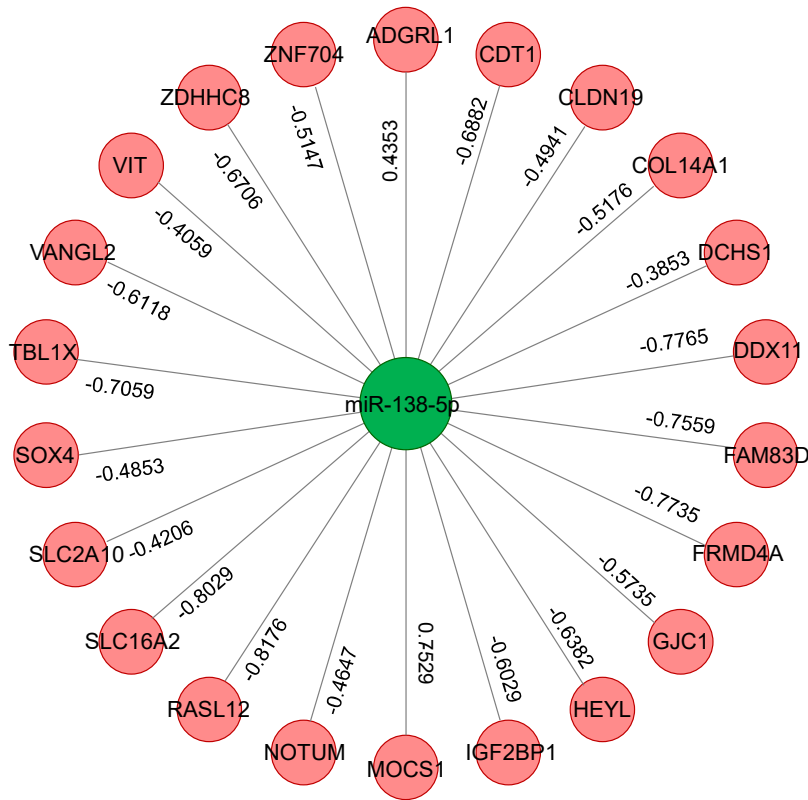


Figure S1 miR-138-5p and its paired mRNAs



22 differentially expressed mRNAs paired to miR-138-5p were identified by using microRNA Target Filter. Upregulated mRNAs are indicated in red, whereas downregulated miRNAs are in green. The negative correlations are connected by grey lines and labeled with Spearman's ρ values.

Table S1. Sequences of qPCR primers used in this study

Gene	Forward primer	Reverse primer
<i>TBL1X</i>	5'-CAGGGCTCCTTATGGTGACT-3'	5'-CATATCAGATGCCTCGCAGA-3'
<i>CLDN19</i>	5'-GGCCTCTATGAAGGGCTCTG-3'	5'-CGCTGATTGGATGTGACCGT-3'
<i>FRMD4A</i>	5'-AGCCTGCTGTCTTCAGGTTC-3'	5'-CAGTTCCTCCAGCCTCTGAC-3'
<i>NOTUM</i>	5'-TGGCTACAAGGTCTACCCGA-3'	5'-ACGTCCTTGAGTGTGTGGC-3'
<i>SLC16A2</i>	5'-CGGCATCCATAACTCTGTGCG-3'	5'-AGCCCAAACGGTCAGTGAA-3'
<i>CCL18</i>	5'-TTGTCCTCGTCTGCACCAT-3'	5'-GGGGCTGGTTTCAGAATAGTCA-3'
<i>HTRA1</i>	5'-AAGGGCAGGAAGATCCCAAC-3'	5'-GCGAAACAATTCGATATGAACCAC-3'
<i>SLC39A6</i>	5'-ACGTGGAAGGGTCTAACAGC-3'	5'-TGGACAACCTGCTTCTTAATCTCCA-3'
<i>BEX1</i>	5'-GAGTCCAAAGAGAAACGAGCAG-3'	5'-ATTCACCAGCATCCAAAGGGAG-3'
<i>EPYC</i>	5'-AGGACTTGTTCTGGGACTTG-3'	5'-GTTCCCTGAAGGCATCACTG-3'
<i>ACTB</i>	5'-GCATCCCCCAAAGTTCACAA-3'	5'-AGGACTGGGCCATTCTCCTT-3'

Table S2. Differentially expressed mRNAs and miRNAs

ID	Exp Log		Entrez Gene Name	Location	Type(s)
	Ratio	Exp p-value			
AADACL3	1.646	0.0012	arylacetamide deacetylase like 3	Other	other
ACTN1	1.209	0.00005	actinin alpha 1	Cytoplasm	transcription regulator
ADAMTS1	1.03	0.00005	ADAM metallopeptidase with thrombospondin type 1 motif 1	Extracellular Space	peptidase
ADAP1	1.01	0.00125	ArfGAP with dual PH domains 1	Nucleus	other
ADGRD1	1.087	0.0001	adhesion G protein-coupled receptor D1	Plasma Membrane	G-protein coupled receptor
ADGRL1	1.078	0.0024	adhesion G protein-coupled receptor L1	Plasma Membrane	G-protein coupled receptor
AEBP1	1.023	0.00005	AE binding protein 1	Nucleus	peptidase
AFAP1	1.354	0.00005	actin filament associated protein 1	Cytoplasm	other
AFAP1L2	1.083	0.00005	actin filament associated protein 1 like 2	Cytoplasm	other
AGR2	-1.23	0.0007	anterior gradient 2, protein disulphide isomerase family member	Extracellular Space	other
AGRN	1.263	0.00005	agrin	Plasma Membrane	other
AMD1	-1.047	0.00005	adenosylmethionine decarboxylase 1	Cytoplasm	enzyme
AMZ1	1.554	0.00015	archaelysin family metallopeptidase 1	Other	peptidase
ANKRD33B	1.036	0.0001	ankyrin repeat domain 33B	Other	other
AOC1	1.351	0.00005	amine oxidase, copper containing 1	Extracellular Space	enzyme
ARHGAP23	1.117	0.00005	Rho GTPase activating protein 23	Cytoplasm	other
ARMS2	-2.211	0.00005	age-related maculopathy susceptibility 2	Cytoplasm	other
ASCL2	1.456	0.00005	achaete-scute family bHLH transcription factor 2	Nucleus	transcription regulator
ATAD1	-1.018	0.00005	ATPase family, AAA domain containing 1	Other	enzyme
ATP7B	1.145	0.00005	ATPase copper transporting beta	Cytoplasm	transporter

