SMC3	-0.73	0.00000	145.91	88.13	-1.32
cl_17654_chr10	hsa-let-7b-5p	1.71	0.000000	786.57	2572.37	TTTGAAAGCTTTGTCAAATCTGGGATTGTACCTCAGTTTGC	TACCTCA	29	12	SMC3	-0.73	0.00000	145.91	88.13	-1.24
cl_17654_chr10	hsa-let-7e-5p	1.57	0.000051	350.23	1042.74	TTTGAAAGCTTTGTCAAATCTGGGATTGTACCTCAGTTTGC	TACCTCA	29	12	SMC3	-0.73	0.00000	145.91	88.13	-1.14
cl_17654_chr10	hsa-let-7f-5p	1.13	0.000287	8944.06	19581.46	TTTGAAAGCTTTGTCAAATCTGGGATTGTACCTCAGTTTGC	TACCTCA	29	12	SMC3	-0.73	0.00000	145.91	88.13	-0.82
cl_17654_chr10	hsa-let-7g-5p	1.85	0.000001	5123.47	18520.87	TTTGAAAGCTTTGTCAAATCTGGGATTGTACCTCAGTTTGC	TACCTCA	29	12	SMC3	-0.73	0.00000	145.91	88.13	-1.35
cl_17654_chr10	hsa-let-7i-5p	1.16	0.000505	4537.30	10130.51	TTTGAAAGCTTTGTCAAATCTGGGATTGTACCTCAGTTTGC	TACCTCA	29	12	SMC3	-0.73	0.00000	145.91	88.13	-0.84
cl_17749_chr10	hsa-miR-4517	-1.60	0.000287	5.06	1.68	CTCGAGCATATTTCAGAACCTGTCCTAGTCTCAATTTCTTG	CATATTT	7	9	GRK5	0.61	0.00422	25.16	38.48	-0.98
cl_17752_chr10	hsa-miR-1254	-1.46	0.000090	5.06	1.83	AAAGAGGATTTCCAGGCTCCTGAAGCGAACGCGGTGACCAA	CCAGGCT	12	7	RGS10	0.54	0.01050	51.33	74.85	-0.79
cl_17782_chr10	hsa-miR-151a-5p	1.39	0.000409	359.84	940.64	ACCTTTCAGTCCTCGAATCCTCTCATCTCCACCACAGCTGC	TCCTCGA	10	12	TACC2	-0.79	0.02326	5.95	3.44	-1.10
cl_17782_chr10	hsa-miR-151b	3.24	0.000000	15.47	146.00	ACCTTTCAGTCCTCGAATCCTCTCATCTCCACCACAGCTGC	TCCTCGA	10	12	TACC2	-0.79	0.02326	5.95	3.44	-2.56
cl_1780_chr1	hsa-miR-582-5p	1.76	0.002936	4.61	15.62	TAAGCCATATTAAAGCTTCATGTACTGTAAAGTCAGGGATG	ACTGTAA	24	11	KCNN3	-1.63	0.00002	30.27	9.76	-2.87
cl_1780_chr1	hsa-miR-135b-5p	1.51	0.007710	1.71	4.91	TAAGCCATATTAAAGCTTCATGTACTGTAAAGTCAGGGATG	AGCCATA	3	11	KCNN3	-1.63	0.00002	30.27	9.76	-2.46
cl_1780_chr1	hsa-miR-125a-5p	1.58	0.000340	2323.77	6956.82	TAAGCCATATTAAAGCTTCATGTACTGTAAAGTCAGGGATG	TCAGGGA	33	11	KCNN3	-1.63	0.00002	30.27	9.76	-2.58
cl_18141_chr11	hsa-miR-4420	-2.03	0.000161	9.58	2.34	CTATCCTCAGAGTTCGACAGTGACGACTGAAGCTGAAGCAA	CAGTGAC	18	10	FAM160A2	0.47	0.00159	22.39	31.01	-0.95
cl_1884_chr1	hsa-miR-365a-5p	-0.99	0.047890	4.19	2.08	CTGGCCTCAGTCCCTAAAAATGATGTGGAAAGGAAAGCCCA	AGTCCCT	9	23	SLAMF8	1.21	0.00022	25.18	58.32	-1.20
cl_18870_chr11	hsa-miR-590-5p	-0.84	0.028628	6.20	3.43	CCGCATAAGCTCCAAAGGCTTGTTGGTATTCAGACCTGAGG	TAAGCTC	6	20	CCND1	1.30	0.00000	8.24	20.32	-1.09
cl_19111_chr11	hsa-miR-369-3p	-1.14	0.016758	3.61	1.65	GCCACAATTGTTTATTATTTTAGAGTTCTACATCCAAGATC	TATTATT	13	30	RAB38	1.21	0.00000	0.83	1.91	-1.37
cl_19111_chr11	hsa-miR-432-5p	-1.20	0.006297	9.90	4.31	GCCACAATTGTTTATTATTTTAGAGTTCTACATCCAAGATC	TCCAAGA	33	30	RAB38	1.21	0.00000	0.83	1.91	-1.44
cl_1917_chr1	hsa-miR-204-5p	-1.38	0.014138	67.02	25.73	ATAATGTACGTAAGGGAAGTTTTTATTAAAATGTCTCTAGA	AAGGGAA	12	14	ATF6	0.35	0.01572	36.99	47.22	-0.49

cl_19274_chr11	hsa-miR-4687-5p	-0.90	0.006179	2.46	1.27	ATCCCGAGGGCTGAAAGGTGTGTCCCTGAGAGGTGGCCCAT	AGGGCTG	7	27	NPAT	0.32	0.03492	39.17	48.90	-0.29
cl_19334_chr11	hsa-miR-3648	-1.65	0.002386	7.08	2.27	GGGGCGGGGGAGGTCGCGGCTCGGGTGGTGCCGCCGCACGG	CGCGGCT	15	53	NCAM1	1.32	0.01354	2.60	6.52	-2.18
cl_19456_chr11	hsa-miR-149-5p	-1.00	0.003123	13.82	6.89	TTGAGCCAGAATCTCACTCTTGTCACCCAGGCTGGAGTACA	AGCCAGA	4	16	THY1	0.80	0.01446	45.69	79.40	-0.80
cl_19456_chr11	hsa-miR-1254	-1.46	0.000090	5.06	1.83	TTGAGCCAGAATCTCACTCTTGTCACCCAGGCTGGAGTACA	CCAGGCT	27	16	THY1	0.80	0.01446	45.69	79.40	-1.16
cl_20048_chr12	hsa-miR-17-5p	-1.37	0.000088	1233.06	477.71	GTCTTCAAAAAGAATCACACTTTGTAGGGTAAGTTCCGAAC	CACTTTG	18	46	CNTN1	1.42	0.00009	1.68	4.48	-1.94
cl_20048_chr12	hsa-miR-20b-5p	-1.12	0.042021	59.74	27.49	GTCTTCAAAAAGAATCACACTTTGTAGGGTAAGTTCCGAAC	CACTTTG	18	46	CNTN1	1.42	0.00009	1.68	4.48	-1.58
cl_20048_chr12	hsa-miR-3609	-2.85	0.000000	596.50	83.01	GTCTTCAAAAAGAATCACACTTTGTAGGGTAAGTTCCGAAC	CACTTTG	18	46	CNTN1	1.42	0.00009	1.68	4.48	-4.03
cl_20048_chr12	hsa-miR-93-5p	-1.06	0.001859	2255.60	1081.01	GTCTTCAAAAAGAATCACACTTTGTAGGGTAAGTTCCGAAC	CACTTTG	18	46	CNTN1	1.42	0.00009	1.68	4.48	-1.50
cl_20136_chr12	hsa-miR-93-3p	-2.56	0.000000	153.44	25.99	GTTCATGGTTCCAGAGTCCGTGCAGCAGTCTCCACTCTGCA	CAGCAGT	23	27	TMBIM6	0.77	0.00000	337.05	575.37	-1.97
cl_20298_chr12	hsa-miR-4781-3p	1.58	0.000108	0.49	1.50	AAAACAAAAGCAGTCTTCTGTTTCAACATTCCCTTTATCCT	CAACATT	24	11	XRCC6BP1	-1.40	0.00000	18.50	7.01	-2.21
cl_20396_chr12	hsa-miR-708-3p	0.98	0.026809	18.72	36.79	TGACCAATCGTACTGTCAATTGATGTCCACTAGTTGTTAAT	CTAGTTG	30	107	CCT2	-1.17	0.00000	389.18	172.41	-1.15
cl_20396_chr12	hsa-miR-3681-5p	5.07	0.000000	1.82	61.30	TGACCAATCGTACTGTCAATTGATGTCCACTAGTTGTTAAT	TCCACTA	26	107	CCT2	-1.17	0.00000	389.18	172.41	-5.96
cl_2061_chr1	hsa-miR-4797-3p	-2.18	0.000008	4.00	0.85	TTCATTCACTGAGAGCTGATTGAGGGCCTCCTGCAGGAAAA	ACTGAGA	8	15	SEC16B	1.61	0.00000	1.33	4.08	-3.52
