SUPPLEMENTAL MATERIAL

Table S1. miRNA primer sets for qRT-PCR

miRNA	**Forward primer sequence (5' to 3')**	**Reverse primer sequence (5' to 3')**
hsa-miR-4433	GGAGCCAGTTGGACAG	GGTCCAGTTTTTTTTTTTTTTTATGTC
hsa-miR-93-5p	GCAAAGTGCTGTTCGTG	GTCCAGTTTTTTTTTTTTTTTCTACCT
hsa-miR-339-5p	CAGTCCCTGTCCTCCAG	GGTCCAGTTTTTTTTTTTTTTTCGT
hsa-miR-3651-5p	CATAGCCCGGTCGCT	GGTCCAGTTTTTTTTTTTTTTTCATGT
hsa-miR-27a	CAGTTCACAGTGGCTAAGTTC	CAGTTTTTTTTTTTTTTTGCGGAA
hsa-miR-27b	CAGTTCACAGTGGCTAAGTTC	TCCAGTTTTTTTTTTTTTTTGCAGA
hsa-miR-15a	CAGTAGCAGCACATAATGGT	GGTCCAGTTTTTTTTTTTTTTTCAC
hsa-miR-125a	CCCTGAGACCCTTTAACCT	GGTCCAGTTTTTTTTTTTTTTTCAC
hsa-miR-4454	GCAGGGATCCGAGTCAC	GGTCCAGTTTTTTTTTTTTTTTGGT
hsa-miR-132-3p	GCAGTAACAGTCTACAGCCA	GTCCAGTTTTTTTTTTTTTTTCGAC
hsa-miR-4463	GCAGGAGACTGGGGTG	GTTTTTTTTTTTTTTTGGCCCCAC
hsa-miR-324	AGAACATTCATTGTTGTCGGT	GGTCCAGTTTTTTTTTTTTTTTACAC
hsa-miR-421	GCAGATCAACAGACATTAATTGG	GTTTTTTTTTTTTTTTGCGCCCA
hsa-mir-4492	GGGCTGGGCGC	GTCCAGTTTTTTTTTTTTTTTGGC
hsa-miR-4793	TGCACTGTGAGTTGGCT	GGTCCAGTTTTTTTTTTTTTTTAGC
hsa-miR-4689	CAGTTGAGGAGACATGGTG	GTTTTTTTTTTTTTTTGGCCCCCA
hsa-miR-4449	GGGGCTGCGCGA	TCCAGTTTTTTTTTTTTTTTGCCT
hsa-miR-1290	CGCAGTGGATTTTTGGATCA	GTCCAGTTTTTTTTTTTTTTTCCCT
hsa-miR-4497	TCCGGGACGGCTG	CCAGTTTTTTTTTTTTTTTGCCCA
hsa-miR-4690-5p	GAGCAGGCGAGGCT	GGTCCAGTTTTTTTTTTTTTTTCAG
hsa-miR-4459	GGAGGCGGAGGAGGT	GGTCCAGTTTTTTTTTTTTTTTCTC
hsa-miR-4674	GCTGGGCTCGGGAC	CCAGTTTTTTTTTTTTTTTAGCCG
hsa-miR-1268	GGGCGTGGTGGTG	GGTCCAGTTTTTTTTTTTTTTTCAC
hsa-miR-3178	GCGCGGCCGGA	GGTCCAGTTTTTTTTTTTTTTTCGAT
hsa-miR-297	GCAGATGTATGTGTGCATGTG	AGGTCCAGTTTTTTTTTTTTTTTCAT
hsa-miR-574	GTGAGTGTGTGTGTGTGAG	CAGGTCCAGTTTTTTTTTTTTTTTACA
hsa-miR-4532	CCCGGGGAGCCC	CAGTTTTTTTTTTTTTTTCGCCG
hsa-miR-4440	TCGTGGGGCTTGCT	CAGTTTTTTTTTTTTTTTCAAGCCA
cel-miR-39	GTCACCGGGTGTAAATCAG	CCAGTTTTTTTTTTTTTTTCAAGCTG

Table S2. Gene onthology and KEGG enrichment analyses of the targets of *miR-4532*, *miR-4463*, *miR-1290* and *miR-4793-3p*

MapID	MapTitle	Pvalue	AdjustedPv	x	y	n	N	EnrichDirect	GeneIDs
map04310	Wnt signaling pathway	0.004095503	0.521424353	5	20	61	1069	Over	ENST00000268459 ENST00000272164 ENST00000374806 ENST00000370828 ENST00000374694
map05217	Basal cell carcinoma	0.008067372	0.521424353	3	8	61	1069	Over	ENST00000272164 ENST00000297261 ENST00000374694
map05205	Proteoglycans in cancer	0.013642665	0.521424353	6	36	61	1069	Over	ENST00000559488 ENST00000272164 ENST00000297261 ENST00000264033 ENST00000355622 ENST00000374694
map04340	Hedgehog signaling pathway	0.015921354	0.521424353	3	10	61	1069	Over	ENST00000308595 ENST00000297261 ENST00000255641
map04924	Renin secretion	0.026893481	0.625634513	3	12	61	1069	Over	ENST00000374806 ENST00000245457 ENST00000368680
map04925	Aldosterone synthesis and secretion	0.028655016	0.625634513	2	5	61	1069	Over	ENST00000302909 ENST00000368680
map04724	Glutamatergic synapse	0.049227337	0.80639532	3	15	61	1069	Over	ENST00000308595 ENST00000382159 ENST00000374806
