Supplementary Material
Reconstructing dynamic microRNA regulated interaction networks

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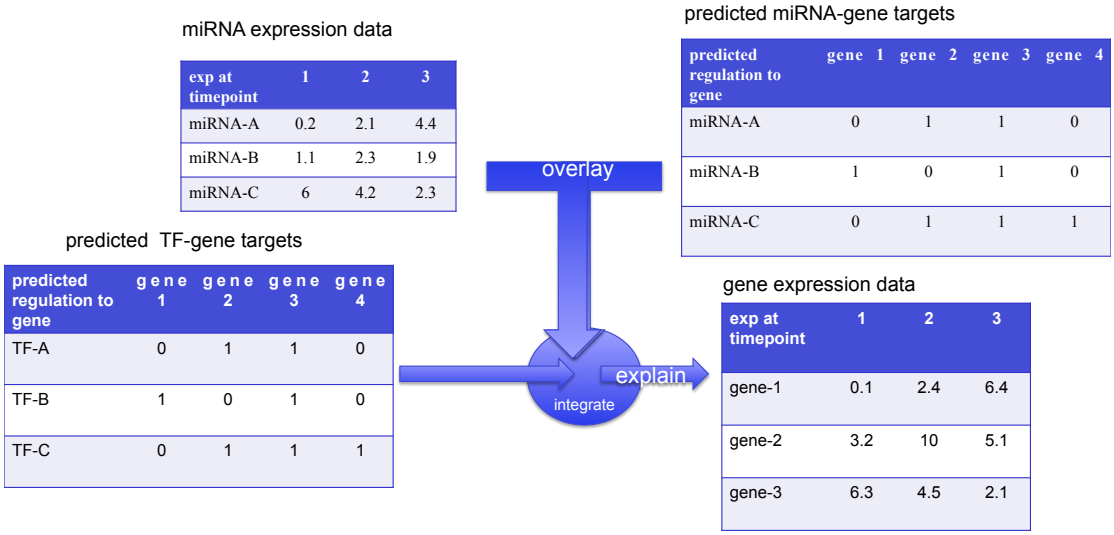
Appendix I – Supplemental Methods

Computational Methods for mirDREM

We introduce a new algorithm to learn a dynamic map of TF and miRNA regulation that jointly considers protein-DNA as well as miRNA-gene regulatory relationships and time series expression data of the regulated genes and the miRNA regulators. The method addresses the fact that miRNAs prevent mRNA translation by primarily acting at the transcriptional level. The next figure illustrates the different data sources that are used.



mirDREM utilizes 4 different data sources. Gene and miRNA expression data sets that measure genome wide expression for each time point part of the investigated process. Further, predicted or experimentally acquired TF-gene and miRNA-gene regulatory relationships are an essential part of mirDREM.

Description of the underlying probabilistic model

mirDREM integrates several different data sources to model the joint effect of TF and miRNA regulation on gene expression measured as a time series. Following Ernst et al.[1] we construct an Input-Output Hidden Markov Model (IOHMM) denoted M. M is a tuple (H,E,ψ,Θ,n,γ). H denotes the set of hidden states, the nodes in the model, and each hidden state *h* is associated with an output distribution of Gaussian form. Θ denotes a set of parameters for the output distributions of the hidden states *h*. Θ_h is a tuple (μ_h,σ_h) of the mean and standard variation of the Gaussian distribution associated to *h*. *n* denotes the number of time points of the model. *E* is the set of directed edges that

connect the states in *H* and are enforced to form a tree where each node has at most γ children. If a state *h* has more than one outgoing edge, it is denoted a *split node*. ψ is a set of transition parameters between hidden states, ψ_h for each *h*. ψ_h has the form of a logistic regression coefficient vector whenever edge *e* emerges out of a split node.
DREM learns the transition parameters of the IOHMM by solving a logistic regression problem. For each hidden state *h*, that has more than one child, *h* maps an input vector X^g, for each gene *g*, to transition probabilities to the child node of *h*. The input vector X^g is different for each time point *t* in mirDREM, therefore denoted $X^{g,t}$, and consists of *T* and *R* input values for TFs and miRNAs, as explained below. This is one of the two major differences between mirDREM and the original version of DREM (the other difference is the requirement for anti-correlation, also below). In DREM X^g is static and contained only TF input values. In mirDREM $X^{g,t}$is time point specific.

Logistic regression classification in DREM
DREM[1] uses a L_1-logistic regression classifier which maps a gene feature vector X={$X_1, \ldots, X_T$} to a class label Y={0,1}, for *T* transcription factors for a binary classification problem. The groups 0 or 1 denote one of the outgoing edges of a binary split node. L_1 – regularized logistic regression, often called lasso regression, promotes sparsity by penalizing features that contribute little to the solution. For the sake of simpler notation we omit the *h* in ψ_h as we are solving one classification problem at a time, one for each state.
In a logistic regression classification framework the probability that a feature vector belongs to class 1 is defined as:

$$P(Y=1|X)=\frac{1}{1+\exp(-\psi_0-\sum_i X_i\psi_i)}\ .$$

In order to solve for the best weight vector $\hat{\psi}=\{\psi_0,\psi_1,..,\psi_T\}$, a L_1-logistic regression classifier optimizes the penalized conditional log-likelihood of *n* training examples $\{(X^j,Y^j)\}_{j=1}^n$ as :

$$\hat{\psi}=\arg\max_{\psi} L(\psi)=\arg\max_{\psi}[l(\psi)+\log p(\psi)] \quad (1)$$

, where $\log p(\psi)$ is the L_1 - regularization term and

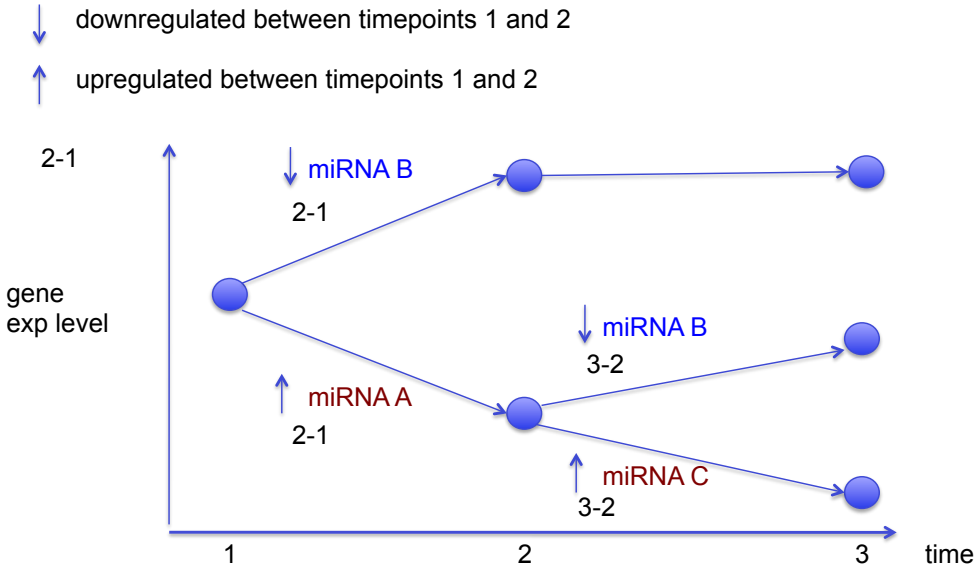
$$l(\psi)=\sum_{j=1}^{n}\log P\left(Y^j\middle|X^j,\psi_j\right) \quad (2)$$

denotes the conditional log-likelihood for logistic regression[2].
The conditional log-likelihood function is convex and can be optimized to obtain a global solution to equation (1).

In DREM the feature vector X^g for gene *g* is defined as an indicator vector, where $X_i^g=1$ if gene *g* is bound by transcription factor *i* and 0 otherwise.

Incorporating miRNA expression levels

While we can obtain expression levels for miRNAs, we cannot obtain direct information about their specific temporal regulation of target mRNAs. Thus, our aim is to integrate the temporal expression data with the static sequence based prediction data to obtain a prior on the effect a specific miRNA has on a specific mRNA at time point *t*. We are particularly interested in finding miRNA regulators that change their expression behavior during the time course and whose targets are changing in response to this change, see Supplementary Figure S1.



Supplementary Figure S1 – Illustrates the relationship of miRNA regulators on genes at split nodes learnt by miRDREM. The figure depicts three hypothetical time points with a model that has two split nodes, where each arrow represents a set of genes that are assigned to this path. Three miRNAs are shown that support an anti correlated expression behavior to the majority of genes assigned to the emerging paths out of the split node. If a miRNA is overexpressed (denoted in blue), the predicted target genes should be found in a path that leads to a node that has a higher expression level than the split node from which it emerges. Vice versa, if a miRNA is underexpressed (in red) its target genes should show a lower expression level compared to the split node.

We define $\mathrm{o}_\mathrm{r}^\mathrm{t}$ as the gene expression log odds ratio for a miRNA *r* at time point *t :*

$$\mathrm{o}_\mathrm{r}^\mathrm{t} = \log \frac{xp_r^t}{xp_r^{t-1}}$$

, where xp_r^t denotes the expression level of miRNA *r* at time point *t*. $\mathrm{o}_\mathrm{r}^\mathrm{t}$ captures the change in expression for two consecutive time points.

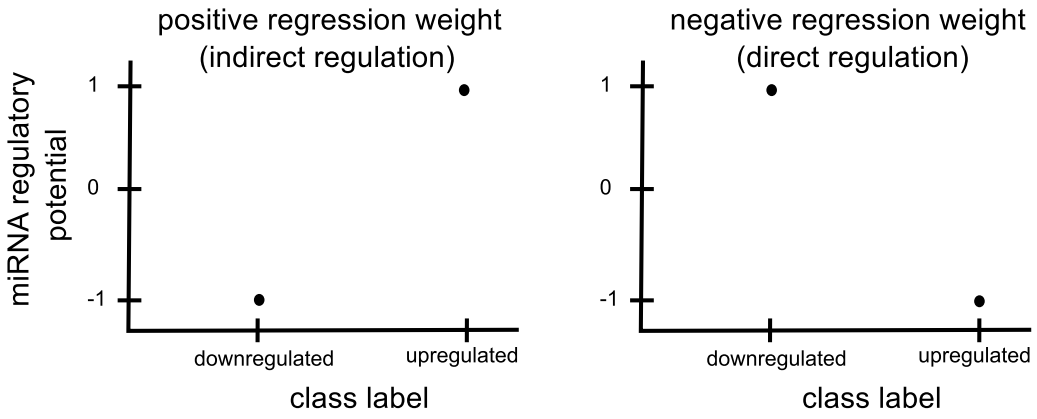
The key idea is that miRNAs that change their expression level change their *regulatory effect* on target genes. For example, a miRNA *r* with increase in expression has a higher copy number in the cell and may affect an increased number of its potential targets. On the other hand, the strength of the regulatory effect for miRNA *r* on a target gene *g* depends on the binding strength denoted b_g^r , where $b_g^r > 0$. Therefore, our formalism can model both aspects and the gene expression odds ratio $\mathrm{o}_\mathrm{r}^\mathrm{t}$ and the binding strength b_g^r are incorporated into the definition of a regulatory effect $RE_g^{r,t}$:

$$RE_g^{r,t} = sign(\mathrm{o}_\mathrm{r}^\mathrm{t}) \begin{cases} \left(\dfrac{2}{1+\exp\left(|\mathrm{o}_\mathrm{r}^\mathrm{t}| b_g^r \phi\right)}\right), & |\mathrm{o}_\mathrm{r}^\mathrm{t}| \geq d \\ 0, & else \end{cases}$$

,where ϕ denotes a scaling weight for combining binding strength and expression odds ratio using a logistic function. If the absolute expression odds ratio is below a minimal change threshold *d*, the regulatory effect is 0 for time point *t*. The regulatory effect can be positive or negative and therefore the sign of the change in expression, $sign(\mathrm{o}_\mathrm{r}^\mathrm{t})$, is included.
This will be important to learn a pattern of anti-correlation at a split node as explained in Supplementary Figure S1.
In our current implementation, the computed $RE_g^{r,t}$ values are rounded to integers and *d* is set to 0.25.

A constraint based approach to lasso logistic regression in mirDREM

In order to include TF and miRNA variables into the logistic regression classification framework in mirDREM, the feature vector *X* is changed in two ways, it is made time point specific and includes *T* features for TFs and *R* features for miRNAs, denoted as $X^{g,t}$=$\{X_1, \ldots, X_T, RE_g^{1,t}, \ldots, RE_g^{R,t}\}$. Therefore, $X^{g,t}$ contains a set of static features for the TFs and a set of time point specific features for miRNAs, where the latter captures the regulatory effect of each miRNA *r o*n a target gene *g* based on its change in expression at time point *t*, see above. The vector of regression weights is changed accordingly $\psi = \{\psi_0, \psi_1, .., \psi_T, \psi_{T+1}, \ldots, \psi_{T+R}\}$.



Supplementary Figure S2: The graphs illustrate the importance of constraining the logistic regression weights to ensure that a regulatory pattern of anti correlation is learnt for miRNA targets by the classifier. (left) If the miRNA shows a positive regulatory effect and its target genes are up regulated the classifier will learn a positive weight, similarly with down regulated targets and a negative regulatory effect. (right) The ideal scenario is if the miRNA shows negative regulatory effect when its targets are up regulated and *vice versa*.

Because we expect that direct regulation by a miRNA leads to inhibition effects of the target gene, we introduce additional constraints for weight values that correspond to miRNA feature values in $X^{g,t}$. We seek to optimize the following equation:

$$\hat{\psi} = \arg\max_{\psi} L(\psi) \qquad (3)$$
$$s.t. \quad \psi_x \leq 0, \forall\, x > T$$

In other words, we only allow for negative regression coefficients for miRNAs, as opposed to TFs that can be either activators or repressors, see Supplementary Figure S2 for explanation. Such a formulation is known as *constrained logistic regression* [3] and in our particular instance *constrained lasso logistic regression*. The reader should not be confused, because the L_1 – regularization term itself is sometimes termed a constraint to logistic regression. However, here the objective function is penalized with the L_1-norm to promote sparsity and in addition some of the weight terms are constrained as well.

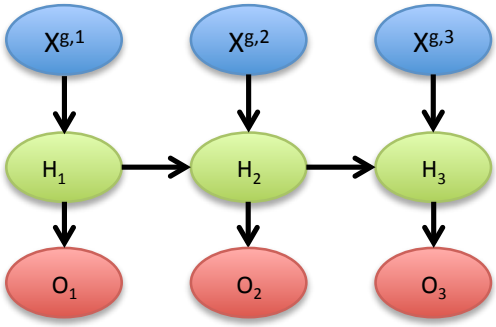
To solve Equation (3) we use a modified version of the approach described by Krishnapuram et al. for lasso logistic regression. In [2] they introduce an efficient iterative method that optimizes one entry in the weight vector ψ at a time. Such an iterative assignment allows us to introduce the non-positivity constraints, because each weight can be forced at its round of optimization to remain smaller than, or equal to, zero. For the unconstrained *TF* variables, $\psi_1, \ldots, \psi_T$, the optimization is not modified. This procedure guarantees that our learning method still converges to a global optimum. Note that our constrained optimization problem has only added linear constraints (≤0) to a convex problem, which means that the convexity of the problem still holds [4].

Likelihood function

Let $o_g = (o_g(1), \ldots, o_g(n-1))$ be the log ratio expression values for gene *g* at time points 1 to *n* − 1 relative to a time point 0 control. Define h_t as the hidden state variable at time *t*, where $t \in \{0,1,\ldots,n-1\}$. Denote the transition probability for a gene *g* to transition to state h_b at time point *t* given that it is in hidden state h_a at time point *t* as $P(H_t = h_b | H_{t-1} = h_a, X^{g,t}.)$. This probability is 0 if h_b is not a child of h_a and set to 1 if it is the only child of h_a. If h_a has two children then the transitions are probabilistic and depend on the input vector $X^{g,t}$. The mapping from input vector $X^{g,t}$ to transition probabilities for a hidden state h_a are determined by a trained logistic regression classifier see above. The likelihood density, *r*, for a set of genes *G* in IOHMM model *M* is

$$r(G|M) = \sum_{g \in G} log \sum_{q \in Q} \prod_{t=1}^{n-1} f_{q(t)}(o_g(t)) \prod_{t=1}^{n-1} P(H_t = q(t) | H_{t-1} = q(t-1), X^{g,t})$$

where *Q* is the set of all possible paths of hidden states of length *n* starting from the root node with non-zero probability.



Depiction of an example IOHMM

Model Learning

The parameters of the model are learnt using the Baum-Welch EM algorithm for a fixed tree structure. During each maximization step of Baum-Welch the logistic regression classifiers are retrained. When training a classifier, for every gene in the training set the classifier is given a weighted example of the gene transition to each child state. The weight of the example is the probability of that gene going through that hidden state based on the current values of all the parameters in the model.
The structure of the network is learned in a greedy fashion. Starting from a linear model with one hidden state per time point, the algorithm explores additions of new hidden states at each time point. The algorithm uses the BIC penalty to the model likelihood to decide if the best hidden state addition is executed and the model structure is changed, in each round of structure learning. A new state is added if the penalized likelihood is larger than in the unchanged model (default penalty 40). After no new addition is made at the end of a structure learning round, it is tested if splits can be delayed or paths merged to simplify the model[1]. After structure learning all genes are parsed through the model and assigned to paths in the model using the Viterbi algorithm.

Enrichment Computation for miRNAs at split nodes

DREM uses the Hypergeometric statistic to assign a transcription factor *f* to an edge *e* in the model[1], denoted H_e^f.
In addition to thresholding the hypergeometric enrichment score H_e^r for miRNA *r* used in DREM for an edge *e* emanating a split node, we make use of the gene expression odds ratio o_r^t for a miRNA to define a secondary filter. Only if the absolute value of the expression ratio o_r^t is greater than threshold T, as defined above, and if the direction of the edge, termed dir(*e*), is opposite to the sign of the expression change:

$$score(e,t,r) = \begin{cases} H_e^r, & |o_r^t| > d \ \wedge \ sign(o_r^t) \neq \ dir(e) \\ 1, & otherwise \end{cases}.$$

As default we consider a miRNA *r* on edge *e* if $score(e,t,r) \ \leq 0.05$.

Rational for experimental time series design

At birth (P0), mice have lungs in the saccular stage of lung development which corresponds to that seen in extremely premature human infants (24-28 weeks of gestation). On the fourth postnatal day (P4), alveolar septation begins with development and elongation of secondary crests that divide the primary saccules into alveoli. Rapid alveolar septation occurs between postnatal days 7 and 14 (P7-P14), and the majority of alveolar septation is complete by P14, although some alveoli are added until P28. Adult mice (P42) have completed alveolar septation and maturation of their alveolar capillary network.

