

Table SI. miR target sequences used in miR array.

miRname	miR target sequence (5'-3')
hsa-let-7a-5p	UGAGGUAGUAGGUUGUAUAGUU
hsa-let-7b-5p	UGAGGUAGUAGGUUGUGUGGUU
hsa-let-7c-5p	UGAGGUAGUAGGUUGUAUGGUU
hsa-let-7d-5p	AGAGGUAGUAGGUUGCAUAGUU
hsa-miR-200a-3p	U AACACUGUCUGGUAACGAUGU
hsa-let-7g-5p	UGAGGUAGUAGUUUGUACAGUU
hsa-let-7i-5p	UGAGGUAGUAGUUUGUGCUGUU
hsa-miR-1	UGGAAUGUAAAGAAGUAUGUAU
hsa-miR-100-5p	AACCCGUAGA UCCGAACUUGUG
hsa-let-7f-5p	UGAGGUAGUAGAUUGUAUAGUU
hsa-miR-101-3p	UACAGUACUGUGAU AACUGAA
hsa-miR-103a-3p	AGCAGCAUUGUACAGGGCUAUGA
hsa-miR-106a-5p	AAAAGUGCUUACAGUGCAGGUAG
hsa-miR-106b-5p	UAAAGUGCUGACAGUGCAGAU
hsa-miR-107	AGCAGCAUUGUACAGGGCUAUCA
hsa-miR-125b-5p	UCCCUGAGACCCUAACUUGUGA
hsa-miR-126-3p	UCGUACCGUGAGUAAUAAUGCG
hsa-miR-130a-3p	CAGUGCAAUGUUAAAAGGGCAU
hsa-miR-132-3p	U AACAGUCUACAGCCAUGGUCG
hsa-miR-10b-5p	UACCCUGUAGAACCGAAUUUGUG
hsa-miR-133a-3p	UUUGGUCCCCUUCAACCAGCUG
hsa-miR-141-3p	U AACACUGUCUGGUAAGAUGG
hsa-miR-143-3p	UGAGAUGAAGCACUGUAGCUC
hsa-miR-145-5p	GUCCAGUUU UCCCAGGAAUCCCU
hsa-miR-146a-5p	UGAGAACUGAAU UCCAUGGGUU
hsa-miR-26a-5p	UUCAAGUAAUCCAGGAUAGGCU
hsa-miR-150-5p	UCUCCCAACCCUUGUACCAGUG
hsa-miR-155-5p	UUA AUGCUAAUCGUGAUAGGGGU
hsa-miR-15a-5p	UAGCAGCACAUAAUGGUUUGUG
hsa-miR-15b-5p	UAGCAGCACAUCAUGGUUUACA
hsa-miR-149-3p	AGGGAGGGACGGGGCUGUGC
hsa-miR-16-5p	UAGCAGCACGUAAAUAUUGGCG
hsa-miR-17-5p	CAAAGUGCUUACAGUGCAGGUAG
hsa-miR-181a-5p	AACA UUCAACGCUGUCGGUGAGU
hsa-miR-181b-5p	AACA UUCAUUGCUGUCGGUGGGU
hsa-miR-182-5p	UUUGGCAAUGGUAGAACUCACACU
hsa-miR-27a-3p	UUCACAGUGGCUAAGU UCCGC
hsa-miR-186-5p	CAAAGAAUUCUCCUUUUGGGCU
hsa-miR-18a-5p	UAAGGUGCAUCUAGUGCAGAUAG
hsa-miR-191-5p	CAACGGAAUCCCAAAGCAGCUG
hsa-miR-192-5p	CUGACCUAUGAAUUGACAGCC
hsa-miR-148a-3p	UCAGUGCACUACAGAACUUUGU
hsa-miR-194-5p	UGU AACAGCAACUCCAUGUGGA
hsa-miR-195-5p	UAGCAGCACAGAAAU AUUGGC
hsa-miR-196a-5p	UAGGUAGUUUCAUGUUGUUGGG
hsa-miR-19a-3p	UGUGCAAAUCUAUGCAAAACUGA
hsa-miR-19b-3p	UGUGCAAAUCCAUGCAAAACUGA
hsa-miR-200b-3p	UAAUACUGCCUGGUA AUGAUGA
hsa-miR-200c-3p	UAAUACUGCCGGGUA AUGAUGGA
hsa-miR-202-3p	AGAGGU AUAGGGCAUGGGAA
hsa-miR-10a-5p	UACCCUGUAGA UCCGAUUUGUG
hsa-miR-205-5p	UCCUUCAU UCCACCGGAGUCUG
hsa-miR-206	UGGAAUGUAAGGAUGUGUGG
hsa-miR-20a-5p	UAAAGUGCUUAUAGUGCAGGUAG
hsa-miR-20b-5p	CAAAGUGCUC AUAGUGCAGGUAG