cl_20837_chr12	hsa-miR-204-5p	-1.38	0.014138	67.02	25.73	TATCATTGGTCAAACCCAACTGAAAGCCGGGGTAAGGGAAC	AAGGGAA	34	5	TBX3	1.03	0.00123	1.62	3.31	-1.42
cl_21247_chr13	hsa-miR-3200-3p	1.32	0.046718	6.16	15.43	TACATGCTAGAATTGTACCTTTCCAAGGTGAACAGAACAGC	CAAGGTG	24	6	NUPL1	-0.42	0.01829	82.94	62.03	-0.55
cl_2190_chr1	hsa-miR-3940-3p	-0.81	0.023652	4.97	2.86	TGCCAAAGGAGATTAACATGTGAGTCAACGGGCTGGGAAAG	CGGGCTG	29	6	PLA2G4A	1.33	0.00000	2.24	5.63	-1.08
cl_22095_chr14	hsa-miR-199a-5p	1.59	0.000007	181.97	548.37	CACTGGGTTCACGTTTCGATTCCGTCTGACTCTTCTGCTCA	CACTGGG	1	16	CTSG	-3.77	0.00000	23.11	1.70	-5.99
cl_22305_chr14	hsa-miR-9-3p	2.32	0.000225	2.29	11.53	GCTTTATTATTACTTATAGGTTGTAAATTTAAAGATGTTAG	GCTTTAT	1	8	CDKN3	-1.90	0.00000	69.03	18.44	-4.42
cl_22365_chr14	hsa-miR-199a-3p	0.65	0.033491	809.01	1268.66	TGCCTACTGTTTAATTAAAATATTTATTGTCAAAGTTTGAC	CTACTGT	4	556	PPM1A	-0.58	0.00001	70.25	46.92	-0.38
cl_22365_chr14	hsa-miR-199b-3p	0.65	0.033410	807.77	1267.49	TGCCTACTGTTTAATTAAAATATTTATTGTCAAAGTTTGAC	CTACTGT	4	556	PPM1A	-0.58	0.00001	70.25	46.92	-0.38
cl_22776_chr14	hsa-miR-3136-5p	1.49	0.009911	0.81	2.26	GTCGTGCTCGTCGCCCGGGCTGGAGTGCAGTCAGTGGTATG	CAGTCAG	28	5	PAPOLA	-0.34	0.00489	247.27	195.82	-0.50
cl_22776_chr14	hsa-miR-766-3p	0.67	0.048792	39.23	62.52	GTCGTGCTCGTCGCCCGGGCTGGAGTGCAGTCAGTGGTATG	CTGGAGT	20	5	PAPOLA	-0.34	0.00489	247.27	195.82	-0.23
cl_2314_chr1	hsa-miR-103a-2-5p	-1.50	0.000002	5.75	2.00	CAACAGCAGAAGCTTTGATCTGCGGATGAATTGGAGTCCTG	AGAAGCT	8	10	CHI3L1	2.27	0.00065	21.30	102.42	-3.40
cl_2314_chr1	hsa-miR-5695	-1.35	0.003064	1.44	0.54	CAACAGCAGAAGCTTTGATCTGCGGATGAATTGGAGTCCTG	TTGGAGT	31	10	CHI3L1	2.27	0.00065	21.30	102.42	-3.05
cl_23151_chr15	hsa-miR-125a-3p	1.45	0.000079	1.91	5.30	CTCAGCAGAAGCAGCACCTGTGACTTACCTTCAGGAGCCAG	CACCTGT	15	26	PAK6	-1.38	0.00000	33.22	12.78	-2.00
cl_23217_chr15	hsa-miR-106b-5p	-1.55	0.000000	617.66	211.04	TATTGATATGCTTATACACTTACACTTTATGCACAAAATGT	CACTTTA	23	27	B2M	1.21	0.00000	2723.06	6284.85	-1.87
cl_2361_chr1	hsa-miR-361-3p	1.24	0.003876	615.76	1454.95	GCAGCTGGAACATGAAAATCTGGGGGAGGGGGAAGAGAAAT	TGGGGGA	21	8	CDK18	-0.70	0.00226	13.33	8.22	-0.86
cl_24199_chr16	hsa-miR-17-3p	-2.96	0.000000	2176.96	279.17	GAGTTCTGCAGTCCGATCATTCATTCATTCAACATCCATGT	CTGCAGT	6	9	SNN	0.45	0.04468	32.10	43.77	-1.32
cl_24340_chr16	hsa-miR-577	-1.72	0.000050	660.86	200.99	TGCTTATCTAGAGAATTCCTTAACCTCAACACGGCGTGGTA	TTATCTA	4	24	PRKCB	0.66	0.01255	128.23	202.93	-1.14
cl_25137_chr16	hsa-miR-150-3p	3.38	0.000000	3.49	36.47	CAGCCGATTCAAGGCTGATGTACCAGCACCGCAGGGACCCT	GTACCAG	20	506	CPNE7	-1.66	0.00041	11.98	3.79	-5.62
cl_25269_chr17	hsa-miR-3940-3p	-0.81	0.023652	4.97	2.86	CTCTGAGGTGGGCTCTGGGGTGGTCGGGCTGGGGGCGGGCT	CGGGCTG	25	117	GP1BA	2.62	0.00000	1.96	12.06	-2.12

cl_2572_chr1	hsa-miR-4424	3.24	0.000289	2.58	24.40	GCTTTGAAGTTAACTCTGGGTTTGACTCTAGTTTGACATTT	TAACTCT	11	67	ENAH	-0.92	0.00244	22.95	12.12	-2.98
cl_25774_chr17	hsa-miR-641	-0.72	0.009573	7.16	4.36	GAGCCCTCTAGCCACCCGACTTGTCTTTAATGCCTATAAAA	TGTCTTT	22	11	PLXDC1	1.03	0.00012	7.64	15.58	-0.75
cl_25782_chr17	hsa-miR-3622a-5p	3.06	0.000010	0.23	1.89	CATGTAACTGTGTGTGTATGTGTACACGTGCGCGTGCCTGC	GTGCCTG	34	21	CACNB1	-0.39	0.04198	9.52	7.28	-1.19
cl_26121_chr17	hsa-miR-421	1.18	0.004426	77.75	176.19	ATAAAACAGCACTCCGCAAATGTCTGTTGATCTTATTATTA	TGTTGAT	25	13	MSI2	-0.86	0.00002	192.37	106.13	-1.01
cl_26300_chr17	hsa-miR-369-3p	-1.14	0.016758	3.61	1.65	ATACTACCTATTATTTTACCATTTTTCATAAATCCAAGAAC	TATTATT	9	355	ABCA9	1.00	0.02595	4.27	8.53	-1.14
cl_26300_chr17	hsa-miR-432-5p	-1.20	0.006297	9.90	4.31	ATACTACCTATTATTTTACCATTTTTCATAAATCCAAGAAC	TCCAAGA	33	355	ABCA9	1.00	0.02595	4.27	8.53	-1.19
cl_26499_chr17	hsa-miR-204-5p	-1.38	0.014138	67.02	25.73	CCACCGTGCCCAGCCTCAAATAATGTATGGAAGGGAAGTTC	AAGGGAA	31	6	TBC1D16	0.98	0.00007	5.76	11.33	-1.35
cl_27100_chr18	hsa-miR-1295a	-1.77	0.001363	16.54	4.85	GGTGCAGAGGTCAGGAGGAATATCCATTTCCCTGGCCTAAT	GGCCTAA	34	17	TCF4	1.44	0.00002	126.93	343.87	-2.54
cl_27264_chr18	hsa-miR-211-5p	4.32	0.000000	0.08	1.66	CCTTTTTCTCTGAAGTCTCTTAAGGGAAGAATATATATTTT	AAGGGAA	22	9	CYB5A	-0.82	0.00219	39.78	22.60	-3.53
cl_27296_chr18	hsa-miR-3136-5p	1.49	0.009911	0.81	2.26	ACAACCGGCCTCCCAGTCAGTTCCTTCCCGGGGCTCTCAGA	CAGTCAG	14	24	ZNF516	-1.04	0.00000	33.81	16.43	-1.55
cl_27296_chr18	hsa-miR-30b-3p	1.06	0.009573	2.25	4.76	ACAACCGGCCTCCCAGTCAGTTCCTTCCCGGGGCTCTCAGA	CTCCCAG	10	24	ZNF516	-1.04	0.00000	33.81	16.43	-1.10
cl_27296_chr18	hsa-miR-30c-2-3p	0.84	0.035995	5.28	9.42	ACAACCGGCCTCCCAGTCAGTTCCTTCCCGGGGCTCTCAGA	CTCCCAG	10	24	ZNF516	-1.04	0.00000	33.81	16.43	-0.88
cl_27438_chr19	hsa-miR-3648	-1.65	0.002386	7.08	2.27	CCCCAACAGGCCACCCTGTGTGCGCGCCGCGGCTGCATGGA	CGCGGCT	28	39	APC2	0.62	0.00028	6.56	10.04	-1.01
cl_27438_chr19	hsa-miR-663b	-1.67	0.001109	4.93	1.56	CCCCAACAGGCCACCCTGTGTGCGCGCCGCGGCTGCATGGA	GGCCACC	9	39	APC2	0.62	0.00028	6.56	10.04	-1.02