map04921	Oxytocin signaling pathway	0.049245516	0.80639532	4	25	61	1069	Over	ENST00000374806 ENST00000270458 ENST00000263026 ENST00000368680
map00750	Vitamin B6 metabolism	0.057062675	0.830578942	1	1	61	1069	Over	ENST00000225573
map04120	Ubiquitin mediated proteolysis	0.086326741	0.898333442	4	30	61	1069	Over	ENST00000399816 ENST00000492996 ENST00000264033 ENST00000291582
map04550	Signaling pathways regulating pluripotency of stem cells	0.100843751	0.898333442	3	20	61	1069	Over	ENST00000272164 ENST00000231121 ENST00000374694
map04745	Phototransduction - fly	0.110919583	0.898333442	1	2	61	1069	Over	ENST00000308595
map04122	Sulfur relay system	0.110919583	0.898333442	1	2	61	1069	Over	ENST00000452446
map04390	Hippo signaling pathway	0.113045039	0.898333442	3	21	61	1069	Over	ENST00000272164 ENST00000374694 ENST00000590071
map05412	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	0.146390899	0.898333442	2	12	61	1069	Over	ENST00000559488 ENST00000270458
map04392	Hippo signaling pathway - multiple species	0.161747985	0.898333442	1	3	61	1069	Over	ENST00000590071
map03030	DNA replication	0.161747985	0.898333442	1	3	61	1069	Over	ENST00000308418
map04916	Melanogenesis	0.187886844	0.898333442	2	14	61	1069	Over	ENST00000272164 ENST00000374694
map05414	Dilated cardiomyopathy	0.187886844	0.898333442	2	14	61	1069	Over	ENST00000559488 ENST00000270458
map01100	Metabolic pathways	0.201576085	0.898333442	6	177	61	1069	Under	ENST00000225573 ENST00000216484 ENST00000244043 ENST00000339600 ENST00000340941 ENST00000258873
map05410	Hypertrophic cardiomyopathy (HCM)	0.209219076	0.898333442	2	15	61	1069	Over	ENST00000559488 ENST00000270458
map00910	Nitrogen metabolism	0.209715502	0.898333442	1	4	61	1069	Over	ENST00000454127
map00061	Fatty acid biosynthesis	0.209715502	0.898333442	1	4	61	1069	Over	ENST00000258873
map04976	Bile secretion	0.209715502	0.898333442	1	4	61	1069	Over	ENST00000261196
map00600	Sphingolipid metabolism	0.209715502	0.898333442	1	4	61	1069	Over	ENST00000216484
map04146	Peroxisome	0.230795625	0.898333442	2	16	61	1069	Over	ENST00000396385 ENST00000295030
map05032	Morphine addiction	0.230795625	0.898333442	2	16	61	1069	Over	ENST00000308595 ENST00000382159
map04145	Phagosome	0.242197418	0.898333442	3	30	61	1069	Over	ENST00000559488 ENST00000350896 ENST00000355622

map03022	Basal transcription factors	0.254980623	0.898333442	1	5	61	1069	Over	ENST00000607778
map05340	Primary immunodeficiency	0.254980623	0.898333442	1	5	61	1069	Over	ENST00000291582
map00514	Other types of O-glycan biosynthesis	0.254980623	0.898333442	1	5	61	1069	Over	ENST00000389617
map03013	RNA transport	0.274309765	0.898333442	2	18	61	1069	Over	ENST00000542526 ENST00000281950
map04660	T cell receptor signaling pathway	0.274309765	0.898333442	2	18	61	1069	Over	ENST00000374806 ENST00000264033
map04919	Thyroid hormone signaling pathway	0.296085044	0.898333442	2	19	61	1069	Over	ENST00000559488 ENST00000396671