B3GNT7	1.191	0.00005	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	Cytoplasm	enzyme
BARX2	1.212	0.0008	BARX homeobox 2	Nucleus	transcription regulator
BEX1	-2.14	0.00435	brain expressed X-linked 1	Other	other
BTBD16	-1.141	0.0056	BTB domain containing 16	Other	other
C1orf106	1.643	0.00005	chromosome 1 open reading frame 106	Other	other
CA1	-1.473	0.00005	carbonic anhydrase 1	Cytoplasm	enzyme
CA10	-1.024	0.00005	carbonic anhydrase 10	Other	enzyme
CCL18	-1.574	0.00015	C-C motif chemokine ligand 18	Extracellular Space	cytokine
CCND1	1.086	0.00005	cyclin D1	Nucleus	transcription regulator
CCNF	1.13	0.00085	cyclin F	Nucleus	other
CD22	1.429	0.00035	CD22 molecule	Plasma Membrane	transmembrane receptor
CDH3	1.176	0.0001	cadherin 3	Plasma Membrane	other
CDT1	1.085	0.00015	chromatin licensing and DNA replication factor 1	Nucleus	other
CELSR2	1.184	0.0001	cadherin EGF LAG seven-pass G-type receptor 2	Plasma Membrane	G-protein coupled receptor
CFH	-1.182	0.00005	complement factor H	Extracellular Space	other
CGB2	1.831	0.0023	chorionic gonadotropin beta subunit 2	Other	other
CLDN19	1.593	0.00005	claudin 19	Plasma Membrane	other
CLK1	-1.262	0.00005	CDC like kinase 1	Nucleus	kinase
CNGA1	-1.004	0.00285	cyclic nucleotide gated channel alpha 1	Plasma Membrane	ion channel
COL14A1	1.105	0.00005	collagen type XIV alpha 1 chain	Extracellular Space	other
COL15A1	1.175	0.00005	collagen type XV alpha 1 chain	Extracellular Space	other
COL17A1	1.752	0.00005	collagen type XVII alpha 1	Extracellular Space	other
COL18A1	1.045	0.00005	collagen type XVIII alpha 1 chain	Extracellular Space	other
COL1A1	1.064	0.00005	collagen type I alpha 1	Extracellular Space	other
COL1A2	1.028	0.00005	collagen type I alpha 2 chain	Extracellular Space	other

COL4A1	1.415	0.00005	collagen type IV alpha 1 chain	Extracellular Space	other
COL4A2	1.415	0.00005	collagen type IV alpha 2	Extracellular Space	other
COL5A1	1.42	0.00005	collagen type V alpha 1	Extracellular Space	other
COL5A3	1.367	0.00015	collagen type V alpha 3	Extracellular Space	other
COL6A1	1.142	0.00005	collagen type VI alpha 1	Extracellular Space	other
COL6A3	1.397	0.00005	collagen type VI alpha 3 chain	Extracellular Space	other
COX4I2	1.034	0.001	cytochrome c oxidase subunit 4I2	Cytoplasm	enzyme
CP	-1.394	0.0033	ceruloplasmin (ferroxidase)	Extracellular Space	enzyme
CRABP2	1.41	0.00005	cellular retinoic acid binding protein 2	Cytoplasm	transporter
CRH	-2.069	0.00005	corticotropin releasing hormone	Extracellular Space	cytokine
CRISPLD1	1.233	0.00005	cysteine rich secretory protein LCCL domain containing 1	Cytoplasm	other
CSPG4	1.539	0.00005	chondroitin sulfate proteoglycan 4	Plasma Membrane	other
CST2	-1.842	0.00595	cystatin SA	Extracellular Space	other
CXCL10	-2.218	0.00005	C-X-C motif chemokine ligand 10	Extracellular Space	cytokine
CXCL11	-2.688	0.00235	C-X-C motif chemokine ligand 11	Extracellular Space	cytokine
DCHS1	1.164	0.00005	dachsous cadherin-related 1	Plasma Membrane	other
DDX11	1.09	0.00225	DEAD/H-box helicase 11	Cytoplasm	enzyme
DENND2A	1.401	0.00005	DENN domain containing 2A	Cytoplasm	other
DGKD	1.253	0.00005	diacylglycerol kinase delta	Cytoplasm	kinase
DNMT1	1.241	0.00005	DNA (cytosine-5-)-methyltransferase 1	Nucleus	enzyme
DOCK5	1.003	0.00005	dedicator of cytokinesis 5	Cytoplasm	other
EGFLAM	1.357	0.0006	EGF like, fibronectin type III and laminin G domains	Extracellular Space	other
EGR1	1.056	0.00175	early growth response 1	Nucleus	transcription regulator
ELN	1.228	0.00005	elastin	Extracellular Space	other
ENDOU	-1.018	0.00005	endonuclease, poly(U) specific	Cytoplasm	peptidase

EPYC	-2.776	0.00005	epiphycan	Extracellular Space	other
ERAP2	-1.529	0.00005	endoplasmic reticulum aminopeptidase 2	Cytoplasm	peptidase
ESPN	1.127	0.00245	espin	Cytoplasm	other
EXTL3	1.369	0.00005	exostosin like glycosyltransferase 3	Cytoplasm	enzyme
FAM171B	-1.032	0.00005	family with sequence similarity 171 member B	Other	other
FAM19A4	-2.277	0.0036	family with sequence similarity 19 member A4, C-C motif chemokine like	Extracellular Space	other
FAM78A	1.063	0.00005	family with sequence similarity 78 member A	Other	other
FAM83D	1.048	0.00115	family with sequence similarity 83 member D	Cytoplasm	other
FAT1	1.518	0.00005	FAT atypical cadherin 1	Plasma Membrane	other
FBN1	1.151	0.00005	fibrillin 1	Extracellular Space	other
FBXL18	1.019	0.00015	F-box and leucine rich repeat protein 18	Other	enzyme
FCGBP	1.01	0.00015	Fc fragment of IgG binding protein	Extracellular Space	other
FGF12	-1.11	0.0001	fibroblast growth factor 12	Extracellular Space	other
FKBP10	1.358	0.00005	FK506 binding protein 10	Cytoplasm	enzyme
FLJ41278	-2.781	0.00005	uncharacterized LOC400046	Other	other
FLNA	1.001	0.00005	filamin A	Cytoplasm	other
FLNB	1.531	0.00005	filamin B	Cytoplasm	other
FN1	2.283	0.00005	fibronectin 1	Extracellular Space	enzyme
FOXF1	1.018	0.00045	forkhead box F1	Nucleus	transcription regulator
FO XK1	1.003	0.00005	forkhead box K1	Nucleus	transcription regulator
FRAS1	1.695	0.00005	Fraser extracellular matrix complex subunit 1	Extracellular Space	other
FREM2	1.081	0.00005	FRAS1 related extracellular matrix protein 2	Extracellular Space	other
FRMD4A	1.036	0.00005	FERM domain containing 4A	Plasma Membrane	other
FSTL3	1.06	0.00005	folistatin like 3	Extracellular Space	other
FZD5	1.003	0.00005	frizzled class receptor 5	Plasma Membrane	G-protein coupled receptor