cl_27561_chr19	hsa-miR-3194-5p	-1.19	0.004724	6.37	2.74	AGAGCTCCGGGGTCGTGGGATCCTGAGGCTGGCCTTGCCCC	GCTGGCC	28	17	STAP2	1.47	0.00000	1.93	5.34	-1.75
cl_27724_chr19	hsa-miR-2467-5p	1.46	0.003890	3.95	10.85	ACTGTTCAATGGAGCCTCAATGGCCTCACCCTACTTTTCTA	AGCCTCA	13	20	SMARCA4	-2.37	0.00000	603.25	116.79	-3.46
cl_27741_chr19	hsa-miR-3605-3p	0.78	0.043923	3.22	5.54	CCATGGCTACGGGGAGCTGGTAAAAACTGCCACGGAGGCAA	ACGGAGG	32	439	ECSIT	-1.00	0.00000	62.21	31.13	-0.78
cl_27741_chr19	hsa-miR-34a-5p	1.22	0.000260	144.34	336.94	CCATGGCTACGGGGAGCTGGTAAAAACTGCCACGGAGGCAA	ACTGCCA	26	439	ECSIT	-1.00	0.00000	62.21	31.13	-1.22
cl_27987_chr19	hsa-miR-873-5p	2.65	0.000001	0.27	1.79	GTTTATTTAATATGGCCGTTTTTACTTCCTGCAGAAAGGGT	TTCCTGC	26	18	ZNF726	-1.22	0.00001	12.52	5.38	-3.24
cl_27988_chr19	hsa-miR-708-3p	0.98	0.026809	18.72	36.79	TATTTGTTAATGTACATAAATGTTGCCAACTAGTTGTAATG	CTAGTTG	30	13	ZNF726	-1.22	0.00001	12.52	5.38	-1.19
cl_28234_chr19	hsa-miR-2355-5p	0.92	0.009772	10.03	18.95	TGTTCGTTGGGGATTCAACATGGCGGCGGGAGTGTCCGCGG	TGGGGAT	8	37	PAK4	-0.54	0.00004	19.47	13.37	-0.50
cl_28628_chr19	hsa-miR-374b-3p	0.94	0.035995	6.48	12.41	AGTCGGAATCTGCTAAGGAGTGTGTAATAGCCCAACTGCTG	TGCTAAG	11	63	FCAR	-1.22	0.00904	2.38	1.02	-1.15
cl_2878_chr2	hsa-miR-361-5p	0.91	0.009573	96.05	180.08	AGTAGAACAAATGTTTTTACTCTACTGATAAAGTACAGGAA	CTGATAA	25	6	TMEM18	-0.44	0.00450	32.72	24.19	-0.39
cl_28867_chr20	hsa-miR-4687-5p	-0.90	0.006179	2.46	1.27	TTCAAAGCTCAAAGGATCTTTTGGTATGCCTAGGGCTGGGA	AGGGCTG	32	18	PLCB4	1.07	0.00004	3.46	7.28	-0.96
cl_29355_chr20	hsa-miR-296-3p	-1.98	0.000000	6.56	1.66	TTCCATCCCATAAATCTGTTTGAATCCAACCCTCTCCAGCA	AACCCTC	28	18	KCNG1	1.95	0.00005	0.41	1.58	-3.87
cl_29374_chr20	hsa-miR-335-3p	-2.49	0.000000	566.47	100.76	ATGAAAAAAAAAAAAGAACTTTTCTGCTAGGAAGATTATAC	TGAAAAA	2	14	TSHZ2	1.88	0.00000	4.94	18.12	-4.67
cl_29517_chr20	hsa-miR-4755-3p	-1.99	0.000050	2.99	0.74	CCTGGCTCTGCTCAGGTGACTGGTCTGAAAGGCGCTCTGAG	CCTGGCT	1	5	OSBPL2	0.46	0.00055	23.15	31.92	-0.92
cl_30430_chr22	hsa-miR-625-5p	-1.31	0.000026	20.75	8.38	TCCCTCTCCCTCTCTCTCTCTCCCCCTCCCTCTTTCTCTCT	TCCCCCT	21	13	SSTR3	1.83	0.00003	0.99	3.53	-2.40
cl_30489_chr22	hsa-miR-361-3p	1.24	0.003876	615.76	1454.95	AGTCAGGCTGGGGGACTTGTTTGAAAGAAAGAGGAGTGGAA	TGGGGGA	9	19	TAB1	-0.32	0.00659	32.80	26.27	-0.40
cl_30740_chr22	hsa-miR-4487	-1.24	0.005006	1.62	0.68	TGTGTGCCCACCGTGGCTGTTGTCAGCTCTTGTCCTGCGGC	CAGCTCT	24	20	SHANK3	0.77	0.00854	11.89	20.26	-0.96
cl_31173_chrX	hsa-miR-424-5p	-1.81	0.000003	177.32	50.51	CGAGGCTGCTGGGAAAACCCTGACTTCTGGCAGGGCACCCC	GCTGCTG	5	5	ZXDA	0.80	0.00001	4.00	6.96	-1.45

cl_3123_chr2	hsa-miR-4687-5p	-0.90	0.006179	2.46	1.27	GCCACTCTGCTCAGATGCCGTGGAGGGCTGCAACTTCTCAG	AGGGCTG	24	25	KLHL29	0.97	0.00202	4.77	9.33	-0.87
cl_31402_chrX	hsa-miR-204-5p	-1.38	0.014138	67.02	25.73	TGAAGGGAAGGACACAATCCTGGCTGGCTCCACCACCTGCT	AAGGGAA	3	17	ARMCX2	2.22	0.00000	4.98	23.20	-3.07
cl_31402_chrX	hsa-miR-4755-3p	-1.99	0.000050	2.99	0.74	TGAAGGGAAGGACACAATCCTGGCTGGCTCCACCACCTGCT	CCTGGCT	19	17	ARMCX2	2.22	0.00000	4.98	23.20	-4.41
cl_31548_chrX	hsa-miR-19a-3p	-2.41	0.000000	1852.64	349.18	GCATTTATCACTTCCAAATCTAACTTTGCACAAGTAACCCA	TTGCACA	26	10	UBE2A	0.64	0.00014	52.47	81.77	-1.54
cl_31548_chrX	hsa-miR-19b-3p	-1.82	0.000000	1655.38	468.75	GCATTTATCACTTCCAAATCTAACTTTGCACAAGTAACCCA	TTGCACA	26	10	UBE2A	0.64	0.00014	52.47	81.77	-1.16
cl_31919_chrY	hsa-miR-345-5p	1.22	0.000700	68.98	161.32	CCTATGTTCACTCAAGGCCCTAGAGTTCTACAGTCAGCAGA	AGTCAGC	32	22	TMSB4Y	-1.02	0.03634	1.59	0.78	-1.25
cl_31919_chrY	hsa-miR-3136-5p	1.49	0.009911	0.81	2.26	CCTATGTTCACTCAAGGCCCTAGAGTTCTACAGTCAGCAGA	CAGTCAG	31	22	TMSB4Y	-1.02	0.03634	1.59	0.78	-1.52
cl_328_chr1	hsa-miR-190b	1.18	0.000093	1.38	3.12	AAAGTCTCAGGTCTTGTTCTTGAATTTACATATCAATATTA	CATATCA	29	24	PEX14	-0.39	0.00157	22.59	17.23	-0.46
cl_328_chr1	hsa-miR-548b-3p	2.90	0.000000	0.27	2.10	AAAGTCTCAGGTCTTGTTCTTGAATTTACATATCAATATTA	GTTCTTG	16	24	PEX14	-0.39	0.00157	22.59	17.23	-1.13
cl_336_chr1	hsa-miR-27b-5p	-0.99	0.003393	21.19	10.62	CCCCAAGCTCTCTCGAGTCCTGTCCCTTCCGCCATTCCTCT	AAGCTCT	5	102	CASZ1	0.55	0.02186	7.31	10.72	-0.55
cl_3881_chr2	hsa-miR-708-5p	1.88	0.000003	14.78	54.47	GGCTCCTTTTTGTGAATCCTTAAAAACTCAACTCTAGGAAG	GCTCCTT	2	16	EIF5B	-0.68	0.00006	199.47	124.38	-1.28
cl_4174_chr2	hsa-miR-4797-3p	-2.18	0.000008	4.00	0.85	CAAACATTGACACTGAGATTTGCAGTGAGAGAAAGAAAGGT	ACTGAGA	12	13	BIN1	1.04	0.00041	31.57	64.86	-2.27
cl_4174_chr2	hsa-miR-1304-3p	-1.38	0.000040	25.27	9.67	CAAACATTGACACTGAGATTTGCAGTGAGAGAAAGAAAGGT	AGTGAGA	24	13	BIN1	1.04	0.00041	31.57	64.86	-1.44
cl_4174_chr2	hsa-miR-181b-3p	-0.88	0.018103	19.40	10.56	CAAACATTGACACTGAGATTTGCAGTGAGAGAAAGAAAGGT	CAGTGAG	23	13	BIN1	1.04	0.00041	31.57	64.86	-0.92
cl_4301_chr2	hsa-miR-449a	-1.36	0.000063	5.99	2.35	GGAGGGGAGATGGACTGCCATAAAGGAATAACGTGATCACT	ACTGCCA	14	5	MGAT5	0.69	0.00911	72.14	116.59	-0.94