Selection of time points was determined by trying to balance the ability to detect major regulatory events with the resources required for the analysis. It has been known for a long time that 'Secondary crests rapidly elongate after the 4th day, subdividing the primary saccule into alveoli, a process that appears substantially complete by the 14th day'[5].We have also recently shown, using radial alveolar counts, that most (~80%) of lung development in mice is complete by week 2[6]. Thus, we believe that an intermediate time point would not be very helpful, as there are few genetic and phenotypic changes in lung development between 2 and 6 weeks.

Obtaining TF and miRNA gene predictions

TF-gene target rankings for 512 position-specific weight matrices (PWMs) of human TFs were obtained by learning general binding preferences of TFs, using genomic features, conservation and differnet types of Chip-chip experiments, and integrating these preferences with TF motif information[7]. Each PWM was associated with TFs using JASPAR[8] and TRANSFAC[9], the TF name mapped to the Entrez Gene ID of the TF's coding gene. TFs without mapped ID were removed from the set. After mapping 348 unique Entrez Gene IDs were obtained. A TF was said to regulate a gene if it is within the top 1000 predictions for any of the PWM annotations of the TF. Then each gene in the set of TF-gene interactions obtained, was mapped to its corresponding orthologous mouse gene (determined by mapping to the Mouse genome database and HGNC) and the TF interaction transferred. Genes with more than 5 orthologous mappings were discarded. This procedure resulted in 468,319 TF-gene predictions in mouse.

miRanda predictions were obtained from the microcosm website (http://www.ebi.ac.uk/enright-srv/microcosm/) and all mouse predictions with p-value < 0.01 used for prediction.

The targetscan data were downloaded from http://www.targetscan.org/cgi-bin/targetscan/data_download.cgi?db=mmu_61

(Release 6.2 from June 2012) the file "Conserved site context+ scores" that contains mirna-mrna predictions for several species. All predictions for mouse miRNAs were extracted.

Obtaining validated miRNA-gene interactions

We retrieved two gold standard sets of mouse miRNA-gene interactions from miRTarBase[10] (544 interactions for 150 miRNAs and 368 genes, median of 2 targets per miRNA) and miRecords[11] (299 interactions for 97 miRNAs and

173 genes, median 1 gene per miRNA).

Immunoblotting

Cells were lysed in 1ml of M-PER lysis buffer (Pierce, Rockford, IL) and protease inhibitors cocktail (Pierce) for 20 min. The lysates were quantified for protein concentrations using the Bradford assay (Biorad, Hercules, CA). Proteins (15 µg per sample) were separated by SDS-polyacrylamide gel electrophoresis (#456-9034-Biorad) and transferred onto nitrocellulose membranes (Invitrogen, Grand Island, NY). The membranes were blocked with 5% fat free albumin in PBS containing 0.1% Tween-20 (TBS-T) for 40 min and subsequently incubated with FANCD2, GLI3, AURKA or CDT1 (1:200-Santacruz) primary antibodies overnight at 4°C. After washing with PBS-T for 30 minutes at room temperature, the membrane was further incubated with rabbit peroxidase-conjugated secondary antibody 1:10000 for 1.5 hours, followed by 30 minutes of washing with PBS-T. Protein bands were visualized with western lighting Plus-ECL substrate (PerkinElmer).

Appendix II - Supplementary Results

Gene ontology path enrichment of mirDREM paths

path (model figure)	#genes	significant GO terms (corrected p-value <= 0.05)
A	217	carbohydrate binding, drug metabollic process, extracellular region
B	474	immune system process, cell surface, cell activation, MHC protein complex, external side of plasma membrane, cell periphery, immune response, response to stimulus, regulation of immune system process, membrane, cell killing, multi-organism process, regulation of cell activation, membrane part, leukocyte differentiation, plasma membrane part, regulation of cell killing, positive regulation of biological process, receptor complex, antigen binding, cell communication, cytokine production, signaling, receptor activity, response to

		organic substance, positive regulation of cell killing, regulation of leukocyte proliferation, positive regulation of cellular process, peptidyl-tyrosine phosphorylation, positive regulation of protein phosphorylation, positive regulation of immune system process, positive regulation of response to stimulus, defense response, receptor tyrosine kinase binding, hematopoietic or lymphoid organ development, regulation of immune response, leukocyte proliferation, antigen processing and presentation, positive regulation of macromolecule metabolic process, plasma membrane, positive regulation of DNA recombination, intracellular membrane-bounded organelle, positive regulation of programmed cell death, positive regulation of apoptotic process, G-protein coupled chemoattractant receptor activity, cellular response to cytokine stimulus, biological regulation
C	76	-
D	1035	-
E	466	regulation of immune system process
F	209	-
G	266	negative regulation of cell growth, regulation of cell growth, regulation of cell ,morphogenesis, cell growth, negative regulation of growth
H	865	nucleic acid binding, membrane-enclosed lumen, nitrogen compound metabolic process, nucleobase-containing compound metabolic process, organelle, organelle part, nucleus, nuclear part, macromolecule biosynthetic process, embryonic organ development, biosynthetic process, cellular metabolic process, cellular macromolecule metabolic process, cellular component organization or biogenesis, S phase, cellular nitrogen compound metabolic process, chromatin binding, skeletal system development, gene expressio
I	462	cell cycle, cell division, cell cycle process, non-membrane-bounded organelle, intracellular non-membrane-bounded organelle, chromosome segregation, DNA metabolic process, organelle fission, chromosomal part, organelle part, kinetochore, regulation of cell cycle, nucleus, microtubule-based process, spindle, midbody, chromosome, intracellular, cellular component organization or biogenesis, cellular response to stress, intracellular part, intracellular organelle part, macromolecular complex, microtubule cytoskeleton, regulation of chromosome segregation, macromolecule metabolic process, DNA replication, organelle, cytokinesis, cellular component organization, cellular component organization or biogenesis, DNA-dependent ATPase activity, microtubule cytoskeleton organization, regulation of microtubule-based process, establishment of organelle localization, condensed chromosome outer

		kinetochore, maintenance of location in cell, cellular process involved in reproduction, microtubule organizing center, cellular macromolecule metabolic process, M phase of mitotic cell cycle, response to DNA damage stimulus, DNA packaging, maintenance of protein location, organelle organization, protein localization to chromosome, establishment of chromosome localization, microtubule, regulation of cell division, cytoskeletal part, maintenance of location, mitosis, reproductive process, reproduction, multicellular organismal development, protein localization to organelle, membrane-enclosed lumen, sister chromatid segregation, regulation of attachment of spindle microtubules to kinetochore, nucleobase-containing compound metabolic process, structural molecule activity, organelle localization, chromatin assembly or disassembly, cartilage condensation, chromosome centromeric region, regulation of organelle organization, M phase

Supplementary Table S1: GO enrichment (Gene ontologizer 2.0, parent-child-union method[12]) of all genes annotated to one of the 9 paths in the miRDREM model. The GO terms are listed in order of significance.

Overlap with validated miRNA-gene interactions

Method	miR	gene	in miRecords?	in miRTarBase ?
Correlation	miR-29a	FBN1	1	1
Correlation	miR-29b	BAK1	1	0
GenMiR++	miR-21	PDCD4	1	1
GenMiR++	miR-21	PELI1	1	1
GenMiR++	miR-1	TMSB4X	0	1
GenMiR++	miR-1	FN1	1	0
mirDREM	miR-29a	ELN	1	1
mirDREM	miR-29a	FBN1	1	1
mirDREM	miR-29b	ELN	1	1
mirDREM	miR-29b	FBN1	1	1

Supplementary Table S2: List of experimentally validated miRNA-gene interactions as listed in miRecords[11] and/or miRTarBase[10]. For each method tested, Correlation, GenMiR++ and

miRDREM, the miRNA (2nd col) and the target gene (3rd col) relationship that are experimentally validated in miRecords (4th col) or miRTarBase (last col) are denoted with a 1.

GO analysis of top-300 ranked genes by different methods

GO ID	adjusted p-value	GO term
GO:0002376	2.38E-05	immune system process
GO:0048534	2.38E-05	hematopoietic or lymphoid organ development
GO:0019222	0.000707202	regulation of metabolic process
GO:0002520	0.002186906	immune system development
GO:0002521	0.002186906	leukocyte differentiation

Supplemental Table S3 – Top 5 enriched significant (adj. $p < 0.05$) GO terms for rankings obtained with mirDREM (miRanda) (all significant GO terms can be found in SI Appendix III, Dataset S2).

GO ID	adjusted p-value	GO term
GO:0032991	5.42E-15	macromolecular complex
GO:0044391	1.51E-14	ribosomal subunit
GO:0043226	8.24E-14	organelle
GO:0005840	1.34E-12	ribosome
GO:0044445	4.06E-12	cytosolic part

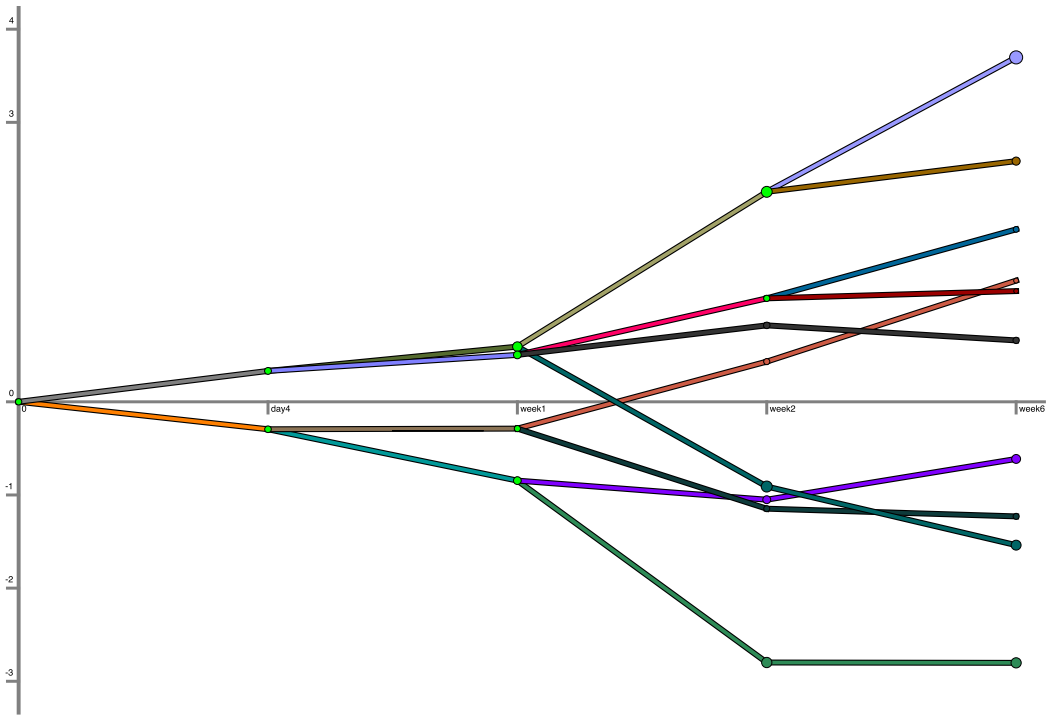
Supplemental Table S4 – Top 5 enriched significant (adj. $p < 0.05$) GO terms for rankings obtained with GenMiR++ (all significant GO terms can be found in SI Appendix III, Dataset S2).

GO ID	adjusted p-value	GO term
GO:0005057	0.000732251	receptor signaling protein activity
GO:0019955	0.013441651	cytokine binding
GO:0004896	0.047327904	cytokine receptor activity

Supplemental Table S5 – Top 5 enriched significant (adj. $p < 0.05$) GO terms for rankings obtained with Pearson Correlation.

GO ID	adjusted p-value	GO term
GO:0007049	0.0007	cell cycle
GO:0042101	0.002	T cell receptor complex
GO:0002376	0.004	immune system process
GO:0035556	0.004	intracellular signal transduction
GO:0005488	0.007	binding

Supplemental Table S6 – Top 5 enriched significant (adj. $p < 0.05$) GO terms for rankings obtained with model without negative regulatory constraints for miRNAs (all significant GO terms can be found in SI Appendix III, Dataset S2).



Supplementary Figure S3: Network structure of mirDREM modelfor learning without negativity constraints. In Supplementary Table S7 (below) are the miRNAs associated to split nodes.

let-7a ,let-7a* ,let-7b ,let-7b* ,let-7c ,let-7c-1* ,let-7d ,let-7d* ,let-7e ,let-7f ,let-7f* ,let-7g ,let-7g* ,let-7i ,let-7i* ,miR-1 ,miR-100 ,miR-101a ,miR-101a* ,miR-101b ,miR-103 ,miR-106a ,miR-106b ,miR-107 ,miR-10a* ,miR-10b ,miR-124 ,miR-125a-3p ,miR-125a-5p ,miR-125b-3p ,miR-125b-5p ,miR-126-3p ,miR-127 ,miR-127* ,miR-128a ,miR-130b* ,miR-132 ,miR-133a ,miR-133b ,miR-134 ,miR-135b ,miR-137 ,miR-138 ,miR-139-3p ,miR-139-5p ,miR-140 ,miR-141 ,miR-146a ,miR-147 ,miR-148a* ,miR-149 ,miR-150 ,miR-150* ,miR-151-3p ,miR-151-5p ,miR-152 ,miR-154 ,miR-154* ,miR-155 ,miR-15a ,miR-15b ,miR-15b* ,miR-16 ,miR-16* ,miR-17 ,miR-181a-2* ,miR-181b ,miR-181c ,miR-181d ,miR-184 ,miR-186 ,miR-187 ,miR-188-3p ,miR-188-5p ,miR-18a ,miR-18a* ,miR-18b ,miR-190 ,miR-190b ,miR-192 ,miR-193 ,miR-193* ,miR-196b ,miR-199a-3p ,miR-199a-5p ,miR-19a ,miR-19a* ,miR-19b ,miR-200c ,miR-202-3p ,miR-204 ,miR-207 ,miR-208 ,miR-208b ,miR-20a ,miR-20a* ,miR-20b ,miR-21 ,miR-212 ,miR-214 ,miR-216a ,miR-216b ,miR-217 ,miR-218-2* ,miR-219 ,miR-22 ,miR-222 ,miR-223 ,miR-224 ,miR-23a ,miR-23b ,miR-24 ,miR-25 ,miR-26b ,miR-26b* ,miR-27a ,miR-27b ,miR-27b* ,miR-28 ,miR-28* ,miR-290-3p ,miR-290-5p ,miR-291a-5p ,miR-291b-5p ,miR-292-3p ,miR-293 ,miR-294 ,miR-295 ,miR-296-3p ,miR-296-5p ,miR-297a ,miR-297b-5p ,miR-297c ,miR-298 ,miR-29a ,miR-29a* ,miR-29b ,miR-29c ,miR-29c* ,miR-301a ,miR-301b ,miR-302a* ,miR-302c ,miR-302c* ,miR-30a ,miR-30b* ,miR-30c-1* ,miR-30d ,miR-30e ,miR-31 ,miR-31* ,miR-32 ,miR-322 ,miR-323-3p ,miR-323-5p ,miR-324-3p ,miR-324-5p ,miR-325 ,miR-325* ,miR-326 ,miR-327 ,miR-328 ,miR-330 ,miR-331-5p ,miR-335-3p ,miR-337-3p ,miR-337-5p ,miR-338-5p ,miR-339-3p ,miR-339-5p ,miR-340-3p ,miR-340-5p ,miR-341 ,miR-342-3p ,miR-342-5p ,miR-343 ,miR-344 ,miR-345-3p ,miR-345-5p ,miR-34a ,miR-34b-3p ,miR-34c ,miR-34c* ,miR-350 ,miR-361 ,miR-362-3p ,miR-363 ,miR-365 ,miR-367 ,miR-369-3p ,miR-376a* ,miR-376b*

,miR-376c* ,miR-377 ,miR-378 ,miR-379 ,miR-380-3p ,miR-381 ,miR-382* ,miR-383 ,miR-384-3p ,miR-384-5p ,miR-411* ,miR-412 ,miR-423-3p ,miR-423-5p ,miR-425 ,miR-429 ,miR-431 ,miR-431* ,miR-433 ,miR-433* ,miR-449a ,miR-449c ,miR-450a-3p ,miR-450a-5p ,miR-450b-3p ,miR-450b-5p ,miR-452 ,miR-453 ,miR-455 ,miR-455* ,miR-463 ,miR-465a-3p ,miR-465a-5p ,miR-466a-3p ,miR-466a-5p ,miR-466b-3-3p ,miR-466b-5p ,miR-466c-5p ,miR-466d-3p ,miR-466e-5p ,miR-466f-3p ,miR-466f-5p ,miR-466g ,miR-467a ,miR-467a* ,miR-467b* ,miR-467c ,miR-467d ,miR-467e ,miR-467e* ,miR-468 ,miR-469 ,miR-471 ,miR-483 ,miR-484 ,miR-485 ,miR-486 ,miR-488 ,miR-488* ,miR-489 ,miR-490 ,miR-493 ,miR-494 ,miR-495 ,miR-497 ,miR-500 ,miR-501-3p ,miR-503 ,miR-503* ,miR-505 ,miR-509-3p ,miR-511 ,miR-532-3p ,miR-532-5p ,miR-539 ,miR-540-3p ,miR-551b ,miR-568 ,miR-574-3p ,miR-582-5p ,miR-590-3p ,miR-590-5p ,miR-615-3p ,miR-615-5p ,miR-652 ,miR-654-3p ,miR-654-5p ,miR-665 ,miR-666-3p ,miR-666-5p ,miR-667 ,miR-668 ,miR-669a ,miR-669b ,miR-670 ,miR-671-3p ,miR-671-5p ,miR-673-3p ,miR-673-5p ,miR-675-5p ,miR-676 ,miR-676* ,miR-677 ,miR-680 ,miR-681 ,miR-682 ,miR-684 ,miR-685 ,miR-686 ,miR-687 ,miR-688 ,miR-689 ,miR-690 ,miR-691 ,miR-692 ,miR-693-5p ,miR-694 ,miR-695 ,miR-696 ,miR-697 ,miR-700 ,miR-701 ,miR-702 ,miR-703 ,miR-705 ,miR-707 ,miR-709 ,miR-711 ,miR-714 ,miR-715 ,miR-717 ,miR-718 ,miR-720 ,miR-742 ,miR-743a ,miR-743b-3p ,miR-743b-5p ,miR-744 ,miR-758 ,miR-759 ,miR-760 ,miR-761 ,miR-762 ,miR-764-3p ,miR-764-5p ,miR-770-3p ,miR-7a* ,miR-7b ,miR-801 ,miR-804 ,miR-805 ,miR-872 ,miR-872* ,miR-873 ,miR-875-5p ,miR-876-3p ,miR-876-5p ,miR-877* ,miR-879 ,miR-880 ,miR-881 ,miR-882 ,miR-883b-3p ,miR-883b-5p ,miR-9 ,miR-9* ,miR-92a ,miR-92a* ,miR-92b ,miR-93* ,miR-96 ,miR-98 ,miR-99a ,miR-99b*

Supplementary Table S7: Predicted miRNAs in the mirDREM model without negativity constraints (for learning and path assignments) for the lung development data.

