

Supplementary Information

Table S1. Synthesized oligonucleotides for miRNA duplexes.

Duplex	One strand	Sequence *	Opposite strand	Sequence *
let-7b	let-7b-5p	UGAGGUAGUAGGUUGUGUGGUU	let-7b-3p	CUAUACAACCUACUGCCUUC
miR-1	miR-1-5p	UGGAAUGUAAAAGAAGUAUGUAU	miR-3p	ACAUACUUCUUUAUAUGCCC
miR-21	miR-21-5p	UAGCUUAUCAGACUGAUGUUGA	miR-21-3p	CAACACCAGUCGAUGGGCUGU
miR-22	miR-22-3p	AAGCUGCCAGUUGAAGAACUGU	miR-22-5p	AGUUCUUCAGUGGCAAGCUU
miR-28	miR-28-5p	AAGGAGCUCACAGUCUAUUGAG	miR-28-3p	CACUAGAUUGUGAGCUCCUGG
miR-30c-1	miR-30c-5p	UGUAAACAUCCUACACUCUCAGC	miR-30c-1-3p	CUGGGAGAGGGUUGUUACUCC
miR-186	miR-186-5p	CAAAGAAUUCUCCUUUUGGGCU	miR-186-3p	GCCCAAAGGUGAAUUUUUUGG
miR-199b	miR-199b-3p	ACAGUAGUCUGCACAUUGGUUA	miR-199b-5p	CCCAGGUUUAGACUAUCUGUUC
miR-200b	miR-200b-3p	UAAUACUGCCUGGUAAUGAUGA	miR-200b-5p	CAUCUUACUGGGCAGCAUUGG
miR-330	miR-330-5p	UCUCUGGGCCUGUGUCUUAGGC	miR-330-3p	GCAAAGCACACGCCUGCAGAGA
miR-335	miR-335-5p	UCAAGAGCAAUAACGAAAAAUG	miR-335-3p	UUUUUCAUUAUUGCUCCUGACC
miR-346	miR-346-5p	UGUCUGCCCGCAUGCCUGCCUCU	miR-3460-3p	AGGCAGGGCUGGGCCUGCAGC
miR-466	miR-466-5p	AUACACAUACACGCAACACACAU	miR-465-3p	GUGUGUUGCAUGUGUGUAUAUGU
miR-574	miR-574-5p	UGAGUGUGUGUGUGAGUGUGU	miR-574-3p	CACGCUCAUGCACACACCCACA
miR-3126	miR-3126-5p	UGAGGGACAGAUGCCAGAAGCA	miR-3126-3p	CAUCUGGCAUCCGUCACACAGA
miDNA	miDNA	taatactgcctggtaatgtga	miDNA *	catcttactggcagcattgga

* Upper character indicates RNA. Lower character, DNA. s* indicates miRNA strand which is not assigned in miRBase.

Table S2. Oligonucleotide sequences for construction of miRNA target reporters. Each oligonucleotide contains completely matched target sequence of each miRNA (22 nt) with 2 nt excessive sequences (upper cases) at both ends, and the overhang sequence of restriction enzyme (4 nt, lower cases) at 5' end.

	Sense strand	Antisense strand
let-7b-5p target	tcgaGAAACCACACAAACCTACTACCTeacc	aattGGTGGAGGTAGTAGGTTGTGTTGtttc
miR-21-5p target	tcgaAGTCAACATCAGTCTGATAAGCtacc	aattGGTAGCTTATCAGACTGATGTTgact
miR-200b-3p target	tcgaCGTCATCATTACCAGGCAGTAttaga	aattTCTAATACTGCCTGGTAATGATgacg
miR-330-5p target	tcgaGAGCCTAAGACACAGGCCAGAgagg	aattCCTCTCTGGGCCTGTGCTTAGgctc

Table S3. qRT-PCR was carried out using the Forward and the Reverse primers.

Gene name	Forward primer (5'→3')	Reverse primer (5'→3')
HDHD1A	GACGGACTTCTTCTGGATACTG	CCATAACCAGGGACTTACATC
UBQLN1	CAGCTACAGAACATCCAGAACAGTCAG	CCCAGTAACCTTTCAATAGCTG
PBX2	GGAGGCAAACATCTATGCTG	CCAGATCCTGAGAGATTGAAAG
ZC3H11A	CAGTCCTCTTCAGATTCTCAC	AAATCATCCTCCACAGAGAGTG
SKA2	CCAGGTTCAAGCAGTTCTCTG	GGATCACCATCAGGAGTTAAAG
CASP7	ATCAGGGCTGTATTGAAGAGC	TACTGAAGAGGGACGGTACAAAC
SLC11A2	CTTGGTCCTTATCATCTGTTCC	CAACCCAAGTAGAACACAAAGC
UBR3	CGACTAAATAGCTGCTCTTCC	ACCACACTTACAATGGTCTGG
RARG	ATCAGCACTAAGGGAGCTGAAAG	CTCAAACATTTCAGGGTTCTCC
SPAST	GTGAAGAATATGTCTGCCAGTG	CTTCTAAAGTTGAGGGCTGAC
METTL7A	CTATTTCATGGAGCATGTGG	AGCTCTCTGGTCAGGTTG
SEC23A	CGGTTCTTCTTGATAGCAGTAGC	CATATCCTGGTATCCTGACTTCC
HMGN4	GCTCGGTTGTCTGCTAAACC	CTTTCCAGCATCTGCTTCC
ZNF652	GAGTAAGGAAATGCTCTCACCC	GTAACTGACAGAGAGGGAGCAC
SLC39A1	GTCACCTCTGGAGGAAACAAG	CAGGGAGAACACCAAGTACACAG
OTUD4	TTCAGCCATCCTAGAAAATAGC	ACACTAGAGTGGACCTTGCTTAG
USP37	CCTAACACCAAGATTCAAGTCAC	CTTGCAAGAGTGCATTACTCAG
AP1S2	TGAGCACTGTCTTATCACATCG	CAGCAGCTCTGCATAGTTGAC
OSTM1	TCAAGAGATCCTCCTGCCTTAG	CCAAGTAGACTCTGGGCTACAC
SHCBP1	CAAGGAAGGGATCCTCATTAAAG	TCACCAAGACAACACCATAACC
PGM2L1	CTACCTTCCAAGTGAGTCACAAC	CCTCACCATACATAGAACAGAG
TOMM34	TCAGAAGAGGTGGAATTCTTG	TTGCCTTCTCCTTCAGAACTC
SPRYD3	GTCTGTGGCTTATCATGCAGAC	ATTCCACAGCCCATGATGTC
SRPR	TCAAAGAGCTTGAGTCGTGAAG	CAACAGATTCACAGAGCTGGAC
B4GALT1	GGGAGTTGTGGAAATAAGAAG	AAGTTACCACTCAGGGATTG
SLC7A11	GCATCTGCTACCTTGAGAGTG	CTGCCCATACCAGAAAGCTC
NHLRC3	CAGGTTTACTCCTGATGGGAAG	TGATCTGCTAGTTGGATTGTGC
CLDN12	GTACTCCCATCCACCCAGTATG	CCCATTAAAGTGGTGTGAAAC