cl_4330_chr2	hsa-miR-92a-3p	-1.64	0.000068	115704.25	37245.94	CCTATCATCTGCAATATTAATGTAATTAGACAATATAACAT	TGCAATA	10	15	SPOPL	0.44	0.01271	25.42	34.55	-0.72
cl_4454_chr2	hsa-miR-4755-3p	-1.99	0.000050	2.99	0.74	ACAGAACTTTAACCTGGCTTTGCCAGTCCGACGCTCTCAAC	CCTGGCT	13	6	GPD2	0.50	0.02392	19.89	28.05	-0.99
cl_4606_chr2	hsa-miR-944	3.11	0.000048	7.33	63.31	CAGCTTTGCTTCTGATAATTTTGCAAACACGGTAAGTGCTG	ATAATTT	15	24	CDCA7	-1.69	0.00000	223.39	69.27	-5.25
cl_4606_chr2	hsa-miR-361-5p	0.91	0.009573	96.05	180.08	CAGCTTTGCTTCTGATAATTTTGCAAACACGGTAAGTGCTG	CTGATAA	12	24	CDCA7	-1.69	0.00000	223.39	69.27	-1.53
cl_4774_chr2	hsa-miR-944	3.11	0.000048	7.33	63.31	AATTTTGTTATCCATGTGCATAATTTACCTCATGATTTCTT	ATAATTT	20	18	MARS2	-0.69	0.00001	15.27	9.49	-2.13
cl_4774_chr2	hsa-let-7a-5p	1.81	0.000004	5051.85	17753.96	AATTTTGTTATCCATGTGCATAATTTACCTCATGATTTCTT	TACCTCA	26	18	MARS2	-0.69	0.00001	15.27	9.49	-1.24
cl_4774_chr2	hsa-let-7b-5p	1.71	0.000000	786.57	2572.37	AATTTTGTTATCCATGTGCATAATTTACCTCATGATTTCTT	TACCTCA	26	18	MARS2	-0.69	0.00001	15.27	9.49	-1.17
cl_4774_chr2	hsa-let-7e-5p	1.57	0.000051	350.23	1042.74	AATTTTGTTATCCATGTGCATAATTTACCTCATGATTTCTT	TACCTCA	26	18	MARS2	-0.69	0.00001	15.27	9.49	-1.08
cl_4774_chr2	hsa-let-7f-5p	1.13	0.000287	8944.06	19581.46	AATTTTGTTATCCATGTGCATAATTTACCTCATGATTTCTT	TACCTCA	26	18	MARS2	-0.69	0.00001	15.27	9.49	-0.78
cl_4774_chr2	hsa-let-7g-5p	1.85	0.000001	5123.47	18520.87	AATTTTGTTATCCATGTGCATAATTTACCTCATGATTTCTT	TACCTCA	26	18	MARS2	-0.69	0.00001	15.27	9.49	-1.27
cl_4774_chr2	hsa-let-7i-5p	1.16	0.000505	4537.30	10130.51	AATTTTGTTATCCATGTGCATAATTTACCTCATGATTTCTT	TACCTCA	26	18	MARS2	-0.69	0.00001	15.27	9.49	-0.80
cl_5545_chr3	hsa-miR-335-5p	-1.09	0.000328	118.94	55.71	TGACTGCTAAAGGATACTCTTGAGAGTACTCTTAAGTACTC	CTCTTGA	17	14	EOMES	1.42	0.00043	8.75	23.44	-1.55
cl_5563_chr3	hsa-miR-4487	-1.24	0.005006	1.62	0.68	AAAAGGTCACAGCTCTAGTCTGACGATCTTCTCTACAGCTA	CAGCTCT	10	16	TGFBR2	0.87	0.00013	71.25	130.06	-1.08
cl_568_chr1	hsa-miR-20a-3p	-2.86	0.000000	28.86	3.93	GTTTGGGGGAGTCGGGAGGATGCAGTCTCTTTGCAGCAGTG	ATGCAGT	20	339	RUNX3	0.43	0.02380	59.56	80.13	-1.23
cl_568_chr1	hsa-miR-93-3p	-2.56	0.000000	153.44	25.99	GTTTGGGGGAGTCGGGAGGATGCAGTCTCTTTGCAGCAGTG	CAGCAGT	34	339	RUNX3	0.43	0.02380	59.56	80.13	-1.10
cl_5974_chr3	hsa-miR-34a-3p	0.99	0.002408	1.08	2.19	ATAAATCCAGCCGTCCCGACTAATGCCTGATTGCATATTTA	CTGATTG	27	21	CADPS	-4.03	0.00000	74.14	4.55	-4.00

cl_601_chr1	hsa-miR-145-5p	-1.46	0.002408	414.75	150.53	CTTTGTCCTGAATGTGCTATTGCTACATGACTGGACTAGGC	ACTGGAC	30	18	PIGV	0.47	0.00257	7.90	10.94	-0.69
cl_6214_chr3	hsa-miR-9-3p	2.32	0.000225	2.29	11.53	TTTTATCTATAATAGCTTTATCAACTCTTTTTCCGATGCTC	GCTTTAT	15	13	TOMM70A	-0.34	0.04086	80.97	64.16	-0.78
cl_6383_chr3	hsa-miR-641	-0.72	0.009573	7.16	4.36	TCTTGTCTTTGGTTTCAGAGTGGGGTATGTAAGCGAGGTAT	TGTCTTT	4	24	ILDR1	1.82	0.00000	2.27	8.00	-1.32
cl_648_chr1	hsa-miR-378a-3p	-1.54	0.000000	2405.55	827.87	TAGAGTCCAGTGAAGAATGATGCGGTAGCCTTGACCACATC	GTCCAGT	5	5	PTPRU	1.00	0.00078	2.27	4.55	-1.54
cl_648_chr1	hsa-miR-378c	-1.27	0.000000	300.43	124.57	TAGAGTCCAGTGAAGAATGATGCGGTAGCCTTGACCACATC	GTCCAGT	5	5	PTPRU	1.00	0.00078	2.27	4.55	-1.28
cl_648_chr1	hsa-miR-378d	-1.10	0.003182	14.73	6.83	TAGAGTCCAGTGAAGAATGATGCGGTAGCCTTGACCACATC	GTCCAGT	5	5	PTPRU	1.00	0.00078	2.27	4.55	-1.10
cl_648_chr1	hsa-miR-378i	-2.12	0.000031	7.69	1.78	TAGAGTCCAGTGAAGAATGATGCGGTAGCCTTGACCACATC	GTCCAGT	5	5	PTPRU	1.00	0.00078	2.27	4.55	-2.13
cl_6528_chr3	hsa-miR-135b-5p	1.51	0.007710	1.71	4.91	GATCGATACAGCCATAACTCTTCTCTCGTCTGTGGTTCACT	AGCCATA	10	16	COL6A6	-2.17	0.00000	6.96	1.55	-3.27
cl_6528_chr3	hsa-miR-4424	3.24	0.000289	2.58	24.40	GATCGATACAGCCATAACTCTTCTCTCGTCTGTGGTTCACT	TAACTCT	15	16	COL6A6	-2.17	0.00000	6.96	1.55	-7.01
cl_6580_chr3	hsa-miR-708-5p	1.88	0.000003	14.78	54.47	CTGCCTGTCTGGGATCTGTGTGTCTGGATCAGCTCCTTTTA	GCTCCTT	32	48	PPP2R3A	-0.39	0.03582	6.43	4.90	-0.74
cl_6601_chr3	hsa-miR-1304-3p	-1.38	0.000040	25.27	9.67	GGTCTCTGTTCTACATCAGCTGATCTGCTTCCAGTGAGACT	AGTGAGA	33	8	MRAS	0.66	0.01123	6.48	10.25	-0.92
cl_6601_chr3	hsa-miR-181b-3p	-0.88	0.018103	19.40	10.56	GGTCTCTGTTCTACATCAGCTGATCTGCTTCCAGTGAGACT	CAGTGAG	32	8	MRAS	0.66	0.01123	6.48	10.25	-0.58
cl_6952_chr3	hsa-miR-641	-0.72	0.009573	7.16	4.36	TTGAAGTGTTTGTGATGCTTTACAAATGTCTTTTTTAGTGT	TGTCTTT	27	18	TTC14	0.94	0.00000	71.79	137.32	-0.68
cl_7186_chr3	hsa-miR-2467-5p	1.46	0.003890	3.95	10.85	TTAATGGCACCCACCGGGCCTGGGTGGAGCCTCAGCACCAC	AGCCTCA	28	5	DLG1	-0.38	0.00692	94.72	72.84	-0.55
cl_7449_chr4	hsa-miR-101-5p	1.15	0.002105	4.96	11.04	ATAACTGGGCTTAAAGGGCATTGAAAAGGATGAATTCTGGT	ATAACTG	1	20	GPR125	-1.08	0.00444	8.24	3.89	-1.25
cl_7963_chr4	hsa-miR-204-5p	-1.38	0.014138	67.02	25.73	GACCCAAGGGAACCCTGTACTGCCCACCCTTAGAGATACTA	AAGGGAA	6	23	FAM13A	0.62	0.01100	9.41	14.43	-0.85
