

	Predicted consequential pairing of target region (top) and miRNA (bottom)	Site type	Context++ score	Context++ score percentile	Weighted context++ score	Conserved branch length	P _{CT}
Position 1042-1048 of NQO1 3' UTR hsa-miR-129-5p	5' ...AAAAUAGUCUCCACAAAAAU... 3' CGUUCGGGUCUGGCUUUUUC	7mer-A1	-0.03	47	0.00	0.635	< 0.1
Position 381-387 of NQO1 3' UTR hsa-miR-211-5p	5' ...UGUAGUUUAUGGCAGAAGGGAAU... 3' UCCGCUUCCUACUGUUUCCUU	7mer-A1	-0.08	76	-0.01	3.379	< 0.1
Position 764-770 of NQO1 3' UTR hsa-miR-214-5p	5' ...CCUAGUAGCUGGGGAUGACAGGCG... 3' CGUGUCGUUCACAUCUGUCCGU	7mer-m8	-0.03	61	0.00	0.122	< 0.1
Position 514-520 of NQO1 3' UTR hsa-miR-218-5p	5' ...GUUACUAAUUGCCUAGCACAAG... 3' UGUACCAAUUCUAGUUCGUGUU	7mer-A1	-0.12	78	-0.02	0.076	< 0.1

Figure S1. Predicted binding sites in NQO1 3'-UTR among the NEAT1 interacting miRNAs. Three NEAT1 interacting miRNAs including miR-129-5p, miR-211-5p, **miR-214-5p**, or miR-218-5p were selected and the binding sites in NQO1 3'-UTR region were predicted by TargetScan website (http://www.targetscan.org/vert_72/).