

Table S2: Summary of miRNA Targets Binding sites analysis along with query and reference sequences. miRNAs that are expressed at relatively low level as compared to miRNA from opposite/guided standard : marked with star (*).

miRNA	Alignment	Gene Symbol	Energy
hsa-miR-432*	Query: 3' UCUGUAC---CUCCUCGGUAGGuc 5' :: Ref: 5' AGATGGGACTGAGGATCCATCCtt 3'	PALMD	-22.84
	Query: 3' ucUGUACCUCCUCGG-UAGGUC 5' Ref: 5' ctAAATGGCGCAGCCAATCCAG 3'	RAPGEF5	-22.56
	Query: 3' UCUGUAC-CUCC---UCGGUAGGUC 5' : Ref: 5' AGACAAGAGAGGGCAAGTCAGCCAG 3'	LOC90139	-24.93
	Query: 3' uCUGUACCUCCUCGGUAGGUC 5' : Ref: 5' gGCCATGGGGCAGCC-TCCAG 3'	MYLK	-28.26
	Query: 3' uCUGUAC-CUC-----CUC-GGUAGGUC 5' Ref: 5' tGAC-TGAGAGCAGCTCCGAGTCCATCCAG 3'	CETP	-24.84
	Query: 3' UCUGUACCUCCUCGGUAGGUC 5' : Ref: 5' AGGCCT-GAGCTGCCATCCAG 3'	TIE1	-25.91
	Query: 3' ucuGUACCUCCUCGGUAGGUC 5' Ref: 5' cttCATCCACGAACCATCCAG 3'	GLCE	-17.77
	Query: 3' uCUGUACCU-CCUC-GGUAGGUC 5' Ref: 5' cGACACGGACGGAGCCCATGCAG 3'	VWF	-27.82
	Query: 3' UCUGUACCUCC--UCG--GUAGGUC 5' Ref: 5' AGACATGGAGGTCAGCCACACCCAG 3'	ROBO4	-34.25
	Query: 3' uCUGUACCUC---C---UCGGUAGGuc 5' Ref: 5' gGACAGGGAGACAGCACAGCCATCCct 3'	KIAA1274	-23.2
	Query: 3' UCUGUACCUCCUCGGUAGGUc 5' :: Ref: 5' AGGTATGAATGAGCCAGCCAt 3'	PDE2A	-20.07
hsa-miR-132	Query: 3' gCUGGUACCGACAUCUGACAAu 5' : Ref: 5' tGATCTT---TGTAGACTGTTc 3'	IL1RL1	-22.12
	Query: 3' GCUGGUACCGACAUCUGACAAU 5' : Ref: 5' CGACCGT--CTTCAGACTGTTA 3'	CXorf36	-24.85
	Query: 3' gCUGGU-ACCGAC-AUCUGACAAu 5' : Ref: 5' gGTCCACTGGAGGATGGACTGTTc 3'	LOC90139	-21.72
	Query: 3' GCUGGUACCGACA-UCUGACAau 5' : : Ref: 5' CGTCCGTGTCTGTCTCAGGCTGTct 3'	SLC29A1	-25.41
	Query: 3' gcugGUACCGACA---UCUGACAAu 5' : Ref: 5' cccaCGTGGCTATGACAGACTGTTt 3'	IPO11	-22.5
	Query: 3' gcUGGUA-CCGAC--AUCUGACAAU 5' : : : Ref: 5' gcACCGTACGTTGAATGGACTGTTA 3'	LOC116441	-22.1
hsa-miR-188	Query: 3' uGGGAG-GUGGUACGUUCCCUAc 5' Ref: 5' cCCCTCACAC--TGCAAGGGAtt 3'	CDH5	-29.85
	Query: 3' uGGGAGG--UGGUA-CGUUCCCUAC 5' : Ref: 5' gCTCCCCAGACCCTGGCATGGGATG 3'	EGFL7	-25.88