Robustness analysis of mirDREM

Parameter robustness

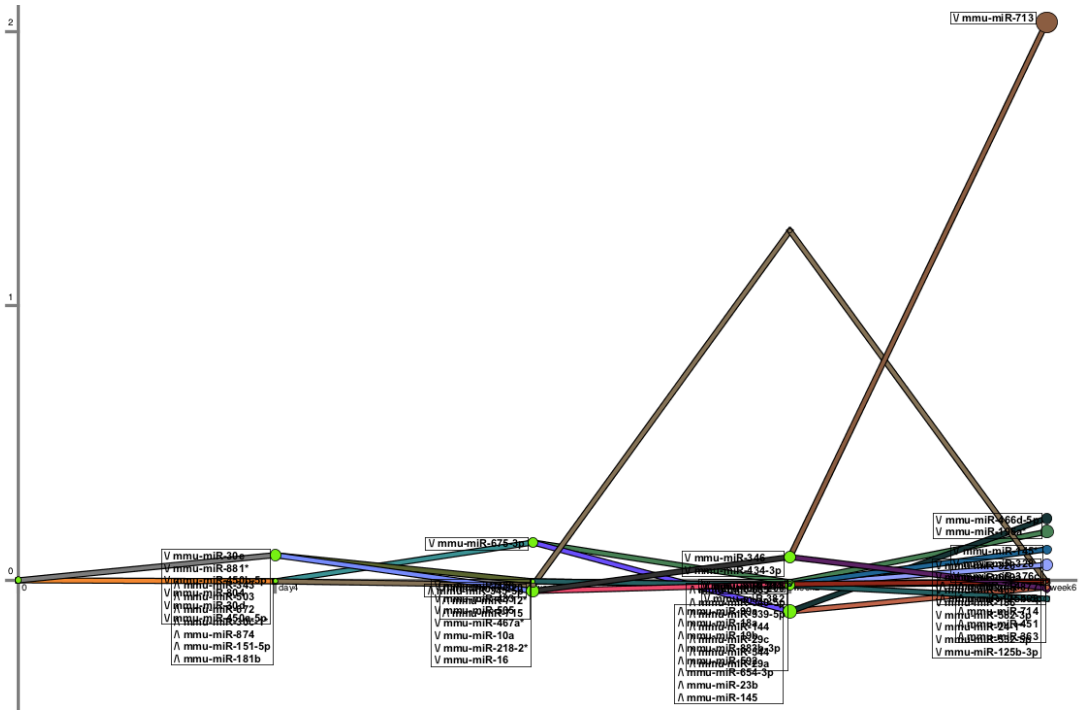
Penalty	paths	sign. miRs	Overlap with default
20	9	58	49
25	9	58	49
30	9	58	49
35	9	58	49
40	9	56	56
45	9	56	56
50	9	55	47

Supplementary Table S8: Effect of the AIC penalty term (1st column) for the model structure search (number of paths in the model, 2nd column), the number of predicted miRNAs (3rd column) and the overlap with default parameters (4th column).

scaling weight	paths	sign. miRs	Overlap with default
1	9	56	56

1.5	9	56	56
0.5	9	56	56

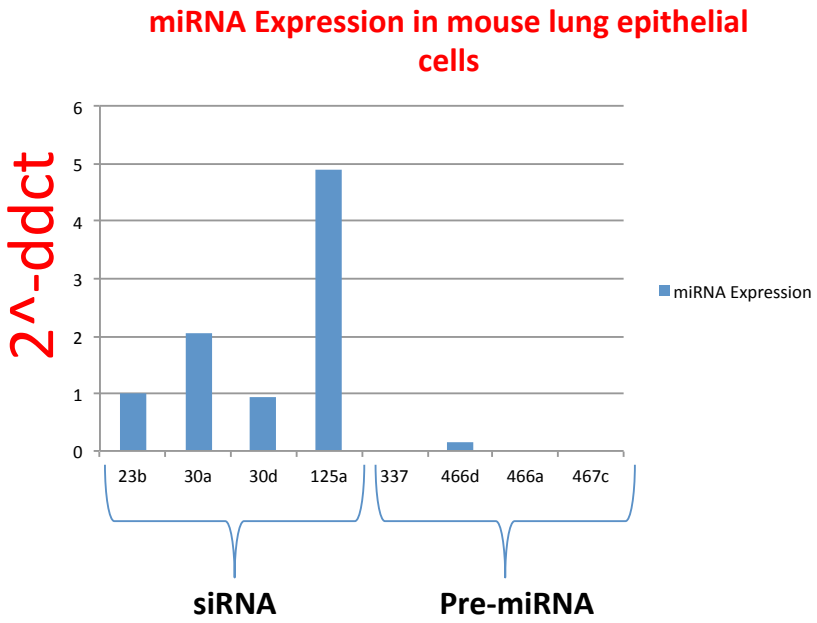
Supplementary Table S9: Effect of the scaling weight (1st column) in the regulatory potential score on network learning (number of paths in the model, 2nd column), the number of predicted miRNAs (3rd column) and the overlap with default parameters (4th column).



Supplementary Figure S4: mirDREM model on randomly shuffled gene expression ratios. No significant enrichment of GO terms could be found in the top300 genes (Analysis as in Supplementary Tables S3-S5). Supporting the fact that the model does not recover important and relevant biological properties.

RT-qPCR of selected miRNAs in lung epithelial cells

RT-qPCR experiments were conducted in order to decide if we design the transfection experiments as a miRNA over expression or miRNA knock down experiment. The resulting expression levels are shown in Supplementary Figure S5.



Supplementary Figure S5: qPCR measurement of the 8 investigated miRNAs in a lung epithelial cell line. miR 23b, 30a, 30d, and 125a were sufficiently expressed and therefore siRNAs against the mature miRNA sequences were designed to observe the effect of knockdown. For miR-337, 466d, 466a, and 467c all of which occurred at low expression level, additional pre-miRNA molecules were introduced to measure the effect of overexpression in the cell line.

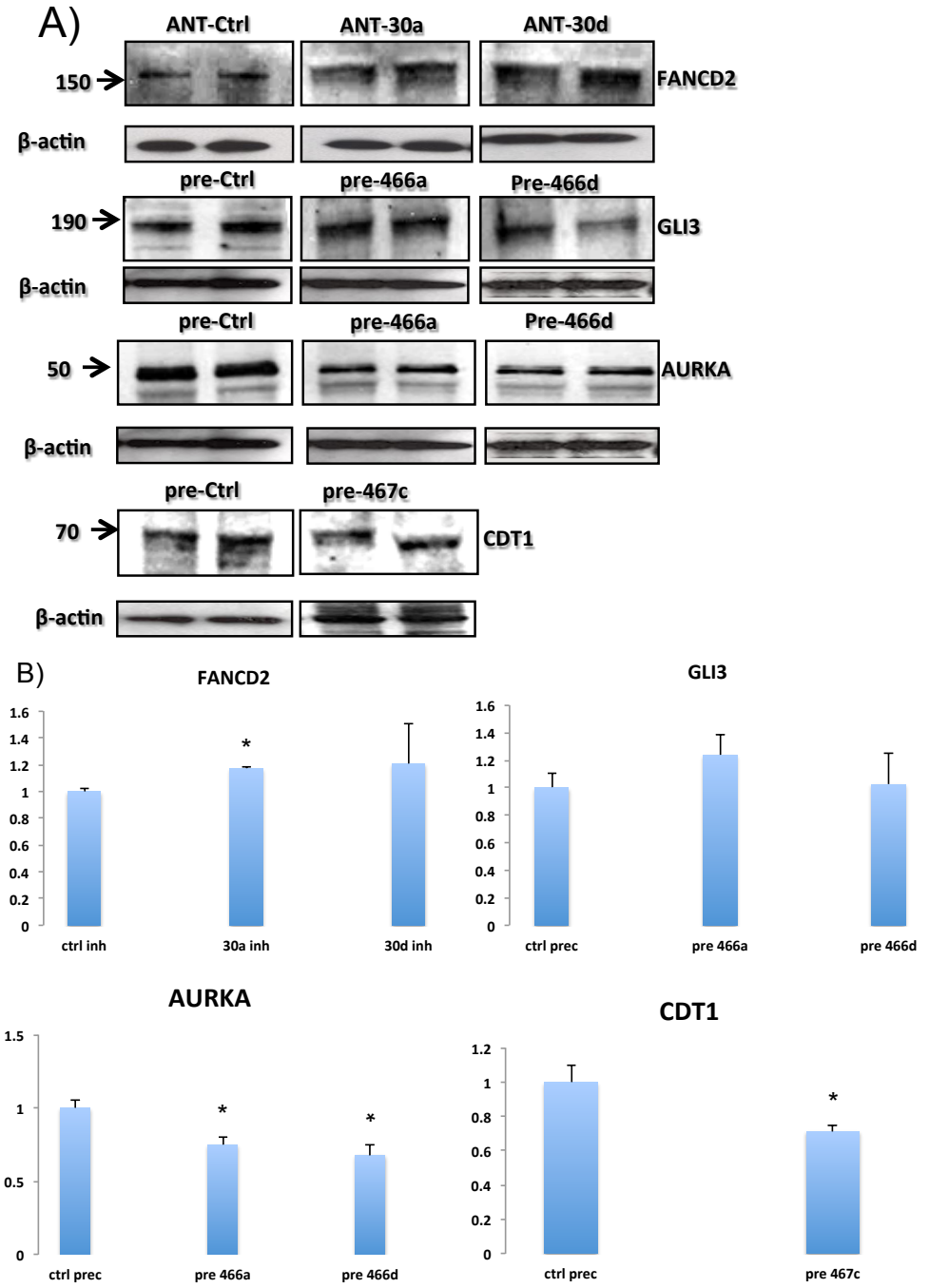
Validation of mirDREM paths by miRNA transfection

Below we list an additional result concerning the hypergeometric enrichment of affected miRNA targets after miRNA transfection in MLE-12 cells in the mirDREM paths (Table 1).

miRNA	significant paths in opposite direction		
	Top 1000	Top 500	Top 3000
miR-125a-5p	A,B,C+E	A,B,C+E	A,B,C+E,F
miR-337-5p	B,C+E	B, C+E	B, C+E,F
miR-467c	D	-	D
miR-466a-3p	D	-	D
miR-466d-3p	D	D	D,H
miR-30d	H	-	H
miR-30a	-	-	-
miR-23b	-	-	-

Supplementary Table S10: Significantly enriched mirDREM paths (Figure 2) after miRNA transfection for different cutoffs of top (500,1000,3000) genes using the hypergeometric enrichment test with multiple testing correction and p <= 0.05.

Validation of individual miRNA-gene targets by transfection and immunoblotting



Supplementary Figure S6: Results of miRNA transfection in MLE-12 cells and subsequent immunoblotting with antibodies against proteins for corresponding miRNA targets. A) Pictures of protein bands after transfection of miR-30a/d antagonists and miR-466a/d,miR-467c precursors with two replicates. The first column in each row denotes the control without transfection of antagonist/precursor. Levels of beta-actin, shown below, serve for normalization. B) Bar plot with standard deviation of quantified blotting intensity from pictures in A). Results that are significant with p-value <0.05 are denoted with * above the bar.

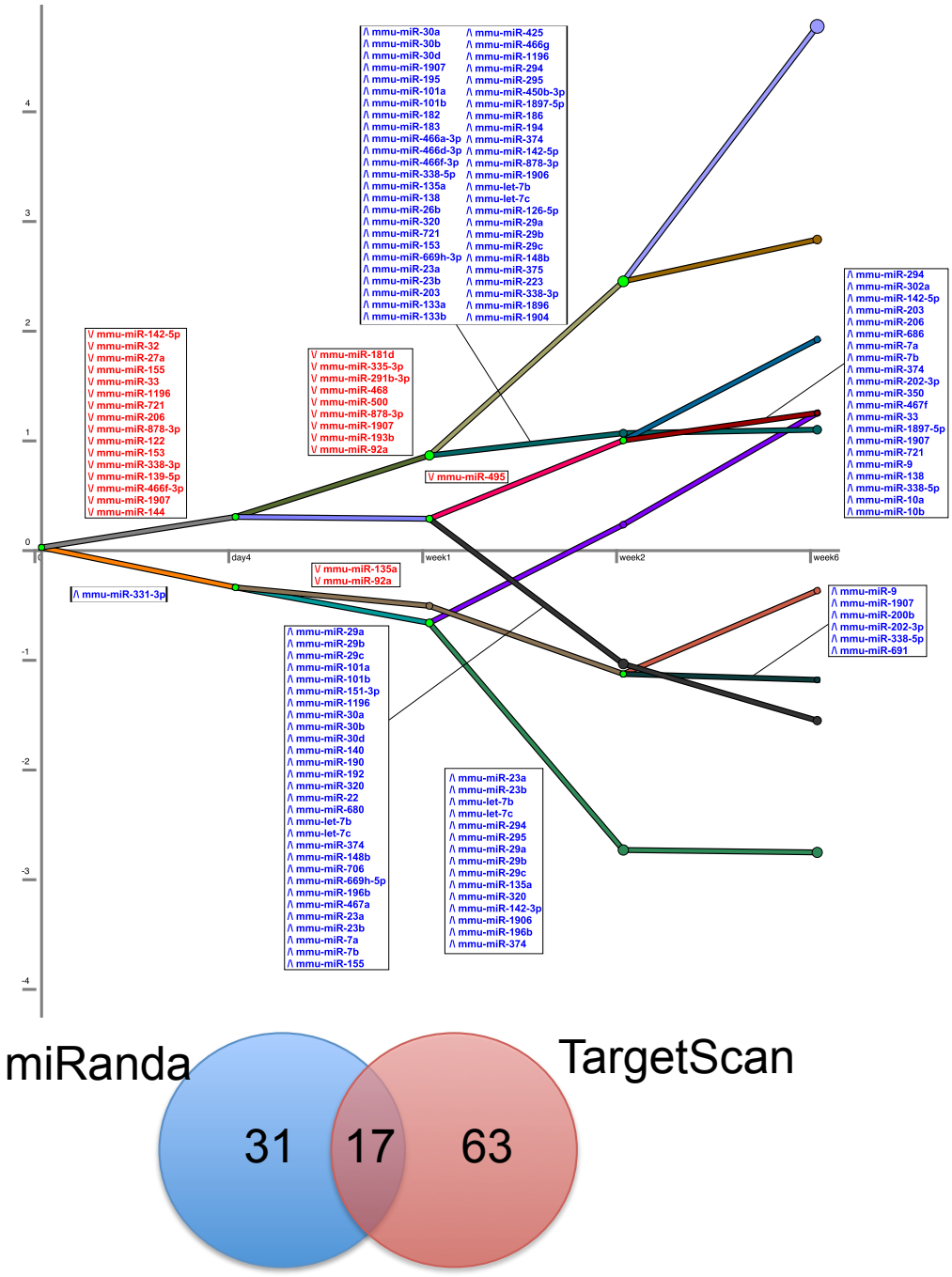
Analysis of significant miRNAs in patients with Idiopathic Pulmonary Fibrosis (IPF)

Patient Cohort	1	2	3	Mouse model
	142 control vs 162 IPF (LGRC http://www.lung-genomics.org)	28 control vs 33 IPF (TissueBank)	10 control vs 10 IPF (TissueBank)	bleomycin at 14d (Liu et al. [15])
miR-125a	-	-	down	down
miR-30a	down	down	down	down
miR-30d	down	down	down	down
miR-467c	-	-	-	-
miR-337	up	up	-	-
miR-466a-3p	-	-	-	down
miR-466d-3p	-	-	-	down

Supplementary Table S11: Expression of the 7 candidate miRNAs for lung development in 4 public data sets of idiopathic pulmonary fibrosis (IPF). 6 out of 7 miRNAs are found to be de-regulated (significantly down- or up-regulated) in at least one of the data sets, highlighting a potential role in IPF progression.

Using TargetScan predictions for network construction

We have also tested mirDREM using a different computationally predicted set of miRNA-mRNA interactions (TargetScan[13]). Roughly a third of the 56 miRNAs are predicted by both networks, an overlap that is similar to previous analyses comparing computationally derived miRNA-gene interactions [14]. While this overlap is not very large, several of the miRNAs we experimentally validated were also included in the TargetScan results and similar GO terms are enriched. This indicates that using the intersection of miRNAs identified by multiple computational methods may improve the accuracy of regulatory models for miRNA regulation. The results are summarized in Supplementary Figure S7 and Supplementary Tables S12-14.



Supplementary Figure S7. (Top) Network model learnt with mirDREM and predicted TargetScan interactions. (Bottom) Overlap of predicted miRNAs in dynamic networks created with miRDREM using either miRanda or TargetScan predictions.