cl_7967_chr4	hsa-miR-641	-0.72	0.009573	7.16	4.36	GAGTTCTACAGCCCCATGATTAGGTCTGTCTTTTAGTGAGC	TGTCTTT	27	10	FAM13A	0.62	0.01100	9.41	14.43	-0.45
cl_8073_chr4	hsa-miR-1295a	-1.77	0.001363	16.54	4.85	GTGAGCACAATGCTAGGGCCTAAAAGATGGTGAACTATGCC	GGCCTAA	17	1519	DKK2	0.66	0.00754	1.00	1.58	-1.17
cl_8148_chr4	hsa-miR-4767	1.69	0.000000	1.09	3.49	GCCCGCGCGACTCTCGACAATGGACAGTGTACAGTGGTGGC	GCCCGCG	1	19	UGT8	-1.45	0.00000	15.21	5.56	-2.45
cl_8417_chr4	hsa-miR-378a-3p	-1.54	0.000000	2405.55	827.87	TCCCCCCATGCCCACCCACCTGACCCCTCTTGTCCAGTCCA	GTCCAGT	32	11	TRIM2	0.84	0.00027	6.23	11.13	-1.29
cl_8417_chr4	hsa-miR-378c	-1.27	0.000000	300.43	124.57	TCCCCCCATGCCCACCCACCTGACCCCTCTTGTCCAGTCCA	GTCCAGT	32	11	TRIM2	0.84	0.00027	6.23	11.13	-1.06
cl_8417_chr4	hsa-miR-378d	-1.10	0.003182	14.73	6.83	TCCCCCCATGCCCACCCACCTGACCCCTCTTGTCCAGTCCA	GTCCAGT	32	11	TRIM2	0.84	0.00027	6.23	11.13	-0.92
cl_8417_chr4	hsa-miR-378i	-2.12	0.000031	7.69	1.78	TCCCCCCATGCCCACCCACCTGACCCCTCTTGTCCAGTCCA	GTCCAGT	32	11	TRIM2	0.84	0.00027	6.23	11.13	-1.78
cl_8476_chr4	hsa-miR-641	-0.72	0.009573	7.16	4.36	GAAACGTGTGCCCTATCGATTCTTTGTCTTTGGATTCCTGA	TGTCTTT	25	15	RAPGEF2	0.54	0.01964	19.98	29.01	-0.39
cl_8478_chr4	hsa-miR-4517	-1.60	0.000287	5.06	1.68	TTTTGTTCATTGTTAAGTATTCATATTTTTGTACTCGGCTG	CATATTT	22	5	RAPGEF2	0.54	0.01964	19.98	29.01	-0.86
cl_8478_chr4	hsa-miR-3613-3p	-0.59	0.049047	4.41	2.92	TTTTGTTCATTGTTAAGTATTCATATTTTTGTACTCGGCTG	TTTTTGT	26	5	RAPGEF2	0.54	0.01964	19.98	29.01	-0.32
cl_8601_chr4	hsa-miR-211-5p	4.32	0.000000	0.08	1.66	CGAAGGGAAGGACTCAGTCCTAGCATACTCCTCTTTCCCTC	AAGGGAA	3	16	SPCS3	-0.38	0.00566	120.61	92.93	-1.63
cl_9065_chr5	hsa-miR-132-3p	-0.85	0.002610	123.76	68.55	TACAATTTTCATTTATAACGTGGAAAAGTTAACTGTTAGGT	ACTGTTA	32	14	LIFR	2.68	0.00000	6.19	39.77	-2.28
cl_9231_chr5	hsa-miR-3157-3p	0.92	0.008752	0.73	1.44	GGTCTAATATGTTATAAAAATAATGTATGTAAGGGCAGAAA	AGGGCAG	32	5	NLN	-0.69	0.00747	36.39	22.54	-0.64
cl_9251_chr5	hsa-miR-3667-3p	-1.36	0.008075	1.56	0.64	GTTACAAGCTTCCAGGAAGGTTCTGAGATAGCTGGTTCTGG	GGAAGGT	15	26	CD180	0.69	0.03903	50.22	81.05	-0.94
cl_9251_chr5	hsa-miR-589-3p	-1.73	0.000002	17.95	5.34	GTTACAAGCTTCCAGGAAGGTTCTGAGATAGCTGGTTCTGG	GTTCTGA	20	26	CD180	0.69	0.03903	50.22	81.05	-1.19

cl_9476_chr5	hsa-miR-200c-3p	3.71	0.000013	13.86	181.49	ACCGCTCGGAATAGTTTAAATGTAGTATTAACTATGAAGAG	AGTATTA	24	5	ANKRD32	-0.60	0.00000	33.05	21.73	-2.25
cl_9476_chr5	hsa-miR-615-3p	2.51	0.000000	2.50	14.25	ACCGCTCGGAATAGTTTAAATGTAGTATTAACTATGAAGAG	GCTCGGA	4	5	ANKRD32	-0.60	0.00000	33.05	21.73	-1.52
cl_9645_chr5	hsa-miR-4677-3p	2.36	0.000008	6.84	35.21	GGCAACCTCAACCAATTTGTTGCCATGTTCACAGAAAACTT	TCACAGA	29	14	CCDC112	-0.89	0.00000	17.86	9.64	-2.10
cl_10531_chr6	hsa-miR-4755-3p	-1.99	0.000050	2.99	0.74	TGTCCTCTGAACGCACAGCCTGGCAGAGTGGAACGAAGCCA	GCCTGGC	18	5	RREB1	0.58	0.00256	19.49	29.03	-1.14
cl_10546_chr6	hsa-miR-485-5p	-1.88	0.001384	12.78	3.45	CCAGCCTCGTGTCTGACCTTTGGGGCAATGTTTACTTTGGC	CAGCCTC	2	35	SLC35B3	0.36	0.00855	26.59	34.13	-0.68
cl_10881_chr6	hsa-miR-4767	1.69	0.000000	1.09	3.49	CTCCGCGAGCGGCTCCGGGGTGACGCCCGCCGGAGAGCTGG	CGCCCGC	24	8	ITPR3	-0.46	0.00832	180.31	131.23	-0.77
cl_11017_chr6	hsa-miR-4662a-5p	1.64	0.000301	0.82	2.46	GCCTCTGGCAGGTACTGGATTGGCTAGGGAGACTAGGAGGG	TTGGCTA	20	9	MRPS10	-0.38	0.01960	22.58	17.36	-0.62
cl_11334_chr6	hsa-miR-299-3p	-1.46	0.003877	4.09	1.48	TGCCCACATCGTTCTACAGATCGACAATGCCCGTCTTGCTG	CCCACAT	3	64	NT5E	0.92	0.00981	4.87	9.18	-1.34
cl_11367_chr6	hsa-let-7b-3p	1.17	0.001317	16.34	36.79	TATTTGTATACTTCTAGGGGTCTGGTGGTTCTAGCGACTGA	TTGTATA	4	41	PM20D2	-1.10	0.00000	57.20	26.62	-1.29
cl_11448_chr6	hsa-miR-30c-2-3p	0.84	0.035995	5.28	9.42	CTCTCTCCCACCCCTCCCCCTCACAGATCCTTCCCTCCCCG	TCTCCCA	4	26	CCNC	-0.37	0.02256	87.35	67.57	-0.31
cl_11508_chr6	hsa-miR-374c-5p	3.26	0.001459	0.66	6.22	CCCAGGTGTATTAAGTTATCTGCCTGGGGTCATATAACTCC	TGTATTA	7	14	ARMC2	-1.00	0.00000	54.26	27.17	-3.25
cl_12122_chr7	hsa-miR-181b-3p	-0.88	0.018103	19.40	10.56	GCTGTGGAGGGGGTTGGAACTGGCTGGGAGAGTCAGTGACG	TCAGTGA	33	25	PDGFA	1.26	0.00026	2.97	7.09	-1.11
cl_12492_chr7	hsa-miR-365a-5p	-0.99	0.047890	4.19	2.08	TCTCTGCTTAAGTCCCAGAATTTAGCAGAGATGCTTTTTTT	AAGTCCC	10	30	WIPF3	0.83	0.01049	0.96	1.72	-0.83
cl_13489_chr7	hsa-miR-411-5p	-1.33	0.024549	47.59	18.90	GGACAGTTGGTGCAGTCTACTGGAGAGGACCACACCCTTCC	GTCTACT	15	21	TMEM178B	1.29	0.00008	2.65	6.48	-1.71
cl_13581_chr7	hsa-miR-29a-3p	0.97	0.019370	4902.45	9611.91	CACAACCGTGTCGGTCTCACTGGTGCTGTGAGTGCAGCTGA	TGGTGCT	21	21	ZNF777	-0.35	0.01738	15.23	11.94	-0.34
cl_13581_chr7	hsa-miR-29b-3p	1.97	0.000004	156.65	614.17	CACAACCGTGTCGGTCTCACTGGTGCTGTGAGTGCAGCTGA	TGGTGCT	21	21	ZNF777	-0.35	0.01738	15.23	11.94	-0.69
cl_13581_chr7	hsa-miR-29c-3p	1.51	0.002622	1205.13	3424.74	CACAACCGTGTCGGTCTCACTGGTGCTGTGAGTGCAGCTGA	TGGTGCT	21	21	ZNF777	-0.35	0.01738	15.23	11.94	-0.53