map04978	Mineral absorption	0.2976932	0.898333442	1	6	61	1069	Over	ENST00000233202
map03440	Homologous recombination	0.2976932	0.898333442	1	6	61	1069	Over	ENST00000359321
map05031	Amphetamine addiction	0.2976932	0.898333442	1	6	61	1069	Over	ENST00000374806
map05134	Legionellosis	0.2976932	0.898333442	1	6	61	1069	Over	ENST00000355622
map04918	Thyroid hormone synthesis	0.2976932	0.898333442	1	6	61	1069	Over	ENST00000392256
map04341	Hedgehog signaling pathway - fly	0.2976932	0.898333442	1	6	61	1069	Over	ENST00000255641
map04720	Long-term potentiation	0.2976932	0.898333442	1	6	61	1069	Over	ENST00000374806
map04130	SNARE interactions in vesicular transport	0.2976932	0.898333442	1	6	61	1069	Over	ENST00000367568
map04020	Calcium signaling pathway	0.317778521	0.898333442	2	20	61	1069	Over	ENST00000282018 ENST00000374806
map04144	Endocytosis	0.318859077	0.898333442	4	45	61	1069	Over	ENST00000308595 ENST00000264033 ENST00000356956 ENST00000304032
map04080	Neuroactive ligand-receptor interaction	0.33714738	0.898333442	4	47	61	1069	Over	ENST00000282018 ENST00000590320 ENST00000245457 ENST00000396671
map04142	Lysosome	0.339329413	0.898333442	2	21	61	1069	Over	ENST00000233202 ENST00000356956
map04071	Sphingolipid signaling pathway	0.360683922	0.898333442	2	22	61	1069	Over	ENST00000216484 ENST00000590320
map03420	Nucleotide excision repair	0.376019682	0.898333442	1	8	61	1069	Over	ENST00000607778
map03008	Ribosome biogenesis in eukaryotes	0.376019682	0.898333442	1	8	61	1069	Over	ENST00000341162
map04215	Apoptosis - multiple species	0.376019682	0.898333442	1	8	61	1069	Over	ENST00000318407
map01212	Fatty acid metabolism	0.376019682	0.898333442	1	8	61	1069	Over	ENST00000258873
map05014	Amyotrophic lateral sclerosis (ALS)	0.376019682	0.898333442	1	8	61	1069	Over	ENST00000374806
map05144	Malaria	0.41189414	0.898333442	1	9	61	1069	Over	ENST00000355622
map00590	Arachidonic acid metabolism	0.41189414	0.898333442	1	9	61	1069	Over	ENST00000244043
map04662	B cell receptor signaling pathway	0.41189414	0.898333442	1	9	61	1069	Over	ENST00000374806
map04391	Hippo signaling pathway - fly	0.41189414	0.898333442	1	9	61	1069	Over	ENST00000590071
map04360	Axon guidance	0.422132398	0.898333442	3	32	61	1069	Over	ENST00000297261 ENST00000374806 ENST00000245323
map05200	Pathways in cancer	0.442258613	0.898333442	6	78	61	1069	Over	ENST00000382159 ENST00000272164 ENST00000297261 ENST00000264033 ENST00000245457 ENST00000374694
map03320	PPAR signaling pathway	0.445737967	0.898333442	1	10	61	1069	Over	ENST00000258873
map00071	Fatty acid metabolism	0.445737967	0.898333442	1	10	61	1069	Over	ENST00000258873
map04370	VEGF signaling pathway	0.445737967	0.898333442	1	10	61	1069	Over	ENST00000374806
map04922	Glucagon signaling pathway	0.445737967	0.898333442	1	10	61	1069	Over	ENST00000374806

map00280	Valine, leucine and isoleucine degradation	0.445737967	0.898333442	1	10	61	1069	Over	ENST00000340941