GATA4	1.084	0.0033	GATA binding protein 4	Nucleus	transcription regulator
GATA6	1.126	0.00265	GATA binding protein 6	Nucleus	transcription regulator
GBP5	-1.033	0.0004	guanylate binding protein 5	Plasma Membrane	enzyme
GJA4	1.426	0.00005	gap junction protein alpha 4	Plasma Membrane	transporter
GJC1	1.112	0.00005	gap junction protein gamma 1	Plasma Membrane	ion channel
GPC4	1.199	0.00005	glypican 4	Plasma Membrane	transmembrane receptor
GREB1L	1.042	0.0007	growth regulation by estrogen in breast cancer 1 like	Extracellular Space	other
GYS1	1.096	0.0001	glycogen synthase 1	Cytoplasm	enzyme
HAPLN3	1.233	0.0005	hyaluronan and proteoglycan link protein 3	Extracellular Space	other
HBD	-1.3	0.00005	hemoglobin subunit delta	Other	transporter
HBG1	-1.706	0.00005	hemoglobin subunit gamma 1	Cytoplasm	other
HCAR1	1.411	0.00065	hydroxycarboxylic acid receptor 1	Plasma Membrane	G-protein coupled receptor
HEYL	1.188	0.00005	hes related family bHLH transcription factor with YRPW motif-like	Nucleus	transcription regulator
HLA-DQA2	-1.463	0.00095	major histocompatibility complex, class II, DQ alpha 2	Plasma Membrane	transmembrane receptor
HLA-G	2.298	0.00005	major histocompatibility complex, class I, G	Plasma Membrane	other
HN1	1	0.00005	hematological and neurological expressed 1	Nucleus	other
HSPG2	2.095	0.00005	heparan sulfate proteoglycan 2	Extracellular Space	enzyme
HTRA1	-1.449	0.00005	HtrA serine peptidase 1	Extracellular Space	peptidase
HUNK	1.452	0.00005	hormonally up-regulated Neu-associated kinase	Cytoplasm	kinase
IGF2BP1	1.108	0.00005	insulin like growth factor 2 mRNA binding protein 1	Cytoplasm	translation regulator
IGFBP1	-1.05	0.0002	insulin like growth factor binding protein 1	Extracellular Space	other
IGFBP5	1.082	0.00005	insulin like growth factor binding protein 5	Extracellular Space	other
IL13RA2	-1.141	0.00005	interleukin 13 receptor subunit alpha 2	Plasma Membrane	transmembrane receptor
IL17RE	1.356	0.00045	interleukin 17 receptor E	Plasma Membrane	other
IL27RA	1.216	0.00615	interleukin 27 receptor subunit alpha	Plasma Membrane	transmembrane receptor

IL2RB	1.481	0.00005	interleukin 2 receptor subunit beta	Plasma Membrane	transmembrane receptor
ISM2	1.544	0.00005	isthmin 2	Other	other
JAG2	1.413	0.00005	jagged 2	Extracellular Space	growth factor
JCHAIN	-1.713	0.00015	joining chain of multimeric IgA and IgM	Extracellular Space	other
KANK3	1.181	0.00005	KN motif and ankyrin repeat domains 3	Cytoplasm	other
KANK4	1.077	0.00005	KN motif and ankyrin repeat domains 4	Cytoplasm	other
KCNK12	1.15	0.00695	potassium two pore domain channel subfamily K member 12	Plasma Membrane	ion channel
KIAA1161	1.107	0.00005	KIAA1161	Nucleus	other
KIAA1217	1.137	0.00005	KIAA1217	Cytoplasm	other
KIAA1456	-1.46	0.00005	KIAA1456	Cytoplasm	enzyme
KIF26B	1.257	0.00025	kinesin family member 26B	Other	other
KIRREL	1.061	0.00005	kin of IRRE like (Drosophila)	Plasma Membrane	other
KLRB1	-1.03	0.006	killer cell lectin like receptor B1	Plasma Membrane	transmembrane receptor
KRT17	1.166	0.00565	keratin 17	Cytoplasm	other
KRT6A	1.087	0.00445	keratin 6A	Cytoplasm	other
KRTAP26-1	-1.104	0.00005	keratin associated protein 26-1	Other	other
LAIR2	1.693	0.00005	leukocyte associated immunoglobulin like receptor 2	Plasma Membrane	other
LAMA2	1.062	0.00005	laminin subunit alpha 2	Extracellular Space	other
LAMA5	1.631	0.00005	laminin subunit alpha 5	Extracellular Space	other
LAMB1	1.129	0.00005	laminin subunit beta 1	Extracellular Space	other
LAMB4	1.011	0.00005	laminin subunit beta 4	Other	other
LAMC3	1.35	0.00005	laminin subunit gamma 3	Extracellular Space	other
GYLTL1B	1.082	0.00005	LARGE xylosyl- and glucuronyltransferase 2	Cytoplasm	enzyme
LDLR	1.081	0.00005	low density lipoprotein receptor	Plasma Membrane	transporter
LHFP	1.003	0.00005	lipoma HMGIC fusion partner	Other	other

LINC00474	-1.239	0.00065	long intergenic non-protein coding RNA 474	Other	other
LIPG	1.08	0.00005	lipase G, endothelial type	Extracellular Space	enzyme
LOC100507477	-1.483	0.0026	uncharacterized LOC100507477	Other	other
LOC101927354	-2.204	0.00005	uncharacterized LOC101927354	Other	other
LPAR2	1.252	0.00525	lysophosphatidic acid receptor 2	Plasma Membrane	G-protein coupled receptor
LPL	-1.246	0.00005	lipoprotein lipase	Cytoplasm	enzyme
LRIG3	-1.119	0.00005	leucine rich repeats and immunoglobulin like domains 3	Extracellular Space	other
LRP1	1.085	0.00005	LDL receptor related protein 1	Plasma Membrane	transmembrane receptor
LRP2	1.395	0.00005	LDL receptor related protein 2	Plasma Membrane	transporter
LRP5	1.113	0.00005	LDL receptor related protein 5	Plasma Membrane	transmembrane receptor
LRRC4B	1.241	0.00355	leucine rich repeat containing 4B	Plasma Membrane	other
LTBP2	1.044	0.00005	latent transforming growth factor beta binding protein 2	Extracellular Space	other
LTBP4	1.259	0.00005	latent transforming growth factor beta binding protein 4	Extracellular Space	growth factor
LUM	-1.384	0.00005	lumican	Extracellular Space	other
LVCAT8	-1.348	0.00005		Other	other
MAGED1	1.088	0.00005	MAGE family member D1	Plasma Membrane	transcription regulator
MEGF8	1.146	0.00005	multiple EGF like domains 8	Extracellular Space	other
MISP	1.451	0.0012	mitotic spindle positioning	Plasma Membrane	other
MKI67	1.224	0.00005	marker of proliferation Ki-67	Nucleus	other
MKL1	1.038	0.00125	megakaryoblastic leukemia (translocation) 1	Nucleus	transcription regulator
MMP1	-1.054	0.00035	matrix metalloproteinase 1	Extracellular Space	peptidase
MMP12	2.025	0.00005	matrix metalloproteinase 12	Extracellular Space	peptidase
MMP14	1.057	0.00005	matrix metalloproteinase 14	Extracellular Space	peptidase
MMP2	1.253	0.00005	matrix metalloproteinase 2	Extracellular Space	peptidase
MOCS1	1.087	0.00005	molybdenum cofactor synthesis 1	Cytoplasm	other