cl_13745_chr7	hsa-miR-127-5p	-1.65	0.000512	10.82	3.43	AGCGGCTAATGAGCTTCACATAGACTTTTAAATGTCCAGAA	AGCTTCA	12	31	PTPRN2	0.93	0.00066	8.05	15.36	-1.54
cl_13801_chr8	hsa-miR-641	-0.72	0.009573	7.16	4.36	ATGTCTTAAAGTTCCTAACCTGGGGAACTGATACATCCCTC	ATGTCTT	1	8	ARHGEF10	1.05	0.00023	6.25	13.00	-0.76
cl_13910_chr8	hsa-miR-4677-3p	2.36	0.000008	6.84	35.21	TGTTCCACTGTCCGACGATTTGGGAATGAGACTCACAGTTC	CTCACAG	32	148	FAM167A	-3.14	0.00000	88.76	10.07	-7.42
cl_144_chr1	hsa-miR-296-5p	-1.00	0.001384	13.99	7.04	GCCCTAGTAAGTCCAAACGGTACCACCAGGAGTGGGGCCCC	GGGGCCC	34	17	CCR6	1.54	0.00369	6.12	17.76	-1.53
cl_1462_chr1	hsa-miR-625-3p	-0.95	0.012667	40.61	21.02	AGCAATGTTGTCATGGTTCCTCTATAGTGATTCGTATGAAG	CTATAGT	22	23	NTNG1	1.17	0.02029	2.38	5.34	-1.11
cl_14669_chr8	hsa-miR-151a-3p	0.87	0.011732	2221.72	4062.80	CTTTTATTGGATAAAAGTTATTGCAGTCTAATACAATTTTT	CAGTCTA	24	9	MMP16	-0.86	0.00792	2.21	1.22	-0.74
cl_14854_chr8	hsa-miR-181b-3p	-0.88	0.018103	19.40	10.56	GTGAAGGTGACTGGCTTCAGTGAAGGTGTGGCAGGTGGTGT	TCAGTGA	17	6	ZFPM2	0.94	0.00126	2.86	5.50	-0.83
cl_14854_chr8	hsa-miR-4420	-2.03	0.000161	9.58	2.34	GTGAAGGTGACTGGCTTCAGTGAAGGTGTGGCAGGTGGTGT	TCAGTGA	17	6	ZFPM2	0.94	0.00126	2.86	5.50	-1.91
cl_15932_chr9	hsa-miR-548s	1.29	0.011693	0.70	1.77	TGGGCAGTCCCGAAAGCTCATTGGCCAAGCGCTCCTTCAGG	TTGGCCA	21	32	GALNT12	-0.54	0.02726	9.95	6.87	-0.69
cl_16040_chr9	hsa-miR-3940-3p	-0.81	0.023652	4.97	2.86	GGGCCGGGCTCGGCTGGCGGTGGGGCGGGGGCCGCCGGGAC	CCGGGCT	4	7	LPAR1	2.25	0.00000	4.11	19.50	-1.82
cl_16040_chr9	hsa-miR-3194-5p	-1.19	0.004724	6.37	2.74	GGGCCGGGCTCGGCTGGCGGTGGGGCGGGGGCCGCCGGGAC	GGCTGGC	12	7	LPAR1	2.25	0.00000	4.11	19.50	-2.68
cl_16303_chr9	hsa-miR-130b-5p	-2.01	0.000006	211.10	52.39	AGCCACACATGGCTTCTGTGTTGGAAAGAGCGGCCATAGAA	GAAAGAG	24	11	FNBP1	1.91	0.00000	77.52	291.85	-3.84
cl_16342_chr9	hsa-miR-296-5p	-1.00	0.001384	13.99	7.04	GAGGCCCGGGGCCCAGGGAGTGAGACCCTTGCTTCTGACTT	GGGGCCC	8	16	NTNG2	1.18	0.00012	3.25	7.38	-1.18
cl_17100_chr10	hsa-miR-132-3p	-0.85	0.002610	123.76	68.55	AAAGACATTTTAGGGACTGTTGGGGGCATTTGAAAATGTCT	GACTGTT	15	5	ANK3	1.00	0.00316	7.32	14.68	-0.85

cl_17705_chr10	hsa-miR-146a-5p	3.62	0.000000	9075.99	111335.84	AGTTCTCCAGGTCCAACGATTACCCTTCTGTTCCGGTCCTG	AGTTCTC	1	8	TRUB1	-0.29	0.02493	23.71	19.40	-1.05
cl_17705_chr10	hsa-miR-146b-5p	1.74	0.002333	17080.92	57155.72	AGTTCTCCAGGTCCAACGATTACCCTTCTGTTCCGGTCCTG	AGTTCTC	1	8	TRUB1	-0.29	0.02493	23.71	19.40	-0.50
cl_18109_chr11	hsa-miR-149-5p	-1.00	0.003123	13.82	6.89	CGCAGCCCCGGCGGACCCACTGTTGGACCTGAGGAGCCAGC	GAGCCAG	34	16	MIR4687	0.90	0.00003	0.52	0.98	-0.90
cl_18501_chr11	hsa-miR-5695	-1.35	0.003064	1.44	0.54	AAAAAAAAAAGTTGGGGGCTTGGAGATGAAAGACTTGGAGG	CTTGGAG	34	18	CD82	1.77	0.00000	58.84	201.31	-2.39
cl_18870_chr11	hsa-miR-27b-5p	-0.99	0.003393	21.19	10.62	CCGCATAAGCTCCAAAGGCTTGTTGGTATTCAGACCTGAGG	TAAGCTC	6	20	CCND1	1.30	0.00000	8.24	20.32	-1.29
cl_19020_chr11	hsa-miR-424-5p	-1.81	0.000003	177.32	50.51	ACTGAGGCCTCCCAATTCGATGTTGGATCATGCTGCTCTCA	TGCTGCT	31	31	PAK1	0.69	0.00574	38.08	61.41	-1.25
cl_19274_chr11	hsa-miR-4518	-1.83	0.000964	8.95	2.49	ATCCCGAGGGCTGAAAGGTGTGTCCCTGAGAGGTGGCCCAT	CCCTGAG	24	27	NPAT	0.32	0.03492	39.17	48.90	-0.59
cl_19314_chr11	hsa-miR-140-3p	0.74	0.009811	2206.05	3679.70	GAAGGGGAGGCGGGGAATGCTCCGCGAGGGGCTGTGGTGAC	CTGTGGT	32	57	PPP2R1B	-0.49	0.00153	59.54	42.38	-0.36
cl_19546_chr11	hsa-miR-3922-3p	1.24	0.017898	0.75	1.82	CGCCCGGGGGCGCGCAGGACTGACGTATCGCAAGGCCAGCC	AGGCCAG	33	19	FOXRED1	-0.62	0.00040	49.43	32.06	-0.78
cl_19660_chr12	hsa-miR-3648	-1.65	0.002386	7.08	2.27	GCCCGGCCGCCGCGGCCTCTTCCGCCCGGCGCCCGCGCATT	CCGCGGC	10	7	NINJ2	1.25	0.00000	8.11	19.29	-2.06
cl_19905_chr12	hsa-miR-590-5p	-0.84	0.028628	6.20	3.43	TGCTTTTCCAAGGTCGGGGTTGCGATAAGCTTATCGCTTAT	ATAAGCT	25	12	ST8SIA1	1.48	0.00000	11.61	32.45	-1.24
cl_20286_chr12	hsa-miR-432-5p	-1.20	0.006297	9.90	4.31	TAAACGTGGCTCCAAGGTCCTGGGGAGGTGGATCACGACGA	CTCCAAG	10	17	OS9	0.50	0.00014	180.32	255.15	-0.60
cl_20392_chr12	hsa-miR-361-3p	1.24	0.003876	615.76	1454.95	CGTGGCAACCGGCTCCGGGATGGCTGGCTGGGGGGCCTAGT	CTGGGGG	28	9403	MDM2	-1.40	0.00000	216.24	82.20	-1.73
cl_20396_chr12	hsa-miR-4645-3p	0.66	0.038686	3.63	5.68	TGACCAATCGTACTGTCAATTGATGTCCACTAGTTGTTAAT	TACTGTC	11	107	CCT2	-1.17	0.00000	389.18	172.41	-0.77
cl_20902_chr12	hsa-miR-659-5p	1.29	0.000787	2.67	6.44	CATGGAATCAGAACCTACGTTGTAACAAGGTCCCCAGGTGA	AAGGTCC	27	22	CIT	-1.22	0.00000	45.23	19.42	-1.57
cl_21077_chr12	hsa-miR-484	-1.26	0.000040	1404.88	587.88	GGGCAAGGGAGCCTGGGGGCTGTAGTTCACATGGGCCAGCC	GAGCCTG	9	5	TMEM132C	0.98	0.00321	1.31	2.58	-1.24
cl_21249_chr13	hsa-miR-132-3p	-0.85	0.002610	123.76	68.55	TTTGAGACTGTTCTACAGTCTGACGGCATGAACATCAACGC	GACTGTT	6	30	ATP8A2	0.66	0.00865	2.60	4.12	-0.56