GO ID	adjusted p-value	GO term
GO:0002376	6.43E-07	immune system process
GO:0048534	1.48E-04	hematopoietic or lymphoid organ development
GO:0048518	1.48E-04	positive regulation of biological process
GO:0005488	0.001970531	binding
GO:0002682	0.001970531	regulation of immune system process

Supplemental Table S12 – Top 5 enriched significant (adj. p < 0.05) GO terms for rankings obtained with mirDREM (TargetScan) (all significant GO terms can be found in SI Appendix III, Dataset S2).

validated miR	in TargetScan prediction set	in mirDREM model TargetScan
30a	1	1
30d	1	1
466d-3p	1	1
466a-3p	1	1
337-5p	1 (only 2 targets total)	0
467c	1 (only 10 targets overlap miRanda predictions)	0
125-5p	0	0

Supplementary Table S13: Detailed analysis of validated miRNAs compared to predicted made in the mirDREM TargetScan model. All validated miRs (1st col) that occur in the TargetScan prediction set are denoted with a 1 and 0 otherwise (2nd col), similarly if they occur in the mirDREM model constructed from TargetScan interactions (3rd col).

miR	Gene symbol
155	SATB1,THOC1
23b	MARCKSL1, 6720463M24RIK,FREM1
29a	IBSP, GPR156,9930013L23RIK,COL4A1, ELN,CCDC80,D0H4S114, PPIC, PER3 NPAS3, EMID1,PTX3,FBN1,TMEM132A,GPR37
29b	IBSP,GPR156,9930013L23RIK,COL4A1,ELN, CCDC80,D0H4S114,PPIC,PER3,NPAS3,EMID1,FBN1 CD276,TMEM132A,GPR37,MFAP2
29c	IBSP,GPR156,9930013L23RIK,COL4A1,ELN,CCDC80, D0H4S114,PPIC,PER3,NPAS3,EMID1,PTX3,FBN1 TMEM132A,GPR37
32	IBSP,RHPN2,NPNT,TCF21,EVI5,CD69,BCL11B COL27A1,NOX4,MYO1B,EOMES,RSBN1,PCOLCE2 DNAJB9,GFPT2,KLF2
338-5p	ARHGAP21,RNF19B,KLF2
878-3p	MEF2C,TOP2B

Supplementary Table S14: List of predicted miRNAs and targets that are shared in the mirDREM networks build with either miRanda or TargetScan predictions.

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Appendix III – Supplemental Datasets

Dataset S1: A list of the predicted miRNA-gene interactions for the lung development data with mirDREM and miRanda interactions. The predictions are sorted by split node (see Figure 1 in the paper).We supply the miRNA ID, mouse gene symbol, timepoint after the split node and split node number.

miRNA ID	Gene symbol	time point	associated split node
mmu-miR-551b	PLXNA3	day4	1
mmu-miR-551b	CADM4	day4	1
mmu-miR-551b	SLC45A1	day4	1
mmu-miR-551b	CRLF1	day4	1
mmu-miR-551b	TIPIN	day4	1
mmu-miR-551b	IGF2BP1	day4	1
mmu-miR-551b	TIMM50	day4	1
mmu-miR-551b	SAE1	day4	1
mmu-miR-551b	TRIM72	day4	1
mmu-miR-551b	CITED4	day4	1
mmu-miR-551b	CCHCR1	day4	1
mmu-miR-551b	METRN	day4	1
mmu-miR-551b	DCPP1	day4	1
mmu-miR-551b	BOK	day4	1
mmu-miR-551b	PTK2B	day4	1
mmu-miR-551b	RASL10A	day4	1
mmu-miR-551b	BCL3	day4	1
mmu-miR-551b	A630055G03RIK	day4	1
mmu-miR-551b	POPDC2	day4	1
mmu-miR-551b	TLX2	day4	1
mmu-miR-551b	ICAM1	day4	1
mmu-miR-551b	CENPN	day4	1
mmu-miR-551b	HAPLN3	day4	1
mmu-miR-551b	SLC22A7	day4	1
mmu-miR-551b	OLFML2B	day4	1
mmu-miR-551b	CRTAP	day4	1
mmu-miR-551b	NPL	day4	1
mmu-miR-551b	GIF	day4	1
mmu-miR-551b	AK7	day4	1
mmu-miR-551b	WDR90	day4	1
mmu-miR-551b	NAALAD2	day4	1
mmu-miR-551b	NTS	day4	1
mmu-miR-551b	PLK1	day4	1
mmu-miR-551b	ASPHD2	day4	1
mmu-miR-551b	ABCC3	day4	1
mmu-miR-551b	RPL3L	day4	1
mmu-miR-551b	CHTF18	day4	1
mmu-miR-551b	TCF19	day4	1
mmu-miR-551b	ALOX5	day4	1
mmu-miR-551b	VSIG4	day4	1
mmu-miR-551b	CAR6	day4	1

mmu-miR-551b	RERE	day4	1
mmu-miR-551b	PDZD4	day4	1
mmu-miR-690	PRPH	day4	1
mmu-miR-690	MAD1L1	day4	1
mmu-miR-690	PPP1R14D	day4	1
mmu-miR-690	6330403K07RIK	day4	1
mmu-miR-690	MRE11A	day4	1
mmu-miR-690	CLDN6	day4	1
mmu-miR-690	FCNB	day4	1
mmu-miR-690	ASZ1	day4	1
mmu-miR-690	AURKA	day4	1
mmu-miR-690	KCNIP2	day4	1
mmu-miR-690	AGXT	day4	1
mmu-miR-690	HOXD10	day4	1
mmu-miR-690	CKB	day4	1
mmu-miR-690	GATA1	day4	1
mmu-miR-690	TRAM2	day4	1
mmu-miR-690	TIAM2	day4	1
mmu-miR-690	1700026D08RIK	day4	1
mmu-miR-690	NUDT8	day4	1
mmu-miR-690	KIF4	day4	1
mmu-miR-690	ARMCX4	day4	1
mmu-miR-690	E030010A14RIK	day4	1
mmu-miR-690	ARHGAP9	day4	1
mmu-miR-690	KIF11	day4	1
mmu-miR-690	RCOR2	day4	1
mmu-miR-690	MOSC1	day4	1
mmu-miR-690	EMILIN3	day4	1
mmu-miR-690	WEE1	day4	1
mmu-miR-690	NCAPD2	day4	1
mmu-miR-690	1700011H14RIK	day4	1
mmu-miR-690	GYLTL1B	day4	1
mmu-miR-690	NPY	day4	1
mmu-miR-690	RYR3	day4	1
mmu-miR-690	TROAP	day4	1
mmu-miR-690	HSD11B2	day4	1
mmu-miR-690	PLA2G4C	day4	1
mmu-miR-484	GDF2	day4	1
mmu-miR-484	LZTS1	day4	1
mmu-miR-484	1700026J04RIK	day4	1
mmu-miR-484	SYT5	day4	1
mmu-miR-484	ARSI	day4	1
mmu-miR-484	SUSD2	day4	1
mmu-miR-484	UNC93B1	day4	1
mmu-miR-484	AURKA	day4	1
mmu-miR-484	PRDX2	day4	1

mmu-miR-484	BDKRB2	day4	1
mmu-miR-484	SHF	day4	1
mmu-miR-484	4930451C15RIK	day4	1
mmu-miR-484	2010001M09RIK	day4	1
mmu-miR-484	HIC1	day4	1
mmu-miR-484	SERPINA9	day4	1
mmu-miR-484	NCAPH	day4	1
mmu-miR-484	SLC2A5	day4	1
mmu-miR-484	NFATC4	day4	1
mmu-miR-484	UCK2	day4	1
mmu-miR-484	HHATL	day4	1
mmu-miR-484	LRRC20	day4	1
mmu-miR-484	6230427J02RIK	day4	1
mmu-miR-484	LRRC3	day4	1
mmu-miR-484	SLC8A2	day4	1
mmu-miR-484	SLAMF9	day4	1
mmu-miR-484	LIG1	day4	1
mmu-miR-484	PSRC1	day4	1
mmu-miR-484	SLC6A13	day4	1
mmu-miR-484	FTCD	day4	1
mmu-miR-484	ILF3	day4	1
mmu-miR-484	4930572J05RIK	day4	1
mmu-miR-484	EMILIN2	day4	1
mmu-miR-484	MOXD1	day4	1
mmu-miR-484	MXD3	day4	1
mmu-miR-484	SERPINA3K	day4	1
mmu-miR-484	ITGB1BP3	day4	1
mmu-miR-484	PSORS1C2	day4	1
mmu-miR-484	DUSP9	day4	1
mmu-miR-484	2310043J07RIK	day4	1
mmu-miR-484	MGAT5	day4	1
mmu-miR-484	ADD2	day4	1
mmu-miR-484	PTAFR	day4	1
mmu-miR-484	DMBT1	day4	1
mmu-miR-484	PEG3	day4	1
mmu-miR-485	LDHC	day4	1
mmu-miR-485	PYCRL	day4	1
mmu-miR-485	FXYD2	day4	1
mmu-miR-485	MAD1L1	day4	1
mmu-miR-485	BCMO1	day4	1
mmu-miR-485	TMEM121	day4	1
mmu-miR-485	ACSBG2	day4	1
mmu-miR-485	UNC93B1	day4	1
mmu-miR-485	PKMYT1	day4	1
mmu-miR-485	ACP5	day4	1
mmu-miR-485	CD52	day4	1

mmu-miR-485	E130303B06RIK	day4	1
mmu-miR-485	PRRX2	day4	1
mmu-miR-485	2010001M09RIK	day4	1
mmu-miR-485	MYL9	day4	1
mmu-miR-485	NCAPH	day4	1
mmu-miR-485	FXN	day4	1
mmu-miR-485	HLX	day4	1
mmu-miR-485	COL6A2	day4	1
mmu-miR-485	CDA	day4	1
mmu-miR-485	NGFRAP1	day4	1
mmu-miR-485	NFATC4	day4	1
mmu-miR-485	ATOH8	day4	1
mmu-miR-485	FBN2	day4	1
mmu-miR-485	SULT1E1	day4	1
mmu-miR-485	2310067B10RIK	day4	1
mmu-miR-485	ARHGAP9	day4	1
mmu-miR-485	BC030867	day4	1
mmu-miR-485	CENPN	day4	1
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mmu-miR-485	CDC25C	day4	1
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mmu-miR-485	RGS14	day4	1
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mmu-miR-485	COQ3	day4	1
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mmu-miR-485	WDR67	day4	1
mmu-miR-485	KRT17	day4	1
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mmu-miR-485	GAS2L2	day4	1
mmu-miR-485	CAND2	day4	1
mmu-miR-485	BUB1B	day4	1
mmu-miR-485	HTR2B	day4	1
mmu-miR-485	PRSS22	day4	1
mmu-miR-700	KCNE1L	day4	1
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mmu-miR-700	NOG	day4	1
mmu-miR-700	IMPA2	day4	1
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mmu-miR-700	CLSTN3	day4	1
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mmu-miR-700	LRDD	day4	1
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mmu-miR-700	LTF	day4	1
mmu-miR-700	HIRIP3	day4	1
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mmu-miR-700	GMPR	day4	1
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mmu-miR-214	LRRC51	day4	1
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mmu-miR-214	1190003J15RIK	day4	1
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mmu-miR-214	COL6A2	day4	1
mmu-miR-214	NKX2-5	day4	1
mmu-miR-214	GCHFR	day4	1
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mmu-miR-214	SUV39H1	day4	1
mmu-miR-214	ILF3	day4	1
mmu-miR-214	PMF1	day4	1
mmu-miR-214	FSD1	day4	1
mmu-miR-214	GAS2L2	day4	1
mmu-miR-214	IRF1	day4	1
mmu-miR-214	CMA1	day4	1
mmu-miR-214	SCARA3	day4	1
mmu-miR-214	PSAT1	day4	1
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mmu-miR-324-5p	PRPH	day4	1
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mmu-miR-324-5p	SUSD2	day4	1
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mmu-miR-342-3p	HPCA	day4	1
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mmu-miR-342-3p	5730528L13RIK	day4	1
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mmu-miR-190b	MAMDC2	day4	1
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mmu-miR-190b	EAR1	day4	1
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mmu-miR-190b	IL6	day4	1
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mmu-miR-190b	LMCD1	day4	1
mmu-miR-190b	KIF18A	day4	1
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mmu-miR-190b	PDZRN4	day4	1
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mmu-miR-190b	LIPF	day4	1
mmu-miR-190b	F2R	day4	1
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mmu-miR-669c	PCP4	day4	1
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mmu-miR-669c	TRAF3IP3	day4	1
mmu-miR-669c	TSGA10	day4	1
mmu-miR-669c	2010016I18RIK	day4	1
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mmu-miR-669c	H2-T23	day4	1
mmu-miR-669c	SERPIND1	day4	1
mmu-miR-32	IBSP	day4	1
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mmu-miR-32	INSL5	day4	1
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mmu-miR-32	MTMR1	day4	1
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mmu-miR-32	CD69	day4	1
mmu-miR-32	LRRTM3	day4	1
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mmu-miR-32	COL27A1	day4	1
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mmu-miR-32	EPSTI1	day4	1
mmu-miR-32	RANBP2	day4	1
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mmu-miR-32	NXNL2	day4	1
mmu-miR-32	CYP2D22	day4	1
mmu-miR-32	MYO1B	day4	1
mmu-miR-32	EOMES	day4	1
mmu-miR-32	DMRT2	day4	1
mmu-miR-32	CTSS	day4	1
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mmu-miR-32	RSBN1	day4	1
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mmu-miR-32	ELL2	day4	1
mmu-miR-32	PCF11	day4	1
mmu-miR-32	DNAHC5	day4	1
mmu-miR-32	DNAJB9	day4	1

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mmu-miR-32	GFPT2	day4	1
mmu-miR-32	ZFP677	day4	1
mmu-miR-32	KLF2	day4	1
mmu-miR-32	AGR3	day4	1
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mmu-miR-378	SPP1	week1	2
mmu-miR-378	CAR5A	week1	2
mmu-miR-378	GZMB	week1	2
mmu-miR-378	TRDN	week1	2
mmu-miR-378	CEP290	week1	2
mmu-miR-378	NXNL2	week1	2
mmu-miR-378	ADIPOQ	week1	2
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mmu-miR-378	GRIK4	week1	2
mmu-miR-378	TPO	week1	2
mmu-miR-378	KRT33B	week1	2
mmu-miR-378	COL9A2	week1	2
mmu-miR-378	CDH4	week1	2
mmu-miR-411*	VIP	week1	2
mmu-miR-411*	TBX5	week1	2
mmu-miR-411*	STYX	week1	2
mmu-miR-411*	CCDC80	week1	2
mmu-miR-411*	FABP4	week1	2
mmu-miR-411*	GLB1L3	week1	2
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mmu-miR-188-3p	TLR1	week1	2
mmu-miR-188-3p	SLC22A14	week1	2
mmu-miR-188-3p	KLRK1	week1	2
mmu-miR-188-3p	KMO	week1	2
mmu-miR-188-3p	CCDC37	week1	2
mmu-miR-188-3p	C1S	week1	2
mmu-miR-188-3p	CD74	week1	2
mmu-miR-188-3p	NPDC1	week1	2
mmu-miR-188-3p	KISS1R	week1	2
mmu-miR-188-3p	DOCK2	week1	2
mmu-miR-188-3p	NIPBL	week1	2
mmu-miR-188-3p	SYN2	week1	2
mmu-miR-188-3p	ST3GAL6	week1	2
mmu-miR-188-3p	GUCY1A2	week1	2
mmu-miR-188-3p	ITIH4	week1	2
mmu-miR-188-3p	BCL6	week1	2
mmu-miR-188-3p	ITIH3	week1	2
mmu-miR-188-3p	FBXO24	week1	2
mmu-miR-188-3p	STX11	week1	2
mmu-miR-188-3p	CD27	week1	2

mmu-miR-188-3p	KLRA2	week1	2
mmu-miR-188-3p	SRPK3	week1	2
mmu-miR-188-3p	TBC1D10C	week1	2
mmu-miR-188-3p	4921517D21RIK	week1	2
mmu-miR-188-3p	NRXN2	week1	2
mmu-miR-188-3p	SCUBE1	week1	2
mmu-miR-188-3p	CMAH	week1	2
mmu-miR-188-3p	DOCK9	week1	2
mmu-miR-188-3p	CIDEA	week1	2
mmu-miR-188-3p	RNF207	week1	2
mmu-miR-188-3p	PCM1	week1	2
mmu-miR-188-3p	CDKL5	week1	2
mmu-miR-188-3p	CYP4B1	week1	2
mmu-miR-188-3p	CTSW	week1	2
mmu-miR-188-3p	ARHGAP30	week1	2
mmu-miR-188-3p	TRAF3IP1	week1	2
mmu-miR-188-3p	PNPLA8	week1	2
mmu-miR-188-3p	CD19	week1	2
mmu-miR-188-3p	KCNT1	week1	2
mmu-miR-188-3p	ATF3	week1	2
mmu-miR-188-3p	DUSP1	week1	2
mmu-miR-188-3p	CST7	week1	2
mmu-miR-188-3p	XIRP2	week1	2
mmu-miR-188-3p	SERPINF2	week1	2
mmu-miR-188-3p	CD79B	week1	2
mmu-miR-188-3p	SLC14A1	week1	2
mmu-miR-341	FST	week2	3
mmu-miR-341	4922501L14RIK	week2	3
mmu-miR-341	BDKRB1	week2	3
mmu-miR-341	NR1D1	week2	3
mmu-miR-341	RPRML	week2	3
mmu-miR-341	WFDC6A	week2	3
mmu-miR-341	WFDC6B	week2	3
mmu-miR-341	WFDC1	week2	3
mmu-miR-154*	ASGR1	week2	3
mmu-miR-154*	AKR1B7	week2	3
mmu-miR-154*	4922501L14RIK	week2	3
mmu-miR-154*	DCLK3	week2	3
mmu-miR-154*	SLC10A6	week2	3
mmu-miR-29a	IBSP	week2	3
mmu-miR-29a	GPR156	week2	3
mmu-miR-29a	9930013L23RIK	week2	3
mmu-miR-29a	COL4A1	week2	3
mmu-miR-29a	MMEL1	week2	3
mmu-miR-29a	ELN	week2	3
mmu-miR-29a	CCDC80	week2	3

mmu-miR-29a	ARNTL	week2	3
mmu-miR-29a	4833422F24RIK	week2	3
mmu-miR-29a	ACCN4	week2	3
mmu-miR-29a	D0H4S114	week2	3
mmu-miR-29a	PPIC	week2	3
mmu-miR-29a	PER3	week2	3
mmu-miR-29b	IBSP	week2	3
mmu-miR-29b	GPR156	week2	3
mmu-miR-29b	9930013L23RIK	week2	3
mmu-miR-29b	COL4A1	week2	3
mmu-miR-29b	MMEL1	week2	3
mmu-miR-29b	ABCB11	week2	3
mmu-miR-29b	ELN	week2	3
mmu-miR-29b	CCDC80	week2	3
mmu-miR-29b	ARNTL	week2	3
mmu-miR-29b	PAQR3	week2	3
mmu-miR-29b	4833422F24RIK	week2	3
mmu-miR-29b	AHSG	week2	3
mmu-miR-29b	D0H4S114	week2	3
mmu-miR-29b	ACCN4	week2	3
mmu-miR-29b	PPIC	week2	3
mmu-miR-29b	PER3	week2	3
mmu-miR-29b	ROS1	week2	3
mmu-miR-29c	IBSP	week2	3
mmu-miR-29c	GPR156	week2	3
mmu-miR-29c	9930013L23RIK	week2	3
mmu-miR-29c	COL4A1	week2	3
mmu-miR-29c	MMEL1	week2	3
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mmu-miR-29c	CCDC80	week2	3
mmu-miR-29c	POSTN	week2	3
mmu-miR-29c	ARNTL	week2	3
mmu-miR-29c	PAQR3	week2	3
mmu-miR-29c	4833422F24RIK	week2	3
mmu-miR-29c	AHSG	week2	3
mmu-miR-29c	D0H4S114	week2	3
mmu-miR-29c	ACCN4	week2	3
mmu-miR-29c	PPIC	week2	3
mmu-miR-29c	PER3	week2	3
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mmu-miR-551b	NLRC5	week2	4
mmu-miR-551b	VPREB3	week2	4
mmu-miR-551b	BLK	week2	4
mmu-miR-551b	SLC22A14	week2	4
mmu-miR-551b	CD72	week2	4
mmu-miR-551b	SKAP1	week2	4