MRC2	1.064	0.0001	mannose receptor C type 2	Plasma Membrane	transmembrane receptor
MUC15	-1.266	0.00005	mucin 15, cell surface associated	Extracellular Space	other
MUM1L1	-1.04	0.00005	MUM1 like 1	Cytoplasm	other
MYCN	1.081	0.00005	v-myc avian myelocytomatosis viral oncogene neuroblastoma derived homolog	Nucleus	transcription regulator
MYO7A	1.085	0.00005	myosin VIIA	Cytoplasm	enzyme
NCKAP5L	1.341	0.00005	NCK associated protein 5 like	Cytoplasm	other
NDP	-1.248	0.0006	NDP, norrin cystine knot growth factor	Extracellular Space	growth factor
NES	1.464	0.00005	nestin	Extracellular Space	other
NEURL1B	1.122	0.0005	neuralized E3 ubiquitin protein ligase 1B	Other	enzyme
NFATC1	1.136	0.00265	nuclear factor of activated T-cells 1	Nucleus	transcription regulator
NID2	1.247	0.00005	nidogen 2	Extracellular Space	other
NOG	1.635	0.00005	noggin	Extracellular Space	growth factor
NOTUM	1.852	0.00005	NOTUM, palmitoleoyl-protein carboxylesterase	Extracellular Space	enzyme
NOVA2	1.391	0.0027	NOVA alternative splicing regulator 2	Nucleus	other
NRP2	1.296	0.00005	neuropilin 2	Plasma Membrane	kinase
NUP210	1.213	0.00005	nucleoporin 210	Nucleus	transporter
OLAH	-1.143	0.00005	oleoyl-ACP hydrolase	Cytoplasm	enzyme
OLFM4	-1.297	0.0011	olfactomedin 4	Extracellular Space	other
P3H1	1.069	0.00005	prolyl 3-hydroxylase 1	Nucleus	enzyme
PCDHGC3	1.389	0.00125	protocadherin gamma subfamily C, 3	Plasma Membrane	other
PCOLCE	1.032	0.00075	procollagen C-endopeptidase enhancer	Extracellular Space	other
PCSK6	1.293	0.00005	proprotein convertase subtilisin/kexin type 6	Extracellular Space	peptidase
PDE4A	1.004	0.00145	phosphodiesterase 4A	Cytoplasm	enzyme
PDGFRB	1.048	0.00005	platelet derived growth factor receptor beta	Plasma Membrane	kinase
PENK	-2.046	0.00245	proenkephalin	Extracellular Space	other

PIEZO1	1.166	0.00005	piezo type mechanosensitive ion channel component 1	Cytoplasm	ion channel
PIP	-2.048	0.00045	prolactin induced protein	Extracellular Space	peptidase
PIPOX	1.021	0.0008	pipecolic acid and sarcosine oxidase	Cytoplasm	enzyme
PLA2G2F	-1.181	0.00165	phospholipase A2 group IIF	Extracellular Space	enzyme
PLEKHG2	1.139	0.0003	pleckstrin homology and RhoGEF domain containing G2	Cytoplasm	other
PLK1	1.075	0.00015	polo like kinase 1	Nucleus	kinase
PLVAP	1.166	0.00005	plasmalemma vesicle associated protein	Plasma Membrane	other
PRL	-1.16	0.00065	prolactin	Extracellular Space	cytokine
PROSER2	1.047	0.00635	proline and serine rich 2	Other	other
PROSER2-AS1	1.048	0.00215	PROSER2 antisense RNA 1	Other	other
PSG11	-1.481	0.00005	pregnancy specific beta-1-glycoprotein 11	Extracellular Space	other
PTK7	1.116	0.00005	protein tyrosine kinase 7 (inactive)	Plasma Membrane	kinase
PTPRS	1.222	0.00015	protein tyrosine phosphatase, receptor type S	Plasma Membrane	phosphatase
PYCR1	1.283	0.00005	pyrroline-5-carboxylate reductase 1	Cytoplasm	enzyme
RAMP3	1.204	0.00005	receptor (G protein-coupled) activity modifying protein 3	Plasma Membrane	transporter
RASGRF2	1.459	0.00385	Ras protein specific guanine nucleotide releasing factor 2	Cytoplasm	other
RASL12	1.52	0.00005	RAS like family 12	Other	enzyme
RBM24	-1.587	0.0002	RNA binding motif protein 24	Other	other
RBP4	-1.283	0.00005	retinol binding protein 4	Extracellular Space	transporter
RCN3	1.344	0.00005	reticulocalbin 3	Cytoplasm	other
RGMA	1.08	0.00315	repulsive guidance molecule family member a	Plasma Membrane	other
RIPK4	1.207	0.00005	receptor interacting serine/threonine kinase 4	Nucleus	kinase
RRAD	1.27	0.00005	RRAD, Ras related glycolysis inhibitor and calcium channel regulator	Cytoplasm	enzyme
RTN4RL2	2.443	0.00015	reticulon 4 receptor-like 2	Plasma Membrane	other
RUSC2	1.041	0.0001	RUN and SH3 domain containing 2	Cytoplasm	other

RXFP1	-1.351	0.00005	relaxin/insulin like family peptide receptor 1	Plasma Membrane	G-protein coupled receptor
SCD5	1.084	0.00035	stearoyl-CoA desaturase 5	Cytoplasm	enzyme
SCUBE1	1.709	0.00005	signal peptide, CUB domain and EGF like domain containing 1	Plasma Membrane	transmembrane receptor
SCUBE2	1.269	0.0001	signal peptide, CUB domain and EGF like domain containing 2	Extracellular Space	other
SDK1	1.74	0.00005	sidekick cell adhesion molecule 1	Plasma Membrane	other
SEMA3G	1.269	0.00005	semaphorin 3G	Cytoplasm	other
SERPINB7	-1.28	0.00025	serpin family B member 7	Cytoplasm	other
SERPINE2	1.263	0.00005	serpin family E member 2	Extracellular Space	other
SERPINI1	-1.106	0.00005	serpin family I member 1	Extracellular Space	other
SFRP1	1.8	0.00005	secreted frizzled related protein 1	Plasma Membrane	transmembrane receptor
SH3PXD2B	1.688	0.00005	SH3 and PX domains 2B	Cytoplasm	other
SIGLEC14	2.864	0.00005	sialic acid binding Ig like lectin 14	Plasma Membrane	other
SLAMF7	-1.059	0.00105	SLAM family member 7	Plasma Membrane	other
SLC13A3	1.011	0.0004	solute carrier family 13 member 3	Plasma Membrane	transporter
SLC16A2	1.083	0.00005	solute carrier family 16 member 2	Plasma Membrane	transporter
SLC26A7	-1.219	0.00005	solute carrier family 26 member 7	Plasma Membrane	transporter
SLC27A1	1.115	0.00065	solute carrier family 27 member 1	Plasma Membrane	transporter
SLC2A10	1.354	0.00005	solute carrier family 2 member 10	Plasma Membrane	transporter
SLC39A6	-1.073	0.00005	solute carrier family 39 member 6	Plasma Membrane	transporter
SLCO4A1	1.622	0.00005	solute carrier organic anion transporter family member 4A1	Plasma Membrane	transporter
SLFN5	1.025	0.00005	schlafen family member 5	Nucleus	enzyme
SLIT3	1.009	0.0001	slit guidance ligand 3	Extracellular Space	other
SMTN	1.094	0.0002	smoothelin	Extracellular Space	other
SOX17	1.006	0.00195	SRY-box 17	Nucleus	transcription regulator
SOX4	1.172	0.00005	SRY-box 4	Nucleus	transcription regulator