cl_21256_chr13	hsa-miR-361-3p	1.24	0.003876	615.76	1454.95	CGAGGGACGAGGGCTGGGGGTGGGGAGCGGTGTCTCTGCCC	CTGGGGG	14	49	CDK8	-0.53	0.00034	17.74	12.31	-0.65
cl_21616_chr13	hsa-miR-3136-5p	1.49	0.009911	0.81	2.26	TTCTTCACAATCAAATTCAGTCAATAGCCCAAGACTGATAG	TCAGTCA	17	34	DACH1	-0.85	0.00000	15.77	8.78	-1.26
cl_21642_chr13	hsa-miR-140-3p	0.74	0.009811	2206.05	3679.70	AATCAAGTTCTAGAGTCCAATGATCTTAATCACTGTGGTGT	CTGTGGT	33	8	UCHL3	-0.93	0.00000	41.29	21.64	-0.69
cl_22757_chr14	hsa-miR-181a-5p	1.32	0.014841	7336.45	18322.20	AAAATTCTGATTTAATGAGCTTGAGTTTGAATGTAATCAGA	TGAATGT	28	10	CLMN	-0.56	0.02125	14.83	10.03	-0.74
cl_22757_chr14	hsa-miR-181c-5p	2.83	0.000011	218.96	1560.77	AAAATTCTGATTTAATGAGCTTGAGTTTGAATGTAATCAGA	TGAATGT	28	10	CLMN	-0.56	0.02125	14.83	10.03	-1.60
cl_22933_chr14	hsa-miR-3648	-1.65	0.002386	7.08	2.27	GTAGGTGGCTGCCGCGGCGATGTGGGCGGCTTGCGTGTGGC	CCGCGGC	12	10	GPR132	1.48	0.00000	4.56	12.75	-2.45
cl_23041_chr15	hsa-miR-2467-5p	1.46	0.003890	3.95	10.85	GGCGGGCCAGCGCCGCGGAGTTTCGGGTCCGAGGAGCCTCG	GAGCCTC	34	8	TJP1	-1.07	0.00000	136.54	64.81	-1.57
cl_23199_chr15	hsa-miR-146a-5p	3.62	0.000000	9075.99	111335.84	CTCAGTTCTCCAGTACGACGTTTCCTGTCTTGAGCAGGAGC	AGTTCTC	4	6	STARD9	-0.49	0.00438	20.47	14.60	-1.76
cl_23199_chr15	hsa-miR-146b-5p	1.74	0.002333	17080.92	57155.72	CTCAGTTCTCCAGTACGACGTTTCCTGTCTTGAGCAGGAGC	AGTTCTC	4	6	STARD9	-0.49	0.00438	20.47	14.60	-0.85
cl_24095_chr16	hsa-miR-2110	1.05	0.000723	2.94	6.19	CTGGGCTTCCTTCTTGGGCATTCCCCAGGCCTATCTCCAGA	TTCCCCA	21	23	DNASE1	-0.94	0.00000	185.11	96.73	-0.99
cl_24243_chr16	hsa-miR-485-5p	-1.88	0.001384	12.78	3.45	GCCCTGCAGCCTCGTCAGGCTCAGTCCCCTCCCGATAAACC	CAGCCTC	7	48	KIAA0430	0.61	0.00073	95.43	145.46	-1.14
cl_24793_chr16	hsa-miR-4662a-5p	1.64	0.000301	0.82	2.46	CTTGGCTATACGGATGCTCATGGCGACCTGCTGCCCCTCAC	TTGGCTA	2	23	ACD	-0.41	0.00525	40.14	30.17	-0.68
cl_24965_chr16	hsa-miR-199a-5p	1.59	0.000007	181.97	548.37	GACCCCCTAGCTACACTGGTTGGTACACAGTTGGTACCCAA	ACACTGG	13	8	MPHOSPH6	-0.79	0.00000	43.58	25.18	-1.26
cl_25287_chr17	hsa-miR-150-3p	3.38	0.000000	3.49	36.47	GCGGGCATGAGGAGTGACTGTGTACCATTTCAGCTGTTTCT	TGTACCA	21	339	DHX33	-1.13	0.00000	43.83	20.04	-3.82

cl_25426_chr17	hsa-miR-374c-5p	3.26	0.001459	0.66	6.22	TTGTATTAGAATAGAGCATGTGCTGGATTATGACTGGATGC	TGTATTA	2	16	ELAC2	-0.53	0.00004	142.93	98.66	-1.74
cl_25662_chr17	hsa-miR-3065-3p	-1.21	0.004663	1.20	0.49	AGGAGGTGCTGTGTGAAGTCTGTGCCAGCAGCCGCAGGCTC	GGTGCTG	5	20	CDK5R1	3.58	0.00000	2.41	28.75	-4.34
cl_2572_chr1	hsa-miR-708-3p	0.98	0.026809	18.72	36.79	GCTTTGAAGTTAACTCTGGGTTTGACTCTAGTTTGACATTT	TCTAGTT	27	67	ENAH	-0.92	0.00244	22.95	12.12	-0.90
cl_25906_chr17	hsa-miR-221-5p	1.18	0.015984	188.23	426.85	GTCCCTGCTTTAGAGGTCATTGCCAGGGTTGTTGAGGCAAC	TGCCAGG	21	52	SLC25A39	-0.73	0.00001	178.71	107.89	-0.86
cl_2634_chr1	hsa-miR-4523	-1.05	0.028608	2.00	0.93	TATATAAAAAACATTCTCGGTTGATGCACCATACCAAAATA	TCTCGGT	15	23	RHOU	0.71	0.01537	7.16	11.71	-0.75
cl_26407_chr17	hsa-miR-18a-3p	-2.46	0.000000	88.89	16.14	AGGGACAGAGGGCAGCACGCTGGACCGAGGCGGCGTTCCCA	AGGGCAG	9	5	LLGL2	1.33	0.00000	8.23	20.71	-3.27
cl_26499_chr17	hsa-miR-485-5p	-1.88	0.001384	12.78	3.45	CCACCGTGCCCAGCCTCAAATAATGTATGGAAGGGAAGTTC	CAGCCTC	11	6	TBC1D16	0.98	0.00007	5.76	11.33	-1.83
cl_265_chr1	hsa-miR-485-5p	-1.88	0.001384	12.78	3.45	CCGCGCCAGCCTCCTGGCCTTCGCGGAGGACGCACCACCGT	CAGCCTC	7	5	GPR153	0.73	0.02360	3.68	6.11	-1.37
cl_27718_chr19	hsa-miR-615-3p	2.51	0.000000	2.50	14.25	CTGTGGAGCTTGACTCTGGCTCGGTGAAGAGACATGGGTGA	GGCTCGG	18	9	ILF3	-1.17	0.00000	878.29	389.71	-2.94
cl_28628_chr19	hsa-miR-10b-3p	3.02	0.000000	1.45	11.98	AGTCGGAATCTGCTAAGGAGTGTGTAATAGCCCAACTGCTG	GAATCTG	6	63	FCAR	-1.22	0.00904	2.38	1.02	-3.70
cl_2878_chr2	hsa-miR-222-5p	2.42	0.000036	0.56	3.04	AGTAGAACAAATGTTTTTACTCTACTGATAAAGTACAGGAA	CTACTGA	22	6	TMEM18	-0.44	0.00450	32.72	24.19	-1.06
cl_2879_chr2	hsa-miR-21-3p	2.80	0.000301	738.25	5152.52	GGAGGGAAAGACCAAGGGTTTCCTGTTGGTGTTTTGGCAAC	TGGTGTT	27	23	TMEM18	-0.44	0.00450	32.72	24.19	-1.22
cl_288_chr1	hsa-miR-342-5p	0.77	0.020518	31.43	53.35	CGTGGCACCCCCCTCGCGGCTCTCCCTGCTCCACTGTGGGT	GCACCCC	5	11	CAMTA1	-1.00	0.00000	52.64	26.39	-0.76
cl_29908_chr21	hsa-miR-106b-3p	-1.41	0.000000	1010.79	381.55	GAAACACTCGCGCACACCCCTCAGTGCGCCCCGGGCGGGGG	CAGTGCG	22	54	BACE2	1.88	0.00000	11.14	40.86	-2.64
cl_30740_chr22	hsa-miR-654-5p	-1.68	0.000699	4.43	1.38	TGTGTGCCCACCGTGGCTGTTGTCAGCTCTTGTCCTGCGGC	GCCCACC	6	20	SHANK3	0.77	0.00854	11.89	20.26	-1.29
cl_30740_chr22	hsa-miR-335-5p	-1.09	0.000328	118.94	55.71	TGTGTGCCCACCGTGGCTGTTGTCAGCTCTTGTCCTGCGGC	GCTCTTG	26	20	SHANK3	0.77	0.00854	11.89	20.26	-0.84
cl_31074_chrX	hsa-miR-3065-3p	-1.21	0.004663	1.20	0.49	AGCACCAGAGTGGTGCTGTCTGGGTACTTGGTGCTTAGTGC	GGTGCTG	12	14	PHF16	1.43	0.00065	9.55	25.80	-1.74
cl_31217_chrX	hsa-miR-378a-3p	-1.54	0.000000	2405.55	827.87	TGAGTCCAGGAGATCAAGGCTGTAGTGCCGTGACTGTGCCA	AGTCCAG	3	5	YIPF6	0.58	0.00019	15.68	23.36	-0.89
