

Table S2. Suitable complementarity of sequences in the mouse *Barx1* 3'-UTR to those of known miRNAs

miRNA	Score	Energy	Start	End	Alignment
miR-135	18.438	-32.16	362	385	GCGGUG--CCgaGguuAGGGAUau CGCCACCGGGtgCaggTCCCTATg
miR-203	18.0042	-13.1	68	89	gAucaccAcGAUUuGUAAGUg gTttgctTtCTAAtCATTTCat
miR-689	17.5504	-31.51	20	39	cCuGgGgCgGCUCGCCCCUGc tGgCgCgGtCG-GCGGGACc
miR-764-3p	17.4619	-23.62	421	441	uGUCaACggUGAuACCGGAGGa tCAGcTGatAC-cTGGCCTCCc
miR-7a	16.7304	-17.59	203	225	uguuGuUUuaguGAuCAGAAGGu tggcCgAAgcttCTgGTCTTtCt
miR-293	16.5942	-22.03	228	249	uguGAuGuuUgAgACGCCGuGA gacCTcCgcAgTgTGGGCGcCT
miR-764-3p	16.3773	-16.93	280	301	UGUcAAcggGuaCCGGAGGa ACAcTttatCcccGGCCTCCa
miR-615-5p	16.1604	-32.4	21	42	CuagGCucGugGCCCCUGGGg GgcgCGgtCggCGGGGACCCag
miR-328	15.7265	-22.73	100	121	UgcCuuCccgUcucUCCCCGUC AatGcgGacaAttaAGGGCCAG
miR-689	15.2612	-25.49	340	360	ccuggGGCGgcucgCCCCUGc tacttCCGcgccttGGGGACc

The *Barx1* 3'-UTR reference sequence is aligned in red. Sequence position is numbered according to *Barx1* reference clone ENSMUST0000021813 (MGI: 103124). Complementarity appropriate for miRNA activity of each candidate is delineated in capital letters. Binding energy and miRNA score are derived from EMBL-EBI MicroCosm Target.

Barx1 3'-UTR sequence.

1 GCGTCGCCGAGGATGCGGCTGGCGCGGTGCGGGGACCCAGGAGCTGGCCCTTCCGCGT 60
61 CCATGCCGTTTGCTTTCTAATCATTTCACTACTTTGAATGCAGACAATTAAGGGCCA 120
121 GACAAGGAAGGACACAGGCCCGGAAGCCAATCCAGGTGTCAGCGAGTTCTGTCCCCAG 180
181 TCTGGGAGACTTGTGTCCAGCGTGGCCGAAGCTTCTGGTCTTTCTCGGACCTCCGCAGTG 240
241 TGGGGCGCTCCACGCTATTACGCCCGCTCCTTGCCACACTTTTATCCCCGGCCTCC 300
301 AGCCGGCCTTCTGGGCCCGGACACCGGAGGCACACACTTACTTCCGCGCCTTGGGGACC 360
361 CCGCCACCGGTGCAGTCCCTATGGCCCTGCCCTGCAGAGCAGATCGTCTCTAGCAGA 420
421 TCAGCTGATACCTGGCCTCCCCATGTCGCTGAGGCTTCT 459