Supplementary Table S2. MicroRNAs predicted to target KIT 3' UTR (NM_001093772 - 2158 nt) by TargetScan analysis

MicroRNA	Position in KIT 3'UTR	predicted pairing of target region (top) and miRNA (bottom)	seed match	context + score	context + score percentile	PCT	Validated Kit-targeting?	Validated RUNX1-target?
hsa-miR-218	844-850	5' ...AACAAUAUAACCACAAAGCACAG... ||||||| 3' UGUACCAAUCUAGUUCGUGUU	7mer-m8	-0.1	53	0.42		
hsa-miR-193a-3p	1088-1095	5' ...AUGUCCUGGACACCG--GGCCAGUA... |||| ||||||| 3' UGACCCUGAAACAUCCGGUCAA	8mer	-0.22	72	0.54	YES PMID:21399664	YES PMID:23223432
hsa-miR-193b	1088-1095	5' ...AUGUCCUGGACACCG--GGCCAGUA... |||| ||||||| 3' UCGCCCUGAAACUCCCGGUCAA	8mer	-0.22	72	0.54	YES PMID:21724256	
hsa-miR-19b	1648-1654	5' ...AUCUGGAAGUAACCAUUUGCACU... ||||||| 3' AGUCAAAACGUACCUAAACGUGU	7mer-m8	-0.07	39	0.83		YES PMID:17589498
hsa-miR-19a	1648-1654	5' ...AUCUGGAAGUAACCAUUUGCACU... ||||||| 3' AGUCAAAACGUAUCUAAACGUGU	7mer-m8	-0.07	39	0.83	YES PMID:21880628	YES PMID:17589498
hsa-miR-152	1650-1656	5' ...CUGGAAGUAACCAUUUGCACUGG... ||||||| 3' GGUUCAAGACAGUACGUGACU	7mer-m8	-0.18	72	0.72		
hsa-miR-148b	1650-1656	5' ...CUGGAAGUAACCAUUUGCACUGG... ||||||| 3' UGUUUCAAGACACUACGUGACU	7mer-m8	-0.18	72	0.72		
hsa-miR-148a	1650-1656	5' ...CUGGAAGUAACCAUUUGCACUGG... ||||||| 3' UGUUUCAAGACAUCACGUGACU	7mer-m8	-0.18	71	0.72		
hsa-miR-4295	1649-1655	5' ...UCUGGAAGUAACCAUUUGCACUG... |||| ||||||| 3' UUCCUUUUGU----AACGUGAC	7mer-m8	-0.13	59	0.8		
hsa-miR-454	1649-1655	5' ...UCUGGAAGUAACCAUUUGCACUG... ||| ||||||| 3' UGGGAUAUUCGUUAU--AACGUGAU	7mer-m8	-0.13	57	0.8		
hsa-miR-130a	1649-1655	5' ...UCUGGAAGUAACCAUUUGCACUG... ||||||| 3' UACGGGAAAAUUGUAACGUGAC	7mer-m8	-0.12	53	0.8		
hsa-miR-301b	1649-1655	5' ...UCUGGAAGUAACCAUUUGCACUG... ||||||| 3' CGAAACUGUUAUAGUAACGUGAC	7mer-m8	-0.11	50	0.8		
hsa-miR-301a	1649-1655	5' ...UCUGGAAGUAACCAUUUGCACUG... ||||||| 3' CGAAACUGUUAUGAUAACGUGAC	7mer-m8	-0.11	49	0.8		
hsa-miR-130b	1649-1655	5' ...UCUGGAAGUAACCAUUUGCACUG... ||||||| 3' UACGGGAAAGUAGUAACGUGAC	7mer-m8	-0.11	49	0.8		
hsa-miR-3666	1649-1655	5' ...UCUGGAAGUAACCAUUUGCACUG... ||||||| 3' AGCCGUAGAUGUGAACGUGAC	7mer-m8	-0.1	45	0.8		
hsa-miR-4735-3p	1672-1678	5' ...GAGUUCUAUGCUCUCGCACCUUU... |||| ||||||| 3' UACAGAUUAAACU-CGUGGAAA	7mer-m8	-0.16	71	0.66		
hsa-miR-18a	1672-1678	5' ...GAGUUCUAUGCUCUCGCACCUUU... ||||||| 3' GAUAGACGUGAUCUACGUGGAAU	7mer-m8	-0.15	64	0.66		YES PMID:17589498
hsa-miR-18b	1672-1678	5' ...GAGUUCUAUGCUCUCGCACCUUU... ||||||| 3' GAUUGACGUGAUCUACGUGGAAU	7mer-m8	-0.15	64	0.66		YES PMID:17589498
hsa-miR-199a-5p	1652-1658	5' ...GGAAGUAACCAUUUGCACUGGAG... |||||| 3' CUUGUCCAUCAGACUUGUGACCC	7mer-1A	-0.12	53	0.62		
hsa-miR-199b-5p	1652-1658	5' ...GGAAGUAACCAUUUGCACUGGAG... |||||| 3' CUUGUCUAUCAGAUUUGUGACCC	7mer-1A	-0.11	52	0.62		
hsa-miR-222	1030-1037	5' ...UUAGUUUGGAUUCUUAUGUAGCA... ||||||| 3' UGGGUCAUCGGUCUACAUCGA	8mer	-0.13	57	< 0.1	YES PMID:16330772	YES PMID:21076613
hsa-miR-221	1030-1037	5' ...UUAGUUUGGAUUCUUAUGUAGCA... ||||||| 3' CUUUGGGUCGUCUGUUACAUCGA	8mer	-0.11	49	< 0.1	YES PMID:16330772	YES PMID:21076613
hsa-miR-137	1963-1970	5' ...UAAAUAUUGAAAUGUAGCAAUAA... |||| ||||||| 3' GAUGCGCAUAAGAAU---UCGUUAUU	8mer	-0.33	97	0.92	YES PMID:24412084	

Targetscan analysis - release 6.2 (June 2012) - showing only sites conserved among vertebrates