mmu-miR-551b	AGRP	week2	4
mmu-miR-551b	H2-Q8	week2	4
mmu-miR-337-3p	LY6D	week2	4
mmu-miR-337-3p	KLB	week2	4
mmu-miR-337-3p	9530057J20RIK	week2	4
mmu-miR-337-3p	SLC16A11	week2	4
mmu-miR-337-3p	OASL2	week2	4
mmu-miR-337-3p	CASC4	week2	4
mmu-miR-337-3p	GGT1	week2	4
mmu-miR-337-3p	MESP1	week2	4
mmu-miR-337-3p	PAPSS2	week2	4
mmu-miR-337-3p	H2-Q8	week2	4
mmu-miR-337-3p	HSH2D	week2	4
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mmu-miR-574-3p	EZH1	week2	4
mmu-miR-574-3p	MAP4K1	week2	4
mmu-miR-574-3p	SLFN5	week2	4
mmu-miR-574-3p	ZFP85-RS1	week2	4
mmu-miR-574-3p	SP110	week2	4
mmu-miR-574-3p	ATP6V1B1	week2	4
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mmu-miR-574-3p	ARHGAP12	week2	4
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mmu-miR-574-3p	ENTPD2	week2	4
mmu-miR-574-3p	AATK	week2	4
mmu-miR-574-3p	DEPDC6	week2	4
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mmu-miR-574-3p	TMEM38B	week2	4
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mmu-miR-574-3p	TNNI3K	week2	4
mmu-miR-574-3p	LRMP	week2	4
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mmu-miR-878-3p	ATP1B1	week2	4
mmu-miR-878-3p	MYBPC2	week2	4
mmu-miR-878-3p	GPBP1	week2	4
mmu-miR-878-3p	CRLF3	week2	4
mmu-miR-878-3p	ACOT4	week2	4
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mmu-miR-878-3p	PLLP	week2	4
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mmu-miR-155	LMBRD1	week2	4
mmu-miR-155	SSPO	week2	4
mmu-miR-155	CHPT1	week2	4
mmu-miR-155	GCC2	week2	4

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mmu-miR-155	1700024G13RIK	week2	4
mmu-miR-155	PDE7B	week2	4
mmu-miR-155	TDO2	week2	4
mmu-miR-155	CD46	week2	4
mmu-miR-155	BCAP29	week2	4
mmu-miR-155	RGS7	week2	4
mmu-miR-155	RAPGEF4	week2	4
mmu-miR-155	LRRK2	week2	4
mmu-miR-155	MGST1	week2	4
mmu-miR-155	IFNGR1	week2	4
mmu-miR-155	THOC1	week2	4
mmu-miR-34b-3p	SGPP2	week2	4
mmu-miR-34b-3p	LMO7	week2	4
mmu-miR-34b-3p	ITSN2	week2	4
mmu-miR-34b-3p	VIPR1	week2	4
mmu-miR-34b-3p	BTK	week2	4
mmu-miR-34b-3p	ERO1LB	week2	4
mmu-miR-34b-3p	KISS1R	week2	4
mmu-miR-34b-3p	PLCB4	week2	4
mmu-miR-34b-3p	HEY1	week2	4
mmu-miR-34b-3p	ZFP273	week2	4
mmu-miR-34b-3p	PLTP	week2	4
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mmu-miR-34b-3p	PHKG1	week2	4
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mmu-miR-34b-3p	CYB561	week2	4
mmu-miR-34b-3p	DENND1C	week2	4
mmu-miR-34b-3p	IL6RA	week2	4
mmu-miR-34b-3p	CYBB	week2	4
mmu-miR-34b-3p	SLC7A3	week2	4
mmu-miR-34b-3p	AGTR1A	week2	4
mmu-miR-34b-3p	CCR3	week2	4
mmu-miR-34b-3p	PRICKLE2	week2	4
mmu-miR-34b-3p	CRYM	week2	4
mmu-miR-34b-3p	GRB14	week2	4
mmu-miR-34b-3p	F2R	week2	4
mmu-miR-338-5p	KIFC2	week2	4
mmu-miR-338-5p	PDIA2	week2	4
mmu-miR-338-5p	PTPN20	week2	4
mmu-miR-338-5p	PTTG1	week2	4
mmu-miR-338-5p	CAR5B	week2	4
mmu-miR-338-5p	CD2AP	week2	4
mmu-miR-338-5p	KRT23	week2	4
mmu-miR-338-5p	2310001H12RIK	week2	4

mmu-miR-338-5p	ARHGAP21	week2	4
mmu-miR-338-5p	SFRS18	week2	4
mmu-miR-338-5p	KISS1R	week2	4
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mmu-miR-338-5p	EPSTI1	week2	4
mmu-miR-338-5p	FBXL13	week2	4
mmu-miR-338-5p	DTNA	week2	4
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mmu-miR-338-5p	MAOB	week2	4
mmu-miR-338-5p	KTN1	week2	4
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mmu-miR-338-5p	KLF2	week2	4
mmu-miR-338-5p	MGST1	week2	4
mmu-miR-338-5p	SH3GL2	week2	4
mmu-miR-467e	ENPP5	week2	4
mmu-miR-467e	DNAJC5B	week2	4
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mmu-miR-467e	TNFRSF25	week2	4
mmu-miR-467e	HSD17B1	week2	4
mmu-miR-467e	OLAH	week2	4
mmu-miR-467e	ZFP68	week2	4
mmu-miR-467e	RNF186	week2	4
mmu-miR-467e	ASB11	week2	4
mmu-miR-467e	RABGAP1L	week2	4
mmu-miR-467e	DNAHC12	week2	4
mmu-miR-467e	ANKRD1	week2	4
mmu-miR-467e	LRRC34	week2	4
mmu-miR-467e	LRRC4C	week2	4
mmu-miR-467e	BC005561	week2	4
mmu-miR-467e	HOOK3	week2	4
mmu-miR-467e	CAPS2	week2	4
mmu-miR-467e	TDO2	week2	4
mmu-miR-467e	CCDC66	week2	4
mmu-miR-467e	PDGFD	week2	4
mmu-miR-467e	DOCK10	week2	4
mmu-miR-467e	SRGN	week2	4

mmu-miR-467e	STAG2	week2	4
mmu-miR-467e	TEC	week2	4
mmu-miR-467e	C1GALT1C1	week2	4
mmu-miR-467e	CCPG1	week2	4
mmu-miR-467e	PIK3C2A	week2	4
mmu-miR-467e	YIPF7	week2	4
mmu-miR-467e	MYO1B	week2	4
mmu-miR-467e	CCDC81	week2	4
mmu-miR-467e	TNFRSF13C	week2	4
mmu-miR-467e	DOCK9	week2	4
mmu-miR-467e	LMBRD1	week2	4
mmu-miR-467e	TRIM21	week2	4
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mmu-miR-467e	HSPB1	week2	4
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mmu-miR-467e	WDR69	week2	4
mmu-miR-467e	LRRK2	week2	4
mmu-miR-467e	BCAR3	week2	4
mmu-miR-467a*	ZFP54	week2	4
mmu-miR-467a*	GM129	week2	4
mmu-miR-467a*	HERPUD1	week2	4
mmu-miR-467a*	A930001N09RIK	week2	4
mmu-miR-467a*	AKAP9	week2	4
mmu-miR-467a*	4933421E11RIK	week2	4
mmu-miR-467a*	ANKRD1	week2	4
mmu-miR-467a*	SERPINB1B	week2	4
mmu-miR-467a*	CCDC68	week2	4
mmu-miR-467a*	CTTNBP2	week2	4
mmu-miR-467a*	PCF11	week2	4
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mmu-miR-467a*	RNF19B	week2	4
mmu-miR-467a*	INPP5D	week2	4
mmu-miR-467a*	PDGFD	week2	4
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mmu-miR-467a*	NBEAL1	week2	4
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mmu-miR-467e*	GM129	week2	4
mmu-miR-467e*	HERPUD1	week2	4
mmu-miR-467e*	A930001N09RIK	week2	4
mmu-miR-467e*	AKAP9	week2	4
mmu-miR-467e*	4933421E11RIK	week2	4

mmu-miR-467e*	ANKRD1	week2	4
mmu-miR-467e*	SERPINB1B	week2	4
mmu-miR-467e*	CCDC68	week2	4
mmu-miR-467e*	PCF11	week2	4
mmu-miR-467e*	CTTNBP2	week2	4
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mmu-miR-467e*	LRRK2	week2	4
mmu-miR-467e*	NBEAL1	week2	4
mmu-miR-142-5p	LDHC	week1	5
mmu-miR-142-5p	CKAP2	week1	5
mmu-miR-142-5p	CCDC99	week1	5
mmu-miR-142-5p	NELL1	week1	5
mmu-miR-142-5p	OTX2	week1	5
mmu-miR-142-5p	TTK	week1	5
mmu-miR-142-5p	PBK	week1	5
mmu-miR-142-5p	ORC1L	week1	5
mmu-miR-142-5p	NPHP4	week1	5
mmu-miR-142-5p	CCNB2	week1	5
mmu-miR-142-5p	NCAPG	week1	5
mmu-miR-142-5p	LY6F	week1	5
mmu-miR-142-5p	LRRN1	week1	5
mmu-miR-142-5p	CACNA1G	week1	5
mmu-miR-142-5p	TUBE1	week1	5
mmu-miR-142-5p	TUBB6	week1	5
mmu-miR-142-5p	BUB1B	week1	5
mmu-miR-142-5p	AREG	week1	5
mmu-miR-142-5p	MASTL	week1	5
mmu-miR-142-5p	MELK	week1	5
mmu-miR-142-5p	ERCC6L	week1	5
mmu-let-7f*	KIF22	week1	5
mmu-let-7f*	HMGB2	week1	5
mmu-let-7f*	HIST4H4	week1	5
mmu-let-7f*	OLFML2B	week1	5
mmu-let-7f*	PLAC1	week1	5
mmu-let-7f*	NUF2	week1	5
mmu-let-7f*	NUSAP1	week1	5
mmu-let-7f*	CASC5	week1	5
mmu-let-7f*	BRIP1	week1	5
mmu-let-7f*	GTF2A1L	week1	5
mmu-let-7f*	ECT2	week1	5
mmu-let-7f*	CCL11	week1	5
mmu-let-7f*	POLE2	week1	5
mmu-let-7f*	NPY	week1	5
mmu-let-7f*	OLFR664	week1	5

mmu-let-7f*	FANCI	week1	5
mmu-let-7f*	PLK1	week1	5
mmu-let-7f*	SQLE	week1	5
mmu-let-7f*	KRT15	week1	5
mmu-let-7f*	CRH	week1	5
mmu-let-7f*	SPON2	week1	5
mmu-let-7f*	UBE2T	week1	5
mmu-let-7f*	ASPM	week1	5
mmu-miR-101b	MAGEL2	week1	5
mmu-miR-101b	LMNB1	week1	5
mmu-miR-101b	DBC1	week1	5
mmu-miR-101b	SYCE2	week1	5
mmu-miR-101b	TTK	week1	5
mmu-miR-101b	4833423E24RIK	week1	5
mmu-miR-101b	GTF2A1L	week1	5
mmu-miR-101b	MCM3	week1	5
mmu-miR-101b	AQP3	week1	5
mmu-miR-101b	RAD51	week1	5
mmu-miR-101b	MYCN	week1	5
mmu-miR-101b	SPC25	week1	5
mmu-miR-101b	CHRM3	week1	5
mmu-miR-101b	FANCI	week1	5
mmu-miR-101b	SQLE	week1	5
mmu-miR-101b	AGT	week1	5
mmu-miR-101b	RRM1	week1	5
mmu-miR-101b	LRRN1	week1	5
mmu-miR-101b	MNS1	week1	5
mmu-miR-101b	RAD18	week1	5
mmu-miR-101b	HAS2	week1	5
mmu-miR-181c	CKS1B	week1	5
mmu-miR-181c	JPH3	week1	5
mmu-miR-181c	CCDC99	week1	5
mmu-miR-181c	B3GALT5	week1	5
mmu-miR-181c	LMO3	week1	5
mmu-miR-181c	E2F7	week1	5
mmu-miR-181c	TMEM121	week1	5
mmu-miR-181c	4930547N16RIK	week1	5
mmu-miR-181c	TTK	week1	5
mmu-miR-181c	FHL2	week1	5
mmu-miR-181c	AURKB	week1	5
mmu-miR-181c	H19	week1	5
mmu-miR-181c	INCENP	week1	5
mmu-miR-181c	TGFBI	week1	5
mmu-miR-181c	2310067B10RIK	week1	5
mmu-miR-181c	OLFR530	week1	5
mmu-miR-181c	THBS4	week1	5

mmu-miR-181c	TRPA1	week1	5
mmu-miR-181c	CCNF	week1	5
mmu-miR-181c	SIX2	week1	5
mmu-miR-181c	RACGAP1	week1	5
mmu-miR-181c	RAD54L	week1	5
mmu-miR-181c	6720463M24RIK	week1	5
mmu-miR-181c	ANKRD22	week1	5
mmu-miR-181c	ASPHD2	week1	5
mmu-miR-181c	LRRN1	week1	5
mmu-miR-181c	WIF1	week1	5
mmu-miR-181c	EFNA4	week1	5
mmu-miR-181c	MELK	week1	5
mmu-miR-181c	1700049L16RIK	week1	5
mmu-miR-302c*	CKAP2	week1	5
mmu-miR-302c*	AIPL1	week1	5
mmu-miR-302c*	MKI67	week1	5
mmu-miR-302c*	1500015O10RIK	week1	5
mmu-miR-302c*	INTS2	week1	5
mmu-miR-302c*	AURKA	week1	5
mmu-miR-302c*	ORC1L	week1	5
mmu-miR-302c*	MXD3	week1	5
mmu-miR-302c*	D14ERTD449E	week1	5
mmu-miR-302c*	WBP2NL	week1	5
mmu-miR-302c*	C1QL1	week1	5
mmu-miR-302c*	STAG3	week1	5
mmu-miR-302c*	PPIL5	week1	5
mmu-miR-302c*	COL11A1	week1	5
mmu-miR-302c*	CCNA2	week1	5
mmu-miR-302c*	TUBB3	week1	5
mmu-miR-224	CPNE6	week2	6
mmu-miR-224	WASF1	week2	6
mmu-miR-224	ARSI	week2	6
mmu-miR-224	GDF5	week2	6
mmu-miR-224	CACNB2	week2	6
mmu-miR-224	RANGAP1	week2	6
mmu-miR-224	CDH3	week2	6
mmu-miR-224	DAAM2	week2	6
mmu-miR-224	HOXD10	week2	6
mmu-miR-224	GPC4	week2	6
mmu-miR-224	PYCR1	week2	6
mmu-miR-224	H2AFY2	week2	6
mmu-miR-224	PCNA	week2	6
mmu-miR-224	AP3B2	week2	6
mmu-miR-224	RGN	week2	6
mmu-miR-224	CDA	week2	6
mmu-miR-224	PTX3	week2	6

mmu-miR-224	SLITRK5	week2	6
mmu-miR-224	TWIST2	week2	6
mmu-miR-224	CAR2	week2	6
mmu-miR-126-3p	MAF	week2	6
mmu-miR-126-3p	CADM3	week2	6
mmu-miR-126-3p	HS3ST5	week2	6
mmu-miR-126-3p	GMNN	week2	6
mmu-miR-126-3p	PNCK	week2	6
mmu-miR-126-3p	THOP1	week2	6
mmu-miR-126-3p	PDXP	week2	6
mmu-miR-126-3p	TCEAL5	week2	6
mmu-miR-126-3p	ILF3	week2	6
mmu-miR-126-3p	TPBG	week2	6
mmu-miR-126-3p	CTNNBIP1	week2	6
mmu-miR-126-3p	CASP3	week2	6
mmu-miR-126-3p	COL14A1	week2	6
mmu-miR-126-3p	MPI	week2	6
mmu-miR-126-3p	4930404H21RIK	week2	6
mmu-miR-126-3p	NTS	week2	6
mmu-miR-126-3p	COL6A2	week2	6
mmu-miR-126-3p	SP5	week2	6
mmu-miR-126-3p	C1QL3	week2	6
mmu-miR-126-3p	TMPO	week2	6
mmu-miR-126-3p	PTX3	week2	6
mmu-let-7i*	5530401N12RIK	week2	6
mmu-let-7i*	THOP1	week2	6
mmu-let-7i*	DTYMK	week2	6
mmu-let-7i*	PGAM2	week2	6
mmu-let-7i*	MYBL1	week2	6
mmu-let-7i*	GPC4	week2	6
mmu-let-7i*	CDH22	week2	6
mmu-let-7i*	CRISPLD1	week2	6
mmu-let-7i*	FXN	week2	6
mmu-let-7i*	SPEG	week2	6
mmu-let-7i*	KIRREL	week2	6
mmu-let-7i*	LSM3	week2	6
mmu-let-7i*	NGFRAP1	week2	6
mmu-let-7i*	WDHD1	week2	6
mmu-let-7i*	CRY1	week2	6
mmu-let-7i*	THBS1	week2	6
mmu-let-7i*	CCDC106	week2	6
mmu-let-7i*	ZFP239	week2	6
mmu-let-7i*	CDC42EP5	week2	6
mmu-let-7i*	2610017I09RIK	week2	6
mmu-let-7i*	SLC8A1	week2	6
mmu-let-7i*	TTF2	week2	6

