

Table S1 Top 10 predicted miRNAs that bind the 3'UTR end of *CISD2* in the TargetScan database

miRNA	Position in the UTR	Seed match	Context++ score	Context++ score percentile	Weighted context++ score	Conserved branch length	Pct
hsa-miR-186-5p	22–28	7mer-m8	–0.05	92	–0.05	2.981	N/A
hsa-miR-199a-3p	111–117	7mer-m8	–0.38	97	–0.38	5.303	0.8
hsa-miR-199b-3p	111–117	7mer-m8	–0.38	97	–0.38	5.303	0.8
hsa-miR-335-5p	2495–2502	8mer	–0.21	95	0	2.867	N/A
hsa-miR-320b	2748–2754	7mer-m8	–0.07	79	0	3.492	N/A
hsa-miR-320c	2748–2754	7mer-m8	–0.07	79	0	3.492	N/A
hsa-miR-320d	2748–2754	7mer-m8	–0.07	79	0	3.492	N/A
hsa-miR-320a	2748–2754	7mer-m8	–0.07	79	0	3.492	N/A
hsa-miR-154-5p	2803–2809	7mer-1A	–0.07	71	0	4.568	N/A
hsa-miR-495-3p	2811–2817	7mer-1A	–0.02	77	0	5.12	N/A

miRNA, microRNA; N/A, not applicable; Pct, The score of conservative calculation in interspecies evolution.