	Query: 3' ugGGAGGUGGUACGUUCCCUAc 5' : Ref: 5' tgCCTCCATCAT-AAAGGGAgg 3'	CXorf36	-28.93
	Query: 3' ugggagUGGU-AC--GUUCCCUAc 5' : Ref: 5' gaagaaCACCAGTGTTTAAGGGATG 3'	Hs.382865	-23.85
	Query: 3' UGGGA-GUGGUAC----GUUCCCUac 5' : : Ref: 5' ACCCTATCACCATGTTCTTAAGGGggg 3'	RNASE1	-31.37
	Query: 3' uGGGAGGUGGUACG-UUCCCUAc 5' : : Ref: 5' cCCCCCACTCTGCAGAGGGAag 3'	SEMA6B	-27.6
	Query: 3' UGGGAGGUGGUACGUUCCCUAc 5' ::: : Ref: 5' ACCCTCCGTTTTCCGAGGGAag 3'	ESAM	-29.83
	Query: 3' UGGGAGGUGGU--ACGUUCCCUAc 5' : : Ref: 5' ACCATTCTCCAGCTTCAGGGGATa 3'	RGS3	-25.03
	Query: 3' uggGAGGUGGUAC-GUUCCCUAc 5' : Ref: 5' cgtCTCTCCCATGCCAAGGGCTc 3'	ROBO4	-25.17
	Query: 3' ugGGAGGUGGUACGUUCCCUAc 5' : Ref: 5' ggCCTCTACCA--CAAGGGCTc 3'	HYAL2	-26.55

hsa-miR-331	Query: 3' aaGAUCCUAUCCGGGUCCCCg 5' : :	TXNRD2	-30.36
	Ref: 5' caCAGGGAT-GGCTCAGGGGa 3'		
	Query: 3' aaGAUCCU-AUCCGGGUCCCCg 5' 	LOC90139	-29.41
	Ref: 5' ggCCAGGAGAAGGGCCAGGGGa 3'		
	Query: 3' aagauccuaUCCGGGUCCCCG 5' 	LOC90139	-24.97
	Ref: 5' aagtcatcaAAGCCCAGGGGC 3'		
	Query: 3' aaGAUCC---UAUCC-GGGUCCCCG 5' 	FLJ22746	-32.2
	Ref: 5' aaCCAGGGCAAGAGGTCCCAGGGGC 3'		
	Query: 3' AAGA-UCCUAUC-CG---GGUCCCCG 5' :	BCL6B	-26.36
	Ref: 5' TTCTGAGGAGAGAGCTAGCTAGGGGC 3'		
hsa-miR-296	Query: 3' AAGAUCCUAUCCGGGUCCCCg 5' :	SEMA6B	-28.13
	Ref: 5' TTCCA-GA-AGGCCCGGGGt 3'		
	Query: 3' aaGAUCCUAUCCG--GGUCCCCG 5' 	ESAM	-24.11
	Ref: 5' ccCTTG---AGGCCTCCAGGGGC 3'		
	Query: 3' aagaUCCUAUC-CG--GGUCCCCg 5' 	KIAA1274	-24.36
	Ref: 5' ggggAGGAAAGAGCTTCCAGGGGg 3'		
	Query: 3' aagauccuaUCCGGGUCCCCG 5' 	TBX1	-23.47
	Ref: 5' cgttccccAGCCCCAGGGGC 3'		
	Query: 3' aagaUCCUA-UCCG---GGUCCCCG 5' :	ICAM2	-30.88
	Ref: 5' gaagAGGGTGAGGCTGTCCAGGGGC 3'		
hsa-miR-512-5p	Query: 3' UGU--CCUAACUCCCCCGGGa 5' 	ARHGEF15	-32.3
	Ref: 5' ACAGTGGCTGGCAGGGGGGCCCa 3'		
	Query: 3' uGUCCUAA CUCC-CCCCGGGa 5' 	CDH5	-28.27
	Ref: 5' tCAAGAGGAGGAAGGGGCCCc 3'		
	Query: 3' uGUCCUAA CUCCCCCGGGa 5' 	APLN	-28.27
	Ref: 5' gCAGGACTGA--AGGGGCCCc 3'		