map04750	Inflammatory mediator regulation of TRP channels	0.445737967	0.898333442	1	10	61	1069	Over	ENST00000245457
map04114	Oocyte meiosis	0.445737967	0.898333442	1	10	61	1069	Over	ENST00000374806
map05152	Tuberculosis	0.454617174	0.902346208	3	36	61	1069	Over	ENST00000374806 ENST00000355622 ENST00000256458
map04010	MAPK signaling pathway	0.463909936	0.906592628	3	37	61	1069	Over	ENST00000265080 ENST00000374806 ENST00000270458
map04214	Apoptosis - fly	0.477664298	0.906592628	1	11	61	1069	Over	ENST00000318407
map05166	HTLV-I infection	0.504242149	0.906592628	3	41	61	1069	Over	ENST00000272164 ENST00000374806 ENST00000374694
map04923	Regulation of lipolysis in adipocytes	0.507780062	0.906592628	1	12	61	1069	Over	ENST00000368680
map05140	Leishmaniasis	0.507780062	0.906592628	1	12	61	1069	Over	ENST00000355622
map04920	Adipocytokine signaling pathway	0.507780062	0.906592628	1	12	61	1069	Over	ENST00000258873
map03015	mRNA surveillance pathway	0.536186321	0.906592628	1	13	61	1069	Over	ENST00000238714
map04512	ECM-receptor interaction	0.536186321	0.906592628	1	13	61	1069	Over	ENST00000559488
map04713	Circadian entrainment	0.562978588	0.906592628	1	14	61	1069	Over	ENST00000382159
map05133	Pertussis	0.562978588	0.906592628	1	14	61	1069	Over	ENST00000355622
map04727	GABAergic synapse	0.562978588	0.906592628	1	14	61	1069	Over	ENST00000382159
map05130	Pathogenic Escherichia coli infection	0.562978588	0.906592628	1	14	61	1069	Over	ENST00000355622
map03460	Fanconi anemia pathway	0.562978588	0.906592628	1	14	61	1069	Over	ENST00000294008
map04260	Cardiac muscle contraction	0.562978588	0.906592628	1	14	61	1069	Over	ENST00000270458
map05321	Inflammatory bowel disease (IBD)	0.562978588	0.906592628	1	14	61	1069	Over	ENST00000355622
map04721	Synaptic vesicle cycle	0.588247125	0.906592628	1	15	61	1069	Over	ENST00000263354
map04723	Retrograde endocannabinoid signaling	0.588247125	0.906592628	1	15	61	1069	Over	ENST00000382159
map04620	Toll-like receptor signaling pathway	0.588247125	0.906592628	1	15	61	1069	Over	ENST00000355622
map04726	Serotonergic synapse	0.588247125	0.906592628	1	15	61	1069	Over	ENST00000382159
map05100	Bacterial invasion of epithelial cells	0.612077225	0.921633523	1	16	61	1069	Over	ENST00000264033
map05012	Parkinson's disease	0.612077225	0.921633523	1	16	61	1069	Over	ENST00000339600
map05010	Alzheimer's disease	0.642889256	0.944927224	2	24	61	1069	Over	ENST00000374806 ENST00000339600
map04910	Insulin signaling pathway	0.656299976	0.944927224	2	26	61	1069	Over	ENST00000452015 ENST00000264033
map04022	cGMP-PKG signaling pathway	0.656299976	0.944927224	2	26	61	1069	Over	ENST00000374806 ENST00000368680
map04150	mTOR signaling pathway	0.663613012	0.944927224	2	27	61	1069	Over	ENST00000272164 ENST00000374694
map04380	Osteoclast differentiation	0.663613012	0.944927224	2	27	61	1069	Over	ENST00000559488 ENST00000374806
map04024	cAMP signaling pathway	0.687211007	0.96785942	2	30	61	1069	Over	ENST00000245457 ENST00000368680