hsa-miR-21-5p	UAGCUUAUCAGACUGAUGUUGA
hsa-miR-210-3p	CUGUGCGUGUGACAGCGGCUGA
hsa-miR-214-3p	ACAGCAGGCACAGACAGGCAGU
hsa-miR-215-5p	AUGACCUAUGAAUUGACAGAC
hsa-miR-22-3p	AAGCUGCCAGUUGAAGAACUGU
hsa-miR-221-3p	AGCUACAUUGUCUGCUGGGUUUC
hsa-miR-222-3p	AGCUACAUCUGGCUACUGGGU
hsa-miR-223-3p	UGUCAGUUUGUCAAUACCCCA
hsa-miR-23a-3p	AUCACAUUGCCAGGGAUUUCC
hsa-miR-23b-3p	AUCACAUUGCCAGGGAUUACC
hsa-miR-24-3p	UGGCUCAGUUCAGCAGGAACAG
hsa-miR-25-3p	CAUUGCACUUGUCUCGGUCUGA
hsa-miR-26b-5p	UUCAAGUAAUUCAGGAUAGGU
hsa-miR-27b-3p	UUCACAGUGGCUAAGUUCUGC
hsa-miR-29a-3p	UAGCACCAUCUGAAAUCGGUUA
hsa-miR-29b-3p	UAGCACCAUUUGAAAUCAGUGUU
hsa-miR-29c-3p	UAGCACCAUUUGAAAUCGGUUA
hsa-miR-30b-5p	UGUAAACAUCCUACACUCAGCU
hsa-miR-30c-5p	UGUAAACAUCCUACACUCUCAGC
hsa-miR-30d-5p	UGUAAACAUCCCCGACUGGAAG
hsa-miR-31-5p	AGGCAAGAUGCUGGCAUAGCU
hsa-miR-34a-5p	UGGCAGUGUCUUAGCUGGUUGU
hsa-miR-423-5p	UGAGGGGCAGAGAGCGAGACUUU
hsa-miR-7-5p	UGGAAGACUAGUGAUUUUGUUGU
hsa-miR-9-5p	UCUUUGGUUAUCUAGCUGUAUGA
hsa-let-7e-5p	UGAGGUAGGAGGUUGUAUAGUU
hsa-miR-92b-3p	UAUUGCACUCGUCCCGGCCUCC
hsa-miR-93-5p	CAAAGUGCUGUUCGUGCAGGUAG
hsa-miR-99a-5p	AACCCGUAGAUCCGAUCUUGUG

hsa, *Homo sapiens*; miR, microRNA.

Table SII. Twenty-five common mRNA targets of miR-222-3p predicted using TargetScan 8.0, miRDB and PicTar.

Target gene	Gene name	Total context++ score
CDKN1B	Cyclin-dependent kinase inhibitor 1B (p27, Kip1)	-1.05
EIF5A2	Eukaryotic translation initiation factor 5A2	-0.88
NAP1L5	Nucleosome assembly protein 1-like 5	-0.81
IRX5	Iroquois homeobox 5	-0.70
RIMS3	Regulating synaptic membrane exocytosis 3	-0.67
ARF4	ADP-ribosylation factor 4	-0.58
PAIP2	Poly(A) binding protein interacting protein 2	-0.52
CPNE8	Copine VIII	-0.46
BMF	Bcl2 modifying factor	-0.46
OSBPL3	Oxysterol binding protein-like 3	-0.46
UBE2J1	Ubiquitin-conjugating enzyme E2, J1	-0.45
PDCD10	Programmed cell death 10	-0.42
ANGPTL2	Angiopoietin-like 2	-0.38
YWHAG	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	-0.35
DYRK1A	Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	-0.34
ESR1	Estrogen receptor 1	-0.32
RAB1A	RAB1A, member RAS oncogene family	-0.29
KHDRBS2	KH domain containing, RNA binding, signal transduction associated 2	-0.27
ETS1	v-ETS avian erythroblastosis virus E26 oncogene homolog 1	-0.27
RSBN1L	Round spermatid basic protein 1-like	-0.24
SEMA6D	Sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	-0.22
SLC4A4	Solute carrier family 4 (sodium bicarbonate co-transporter), member 4	-0.20
SHANK2	SH3 and multiple ankyrin repeat domains 2	-0.18
ANKHD1	Ankyrin repeat and KH domain containing 1	-0.17
FAT2	FAT atypical cadherin 2	-0.09