	Query: 3' uguccuAACUCCCCCGGGA 5' 	RNASE1	-30.96
	Ref: 5' atgttcTTAAGGGGGGCCCT 3'		
	Query: 3' uguccuaacUCCCCCGGGa 5' 	Hs.483538	-28.27
	Ref: 5' -----AGGGGGGCCCc 3'		
	Query: 3' uguccuaaCUC-CCCCCGGGa 5' 	SEMA6B	-29.29
	Ref: 5' caccgcgGAGTGGGGGCCCc 3'		
	Query: 3' uGUC-CUAACUCCC-CCCCGGGa 5' :	SEMA6B	-31.19
hsa-miR-512-5p	Ref: 5' gCGGCGAAGGTGGGTGGGGCCCC 3'		
	Query: 3' uGUCCUAA CUCCC-----CC-CGGGa 5' :	ESAM	-31.9
	Ref: 5' tCGGGAGTGAGGGACCCTGGCGGCCG 3'		
	Query: 3' uGUCCUAA-----CUCCC--CCCCGGGa 5' 	ROBO4	-33.53
	Ref: 5' gCAGGACTGGAGGAGGGGTGGGGCCCa 3'		
	Query: 3' UGUCC--UAACUCCC---CCCCGGGa 5' : :	CGNL1	-26.72
	Ref: 5' ATAGGCAGATGTGGGTATGGGGCCCa 3'		
	Query: 3' ugUC-CUAACUCCC---CCCCGGGa 5' :	CGNL1	-31.44
	Ref: 5' ggAGTGGTTGAGGTCTGGGGGCCag 3'		
	Query: 3' cuUUCACGGGA----GUUCCGACUCac 5' : : :	APLN	-31.98
hsa-miR-512-5p	Ref: 5' tgAAGTGCCTTTTCCCGAGGCTGGGgc 3'		
	Query: 3' cUUUCACGGGAGUUCCGACUCac 5' : :	RAPGEF5	-25.2
	Ref: 5' cAGACTTCCCTCACGGCTGGGct 3'		
	Query: 3' CUU-UCACG--GGAGUUCGACUCAC 5' : :	BCL6B	-29.43
	Ref: 5' GAACAGGTTGCCTCTTGGCTGGGTG 3'		
	Query: 3' CUUUC---ACGGGAGUCCGACUCac 5' :	SLCO2A1	-24.81
	Ref: 5' GAAGGCACTGCCTTCA--GCTGAGTt 3'		
	Query: 3' cUUUCACGGGAGUUCCGACUCAC 5' : : :	LOC400451	-27.64
	Ref: 5' cACGGTGACTCAGGCCTGAGTG 3'		
	Query: 3' CUUUCACGGGAGUUCCGACUCac 5' : :: :	KDR	-25.09
hsa-miR-512-5p	Ref: 5' GGAAGGATTTGCAGGGCTGAGTc 3'		
	Query: 3' cUUUCACGGGAGUUCCGACUCac 5' : :	ROBO4	-23.84

	Ref: 5' cAAAGGG--TTCAAGGCTGGGTc 3'		
	Query: 3' cuuucaCGGGAGUCCGACUCac 5' :	FLJ46061	-28.14
hsa-miR-503	Ref: 5' gccatcGCCCTGGAGGCTGAGca 3'		
	Query: 3' GACGUCUUGACAAGGGCGACGAu 5' :	APLN	-25.74
	Ref: 5' CTGCTG--CTGCTGCTGCTGCTg 3'		
	Query: 3' GAC-GUCUU---GACAAGGGCGACGAu 5' :	LOC90139	-24.89
	Ref: 5' CAGCCAGAAGCTCTGTGCCTGCTGCaa 3'		
	Query: 3' GACGUCUUGACAAGGGCGACGAu 5' :	ESAM	-24.81
	Ref: 5' CTGC-GGCCTCTTCCCGCGGcgt 3'		
	Query: 3' GACGUCUUGACAAGG-GCGACgau 5' :	MGC20262	-24.5
	Ref: 5' CTGCGCACCTGTACCACGCTGagc 3'		