map04062	Chemokine signaling pathway	0.695449691	0.96785942	2	31	61	1069	Over	ENST00000308595 ENST00000382159
map05034	Alcoholism	0.716617786	0.96785942	1	35	61	1069	Under	ENST00000382159
map04015	Rap1 signaling pathway	0.716617786	0.96785942	1	35	61	1069	Under	ENST00000559488

map04510	Focal adhesion	0.716659265	0.96785942	1	34	61	1069	Under	ENST00000559488
map04151	PI3K-Akt signaling pathway	1	1	3	60	61	1069	Under	ENST00000559488 ENST00000382159 ENST00000355622
map04066	HIF-1 signaling pathway	1	1	1	17	61	1069	Over	ENST00000355622
map04064	NF-kappa B signaling pathway	1	1	1	17	61	1069	Over	ENST00000355622
map05132	Salmonella infection	1	1	1	17	61	1069	Over	ENST00000355622
map00230	Purine metabolism	1	1	1	20	61	1069	Under	ENST00000368680
map04725	Cholinergic synapse	1	1	1	18	61	1069	Under	ENST00000382159
map04611	Platelet activation	1	1	1	23	61	1069	Under	ENST00000559488
map05142	Chagas disease (American trypanosomiasis)	1	1	1	20	61	1069	Under	ENST00000355622
map04270	Vascular smooth muscle contraction	1	1	1	18	61	1069	Under	ENST00000368680
map05145	Toxoplasmosis	1	1	1	31	61	1069	Under	ENST00000355622
map04014	Ras signaling pathway	1	1	2	42	61	1069	Under	ENST00000265080 ENST00000382159
map04931	Insulin resistance	1	1	1	18	61	1069	Under	ENST00000452015
map05206	MicroRNAs in cancer	1	1	1	23	61	1069	Under	ENST00000559488
map04932	Non-alcoholic fatty liver disease (NAFLD)	1	1	1	26	61	1069	Under	ENST00000339600
map05016	Huntington's disease	1	1	1	29	61	1069	Under	ENST00000339600
map04722	Neurotrophin signaling pathway	1	1	1	20	61	1069	Under	ENST00000256458
map04640	Hematopoietic cell lineage	1	1	1	18	61	1069	Under	ENST00000559488
map05162	Measles	1	1	1	18	61	1069	Under	ENST00000355622
map05323	Rheumatoid arthritis	1	1	1	25	61	1069	Under	ENST00000355622
map04530	Tight junction	1	1	1	31	61	1069	Under	ENST00000216181
map04740	Olfactory transduction	1	1	3	55	61	1069	Under	ENST00000308595 ENST00000382159 ENST00000315453
map04650	Natural killer cell mediated cytotoxicity	1	1	1	20	61	1069	Under	ENST00000374806
map04012	ErbB signaling pathway	1	1	1	20	61	1069	Under	ENST00000264033
map05164	Influenza A	1	1	1	26	61	1069	Under	ENST00000355622
map05161	Hepatitis B	1	1	1	21	61	1069	Under	ENST00000355622
map05146	Amoebiasis	1	1	1	18	61	1069	Under	ENST00000355622
map05202	Transcriptional misregulation in cancer	1	1	1	23	61	1069	Under	ENST00000296921
map04810	Regulation of actin cytoskeleton	1	1	2	41	61	1069	Under	ENST00000559488 ENST00000382108
map01120	Microbial metabolism in diverse environments	1	1	1	26	61	1069	Under	ENST00000225573
map04152	AMPK signaling pathway	1	1	1	20	61	1069	Under	ENST00000263026
map04261	Adrenergic signaling in cardiomyocytes	1	1	1	23	61	1069	Under	ENST00000270458
map00190	Oxidative phosphorylation	1	1	1	22	61	1069	Under	ENST00000339600
map05220	Chronic myeloid leukemia	1	1	1	19	61	1069	Under	ENST00000264033
map04728	Dopaminergic synapse	1	1	1	19	61	1069	Under	ENST00000382159