SP6	1.047	0.00005	Sp6 transcription factor	Nucleus	transcription regulator
ST18	-1.397	0.00005	ST18, C2H2C-type zinc finger	Nucleus	transcription regulator
STEAP4	-1.007	0.00005	STEAP4 metalloreductase	Plasma Membrane	enzyme
SYNPR	-1.629	0.00075	synaptoporin	Plasma Membrane	transporter
SYT8	1.308	0.0003	synaptotagmin 8	Cytoplasm	transporter
TAC3	1.025	0.00005	tachykinin 3	Extracellular Space	other
TBL1X	1.002	0.00005	transducin (beta)-like 1X-linked	Nucleus	transcription regulator
TBX2	1.077	0.00005	T-box 2	Nucleus	transcription regulator
TBX5-AS1	1.136	0.00725	TBX5 antisense RNA 1	Other	other
TC2N	-1.006	0.00005	tandem C2 domains, nuclear	Nucleus	transporter
TCF7L1	1.261	0.0011	transcription factor 7 like 1	Nucleus	transcription regulator
TCF7L2	1.216	0.00005	transcription factor 7 like 2	Nucleus	transcription regulator
TCHH	-1.147	0.00005	trichohyalin	Extracellular Space	other
TENM3	1.18	0.00005	teneurin transmembrane protein 3	Plasma Membrane	other
TFRC	-1.244	0.00225	transferrin receptor	Plasma Membrane	transporter
TNFRSF10D	-1.098	0.00055	TNF receptor superfamily member 10d	Plasma Membrane	transmembrane receptor
TNFRSF11B	-1.074	0.0028	TNF receptor superfamily member 11b	Plasma Membrane	transmembrane receptor
TNNI2	2.024	0.0001	troponin I2, fast skeletal type	Cytoplasm	enzyme
TOB2P1	-1.214	0.00005	transducer of ERBB2, 2 pseudogene 1	Other	other
TRAM2-AS1	-1.238	0.00005	TRAM2 antisense RNA 1 (head to head)	Other	other
UBASH3B	1.067	0.00005	ubiquitin associated and SH3 domain containing B	Other	enzyme
UBD	-2.334	0.00005	ubiquitin D	Nucleus	other
VANGL2	1.11	0.0005	VANGL planar cell polarity protein 2	Plasma Membrane	other
VAV2	1.124	0.00005	vav guanine nucleotide exchange factor 2	Cytoplasm	transcription regulator
VIT	1.597	0.0007	vitrin	Extracellular Space	other

VNN1	-1.16	0.0005	vanin 1	Plasma Membrane	enzyme
VWCE	1.737	0.00005	von Willebrand factor C and EGF domains	Other	other
WNK2	1.037	0.00005	WNK lysine deficient protein kinase 2	Cytoplasm	kinase
WNT3A	1.43	0.00115	Wnt family member 3A	Extracellular Space	cytokine
WNT6	1.347	0.0041	Wnt family member 6	Extracellular Space	other
XIST	-1.265	0.00005	X inactive specific transcript (non-protein coding)	Nucleus	other
ZBTB6	-1.061	0.00005	zinc finger and BTB domain containing 6	Nucleus	other
ZDHHC8	1.075	0.00005	zinc finger DHHC-type containing 8	Cytoplasm	enzyme
ZNF433	-1.028	0.00015	zinc finger protein 433	Nucleus	other
ZNF704	1.034	0.00005	zinc finger protein 704	Nucleus	other
ZSCAN9	-1.392	0.00005	zinc finger and SCAN domain containing 9	Nucleus	transcription regulator
hsa-miR-4500	-1.436	0.0389			
hsa-miR-1208	-1.066	0.00248			
hsa-miR-4488	-1.856	0.00169			
hsa-miR-1273h-5p	2.722	0.00574			
hsa-miR-216a-3p	-3.33	0.00496			
hsa-miR-1291	-1.212	0.0257			
hsa-miR-138-1-3p	-1.157	0.0126			
hsa-miR-138-5p	-1.386	0.000372			
hsa-miR-1469	-4.005	1.28E-13			
hsa-miR-187-3p	3.026	0.0321			
hsa-miR-202-5p	1.567	0.028			
hsa-miR-203b-3p	-3.721	0.00144			
hsa-miR-205-3p	1.525	0.0432			
hsa-miR-2114-5p	-1.809	0.00923			

hsa-miR-210-5p	-1.398	0.0225
hsa-miR-3130-3p	-3.751	0.0124
hsa-miR-3158-3p	-1.259	0.0204
hsa-miR-4685-3p	-1.453	0.0418
hsa-miR-3914	-3.179	0.0142
hsa-miR-4732-3p	-1.1	0.0356
hsa-miR-4763-5p	1.643	0.0361
hsa-miR-4792	-1.878	0.00000415
hsa-miR-5096	2.784	0.00102
hsa-miR-548at-5p	-1.602	0.0392
hsa-miR-6824-5p	1.395	0.0256
hsa-miR-6844	2.076	0.0345
hsa-miR-6892-3p	-3.264	0.0145
hsa-miR-718	-4.287	0.0000523
hsa-miR-4492	-2.449	0.011
hsa-miR-767-3p	2.422	0.00882
hsa-miR-7975	-1.007	0.0395
hsa-miR-95-3p	-1.372	0.0278

Table S3. Functional analysis for the differentially expressed mRNAs and miRNAs in GDM group compared with control.

Top Diseases and Bio Functions	<i>p</i>-value^a	# of genes
<i>Diseases and Disorders</i>		
Connective Tissue Disorders	2.53E-15-3.6E-04	87
Organismal Injury and Abnormalities	2.53E-15-4.74E-04	274
Cancer	1.21E-14-4.74E-04	267
Reproductive System Disease	6.65E-14-4.74E-04	171
Dermatological Diseases and Conditions	1.77E-13-1.83E-04	171
Endocrine System Disorders	6.09E-13-4.74E-04	144
Gastrointestinal Disease	6.09E-13-3.68E-04	241
Metabolic Disease	6.09E-13-3.68E-04	52
Skeletal and Muscular Disorders	6.09E-13-4.71E-04	118
Cardiovascular Disease	7.16E-12-4.13E-04	57
<i>Molecular and Cellular Functions</i>		
Cellular Growth and Proliferation	2.56E-14-4.71E-04	140
Cellular Movement	2.71E-09-4.68E-04	86
Cell Morphology	8.99E-09-4.65E-04	78
Cellular Development	4.5E-08-4.71E-04	113
Cell Death and Survival	1.24E-06-6.59E-05	107
Post-Translational Modification	1.79E-06-3.6E-04	17
Protein Degradation	1.79E-06-3.6E-04	25
Protein Synthesis	1.79E-06-4.65E-04	36
Cell-To-Cell Signaling and Interaction	3.38E-06-4.13E-04	69
Cellular Function and Maintenance	1.33E-05-4.18E-04	30
<i>Physiological System Development and Function</i>		
Cardiovascular System Development and Function	4.58E-15-4.18E-04	74
Embryonic Development	2.52E-14-4.49E-04	108
Organismal Development	2.52E-14-4.49E-04	128

Organ Development	4.73E-12-4.49E-04	99
Tissue Development	4.73E-12-4.65E-04	145
Tissue Morphology	7.16E-12-4.49E-04	92
Organismal Survival	4.8E-10-1.32E-09	89
Digestive System Development and Function	5.96E-10-2.61E-04	45
Skeletal and Muscular System Development and Function	8.5E-10-4.71E-04	72
Respiratory System Development and Function	1.22E-09-2.97E-04	28

^a Range of *p*-values indicates higher level functions that contained multiple lower level functions.