	Query: 3' gACGUCUUG---ACAAGGGCGACGAu 5' : :	VWF	-30.72
	Ref: 5' gTGCAGGACCAGTGCTCCTGCTGCTc 3'		
	Query: 3' GACGUCUUGA-----CAAGGGCGACGAu 5' :	VWF	-29.88
	Ref: 5' CTGCAG--CTGCATGGGTGCCTGCTGCTg 3'		
	Query: 3' gaCGUCUUGACAAGGGCGACGAu 5' :	ROBO4	-25.42
	Ref: 5' gaGCAGCCCTG--CCTGCTGCTc 3'		
	Query: 3' gACGUCUUGAC--AAGG-GCGACGAu 5' :	ZDHC14	-23.3
	Ref: 5' gTGTGGATCTGCATGCCACGCTGCcg 3'		
hsa-miR-518e	Query: 3' uGUGAGACUUC-----CUUCGCGAAA 5' : :	LAMP3	-27.24
	Ref: 5' ACTCTCTGGAGGGAGACTGAGGGGCTTT 3'		
	Query: 3' uGUGAGACUUC-CCUUCGCGAAa 5' :	NOTCH4	-26.27
	Ref: 5' cCACTGTGGGGATGAAGCGCTTc 3'		
	Query: 3' uguGAGA-CUUCUU-UCGCGAAa 5' :	BCL6B	-26.71
	Ref: 5' ttCTCTAGAAAGGGATGCTGCTTg 3'		
hsa-miR-520a*	Query: 3' uGUGAGACUUCUUUCGCGAAA 5' : :	GLCE	-23.43
	Ref: 5' cCCTTCTGAAGGGTAGTCCTTT 3'		
	Query: 3' uGUGAGAC--UUCCUUCGCGaaa 5' :	SEMA6B	-29.7
	Ref: 5' cCACTCTGCAGAGGGAAGCGggga 3'		
	Query: 3' uCUUUCAUG---AAGGGA-GACCUC 5' :	EGFL7	-31.27
	Ref: 5' gGAAGGTACGAGCTCCCTGCTGGAG 3'		
	Query: 3' ucuuuCAUGAAG--GGAGACCUc 5' :	FLJ10241	-24.75
	Ref: 5' tggttGTGCTTCTGCCTCTGGAc 3'		
	Query: 3' UCUUUCAUGAAG-GGAGACCUC 5' :	APLN	-21.67
	Ref: 5' AGATTGGTCTGCTTCTCTGGAG 3'		
hsa-miR-345	Query: 3' uCUUUC-----UGAAGGAGACCUC 5' 	ABCA4	-20.32
	Ref: 5' tGAAAGTCATGACCTCCCTCTGCac 3'		
	Query: 3' UCUUUC AUGAAGGGAGACCuc 5' :	HSD17B2	-20.14
	Ref: 5' AGCAAGGACTTCTCTCCGGtg 3'		
	Query: 3' UCUUUC AUGAAG-GGAGACCUC 5' : :	SHANK3	-21.7
	Ref: 5' AGAAGCCGCTGCAGCTCTGGAG 3'		
	Query: 3' UCUUUC AUGAAG-GGAGACCUC 5' 	ESAM	-18.46
	Ref: 5' AGAAA-T-CTGCGCCTCTGGAt 3'		
	Query: 3' UCUUUC AUGAAGGA-GACCUC 5' 	CGNL1	-20.1
	Ref: 5' AAAAATTCCTCCCCTCCTGGAG 3'		
hsa-miR-345	Query: 3' CG-GGAC--C-UGAUCC-UCAGUCGU 5' :	FLJ10241	-24.51
	Ref: 5' GCTCCTGAAGCACCAAGCGGTCAGCA 3'		
	Query: 3' CGGGACCUGAUCCUCAGUCGU 5' : :	RAPGEF5	-26.13
	Ref: 5' GCCCT-GCTTAGAAGTTAGCA 3'		
	Query: 3' CGGGACCUGAU-CCUCAGUCGU 5' : : :	MYLK2	-26.11
	Ref: 5' GCCTCAGATGATGGGTCAGCA 3'		
	Query: 3' cGGGAC-CUGA-UCCUCAGUCGU 5' 	ADCY4	-25.54
	Ref: 5' tCCAAGTGACTGAGGAGACAGCA 3'		