mmu-let-7i*	SUV39H2	week2	6
mmu-let-7i*	PPA1	week2	6
mmu-let-7i*	CDKN1C	week2	6
mmu-let-7i*	SMTN	week2	6
mmu-let-7i*	DNMT1	week2	6
mmu-let-7i*	ZMYND19	week2	6
mmu-let-7i*	PLA2G4C	week2	6
mmu-miR-29a	1500010J02RIK	week2	6
mmu-miR-29a	PLXNA3	week2	6
mmu-miR-29a	BLM	week2	6
mmu-miR-29a	DBF4	week2	6
mmu-miR-29a	TSPAN6	week2	6
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mmu-miR-29a	SLC7A9	week2	6
mmu-miR-29a	CHEK2	week2	6
mmu-miR-29a	TGFB2	week2	6
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mmu-miR-29a	PAFAH1B3	week2	6
mmu-miR-29a	COL6A2	week2	6
mmu-miR-29a	TUBB5	week2	6
mmu-miR-29a	RANBP1	week2	6
mmu-miR-29a	TBC1D7	week2	6
mmu-miR-29a	NFATC4	week2	6
mmu-miR-29a	GPX7	week2	6
mmu-miR-29a	PTX3	week2	6
mmu-miR-29a	GCHFR	week2	6
mmu-miR-29a	CDC7	week2	6
mmu-miR-29a	LRRC3	week2	6
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mmu-miR-29a	FBN1	week2	6
mmu-miR-29a	COL15A1	week2	6
mmu-miR-29a	TMEM132A	week2	6
mmu-miR-29a	BRCA2	week2	6
mmu-miR-29a	COL16A1	week2	6
mmu-miR-29a	KITL	week2	6
mmu-miR-29a	WDR90	week2	6
mmu-miR-29a	CDK2	week2	6
mmu-miR-29a	CCDC77	week2	6
mmu-miR-29a	BLMH	week2	6
mmu-miR-29a	FREM3	week2	6
mmu-miR-29a	GPR37	week2	6

mmu-miR-29a	SFPQ	week2	6
mmu-miR-29a	PSORS1C2	week2	6
mmu-miR-29a	TDG	week2	6
mmu-miR-29a	ROR1	week2	6
mmu-miR-29a	FKBP10	week2	6
mmu-miR-29a	2700094K13RIK	week2	6
mmu-miR-29b	1500010J02RIK	week2	6
mmu-miR-29b	PLXNA3	week2	6
mmu-miR-29b	BLM	week2	6
mmu-miR-29b	DBF4	week2	6
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mmu-miR-29b	CHEK2	week2	6
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mmu-miR-29b	CRISPLD1	week2	6
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mmu-miR-29b	CDC7	week2	6
mmu-miR-29b	BMP1	week2	6
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mmu-miR-29b	FBN1	week2	6
mmu-miR-29b	CD276	week2	6
mmu-miR-29b	TMEM132A	week2	6
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mmu-miR-29b	CDK2	week2	6
mmu-miR-29b	CCDC77	week2	6
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mmu-miR-29b	GPR37	week2	6
mmu-miR-29b	SFPQ	week2	6
mmu-miR-29b	PSORS1C2	week2	6
mmu-miR-29b	TDG	week2	6
mmu-miR-29b	ROR1	week2	6
mmu-miR-29b	MFAP2	week2	6

mmu-miR-29b	FKBP10	week2	6
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mmu-miR-29c	1500010J02RIK	week2	6
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mmu-miR-29c	BLM	week2	6
mmu-miR-29c	DBF4	week2	6
mmu-miR-29c	TSPAN6	week2	6
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mmu-miR-29c	SLC7A9	week2	6
mmu-miR-29c	CHEK2	week2	6
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mmu-miR-29c	PSORS1C2	week2	6
mmu-miR-29c	TDG	week2	6
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mmu-miR-29c	FKBP10	week2	6
mmu-miR-29c	2700094K13RIK	week2	6

mmu-miR-467a	FGD1	week2	6
mmu-miR-467a	NDN	week2	6
mmu-miR-467a	WASF1	week2	6
mmu-miR-467a	NANOS1	week2	6
mmu-miR-467a	MED25	week2	6
mmu-miR-467a	SNRPD1	week2	6
mmu-miR-467a	CCDC34	week2	6
mmu-miR-467a	NEO1	week2	6
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mmu-miR-467a	ODC1	week2	6
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mmu-miR-467a	SUV39H1	week2	6
mmu-miR-467a	COL15A1	week2	6
mmu-miR-467a	CHST2	week2	6
mmu-miR-467a	IGF1	week2	6
mmu-miR-467a	RNASEH2B	week2	6
mmu-miR-467a	WDR90	week2	6
mmu-miR-467a	SUV39H2	week2	6
mmu-miR-467a	THSD7A	week2	6
mmu-miR-467a	COQ3	week2	6
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mmu-miR-467a	IGF2R	week2	6
mmu-miR-467a	GNAS	week2	6
mmu-miR-467a	DIAP3	week2	6
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mmu-miR-423-5p	1500010J02RIK	week2	6
mmu-miR-423-5p	KCNMB4	week2	6
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mmu-miR-423-5p	ASB16	week2	6
mmu-miR-423-5p	NRADD	week2	6
mmu-miR-423-5p	ZFP580	week2	6
mmu-miR-423-5p	APLP1	week2	6
mmu-miR-423-5p	METRN	week2	6
mmu-miR-423-5p	SPEG	week2	6
mmu-miR-423-5p	ADH1	week2	6
mmu-miR-423-5p	TUBB5	week2	6
mmu-miR-423-5p	AP3B2	week2	6
mmu-miR-423-5p	UCK2	week2	6

mmu-miR-423-5p	ACADS	week2	6
mmu-miR-423-5p	CRTAP	week2	6
mmu-miR-423-5p	CHST5	week2	6
mmu-miR-423-5p	TAF6L	week2	6
mmu-miR-423-5p	TRERF1	week2	6
mmu-miR-423-5p	CDC25B	week2	6
mmu-miR-423-5p	MMP11	week2	6
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mmu-miR-423-5p	PFDN1	week2	6
mmu-miR-423-5p	KIF1A	week2	6
mmu-miR-423-5p	PODXL2	week2	6
mmu-miR-423-5p	SMYD5	week2	6
mmu-miR-423-5p	MFAP2	week2	6
mmu-miR-451	CTHRC1	week2	6
mmu-miR-451	SLC38A4	week2	6
mmu-miR-451	WASF1	week2	6
mmu-miR-451	ILF3	week2	6
mmu-miR-451	NID2	week2	6
mmu-miR-451	SHF	week2	6
mmu-miR-451	TMEM26	week2	6
mmu-miR-451	CDKN1C	week2	6
mmu-miR-451	MTHFD2	week2	6
mmu-miR-451	MPHOSPH9	week2	6
mmu-miR-451	CRISPLD1	week2	6
mmu-miR-451	ANK2	week2	6
mmu-miR-451	GPR37	week2	6
mmu-miR-451	ROR1	week2	6
mmu-miR-451	MBOAT2	week2	6
mmu-miR-451	NPM3	week2	6
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mmu-miR-451	2700094K13RIK	week2	6
mmu-miR-451	MYC	week2	6
mmu-miR-451	CASQ1	week2	6
mmu-miR-451	GFRA2	week2	6
mmu-miR-345-5p	6330439K17RIK	week2	6
mmu-miR-345-5p	CADM4	week2	6
mmu-miR-345-5p	SIT1	week2	6
mmu-miR-345-5p	SLAMF9	week2	6
mmu-miR-345-5p	WDFY4	week2	6
mmu-miR-345-5p	TNFSF14	week2	6
mmu-miR-345-5p	TRIM72	week2	6
mmu-miR-345-5p	SERPINA3K	week2	6
mmu-miR-345-5p	RASSF4	week2	6
mmu-miR-345-5p	ACSM1	week2	6
mmu-miR-345-5p	DHRS3	week2	6
mmu-miR-345-5p	NR1I2	week2	6

mmu-miR-345-5p	OIT1	week2	6
mmu-miR-345-5p	B3GNT4	week2	6
mmu-miR-345-5p	BNC1	week2	6
mmu-miR-345-5p	BCL3	week2	6
mmu-miR-345-5p	E230008N13RIK	week2	6
mmu-miR-345-5p	ALOX5	week2	6
mmu-miR-345-5p	RASD1	week2	6
mmu-miR-345-5p	PTAFR	week2	6
mmu-miR-199a-3p	PTPN6	week2	6
mmu-miR-199a-3p	SIT1	week2	6
mmu-miR-199a-3p	GCLC	week2	6
mmu-miR-199a-3p	HIST1H2BE	week2	6
mmu-miR-199a-3p	TTC25	week2	6
mmu-miR-199a-3p	9930023K05RIK	week2	6
mmu-miR-199a-3p	ALOX12E	week2	6
mmu-miR-199a-3p	TNFSF14	week2	6
mmu-miR-199a-3p	KIF9	week2	6
mmu-miR-199a-3p	RRAGB	week2	6
mmu-miR-199a-3p	ESPN	week2	6
mmu-miR-199a-3p	ARHGAP4	week2	6
mmu-miR-199a-3p	PTK2B	week2	6
mmu-miR-199a-3p	RASL10A	week2	6
mmu-miR-199a-3p	BCL3	week2	6
mmu-miR-199a-3p	PLCD4	week2	6
mmu-miR-199a-3p	QPRT	week2	6
mmu-miR-199a-3p	SUSD3	week2	6
mmu-miR-199a-3p	JAK3	week2	6
mmu-miR-199a-3p	MTMR7	week2	6
mmu-miR-127	PPP1R14D	week2	6
mmu-miR-127	TTC25	week2	6
mmu-miR-127	NFKBIE	week2	6
mmu-miR-127	FBXO2	week2	6
mmu-miR-127	ITGB2	week2	6
mmu-miR-127	CLNK	week2	6
mmu-miR-127	RGS14	week2	6
mmu-miR-127	MARCO	week2	6
mmu-miR-127	A530016L24RIK	week2	6
mmu-miR-127	TRIM54	week2	6
mmu-miR-127	BCL3	week2	6
mmu-miR-127	JAK3	week2	6
mmu-miR-127	HTR2B	week2	6
mmu-miR-127	RASA4	week2	6
mmu-miR-127	LIPE	week2	6
mmu-miR-184	SNCG	week6	7
mmu-miR-184	OLIG3	week6	7
mmu-miR-184	TNFRSF17	week6	7

mmu-miR-184	MOSC1	week6	7
mmu-miR-380-3p	SLCO4A1	week6	7
mmu-miR-380-3p	MYL1	week6	7
mmu-miR-380-3p	OAS1A	week6	7
mmu-miR-192	CKAP2	week2	8
mmu-miR-192	CCDC99	week2	8
mmu-miR-192	NSL1	week2	8
mmu-miR-192	RRM1	week2	8
mmu-miR-192	IQGAP3	week2	8
mmu-miR-192	CASC5	week2	8
mmu-miR-192	LOXL2	week2	8
mmu-miR-192	E130306D19RIK	week2	8
mmu-miR-466d-3p	KIF23	week2	8
mmu-miR-466d-3p	KIFC1	week2	8
mmu-miR-466d-3p	LMNB1	week2	8
mmu-miR-466d-3p	SCML2	week2	8
mmu-miR-466d-3p	AURKA	week2	8
mmu-miR-466d-3p	PRRX2	week2	8
mmu-miR-466d-3p	AURKB	week2	8
mmu-miR-466d-3p	RNF182	week2	8
mmu-miR-466d-3p	GLI3	week2	8
mmu-miR-466d-3p	TRIM67	week2	8
mmu-miR-466d-3p	POLE2	week2	8
mmu-miR-466d-3p	BUB1	week2	8
mmu-miR-466d-3p	DEPDC1A	week2	8
mmu-miR-466d-3p	COL11A1	week2	8
mmu-miR-466d-3p	ASPM	week2	8
mmu-miR-466d-3p	MAGEL2	week2	8
mmu-miR-466d-3p	OLFML2B	week2	8
mmu-miR-466d-3p	EME1	week2	8
mmu-miR-466d-3p	TPX2	week2	8
mmu-miR-466d-3p	BIRC5	week2	8
mmu-miR-466d-3p	CDC20	week2	8
mmu-miR-466d-3p	MCM3	week2	8
mmu-miR-466d-3p	ORC1L	week2	8
mmu-miR-466d-3p	CENPI	week2	8
mmu-miR-466d-3p	NME4	week2	8
mmu-miR-466d-3p	CCNB2	week2	8
mmu-miR-466d-3p	6230409E13RIK	week2	8
mmu-miR-466d-3p	CACNA1G	week2	8
mmu-miR-466d-3p	WIF1	week2	8
mmu-miR-466d-3p	UBE2T	week2	8
mmu-miR-466a-3p	KIF23	week2	8
mmu-miR-466a-3p	KIFC1	week2	8
mmu-miR-466a-3p	LMNB1	week2	8
mmu-miR-466a-3p	SCML2	week2	8

mmu-miR-466a-3p	AURKA	week2	8
mmu-miR-466a-3p	PRRX2	week2	8
mmu-miR-466a-3p	AURKB	week2	8
mmu-miR-466a-3p	RNF182	week2	8
mmu-miR-466a-3p	GLI3	week2	8
mmu-miR-466a-3p	CCNE1	week2	8
mmu-miR-466a-3p	POLE2	week2	8
mmu-miR-466a-3p	BUB1	week2	8
mmu-miR-466a-3p	DEPDC1A	week2	8
mmu-miR-466a-3p	ASF1B	week2	8
mmu-miR-466a-3p	COL11A1	week2	8
mmu-miR-466a-3p	ASPM	week2	8
mmu-miR-466a-3p	MAGEL2	week2	8
mmu-miR-466a-3p	OLFML2B	week2	8
mmu-miR-466a-3p	EME1	week2	8
mmu-miR-466a-3p	TPX2	week2	8
mmu-miR-466a-3p	BIRC5	week2	8
mmu-miR-466a-3p	CDC20	week2	8
mmu-miR-466a-3p	MCM3	week2	8
mmu-miR-466a-3p	ORC1L	week2	8
mmu-miR-466a-3p	CENPI	week2	8
mmu-miR-466a-3p	CCNB2	week2	8
mmu-miR-466a-3p	CACNA1G	week2	8
mmu-miR-466a-3p	WIF1	week2	8
mmu-miR-466a-3p	UBE2T	week2	8
mmu-miR-467c	STIL	week2	8
mmu-miR-467c	CENPN	week2	8
mmu-miR-467c	HIST4H4	week2	8
mmu-miR-467c	CCDC99	week2	8
mmu-miR-467c	SOX3	week2	8
mmu-miR-467c	KEL	week2	8
mmu-miR-467c	EME1	week2	8
mmu-miR-467c	1500015O10RIK	week2	8
mmu-miR-467c	CENPF	week2	8
mmu-miR-467c	APCDD1	week2	8
mmu-miR-467c	CENPI	week2	8
mmu-miR-467c	CDT1	week2	8
mmu-miR-467c	CENPH	week2	8
mmu-miR-467c	NME4	week2	8
mmu-miR-467c	WBP2NL	week2	8
mmu-miR-467c	HTRA1	week2	8
mmu-miR-467c	SPAG4	week2	8
mmu-miR-467c	MASTL	week2	8
mmu-miR-467c	POLQ	week2	8
mmu-miR-467c	UBE2T	week2	8
mmu-miR-467c	ASPM	week2	8

mmu-miR-467c	SHCBP1	week2	8
mmu-miR-23b	MARCKSL1	week2	8
mmu-miR-23b	ZFP428	week2	8
mmu-miR-23b	SKP2	week2	8
mmu-miR-23b	SYCE2	week2	8
mmu-miR-23b	4833423E24RIK	week2	8
mmu-miR-23b	ESPL1	week2	8
mmu-miR-23b	GTSE1	week2	8
mmu-miR-23b	6720463M24RIK	week2	8
mmu-miR-23b	CENPH	week2	8
mmu-miR-23b	WBP2NL	week2	8
mmu-miR-23b	FREM1	week2	8
mmu-miR-23b	NPPC	week2	8
mmu-miR-23b	FBXO5	week2	8
mmu-miR-23b	SLC27A6	week2	8
mmu-miR-23b	H2AFX	week2	8
mmu-miR-23b	UBE2T	week2	8
mmu-miR-467e	HIST4H4	week2	8
mmu-miR-467e	CCDC99	week2	8
mmu-miR-467e	NELL1	week2	8
mmu-miR-467e	CENPF	week2	8
mmu-miR-467e	PBK	week2	8
mmu-miR-467e	GTSE1	week2	8
mmu-miR-467e	ORC1L	week2	8
mmu-miR-467e	NME4	week2	8
mmu-miR-467e	WBP2NL	week2	8
mmu-miR-467e	CCNB2	week2	8
mmu-miR-467e	HTRA1	week2	8
mmu-miR-467e	SPAG4	week2	8
mmu-miR-467e	NSL1	week2	8
mmu-miR-467e	BUB1	week2	8
mmu-miR-467e	BUB1B	week2	8
mmu-miR-467e	DEPDC1A	week2	8
mmu-miR-467e	ASPM	week2	8
mmu-miR-467e	TRIP13	week2	8
mmu-miR-22	KCNE1L	week2	8
mmu-miR-22	PRC1	week2	8
mmu-miR-22	LGALS1	week2	8
mmu-miR-22	PCDH20	week2	8
mmu-miR-22	PASK	week2	8
mmu-miR-22	NTNG1	week2	8
mmu-miR-22	4833423E24RIK	week2	8
mmu-miR-22	APCDD1	week2	8
mmu-miR-22	E130306D19RIK	week2	8
mmu-miR-22	RFC5	week2	8
mmu-miR-22	UHRF1	week2	8

mmu-miR-22	CDCA7	week2	8
mmu-miR-22	WBP2NL	week2	8
mmu-miR-22	FBLN2	week2	8
mmu-miR-22	F630043A04RIK	week2	8
mmu-miR-22	VSTM2L	week2	8
mmu-miR-22	KRT4	week2	8
mmu-miR-22	EFNA4	week2	8
mmu-miR-30a	NEIL3	week2	8
mmu-miR-30a	CCNF	week2	8
mmu-miR-30a	KNTC1	week2	8
mmu-miR-30a	TMEM121	week2	8
mmu-miR-30a	ZCWPW1	week2	8
mmu-miR-30a	COL25A1	week2	8
mmu-miR-30a	UPK3A	week2	8
mmu-miR-30a	CENPK	week2	8
mmu-miR-30a	RAD54L	week2	8
mmu-miR-30a	MAD2L1	week2	8
mmu-miR-30a	FANCD2	week2	8
mmu-miR-30a	STAG3	week2	8
mmu-miR-30a	SLC27A6	week2	8
mmu-miR-30a	UBE2T	week2	8
mmu-miR-30d	HIST4H4	week2	8
mmu-miR-30d	NEIL3	week2	8
mmu-miR-30d	CCNF	week2	8
mmu-miR-30d	KNTC1	week2	8
mmu-miR-30d	TMEM121	week2	8
mmu-miR-30d	ZCWPW1	week2	8
mmu-miR-30d	BC055324	week2	8
mmu-miR-30d	UPK3A	week2	8
mmu-miR-30d	CENPK	week2	8
mmu-miR-30d	RAD54L	week2	8
mmu-miR-30d	6720463M24RIK	week2	8
mmu-miR-30d	SPC24	week2	8
mmu-miR-30d	RFC3	week2	8
mmu-miR-30d	MAD2L1	week2	8
mmu-miR-30d	HTRA1	week2	8
mmu-miR-30d	FANCD2	week2	8
mmu-miR-30d	CKAP2L	week2	8
mmu-miR-30d	SLC27A6	week2	8
mmu-miR-30d	UBE2T	week2	8
mmu-miR-714	GUCA1A	week2	8
mmu-miR-714	PRPH	week2	8
mmu-miR-714	STMN3	week2	8
mmu-miR-714	FA2H	week2	8
mmu-miR-714	SLC6A13	week2	8
mmu-miR-714	TRPA1	week2	8