Table S4. Canonical pathway analysis for the differentially expressed mRNAs and miRNAs in GDM group compared with control.

Top Canonical Pathways	-log(p-value)	# of genes
Hepatic Fibrosis / Hepatic Stellate Cell Activation	9.4	17
Wnt/ β -catenin Signaling	6.36	13
Inhibition of Matrix Metalloproteases	4.93	6
Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis	4.84	13
Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis	4.15	14
Colorectal Cancer Metastasis Signaling	3.92	12
Factors Promoting Cardiogenesis in Vertebrates	3.65	7
Regulation of the Epithelial-Mesenchymal Transition Pathway	3.65	10
Atherosclerosis Signaling	3.53	8
Intrinsic Prothrombin Activation Pathway	3.26	4

Table S5. Co-expressed mRNAs and miRNAs

miRNAs	Exp Log		Source	Confidence	mRNAs	Exp Log		Exp False
	Ratio	Exp p-value				Ratio	Exp p-value	Discovery
								Rate
								(q-value)
hsa-miR-1273h-5p	2.722	0.00574	TargetScan Human	Moderate (predicted)	CXCL10	-2.218	0.00005	0.00135
hsa-miR-1273h-5p	2.722	0.00574	TargetScan Human	High (predicted)	RBM24	-1.587	0.0002	0.00401
hsa-miR-1273h-5p	2.722	0.00574	TargetScan Human	Moderate (predicted)	VNN1	-1.16	0.0005	0.00809
hsa-miR-216a-3p	-3.33	0.00496	TargetScan Human	High (predicted)	ADGRD1	1.087	0.0001	0.00239
hsa-miR-216a-3p	-3.33	0.00496	TargetScan Human	High (predicted)	AFAP1	1.354	0.00005	0.00135
hsa-miR-216a-3p	-3.33	0.00496	TargetScan Human	High (predicted)	AGRN	1.263	0.00005	0.00135
hsa-miR-216a-3p	-3.33	0.00496	TargetScan Human	High (predicted)	ARHGAP23	1.117	0.00005	0.00135
hsa-miR-216a-3p	-3.33	0.00496	TargetScan Human	High (predicted)	B3GNT7	1.191	0.00005	0.00135
hsa-miR-216a-3p	-3.33	0.00496	TargetScan Human	High (predicted)	COL5A1	1.42	0.00005	0.00135
hsa-miR-216a-3p	-3.33	0.00496	TargetScan Human	High (predicted)	FAM78A	1.063	0.00005	0.00135
hsa-miR-216a-3p	-3.33	0.00496	TargetScan Human	High (predicted)	FRMD4A	1.036	0.00005	0.00135
hsa-miR-216a-3p	-3.33	0.00496	TargetScan Human	High (predicted)	GATA6	1.126	0.00265	0.0255
hsa-miR-216a-3p	-3.33	0.00496	TargetScan Human	High (predicted)	HUNK	1.452	0.00005	0.00135
hsa-miR-216a-3p	-3.33	0.00496	TargetScan Human,miRecords	Experimentally Observed,High (predicted)	LDLR	1.081	0.00005	0.00135
hsa-miR-216a-3p	-3.33	0.00496	TargetScan Human	High (predicted)	NEURL1B	1.122	0.0005	0.00809
hsa-miR-216a-3p	-3.33	0.00496	TargetScan Human	High (predicted)	NRP2	1.296	0.00005	0.00135
hsa-miR-216a-3p	-3.33	0.00496	TargetScan Human	High (predicted)	NUP210	1.213	0.00005	0.00135
hsa-miR-216a-3p	-3.33	0.00496	TargetScan Human	Moderate (predicted)	PROSER2	1.047	0.00635	0.046

hsa-miR-216a-3p	-3.33	0.00496	TargetScan Human	Moderate (predicted)	RASL12	1.52	0.00005	0.00135
hsa-miR-216a-3p	-3.33	0.00496	TargetScan Human	High (predicted)	SFRP1	1.8	0.00005	0.00135
hsa-miR-216a-3p	-3.33	0.00496	TargetScan Human	Moderate (predicted)	SLFN5	1.025	0.00005	0.00135
hsa-miR-216a-3p	-3.33	0.00496	TargetScan Human	High (predicted)	VANGL2	1.11	0.0005	0.00809
hsa-miR-216a-3p	-3.33	0.00496	TargetScan Human	High (predicted)	WNT3A	1.43	0.00115	0.0147
hsa-miR-216a-3p	-3.33	0.00496	TargetScan Human	High (predicted)	ZNF704	1.034	0.00005	0.00135
hsa-miR-138-5p	-1.386	0.000372	TargetScan Human	High (predicted)	ADGRL1	1.078	0.0024	0.0239
hsa-miR-138-5p	-1.386	0.000372	TargetScan Human	Moderate (predicted)	CDT1	1.085	0.00015	0.0032
hsa-miR-138-5p	-1.386	0.000372	TargetScan Human	High (predicted),Moderate (predicted)	CLDN19	1.593	0.00005	0.00135
hsa-miR-138-5p	-1.386	0.000372	TargetScan Human	Moderate (predicted)	COL14A1	1.105	0.00005	0.00135
hsa-miR-138-5p	-1.386	0.000372	TargetScan Human	High (predicted)	DCHS1	1.164	0.00005	0.00135
hsa-miR-138-5p	-1.386	0.000372	TargetScan Human	High (predicted)	DDX11	1.09	0.00225	0.0229
hsa-miR-138-5p	-1.386	0.000372	TargetScan Human	High (predicted)	FAM83D	1.048	0.00115	0.0147
hsa-miR-138-5p	-1.386	0.000372	TargetScan Human	High (predicted)	FRMD4A	1.036	0.00005	0.00135
hsa-miR-138-5p	-1.386	0.000372	TargetScan Human	High (predicted)	GJC1	1.112	0.00005	0.00135
hsa-miR-138-5p	-1.386	0.000372	TargetScan Human	Moderate (predicted)	HEYL	1.188	0.00005	0.00135
hsa-miR-138-5p	-1.386	0.000372	TargetScan Human	High (predicted)	IGF2BP1	1.108	0.00005	0.00135
hsa-miR-138-5p	-1.386	0.000372	TargetScan Human	High (predicted)	MOCS1	1.087	0.00005	0.00135
hsa-miR-138-5p	-1.386	0.000372	TargetScan Human	High (predicted)	NOTUM	1.852	0.00005	0.00135
hsa-miR-138-5p	-1.386	0.000372	TargetScan Human	High (predicted)	RASL12	1.52	0.00005	0.00135
hsa-miR-138-5p	-1.386	0.000372	TargetScan Human	High (predicted)	SLC16A2	1.083	0.00005	0.00135
hsa-miR-138-5p	-1.386	0.000372	TargetScan Human	High (predicted)	SLC2A10	1.354	0.00005	0.00135
hsa-miR-138-5p	-1.386	0.000372	TargetScan Human	High (predicted)	SOX4	1.172	0.00005	0.00135
hsa-miR-138-5p	-1.386	0.000372	TargetScan Human	High (predicted)	TBL1X	1.002	0.00005	0.00135
hsa-miR-138-5p	-1.386	0.000372	TargetScan Human	Moderate (predicted)	VANGL2	1.11	0.0005	0.00809