cl_31217_chrX	hsa-miR-378c	-1.27	0.000000	300.43	124.57	TGAGTCCAGGAGATCAAGGCTGTAGTGCCGTGACTGTGCCA	AGTCCAG	3	5	YIPF6	0.58	0.00019	15.68	23.36	-0.73
cl_31217_chrX	hsa-miR-378d	-1.10	0.003182	14.73	6.83	TGAGTCCAGGAGATCAAGGCTGTAGTGCCGTGACTGTGCCA	AGTCCAG	3	5	YIPF6	0.58	0.00019	15.68	23.36	-0.63
cl_31217_chrX	hsa-miR-378i	-2.12	0.000031	7.69	1.78	TGAGTCCAGGAGATCAAGGCTGTAGTGCCGTGACTGTGCCA	AGTCCAG	3	5	YIPF6	0.58	0.00019	15.68	23.36	-1.22
cl_31402_chrX	hsa-miR-3194-5p	-1.19	0.004724	6.37	2.74	TGAAGGGAAGGACACAATCCTGGCTGGCTCCACCACCTGCT	GGCTGGC	22	17	ARMCX2	2.22	0.00000	4.98	23.20	-2.65
cl_31919_chrY	hsa-miR-628-5p	1.10	0.000433	4.00	8.61	CCTATGTTCACTCAAGGCCCTAGAGTTCTACAGTCAGCAGA	GTCAGCA	33	22	TMSB4Y	-1.02	0.03634	1.59	0.78	-1.12
cl_3262_chr2	hsa-miR-455-3p	1.26	0.000225	16.17	38.86	GTGGACTGAGACAACACATGTGAGACGGACTGTATGTGAGA	TGGACTG	2	26	LTBP1	-1.48	0.00000	106.35	38.19	-1.87
cl_3669_chr2	hsa-miR-5683	3.73	0.000404	2.16	28.60	CAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGA	CATCTGT	33	13	SMYD5	-0.54	0.00004	42.34	29.16	-2.01
cl_4440_chr2	hsa-miR-3667-3p	-1.36	0.008075	1.56	0.64	AAAGTCAAAAGAGGAAGGAATACCAGTGGCAAAAATCATTT	AGGAAGG	12	539	GALNT1	0.44	0.00945	59.79	81.18	-0.60
cl_4499_chr2	hsa-miR-21-3p	2.80	0.000301	738.25	5152.52	GTATGGTGGTGTTATATGCGTGGCATAGTTTAACTGTTCAA	TGGTGTT	7	6	SLC4A10	-0.45	0.00031	32.77	23.95	-1.27
cl_4698_chr2	hsa-miR-873-3p	1.68	0.006278	0.67	2.18	ATGCTCGCCGCGCTCTCCCCTCAGTCTCTCGCTCCTGTTTC	CAGTCTC	22	356	ZNF804A	-0.94	0.03219	27.14	14.19	-1.57
cl_5584_chr3	hsa-miR-376a-3p	-2.14	0.000001	3.89	0.86	TTTAGGTTCCAGGAAATAGCTCCACCCAAAGTCTATGAATG	TCTATGA	32	69	GLB1	1.00	0.00000	45.40	90.64	-2.14
cl_5680_chr3	hsa-miR-376a-3p	-2.14	0.000001	3.89	0.86	AGAACAAGAGTTTCTATGACTGAAGTAATGAAAGTTGAACA	TCTATGA	13	30	KRBOX1	0.72	0.00059	3.05	5.04	-1.55
cl_5704_chr3	hsa-miR-615-3p	2.51	0.000000	2.50	14.25	ATCTTCTTGGGCTTCTGGGTTGGTGGCTCGGTGGTGACCTG	GGCTCGG	25	22	CLEC3B	-0.32	0.04973	26.07	20.91	-0.80

cl_5818_chr3	hsa-miR-145-5p	-1.46	0.002408	414.75	150.53	TGCCAGGGTGGGAACTGGAGTGTGGATTAGGTCCCTGCCCT	AACTGGA	13	61	CISH	2.52	0.00000	1.64	9.41	-3.68
cl_5974_chr3	hsa-miR-92b-5p	0.98	0.008992	0.54	1.12	ATAAATCCAGCCGTCCCGACTAATGCCTGATTGCATATTTA	CCGTCCC	11	21	CADPS	-4.03	0.00000	74.14	4.55	-3.93
cl_601_chr1	hsa-miR-3942-5p	-0.98	0.015065	2.95	1.47	CTTTGTCCTGAATGTGCTATTGCTACATGACTGGACTAGGC	TATTGCT	18	18	PIGV	0.47	0.00257	7.90	10.94	-0.46
cl_6528_chr3	hsa-miR-4999-5p	1.47	0.000026	0.45	1.31	GATCGATACAGCCATAACTCTTCTCTCGTCTGTGGTTCACT	ATACAGC	6	16	COL6A6	-2.17	0.00000	6.96	1.55	-3.17
cl_6528_chr3	hsa-miR-140-3p	0.74	0.009811	2206.05	3679.70	GATCGATACAGCCATAACTCTTCTCTCGTCTGTGGTTCACT	CTGTGGT	30	16	COL6A6	-2.17	0.00000	6.96	1.55	-1.60
cl_7562_chr4	hsa-miR-23a-3p	0.83	0.001283	640.05	1134.81	GCAATATCAGTAACCAGATTTTCACGCAATGTGACACTGGC	AATGTGA	28	11	RELL1	-0.90	0.00020	11.62	6.25	-0.74
cl_7562_chr4	hsa-miR-199a-5p	1.59	0.000007	181.97	548.37	GCAATATCAGTAACCAGATTTTCACGCAATGTGACACTGGC	ACACTGG	34	11	RELL1	-0.90	0.00020	11.62	6.25	-1.42
cl_7891_chr4	hsa-miR-4662a-5p	1.64	0.000301	0.82	2.46	TCACTTTTCTTCCTTCTCCATGAGTCGAGTTGTTTGGCTAA	TTGGCTA	34	59	C4orf22	-0.81	0.00073	4.35	2.48	-1.33
cl_7963_chr4	hsa-miR-654-5p	-1.68	0.000699	4.43	1.38	GACCCAAGGGAACCCTGTACTGCCCACCCTTAGAGATACTA	GCCCACC	22	23	FAM13A	0.62	0.01100	9.41	14.43	-1.03
cl_8103_chr4	hsa-miR-31-5p	1.70	0.001088	12.84	41.26	CTCTCGGAAGAAACCGATCTTGCCCACACCTTGATCTCAGA	TCTTGCC	18	26	ELOVL6	-1.93	0.00000	17.11	4.49	-3.27
cl_828_chr1	hsa-miR-27a-3p	0.86	0.011903	616.77	1122.55	CGGTTCATTCGAATCCTGCATAACCCACTGTGATATTGTGA	ACTGTGA	27	19	ZNF684	-0.44	0.00347	5.87	4.31	-0.38
cl_8324_chr4	hsa-miR-204-5p	-1.38	0.014138	67.02	25.73	CAGGCCAGAACACATGCCTCTGTCGTGAAAAGGGAGGAAAA	AAAGGGA	29	362	INPP4B	2.00	0.00000	7.16	28.60	-2.76
cl_8417_chr4	hsa-miR-654-5p	-1.68	0.000699	4.43	1.38	TCCCCCCATGCCCACCCACCTGACCCCTCTTGTCCAGTCCA	GCCCACC	10	11	TRIM2	0.84	0.00027	6.23	11.13	-1.40
cl_883_chr1	hsa-miR-3065-3p	-1.21	0.004663	1.20	0.49	GGTGCTGGGCTCAAACCTCCTGTGGAGCAGCCCCCACCCCA	GGTGCTG	1	74	CCDC24	1.02	0.00303	4.96	10.08	-1.24
cl_889_chr1	hsa-miR-155-5p	3.25	0.000000	1152.30	10989.11	ATTAGCAAAGCATTAGCTGTTGCTTTAGAGAACTCGGGAAG	AGCATTA	9	18	ERI3	-0.75	0.00000	53.09	31.50	-2.45
cl_9147_chr5	hsa-miR-4999-5p	1.47	0.000026	0.45	1.31	TTATAAAGAGCTGATACAGCTCAAGAGTGGAAAAACAAATA	ATACAGC	14	56	NDUFS4	-0.38	0.01006	37.97	29.17	-0.56
cl_9753_chr5	hsa-miR-103a-2-5p	-1.50	0.000002	5.75	2.00	GTGCATCCACACTGCATTCCTGTAGAAGAAGCCCCAGCTGT	AAGAAGC	26	25	CHSY3	0.84	0.01365	1.37	2.45	-1.26
cl_9753_chr5	hsa-miR-3691-5p	-1.17	0.000276	7.92	3.54	GTGCATCCACACTGCATTCCTGTAGAAGAAGCCCCAGCTGT	CATCCAC	4	25	CHSY3	0.84	0.01365	1.37	2.45	-0.98

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