	Query: 3' cgggACCUGAUCC-----UCAGUCGU 5' :	PLSCR4	-27.77

	Ref: 5' aagtTGGATTGGGCTTACAGTCAGCA 3'		
	Query: 3' cgGGACCUG-AUC---CUCAGUCGU 5' :	GJA4	-23.92
	Ref: 5' tgCCTGAGCACAGACAGAGTCAGCA 3'		
	Query: 3' CGG--GACCUGAUCCUCAGUCGu 5' 	RGS3	-22.12
	Ref: 5' GCCTTCTGGACTA--AGGCAGCc 3'		
	Query: 3' CGGGACCUGA-UCCUCAGUCGu 5' :	PDE2A	-25.98
	Ref: 5' GGCCGGGACTCTTGGGTCAGCc 3'		
hsa-miR-490	Query: 3' GUC-GUACCUCA--G---GAGGUCCAAC 5' :	CDH5	-23.7
	Ref: 5' CAGCCTTGGGATAGCAAACCTCCAGGTTc 3'		
	Query: 3' GUC--GUACCUC-AGGAGGUCCaac 5' 	ESAM	-24.5
	Ref: 5' CAGACCACAGAGATCCTCCAGGaaa 3'		
	Query: 3' GUCGUAC-CUCAGGAGGU----CCAAC 5' :	MGC20262	-31.2
	Ref: 5' CGGCAGGAGAGTCCTCCAAGGGGGTTt 3'		
	Query: 3' GUCGUACCUCAGGA---GGU--CCAAC 5' : :	ROBO4	-26.16
	Ref: 5' CAGCGAGGGCTCCTTAGCCAATGGTTG 3'		
	Query: 3' gucgUACCUC--AGGAGGUCCAAC 5' 	FLJ46061	-22.94
	Ref: 5' gacaATGGAGAGAACCCCCAGGTTc 3'		
	Query: 3' guCGUACCUCAGGAGGUCCAAC 5' : : :	MOV10L1	-28.1
	Ref: 5' ggGTGTGGGG-CTGCCAGGTTG 3'		
hsa-miR-299-3p	Query: 3' gUC-GUACCUCAGG-----A-GGUCCAac 5' 	CGNL1	-29.93
	Ref: 5' tAGCCATGGAGTCCCACCTGTGCCAGGTca 3'		
	Query: 3' GUCGUACCUCAGGAGGU-CCAAC 5' 	ICAM2	-23.21
	Ref: 5' CACCATGGTGT--TCCACGGTTG 3'		
	Query: 3' uucgCCA-AAUGGUA-GGGUGUAU 5' 	APLN	-24.05
	Ref: 5' catgGGTGTCCCCATGCCACATA 3'		
	Query: 3' uuCGCCAAAUGGUAGGGUGUAU 5' :	TNFRSF11A	-21.83
	Ref: 5' ctGCGGTTTATTACCAACATA 3'		
	Query: 3' UUCGC-CAAAUGGUAGGGUGuau 5' : :	TIE1	-27.7
	Ref: 5' AGGTGTGTTTCCCATCCCActgc 3'		
	Query: 3' uuCGCCAAAUGGUAGGGUGUAU 5' :	PECAM1	-20.07
	Ref: 5' ggGCTGTTGAATTTCCACATA 3'		
	Query: 3' uucgCCAAAUGGUA-GGGUGUAu 5' 	ROBO4	-20.17
	Ref: 5' cttgGGTGTCCCTTCCCCACATg 3'		
hsa-miR-328	Query: 3' uGCCUUCCCGUCUCUCCCGGuc 5' :	EGFL7	-34.66
	Ref: 5' gCGGAAGGCCAGGCAGGGCCtt 3'		
	Query: 3' uGCCUUCC-----CGUCUC--UCCCGGuc 5' :	CLDN5	-34.48
	Ref: 5' tCGGAGGGGCGGATGCAGAGCCCAGGGCCcc 3'		
	Query: 3' uGCCUUCCC-GUCUC--UCCC-GGUC 5' 	CLDN5	-32.1
	Ref: 5' tCGGCAGGGCCCCGAGCCAGGGACCAG 3'		