hsa-miR-138-5p	-1.386	0.000372	TargetScan Human	Moderate (predicted)	VIT	1.597	0.0007	0.0103
hsa-miR-138-5p	-1.386	0.000372	TargetScan Human	Moderate (predicted)	ZDHH8	1.075	0.00005	0.00135
hsa-miR-138-5p	-1.386	0.000372	TargetScan Human	High (predicted)	ZNF704	1.034	0.00005	0.00135
hsa-miR-203b-3p	-3.721	0.00144	TargetScan Human	Moderate (predicted)	CRISPLD1	1.233	0.00005	0.00135
hsa-miR-203b-3p	-3.721	0.00144	TargetScan Human	Moderate (predicted)	IL2RB	1.481	0.00005	0.00135
hsa-miR-203b-3p	-3.721	0.00144	TargetScan Human	Moderate (predicted)	SLC13A3	1.011	0.0004	0.00687
hsa-miR-2114-5p	-1.809	0.00923	TargetScan Human	Moderate (predicted)	GPC4	1.199	0.00005	0.00135
hsa-miR-2114-5p	-1.809	0.00923	TargetScan Human	Moderate (predicted)	HUNK	1.452	0.00005	0.00135
hsa-miR-2114-5p	-1.809	0.00923	TargetScan Human	Moderate (predicted)	RASL12	1.52	0.00005	0.00135
hsa-miR-2114-5p	-1.809	0.00923	TargetScan Human	Moderate (predicted)	TCF7L1	1.261	0.0011	0.0143
hsa-miR-3130-3p	-3.751	0.0124	TargetScan Human	Moderate (predicted)	AGRN	1.263	0.00005	0.00135
hsa-miR-3130-3p	-3.751	0.0124	TargetScan Human	Moderate (predicted)	B3GNT7	1.191	0.00005	0.00135
hsa-miR-3130-3p	-3.751	0.0124	TargetScan Human	Moderate (predicted)	ELN	1.228	0.00005	0.00135
hsa-miR-3130-3p	-3.751	0.0124	TargetScan Human	Moderate (predicted)	FLNB	1.531	0.00005	0.00135
hsa-miR-3130-3p	-3.751	0.0124	TargetScan Human	Moderate (predicted)	FZD5	1.003	0.00005	0.00135
hsa-miR-3130-3p	-3.751	0.0124	TargetScan Human	Moderate (predicted)	IL27RA	1.216	0.00615	0.0451
hsa-miR-3130-3p	-3.751	0.0124	TargetScan Human	High (predicted)	LPAR2	1.252	0.00525	0.0408
hsa-miR-3130-3p	-3.751	0.0124	TargetScan Human	Moderate (predicted)	MOCS1	1.087	0.00005	0.00135
hsa-miR-3130-3p	-3.751	0.0124	TargetScan Human	Moderate (predicted)	RGMA	1.08	0.00315	0.0287
hsa-miR-3130-3p	-3.751	0.0124	TargetScan Human	Moderate (predicted)	RIPK4	1.207	0.00005	0.00135
hsa-miR-3130-3p	-3.751	0.0124	TargetScan Human	Moderate (predicted)	SDK1	1.74	0.00005	0.00135
hsa-miR-3130-3p	-3.751	0.0124	TargetScan Human	Moderate (predicted)	SP6	1.047	0.00005	0.00135
hsa-miR-3130-3p	-3.751	0.0124	TargetScan Human	Moderate (predicted)	TCF7L2	1.216	0.00005	0.00135
hsa-miR-3158-3p	-1.259	0.0204	TargetScan Human	Moderate (predicted)	BARX2	1.212	0.0008	0.0113
hsa-miR-3158-3p	-1.259	0.0204	TargetScan Human	Moderate (predicted)	C1orf106	1.643	0.00005	0.00135

hsa-miR-3158-3p	-1.259	0.0204	TargetScan Human	Moderate (predicted)	FLNB	1.531	0.00005	0.00135
hsa-miR-3158-3p	-1.259	0.0204	TargetScan Human	Moderate (predicted)	FN1	2.283	0.00005	0.00135
hsa-miR-3158-3p	-1.259	0.0204	TargetScan Human	Moderate (predicted)	ISM2	1.544	0.00005	0.00135
hsa-miR-3158-3p	-1.259	0.0204	TargetScan Human	Moderate (predicted)	MKL1	1.038	0.00125	0.0155
hsa-miR-3158-3p	-1.259	0.0204	TargetScan Human	Moderate (predicted)	NOTUM	1.852	0.00005	0.00135
hsa-miR-3158-3p	-1.259	0.0204	TargetScan Human	Moderate (predicted)	RGMA	1.08	0.00315	0.0287
hsa-miR-3158-3p	-1.259	0.0204	TargetScan Human	High (predicted)	ZNF704	1.034	0.00005	0.00135
hsa-miR-4685-3p	-1.453	0.0418	TargetScan Human	High (predicted)	ADGRL1	1.078	0.0024	0.0239
hsa-miR-4685-3p	-1.453	0.0418	TargetScan Human	Moderate (predicted)	ASCL2	1.456	0.00005	0.00135
hsa-miR-4685-3p	-1.453	0.0418	TargetScan Human	High (predicted)	B3GNT7	1.191	0.00005	0.00135
hsa-miR-4685-3p	-1.453	0.0418	TargetScan Human	High (predicted)	BARX2	1.212	0.0008	0.0113
hsa-miR-4685-3p	-1.453	0.0418	TargetScan Human	Moderate (predicted)	CD22	1.429	0.00035	0.00614
hsa-miR-4685-3p	-1.453	0.0418	TargetScan Human	Moderate (predicted)	COL17A1	1.752	0.00005	0.00135
hsa-miR-4685-3p	-1.453	0.0418	TargetScan Human	High (predicted)	CSPG4	1.539	0.00005	0.00135
hsa-miR-4685-3p	-1.453	0.0418	TargetScan Human	High (predicted)	EGR1	1.056	0.00175	0.0194
hsa-miR-4685-3p	-1.453	0.0418	TargetScan Human	High (predicted)	HUNK	1.452	0.00005	0.00135
hsa-miR-4685-3p	-1.453	0.0418	TargetScan Human	Moderate (predicted)	IGF2BP1	1.108	0.00005	0.00135
hsa-miR-4685-3p	-1.453	0.0418	TargetScan Human	Moderate (predicted)	LRP1	1.085	0.00005	0.00135
hsa-miR-4685-3p	-1.453	0.0418	TargetScan Human	Moderate (predicted)	MEGF8	1.146	0.00005	0.00135
hsa-miR-4685-3p	-1.453	0.0418	TargetScan Human	Moderate (predicted)	MKI67	1.224	0.00005	0.00135
hsa-miR-4685-3p	-1.453	0.0418	TargetScan Human	Moderate (predicted)	MKL1	1.038	0.00125	0.0155
hsa-miR-4685-3p	-1.453	0.0418	TargetScan Human	Moderate (predicted)	NFATC1	1.136	0.00265	0.0255
hsa-miR-4685-3p	-1.453	0.0418	TargetScan Human	Moderate (predicted)	NRP2	1.296	0.00005	0.00135
hsa-miR-4685-3p	-1.453	0.0418	TargetScan Human	High (predicted)	SP6	1.047	0.00005	0.00135
hsa-miR-4685-3p	-1.453	0.0418	TargetScan Human	Moderate (predicted)	VIT	1.597	0.0007	0.0103

