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/).

| Position | Hsa-miR | 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 |
|----------|---------|---------------------------------------------------------------|-----------|----------------|----------------------------|--------------------------|------------------------|-------|
| 1042-1048 of NQO1 3’-UTR | hsa-miR-129-5p | 5’...AAAAAUAGUCUCGCAAAAAAAU...[......]...CGUCCGCGCCGCUU... | 7mer-A1 | -0.03 | 47 | 0.00 | 0.635 | < 0.1 |
| 301-307 of NQO1 3’-UTR | hsa-miR-211-5p | 5’...UCAGGUUUGCGACAGGGAU...[......]...UCCGCUUCCACUGCUUCCGCUU | 7mer-A1 | -0.08 | 76 | -0.01 | 3.379 | < 0.1 |
| 764-770 of NQO1 3’-UTR | hsa-miR-214-5p | 5’...CCUAGUCUCGCUUCCAGCCCG...[......]...CGUCCGCUUCCACUGCUUCCGCUU | 7mer-m8 | -0.03 | 61 | 0.00 | 0.122 | < 0.1 |
| 514-520 of NQO1 3’-UTR | hsa-miR-218-5p | 5’...GUUACCAUAUCUCCAGCAGCA...[......]...UCCUUGCUUCCACUGCUUCCGCUU | 7mer-A1 | -0.12 | 78 | -0.02 | 0.076 | < 0.1 |