	Query: 3' UGCCUUCCG-UCUCUCCCGGUC 5' :	CXorf36	-34.34
	Ref: 5' AGGGAGGGGCAACAGAGGTCCAG 3'		
	Query: 3' ugcCUUCCCGU-CUC-UCCCGGUC 5' 	LOC90139	-27.36
	Ref: 5' agaGATGGCCAGGAGAAGGGCCAG 3'		
	Query: 3' uGCCUUCCCGUCUCUCCCGGu 5' : :	SEMA6B	-29.51
	Ref: 5' cCGGTGGGGAATGGGGGCCAc 3'		
hsa-miR-328	Query: 3' UGCCUUC---CCG-----UCUCUCCCGGUC 5' 	RGS3	-33.5
	Ref: 5' ACGGAAGCGAGGCCTGGACCAAGAGAGGCCCAG 3'		
	Query: 3' UGCCU-UCCCGUC--UCUCCCGGUC 5' 	ROBO4	-25.69
	Ref: 5' AGGGACAGTGCAGATAGAAGGCCAG 3'		
	Query: 3' uGCCUUC-CGUCUCUCCCGGUC 5' :	KIAA1274	-30.14
	Ref: 5' cCGGTGGGAGCAGAAAAGGCCAG 3'		
hsa-miR-525	Query: 3' uCUUUCACGU--AGGGA-GACCUC 5' : :	EGFL7	-27.81
	Ref: 5' gGAAGGTACGAGCTCCCTGCTGGAG 3'		
	Query: 3' ucuuuCACGUAG--GGAGACCUc 5' 	FLJ10241	-22
	Ref: 5' tggttGTGCTTCTGCCTCTGGAc 3'		
	Query: 3' UCUUUC-----ACGUAGG-GAGACCUc 5' :	RAPGEF5	-21.35

	Query: 3' UCUUUC-----ACGUAGG-GAGACCUC 5' :	RAPGEF5	-21.35
	Ref: 5' AGGATGGGCCATGCACCCTCTCTGGAt 3'		
	Query: 3' UCUUUCACGUAGGGAGACCUC 5' :	NOTCH4	-20.64
	Ref: 5' AGAAGCTGCA--GCTCTGGAA 3'		
	Query: 3' ucuUUCACGUAGGGAGACCUC 5' : :	FLJ22746	-23.83
	Ref: 5' cccAGGGGCAT-TCTCTGGAG 3'		
hsa-miR-337	Query: 3' UCUUU-CACGUAGGGAGACCUC 5' :	ESAM	-20.5
	Ref: 5' AGAAATCTGCG--CCTCTGGAt 3'		
	Query: 3' UCUUUCACGUAGGGAGACCUC 5' :	FLJ46061	-20.64
	Ref: 5' AGGAAGGGGCTCACTCTGGcc 3'		
	Query: 3' UUUCCGUAGUAUAUCCUCGACCu 5' : :	RAPGEF5	-26.22
	Ref: 5' AAGGGCATCCTCCA-GGGCTGGt 3'		
	Query: 3' UUUCCGUAGUAUAUCCUCGACCu 5' :	FLJ22746	-29.25
	Ref: 5' AATGGCATC-T-TGGGAGCTGGc 3'		
	Query: 3' uUUCC-GUAGUAUAUCCUCGACCu 5' :	SHANK3	-23.99
	Ref: 5' cAAGGACGACTTCGTGGAGCTGGg 3'		
	Query: 3' UUUCCGU-AGUAUAUCCUCGACCu 5' 	Hs.382865	-25.32
	Ref: 5' AATGGCAGGAACAAAGGAGCTGGg 3'		
	Query: 3' uUUCCGUAGUAU-CCUCGACCUC 5' : :	LOC400451	-20.92
	Ref: 5' gAAGTCAGTCTAGACGGGGCTGGA 3'		
	Query: 3' uUUCCG---UAGU---AUA-----UCCUCGACCu 5' 	PLSCR4	-26.55
	Ref: 5' gAAGGCAGAATCAGACTATCAGGAAAGGAGCTGGc 3'		
	Query: 3' uuUCCGUAGUAUAUCCUCGACCU 5' :	KIAA1274	-26.63
	Ref: 5' ggAGGTTTC-TCAAGGAGCTGGA 3'		