mmu-miR-714	CHRM3	week2	8
mmu-miR-714	CD177	week2	8
mmu-miR-714	C1QL1	week2	8
mmu-miR-714	SCARA3	week2	8
mmu-miR-714	PRIMA1	week2	8
mmu-miR-714	NKX2-5	week2	8
mmu-miR-714	CAR6	week2	8
mmu-miR-431	COL9A1	week2	8
mmu-miR-431	CCK	week2	8
mmu-miR-431	EEF1A2	week2	8
mmu-miR-431	MNS1	week2	8
mmu-miR-431	TLX2	week2	8
mmu-miR-431	AGXT	week2	8
mmu-miR-431	4930415O20RIK	week2	8
mmu-miR-337-3p	RPP25	week2	8
mmu-miR-337-3p	AIPL1	week2	8
mmu-miR-337-3p	NPHP4	week2	8
mmu-miR-337-3p	MRAP	week2	8
mmu-miR-337-3p	TIMP4	week2	8
mmu-miR-337-3p	AGXT	week2	8
mmu-miR-337-3p	AQP3	week2	8
mmu-miR-337-3p	SLC22A1	week2	8
mmu-miR-125a-5p	LCN2	week2	8
mmu-miR-125a-5p	CCDC109A	week2	8
mmu-miR-125a-5p	TNF	week2	8
mmu-miR-125a-5p	NEPN	week2	8
mmu-miR-125a-5p	RHCG	week2	8
mmu-miR-125a-5p	SCN2B	week2	8
mmu-miR-125a-5p	MRAP	week2	8
mmu-miR-125a-5p	GALNT5	week2	8
mmu-miR-125a-5p	ACTN3	week2	8
mmu-miR-125a-5p	FXYD6	week2	8
mmu-miR-125a-5p	AQP3	week2	8
mmu-miR-337-5p	CCDC109A	week2	8
mmu-miR-337-5p	IL17B	week2	8
mmu-miR-337-5p	MRAP	week2	8
mmu-miR-337-5p	SLC22A7	week2	8
mmu-miR-337-5p	TIMP4	week2	8
mmu-miR-337-5p	CFI	week2	8
mmu-miR-337-5p	GMPR	week2	8
mmu-miR-337-5p	EMILIN2	week2	8
mmu-miR-337-5p	AGXT	week2	8
mmu-miR-337-5p	AQP3	week2	8

Dataset S2: Complete Results of GO enrichment analysis using the Ontologizer software for TOP300 ranked genes by 4 different approaches. Using mirDREM with A) miRanda and B) TargetScan miRNA-gene interaction datasets, or C) without anticorrelation constraints and D) using GenMiR++ with miRanda interactions. Listed are the GO ID, the number of genes within the population and study sets as computed by Ontologizer (Pop.term,Study.total,Study.term,Pop.family,Study.family), the enrichment p-value before and after multiple testing correction (p,p.adjusted) and the GO term name.

A) mirDREM (miRanda) Top 300 GO enrichment

ID	Pop.term	Study.total	Study.term	Pop.family	Study.family	p	p.adjusted	GOterm
GO:0002376	1023	296	48	14761	290	1.36E-08	2.38E-05	immune system process
GO:0048534	441	296	28	1796	43	1.41E-08	2.38E-05	hematopoietic or lymphoid organ development
GO:0019222	3596	296	105	9683	193	6.28E-07	0.000707202	regulation of metabolic process
GO:0002520	464	296	28	2821	72	3.15E-06	0.002186906	immune system development
GO:0002521	270	296	20	1996	51	3.23E-06	0.002186906	leukocyte differentiation
GO:0031323	3125	296	92	8937	182	9.40E-06	0.005295652	regulation of cellular metabolic process
GO:0002682	530	296	27	6977	152	2.40E-05	0.011594727	regulation of immune system process
GO:0035556	1381	296	39	3581	62	7.91E-05	0.033439068	intracellular signal transduction
GO:0001775	476	296	23	10356	210	9.62E-05	0.036129902	cell activation
GO:0006955	508	296	23	5325	106	0.000119839	0.040517672	immune response
GO:0002764	114	296	9	3668	65	0.000146214	0.044940821	immune response-regulating signaling pathway
GO:0002768	74	296	6	2387	29	0.000195143	0.04712712	immune response-regulating cell surface receptor signaling pathway
GO:0008641	6	296	3	4196	91	0.000188302	0.04712712	small protein activating enzyme activity
GO:0042101	6	296	3	1296	29	0.000192908	0.04712712	T cell receptor complex

B) mirDREM (TargetScan) Top 300 GO enrichment

ID	Pop.term	Study.total	Study.term	Pop.family	Study.family	p	p.adjusted	GO term name
GO:0002376	1024	290	51	14777	281	1.73E-10	6.43E-07	immune system process
GO:0048534	442	290	27	1798	43	8.36E-08	1.48E-04	hemopoietic or lymphoid organ development
GO:0048518	2603	290	85	14777	281	1.20E-07	1.48E-04	positive regulation of biological process
GO:0005488	8814	290	203	14713	278	2.71E-06	0.001971	binding
GO:0002682	531	290	30	6983	160	2.78E-06	0.001971	regulation of immune system process
GO:0035556	1383	290	46	3586	70	3.17E-06	0.001971	intracellular signal transduction
GO:0042101	6	290	4	1296	32	4.45E-06	0.002368	T cell receptor complex
GO:0008152	7274	290	174	14777	281	1.05E-05	0.004893	metabolic process
GO:0048522	2358	290	77	10397	219	1.50E-05	0.006193	positive regulation of cellular process
GO:0001816	299	290	16	4511	80	5.15E-05	0.017027	cytokine production
GO:0042824	5	290	3	6619	121	5.80E-05	0.017027	MHC class I peptide loading complex
GO:0046977	4	290	3	4952	123	5.88E-05	0.017027	TAP binding
GO:0002691	4	290	3	74	3	6.17E-05	0.017027	regulation of cellular extravasation
GO:0001775	477	290	24	10364	218	6.40E-05	0.017027	cell activation
GO:0003824	4200	290	109	14713	278	7.24E-05	0.017494	catalytic activity
GO:0002520	465	290	27	2823	79	7.52E-05	0.017494	immune system development
GO:0044237	6187	290	156	11062	229	9.25E-05	0.020263	cellular metabolic process
GO:0006955	509	290	26	5330	126	1.09E-04	0.022475	immune response
GO:0048519	2321	290	68	14777	281	1.25E-04	0.02447	negative regulation of biological process
GO:0008283	1092	290	38	14777	281	2.10E-04	0.039183	cell proliferation
GO:0071897	24	290	5	2979	75	2.59E-04	0.045869	DNA biosynthetic process

C)mirDREM (miRanda, no anticorrelation constraints) Top 300 GO enrichment

ID	Pop.term	Study.total	Study.term	Pop.family	Study.family	p	p.adjusted	name
GO:0007049	901	295	41	10374	203	2.21E-07	7.16E-04	cell cycle
GO:0042101	6	295	4	1298	25	1.57E-06	0.002539	T cell receptor complex
GO:0002376	1026	295	41	14799	282	4.96E-06	0.004117	immune system process
GO:0035556	1385	295	42	3587	63	5.09E-06	0.004117	intracellular signal transduction
GO:0005488	8829	295	202	14734	280	1.12E-05	0.007231	binding
GO:0005634	4260	295	103	6929	133	5.73E-05	0.030867	nucleus
GO:0022402	632	295	27	10374	203	1.01E-04	0.046795	cell cycle process

D) GenMIR++ Top 300 GO enrichment

ID	Pop.term	Study.total	Study.term	Pop.family	Study.family	p	p.adjusted	GOterm
GO:0032991	2809	296	118	15050	291	1.76E-18	5.42E-15	macromolecular complex
GO:0044391	101	296	27	3497	123	9.84E-18	1.51E-14	ribosomal subunit
GO:0043226	7731	296	218	15050	291	8.04E-17	8.24E-14	organelle
GO:0005840	161	296	30	5720	185	1.74E-15	1.34E-12	ribosome
GO:0044445	130	296	28	4426	163	6.60E-15	4.06E-12	cytosolic part
GO:0005198	349	296	33	14696	282	3.21E-14	1.65E-11	structural molecule activity
GO:0044424	8879	296	238	12168	263	9.25E-13	4.07E-10	intracellular part
GO:0044422	3446	296	120	15050	291	1.52E-12	5.86E-10	organelle part
GO:0005622	9074	296	239	12168	263	1.15E-11	3.84E-09	intracellular
GO:0015934	62	296	17	3376	119	1.25E-11	3.84E-09	large ribosomal subunit
GO:0006412	319	296	30	4447	105	1.50E-11	4.20E-09	translation
GO:0030529	405	296	37	9119	240	2.16E-11	5.54E-09	ribonucleoprotein complex
GO:0022626	65	296	25	226	33	1.39E-09	3.28E-07	cytosolic ribosome
GO:0044444	4426	296	163	8879	238	2.83E-09	6.21E-07	cytoplasmic part
GO:0005488	8807	296	212	14696	282	3.94E-08	8.08E-06	binding
GO:0008152	7270	296	176	14761	273	2.27E-07	4.37E-05	metabolic process
GO:0015935	40	296	10	3376	119	7.04E-07	0.000127312	small ribosomal subunit
GO:0015078	73	296	11	240	11	1.18E-06	0.00020129	hydrogen ion transmembrane transporter activity
GO:0005829	779	296	53	4426	163	1.85E-06	0.000300307	cytosol
GO:0003735	95	296	21	349	33	4.26E-06	0.000655857	structural constituent of ribosome
GO:0005623	12168	296	263	15050	291	5.21E-06	0.000728171	cell
GO:0044464	12168	296	263	15050	291	5.21E-06	0.000728171	cell part
GO:0005737	6785	296	208	8879	238	1.23E-05	0.001644619	cytoplasm
GO:0009987	10356	296	222	14761	273	1.54E-05	0.001816201	cellular process
GO:0015985	11	296	4	433	8	1.52E-05	0.001816201	energy coupled proton transport, down electrochemical gradient
GO:0019866	299	296	22	8885	238	1.59E-05	0.001816201	organelle inner membrane
GO:0031975	568	296	29	12168	263	1.49E-05	0.001816201	envelope
GO:0015988	24	296	5	433	8	1.72E-05	0.001884063	energy coupled proton transmembrane transport, against electrochemical gradient
GO:0030984	3	296	3	4948	134	1.94E-05	0.002061071	kininogen binding
GO:0044455	91	296	9	5275	96	3.44E-05	0.003522955	mitochondrial membrane part
GO:0003723	577	296	24	2108	43	6.66E-05	0.006418658	RNA binding
GO:0010608	244	296	13	2395	39	6.68E-05	0.006418658	posttranscriptional regulation of gene expression
GO:0045261	4	296	3	8880	238	7.46E-05	0.006745327	proton-transporting ATP synthase complex, catalytic core F(1)
GO:0071840	2853	296	79	14761	273	7.29E-05	0.006745327	cellular component organization or biogenesis
GO:0016469	36	296	6	6603	136	8.01E-05	0.007038849	proton-transporting two-sector ATPase complex
GO:0044446	3376	296	119	8885	238	8.86E-05	0.007572908	intracellular organelle part
GO:0042599	9	296	4	196	8	0.000135914	0.011299239	lamellar body
GO:0033178	14	296	4	6603	136	0.000146829	0.01188539	proton-transporting two-sector ATPase complex,catalytic domain
GO:0045259	13	296	4	8882	239	0.000301863	0.023808496	proton-transporting ATP synthase complex
GO:0000502	53	296	7	9102	240	0.00044482	0.034206662	proteasome complex
GO:0015992	69	296	6	317	7	0.000516007	0.03779135	proton transport
GO:0045182	20	296	4	14696	282	0.00050452	0.03779135	translation regulator activity
GO:0043062	128	296	11	2101	58	0.000541976	0.038770225	extracellular structure organization

Dataset S3: Complete listing of differentially expressed (DE) genes in three cohorts of patients with idiopathic pulmonary fibrosis, A) LGRC cohort, B) TissueBank cohort 1 and C) Tissuebank cohort 2

A) miRNA expression values for the LGRC 142vs162 people cohort

SystematicName	FOLD CHANGE	ttest p-value
hsa-miR-205	7.1293913	3.03367E-23
hsa-miR-449a	5.063085	2.30762E-13
hsa-miR-31	3.8792008	1.44032E-19
hsa-miR-337-5p	3.4510081	1.5128E-41
hsa-miR-495	3.4108387	1.68486E-39
hsa-miR-31*	3.3799198	1.35716E-19
hsa-miR-34b	3.2577955	6.55629E-09
hsa-miR-299-5p	3.2429486	1.73628E-33
hsa-miR-34c-5p	3.1993989	3.14979E-11
hsa-miR-493*	3.0667679	3.53444E-32
hsa-miR-127-3p	2.991683	3.52059E-44
hsa-miR-654-3p	2.9669627	3.0255E-38
hsa-miR-377	2.8830756	1.67284E-48
hsa-miR-136*	2.8524308	8.31101E-34
hsa-miR-381	2.7837672	1.10934E-34
hsa-miR-379	2.6951544	4.07553E-32
hsa-miR-376b	2.6599215	2.93021E-34
hsa-miR-154	2.5929967	5.40412E-34
hsa-miR-409-3p	2.5905765	1.91018E-25
hsa-miR-136	2.5810624	9.87048E-25
hsa-miR-487b	2.5078384	2.29426E-40
hsa-miR-376a	2.4349681	1.3788E-45
hsa-miR-449b	2.3857437	1.9278E-09
hsa-miR-34b*	2.3755193	3.36033E-13
hsa-miR-376c	2.2076699	1.61639E-43
hsa-miR-1	2.2032491	2.4432E-13
hsa-miR-337-3p	2.0864897	5.67821E-20
hsa-miR-199b-5p	2.0815698	2.47439E-35
hsa-miR-21	2.0692109	4.20262E-34
hsa-miR-382	2.0289625	4.41952E-26
hsa-miR-410	1.9569834	1.03336E-19
hsa-miR-432	1.9179516	9.32819E-21
hsa-miR-34c-3p	1.8573862	2.53112E-05
hsa-miR-650	1.8165299	7.49195E-14
hsa-miR-133b	1.7952689	6.22525E-22
hsa-miR-133a	1.7905775	9.02564E-16
hsa-miR-154*	1.7392875	4.38612E-15
hsa-miR-543	1.7092634	4.95084E-21
hsa-miR-10b	1.7061094	2.53788E-10
hsa-miR-129-3p	1.6908133	3.75643E-08
hsa-miR-132	1.6885547	5.84421E-27
hsa-miR-199a-3p	1.6684748	1.66439E-21
hsa-miR-96	1.6403649	1.41672E-12
hsa-miR-135b	1.6359355	9.28846E-14
hsa-miR-214*	1.6102284	4.61216E-20
hsa-miR-143*	1.572132	3.50266E-17
hsa-miR-212	1.553826	1.72015E-10
hsa-miR-369-5p	1.5507507	5.06864E-16

hsa-miR-143	1.514577	9.34585E-18
hsa-miR-155	1.5128667	4.20496E-15
hsa-miR-148a	1.503827	4.11938E-20
hsa-miR-214	1.4897093	1.80752E-28
hsa-miR-411	1.4533674	6.05657E-12
hsa-miR-34a	1.4258337	4.70346E-28
hsa-miR-199a-5p	1.4094814	2.84035E-28
hsa-miR-376a*	1.3941856	4.60027E-12
hsa-miR-183	1.3874263	9.96639E-06
hsa-miR-99a	1.3839542	1.06142E-19
hsa-miR-132*	1.3827385	1.20783E-06
hsa-miR-202	1.372113	0.00865497
hsa-miR-1202	1.3540615	0.001990204
hsa-miR-625	1.3518518	4.18104E-05
hsa-miR-125b-2*	1.3514646	6.5516E-11
hsa-miR-21*	1.3388391	2.67902E-05
hsa-miR-152	1.3382827	1.34175E-16
hsa-miR-125b	1.3368625	1.08498E-18
hsa-miR-370	1.3366984	8.35486E-05
hsa-miR-514	1.3308673	8.1776E-06
hsa-miR-153	1.3175145	2.4905E-05
hsa-miR-34a*	1.3129662	1.13546E-08
hsa-let-7i	1.3117361	6.80895E-15
hsa-miR-139-5p	1.3075617	4.10721E-11
hsa-miR-622	1.304046	0.011525421
hsa-miR-149	1.3021469	1.67992E-05
hsa-miR-139-3p	1.3001388	5.2146E-09
hsa-miR-455-3p	1.289302	4.10366E-09
hsa-miR-27b	1.288598	4.69221E-22
hsa-miR-940	1.2810493	1.8002E-05
hsa-miR-371-5p	1.2783769	0.001875481
hsa-miR-100	1.2777158	1.10458E-13
hsa-miR-1224-5p	1.2772603	4.04388E-05
hsa-miR-939	1.2677454	0.000236899
hsa-miR-145*	1.2676417	3.8035E-07
hsa-miR-24-1*	1.2427535	3.12419E-06
hsa-miR-99b*	1.2341861	0.003182587
hsa-miR-95	1.2242964	0.010956617
hsa-miR-766	1.2204206	0.000251062
hsa-miR-424	1.2135281	0.000551793
hsa-miR-23b	1.2093605	3.19321E-15
hsa-miR-140-5p	1.2092616	1.93977E-08
hsa-miR-582-5p	1.2068513	0.003026432
hsa-miR-145	1.204814	1.1556E-05
hsa-miR-892b	1.1992935	0.039169037
hsa-miR-28-5p	1.1960007	1.72866E-06
hsa-let-7e	1.195751	4.25002E-06
hsa-miR-497	1.1956399	1.89363E-12
hsa-miR-1280	1.1844743	0.000138749
hsa-miR-188-5p	1.1776896	0.019655098
hsa-miR-1305	1.1733126	0.005098589
hsa-miR-1915	1.1694081	0.018581266