hsa-miR-3914	-3.179	0.0142	TargetScan Human	Moderate (predicted)	AFAP1	1.354	0.00005	0.00135
hsa-miR-3914	-3.179	0.0142	TargetScan Human	Moderate (predicted)	EXTL3	1.369	0.00005	0.00135
hsa-miR-3914	-3.179	0.0142	TargetScan Human	Moderate (predicted)	FOXK1	1.003	0.00005	0.00135
hsa-miR-3914	-3.179	0.0142	TargetScan Human	Moderate (predicted)	GPC4	1.199	0.00005	0.00135
hsa-miR-3914	-3.179	0.0142	TargetScan Human	Moderate (predicted)	KIAA1217	1.137	0.00005	0.00135
hsa-miR-3914	-3.179	0.0142	TargetScan Human	Moderate (predicted)	LAMA5	1.631	0.00005	0.00135
hsa-miR-3914	-3.179	0.0142	TargetScan Human	Moderate (predicted)	MOCS1	1.087	0.00005	0.00135
hsa-miR-3914	-3.179	0.0142	TargetScan Human	Moderate (predicted)	NOG	1.635	0.00005	0.00135
hsa-miR-3914	-3.179	0.0142	TargetScan Human	Moderate (predicted)	SFRP1	1.8	0.00005	0.00135
hsa-miR-3914	-3.179	0.0142	TargetScan Human	Moderate (predicted)	SLC2A10	1.354	0.00005	0.00135
hsa-miR-4732-3p	-1.1	0.0356	TargetScan Human	Moderate (predicted)	ANKRD33B	1.036	0.0001	0.00239
hsa-miR-4732-3p	-1.1	0.0356	TargetScan Human	Moderate (predicted)	ATP7B	1.145	0.00005	0.00135
hsa-miR-4732-3p	-1.1	0.0356	TargetScan Human	Moderate (predicted)	CLDN19	1.593	0.00005	0.00135
hsa-miR-4732-3p	-1.1	0.0356	TargetScan Human	Moderate (predicted)	DOCK5	1.003	0.00005	0.00135
hsa-miR-4732-3p	-1.1	0.0356	TargetScan Human	Moderate (predicted)	FLNB	1.531	0.00005	0.00135
hsa-miR-4732-3p	-1.1	0.0356	TargetScan Human	Moderate (predicted)	HUNK	1.452	0.00005	0.00135
hsa-miR-4732-3p	-1.1	0.0356	TargetScan Human	Moderate (predicted)	IL2RB	1.481	0.00005	0.00135
hsa-miR-4732-3p	-1.1	0.0356	TargetScan Human	Moderate (predicted)	KIRREL	1.061	0.00005	0.00135
hsa-miR-4732-3p	-1.1	0.0356	TargetScan Human	Moderate (predicted)	MEGF8	1.146	0.00005	0.00135
hsa-miR-4732-3p	-1.1	0.0356	TargetScan Human	Moderate (predicted)	MKL1	1.038	0.00125	0.0155
hsa-miR-4732-3p	-1.1	0.0356	TargetScan Human	Moderate (predicted)	NUP210	1.213	0.00005	0.00135
hsa-miR-4732-3p	-1.1	0.0356	TargetScan Human	Moderate (predicted)	PDE4A	1.004	0.00145	0.0171
hsa-miR-4732-3p	-1.1	0.0356	TargetScan Human	Moderate (predicted)	SLC2A10	1.354	0.00005	0.00135
hsa-miR-4732-3p	-1.1	0.0356	TargetScan Human	Moderate (predicted)	SLFN5	1.025	0.00005	0.00135
hsa-miR-4732-3p	-1.1	0.0356	TargetScan Human	Moderate (predicted)	UBASH3B	1.067	0.00005	0.00135

hsa-miR-4732-3p	-1.1	0.0356	TargetScan Human	Moderate (predicted)	VAV2	1.124	0.00005	0.00135
hsa-miR-4732-3p	-1.1	0.0356	TargetScan Human	Moderate (predicted)	ZDHHC8	1.075	0.00005	0.00135
hsa-miR-4763-5p	1.643	0.0361	TargetScan Human	Moderate (predicted)	ERAP2	-1.529	0.00005	0.00135
hsa-miR-4763-5p	1.643	0.0361	TargetScan Human	High (predicted)	HTRA1	-1.449	0.00005	0.00135
hsa-miR-4763-5p	1.643	0.0361	TargetScan Human	Moderate (predicted)	LUM	-1.384	0.00005	0.00135
hsa-miR-4763-5p	1.643	0.0361	TargetScan Human	High (predicted)	RBM24	-1.587	0.0002	0.00401
hsa-miR-4763-5p	1.643	0.0361	TargetScan Human	Moderate (predicted)	SLC26A7	-1.219	0.00005	0.00135
hsa-miR-767-3p	2.422	0.00882	TargetScan Human	Moderate (predicted)	ST18	-1.397	0.00005	0.00135
hsa-miR-95-3p	-1.372	0.0278	TargetScan Human	Moderate (predicted)	COL4A2	1.415	0.00005	0.00135
hsa-miR-95-3p	-1.372	0.0278	TargetScan Human	Moderate (predicted)	IL2RB	1.481	0.00005	0.00135
hsa-miR-95-3p	-1.372	0.0278	TargetScan Human	High (predicted)	LAMC3	1.35	0.00005	0.00135
hsa-miR-95-3p	-1.372	0.0278	TargetScan Human	Moderate (predicted)	NUP210	1.213	0.00005	0.00135
hsa-miR-95-3p	-1.372	0.0278	TargetScan Human	Moderate (predicted)	PDE4A	1.004	0.00145	0.0171
hsa-miR-95-3p	-1.372	0.0278	TargetScan Human	High (predicted)	PLVAP	1.166	0.00005	0.00135
hsa-miR-95-3p	-1.372	0.0278	TargetScan Human	Moderate (predicted)	PROSER2	1.047	0.00635	0.046

Table S6. Network analysis shows interactions between mRNA-miRNA pairs

Top Diseases and Functions	Score	Focus Molecules
Cellular Development and Function, Organ Morphology, Organismal Development	77	32
Cancer, Hematological Disease, Hereditary Disorder	52	24
Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry	35	18
Embryonic Development, Organ Development, Organ Morphology	21	12
Cellular Movement, Immune Cell Trafficking, Cell-To-Cell Signaling and Interaction	19	11
Cancer, Cellular Development, Cellular Growth and Proliferation	11	7