hsa-miR-1185	1.1685723	3.09658E-06
hsa-miR-22*	1.1676409	0.000127746
hsa-miR-503	1.1659439	0.006997875
hsa-miR-98	1.1644593	0.01270083
hsa-miR-195	1.1626288	4.32787E-05
hsa-miR-200b	1.1617645	0.017046687
hsa-miR-299-3p	1.1602038	4.44674E-05
hsa-miR-193b	1.1571845	1.2445E-06
hsa-miR-27a	1.1565218	1.63155E-09
hsa-miR-671-5p	1.1552645	0.048945031
hsa-miR-1249	1.1532457	0.028846169
hsa-miR-1914*	1.1525504	0.013950406
hsa-miR-10a	1.1414432	0.022868263
hsa-miR-365	1.1360416	9.41803E-05
hsa-miR-142-3p	1.1300395	0.017788903
hsa-miR-1274a	1.127781	0.001832686
hsa-miR-505	1.1272374	0.000121163
hsa-miR-539	1.1260617	2.93513E-05
hsa-miR-23a	1.1170715	1.16186E-05
hsa-miR-874	1.1153491	0.00209183
hsa-miR-193a-3p	1.1102523	0.019539611
hsa-miR-324-5p	1.100439	3.59458E-06
hsa-miR-22	1.0975774	0.001204535
hsa-miR-148a*	1.0968906	5.15195E-05
hsa-miR-585	1.0920892	0.002398933
hsa-let-7i*	1.0885416	0.002013827
hsa-miR-1274b	1.0794296	0.017577787
hsa-miR-99a*	1.0721051	0.008376302
hsa-miR-130b	1.0714096	0.02513359
hsa-miR-758	1.0705192	0.00244983
hsa-miR-24	1.0703608	9.09463E-07
hsa-let-7c	1.0452351	0.048625865
hsa-miR-361-5p	0.9518967	0.012734076
hsa-miR-374b*	0.9476378	0.035507452
hsa-miR-221	0.9365264	0.005395404
hsa-miR-516b	0.9260915	0.011528498
hsa-miR-664	0.9222753	0.00614909
hsa-let-7d	0.9208279	0.045248898
hsa-miR-425	0.9136974	0.000831698
hsa-miR-624*	0.9096612	0.000503596
hsa-let-7b	0.9095243	2.96935E-05
hsa-miR-190	0.9094514	0.002271303
hsa-miR-200c	0.9093892	0.023923695
hsa-miR-99b	0.9072403	0.004073152
hsa-miR-374b	0.9028216	0.00388473
hsa-miR-29c*	0.9023212	6.35702E-07
hsa-miR-193a-5p	0.9014537	0.000397112
hsa-miR-196b	0.8986968	0.022396399
hsa-miR-93	0.8917991	3.48382E-06
hsa-miR-320c	0.8913643	0.00482169
hsa-miR-26b*	0.8909283	0.000116804
hsa-let-7e*	0.8888603	9.79318E-05

hsa-miR-15a*	0.8873145	0.000379271
hsa-miR-25	0.8800027	1.9493E-07
hsa-miR-29c	0.8772717	7.37996E-06
hsa-miR-219-5p	0.874745	0.023032119
hsa-miR-1469	0.8742756	0.001296515
hsa-miR-29b-2*	0.8697126	6.6976E-07
hsa-miR-221*	0.8696103	0.042484373
hsa-miR-29a*	0.8683593	0.046310967
hsa-miR-521	0.8675575	0.022149205
hsa-miR-106b	0.8635181	2.77377E-06
hsa-miR-526b	0.8602785	0.024283776
hsa-miR-1307	0.8599451	0.002890067
hsa-miR-28-3p	0.8585445	0.04450175
hsa-miR-532-5p	0.8544851	4.51063E-11
hsa-miR-542-5p	0.8529034	0.019485506
hsa-miR-29b-1*	0.8515362	0.029907019
hsa-miR-16	0.8502746	0.000103918
hsa-miR-887	0.8492384	0.001758114
hsa-miR-125b-1*	0.8489163	0.00635047
hsa-miR-186	0.8488241	2.53422E-10
hsa-miR-361-3p	0.8482711	5.82521E-12
hsa-miR-342-3p	0.8474601	1.59974E-06
hsa-miR-30e*	0.8472762	1.34385E-08
hsa-miR-30c	0.8457421	1.36543E-08
hsa-miR-423-5p	0.8410276	4.73599E-09
hsa-miR-151-3p	0.8406515	5.76452E-11
hsa-miR-1229	0.84064	0.003289513
hsa-miR-135a*	0.8373561	0.020997635
hsa-miR-32	0.8357031	0.012059746
hsa-miR-362-5p	0.835701	2.43384E-09
hsa-miR-328	0.8355158	0.00909253
hsa-miR-335*	0.8340746	0.000687108
hsa-miR-19a	0.8332027	3.4388E-07
hsa-miR-342-5p	0.8302539	6.72278E-07
hsa-miR-130a	0.8299604	2.88071E-19
hsa-miR-197	0.8287168	6.81185E-08
hsa-miR-545	0.8271195	0.000221929
hsa-miR-187*	0.8241239	0.034175429
hsa-miR-192	0.8156308	0.002558232
hsa-miR-636	0.812593	0.001852631
hsa-miR-15b	0.8119784	4.86801E-09
hsa-miR-378*	0.80546	0.003191856
hsa-miR-26a	0.8042296	1.83598E-13
hsa-miR-185	0.800098	5.10676E-10
hsa-miR-15b*	0.8000871	5.9024E-08
hsa-miR-339-3p	0.7960417	3.92393E-12
hsa-miR-628-5p	0.7959242	0.000540715
hsa-miR-499-5p	0.7949074	0.000306586
hsa-miR-1182	0.7920752	0.019807636
hsa-let-7a*	0.7901478	0.000353181
hsa-miR-181b	0.7899964	2.35322E-12
hsa-miR-548c-5p	0.7844623	1.50892E-08

hsa-miR-33b*	0.7835252	0.039562629
hsa-miR-486-3p	0.7833796	1.35539E-07
hsa-miR-181d	0.7816962	2.88498E-09
hsa-miR-522	0.7815942	3.88202E-05
hsa-miR-592	0.7802308	8.69327E-07
hsa-miR-532-3p	0.7780998	1.76249E-13
hsa-miR-20a	0.7758642	1.27881E-16
hsa-miR-17	0.7746347	2.37419E-29
hsa-miR-502-3p	0.7742333	2.75023E-17
hsa-miR-20b	0.7707543	8.93179E-13
hsa-miR-215	0.7676281	0.000273248
hsa-miR-877	0.7660874	0.003342239
hsa-miR-498	0.7638078	0.007401953
hsa-miR-19b	0.7636371	1.68139E-17
hsa-miR-223	0.7631369	2.36048E-05
hsa-miR-195*	0.7629457	9.46679E-05
hsa-miR-210	0.7610377	2.94748E-12
hsa-miR-501-5p	0.7597712	2.05195E-05
hsa-miR-335	0.7582564	1.15037E-06
hsa-miR-501-3p	0.7569253	2.62145E-09
hsa-miR-101	0.7555731	3.67576E-14
hsa-miR-218	0.7552044	3.75254E-07
hsa-miR-18a	0.7501252	4.06532E-12
hsa-miR-30c-1*	0.7473582	5.33192E-09
hsa-miR-502-5p	0.7378654	2.16223E-06
hsa-miR-363	0.7319263	4.11212E-06
hsa-miR-629	0.7299718	4.82239E-09
hsa-miR-17*	0.7287575	1.10692E-14
hsa-miR-20a*	0.7280032	3.24573E-07
hsa-miR-564	0.7263443	0.001703763
hsa-miR-181c	0.722518	1.11045E-23
hsa-miR-452	0.719016	3.48486E-16
hsa-miR-627	0.7167879	1.65179E-09
hsa-miR-33a	0.7157097	6.46233E-07
hsa-miR-489	0.7089172	5.73686E-05
hsa-miR-181a*	0.7017014	2.02296E-19
hsa-miR-16-2*	0.6992187	1.29658E-10
hsa-miR-373*	0.6938073	0.000115763
hsa-miR-92a	0.6913641	9.45204E-19
hsa-miR-181a	0.6861564	9.43902E-19
hsa-miR-126*	0.6861172	1.40535E-08
hsa-miR-423-3p	0.683756	1.68808E-11
hsa-miR-18b	0.6818564	2.73281E-15
hsa-miR-224	0.6816851	3.85374E-09
hsa-miR-222	0.6561428	1.50949E-10
hsa-miR-144*	0.6512442	0.000609593
hsa-miR-598	0.6449508	4.52573E-11
hsa-miR-1471	0.6415042	0.001220774
hsa-miR-652	0.6393687	5.22471E-29
hsa-miR-194	0.6393363	5.65101E-14
hsa-miR-19b-1*	0.6390311	4.04396E-16
hsa-miR-451	0.6320514	6.29646E-07

hsa-miR-375	0.6123103	9.10051E-19
hsa-miR-144	0.6082384	3.97627E-06
hsa-miR-30a*	0.6042775	4.72072E-34
hsa-miR-138	0.6012904	1.97526E-12
hsa-miR-126	0.5916438	1.14976E-28
hsa-miR-184	0.5889152	7.2218E-11
hsa-miR-223*	0.5806467	1.76646E-12
hsa-miR-516a-5p	0.5771108	1.57982E-13
hsa-miR-30a	0.574577	4.38051E-26
hsa-miR-181c*	0.5701582	5.09358E-17
hsa-miR-23a*	0.5570637	5.67421E-11
hsa-let-7d*	0.5559762	1.26139E-10
hsa-miR-30b	0.5538375	4.29781E-38
hsa-miR-30c-2*	0.5389168	1.75793E-35
hsa-miR-30b*	0.5354573	4.48087E-36
hsa-miR-135a	0.507142	3.61425E-12
hsa-miR-30d	0.4905563	3.16932E-30
hsa-miR-486-5p	0.4839831	5.18292E-13
hsa-miR-30d*	0.4759795	1.48149E-23
hsa-miR-101*	0.4758409	1.86179E-27
hsa-miR-203	0.4718639	2.80021E-27
hsa-miR-326	0.4498431	9.22808E-43
hsa-miR-517a	0.4041476	5.97017E-22
hsa-miR-517c	0.3872092	4.44642E-22
hsa-miR-338-3p	0.3624987	9.86897E-50

B) miRNA expression classification for the tissuebank 10vs10 people cohort

SystematicName	Directionality of differential expression
hsa-miR-127	up
hsa-miR-132	up
hsa-miR-134	up
hsa-miR-155	up
hsa-miR-182	up
hsa-miR-198	up
hsa-miR-199a	up
hsa-miR-199b	up
hsa-miR-205	up
hsa-miR-214	up
hsa-miR-296	up
hsa-miR-299-5p	up
hsa-miR-31	up
hsa-miR-320	up
hsa-miR-324-3p	up
hsa-miR-330	up
hsa-miR-376a	up
hsa-miR-379	up
hsa-miR-409-3p	up
hsa-miR-487b	up
hsa-miR-491	up
hsa-miR-509	up
hsa-miR-557	up
hsa-miR-622	up
hsa-miR-659	up
hsa-miR-765	up
hsa-miR-92b	up
hsa-miR-99a	up
let-7d	down
miR-125a	down
miR-126	down
miR-138	down
miR-17-3p	down
miR-184	down
miR-197	down
miR-203	down
miR-224	down
miR-26a	down
miR-30a-3p	down
miR-30a-5p	down
miR-30b	down
miR-30c	down
miR-30d	down
miR-338	down
miR-362	down
miR-92	down

C) miRNA expression values for the tissuebank 28vs33 people cohort

systematic_name	ttest p-value	Fold change
ebv-miR-BART19-3p	0.03777896	-3.174329
hsa-let-7a*	0.025036234	-1.92732
hsa-let-7d*	1.29E-04	-4.216877
hsa-let-7i	2.75E-04	1.3513634
hsa-miR-1	0.019660518	2.7677805
hsa-miR-100*	0.029183453	-1.094663
hsa-miR-1208	0.044593595	1.9255959
hsa-miR-1225-3p	0.005024546	-1.695112
hsa-miR-126	0.02290462	-1.416787
hsa-miR-127-3p	1.69E-05	2.7761967
hsa-miR-129-3p	1.04E-04	5.1510506
hsa-miR-1301	0.027926518	-1.096552
hsa-miR-132	0.01462466	1.7530699
hsa-miR-133a	0.006380936	2.9537714
hsa-miR-133b	0.001262683	2.4028838
hsa-miR-136*	0.018198302	3.7110841
hsa-miR-143	0.007679454	1.5495936
hsa-miR-143*	0.034891646	2.6468115
hsa-miR-146a	0.031571478	-1.309501
hsa-miR-146b-3p	0.049409695	-1.081296
hsa-miR-151-3p	0.007337354	-1.176621
hsa-miR-152	0.002781325	1.4117193
hsa-miR-154	3.20E-05	6.2262874
hsa-miR-154*	0.001082135	4.859066
hsa-miR-181a	1.99E-05	-1.600793
hsa-miR-181a*	0.03140997	-1.756231
hsa-miR-181b	1.74E-05	-1.476264
hsa-miR-181c	6.10E-04	-1.484477
hsa-miR-181d	2.45E-06	-1.76169
hsa-miR-184	0.03402577	-2.493711
hsa-miR-197	0.021283349	-1.349257
hsa-miR-199a-3p	0.001225962	1.4606061
hsa-miR-199a-5p	0.001356903	1.3339453
hsa-miR-199b-5p	8.65E-04	1.8152604
hsa-miR-19b-1*	0.009757555	-1.945349
hsa-miR-200c	0.006184558	-1.573176
hsa-miR-203	0.001642949	-2.684027
hsa-miR-205	0.007550371	7.288751
hsa-miR-21	0.004311839	1.809233
hsa-miR-210	0.004271977	-1.453503
hsa-miR-214	0.001519735	1.4578136
hsa-miR-214*	0.03282364	2.2785082
hsa-miR-222	4.16E-06	-1.655521
hsa-miR-23a*	0.019820033	-2.501476
hsa-miR-26a	0.010298942	-1.150247
hsa-miR-27a*	0.025607519	-1.156813
hsa-miR-27b	0.02778398	1.235184
hsa-miR-28-5p	0.041933138	1.2193662
hsa-miR-299-3p	0.003403887	2.2365103
hsa-miR-299-5p	2.12E-08	12.780098

hsa-miR-3065-5p	0.029818505	-3.163163
hsa-miR-30a	0.007145941	-1.57597
hsa-miR-30a*	0.01517245	-1.506528
hsa-miR-30b	3.34E-04	-1.719208
hsa-miR-30b*	0.001300173	-3.342941
hsa-miR-30d	3.77E-08	-2.142806
hsa-miR-30d*	0.024397997	-2.530247
hsa-miR-31	1.89E-04	8.406341
hsa-miR-31*	0.003537798	6.0338273
hsa-miR-3149	0.026241792	-1.101583
hsa-miR-3181	0.025210774	-1.206659
hsa-miR-326	1.05E-05	-4.371048
hsa-miR-335*	0.037128173	-2.769072
hsa-miR-337-3p	4.90E-05	6.140157
hsa-miR-337-5p	3.15E-04	7.0735908
hsa-miR-338-3p	7.00E-04	-3.121669
hsa-miR-342-3p	3.78E-04	-1.52217
hsa-miR-342-5p	0.007822067	-1.475012
hsa-miR-34c-5p	0.036096606	3.7651496
hsa-miR-361-3p	0.021804132	-1.20989
hsa-miR-361-5p	0.04504125	-1.137092
hsa-miR-369-5p	6.73E-05	3.9933183
hsa-miR-371-5p	0.04749839	1.7236831
hsa-miR-375	0.001718156	-2.43139
hsa-miR-376a	5.62E-04	3.0764985
hsa-miR-376a*	0.003773363	2.3229918
hsa-miR-376b	2.90E-05	6.594181
hsa-miR-376c	0.01331366	2.595239
hsa-miR-377	0.006348185	3.4775202
hsa-miR-379	3.60E-06	8.445055
hsa-miR-381	2.77E-04	5.9654484
hsa-miR-382	1.09E-06	7.470548
hsa-miR-409-3p	6.07E-10	21.914793
hsa-miR-410	3.87E-07	8.62512
hsa-miR-411	7.18E-05	4.496815
hsa-miR-421	0.006857577	2.1466932
hsa-miR-4291	0.012117385	-1.249177
hsa-miR-4313	0.041270826	-1.713371
hsa-miR-432	2.24E-06	7.1745667
hsa-miR-4323	0.02434763	-2.203146
hsa-miR-449a	0.021987779	6.4758606
hsa-miR-449b	0.015362001	4.142411
hsa-miR-487b	2.87E-05	4.532046
hsa-miR-489	5.08E-05	-5.945296
hsa-miR-493*	1.28E-10	18.513674
hsa-miR-495	1.26E-05	7.244548
hsa-miR-500a*	0.001440559	-1.329574
hsa-miR-501-5p	0.044711594	-1.928709
hsa-miR-502-3p	8.24E-04	-1.364393
hsa-miR-503	0.018005582	2.1399236
hsa-miR-512-3p	0.034444507	-1.089404
hsa-miR-514	0.001964029	2.5378788

hsa-miR-517b	0.03366402	-1.134578
hsa-miR-532-3p	0.018577604	-1.331933
hsa-miR-539	0.006897023	1.8087255
hsa-miR-543	6.54E-08	8.500724
hsa-miR-548q	0.0488957	-1.314496
hsa-miR-583	0.028516129	-1.096252
hsa-miR-605	0.043752518	1.5499116
hsa-miR-610	0.039703604	1.7031237
hsa-miR-638	0.039814856	-1.313573
hsa-miR-642b	0.029872905	1.4115938
hsa-miR-652	0.046206422	-1.361586
hsa-miR-654-3p	1.05E-07	8.929594
hsa-miR-664	0.024273891	-1.194848
hsa-miR-92a-1*	0.034511182	-1.089352
hsv2-miR-H6	0.01793159	-1.336587