

Table S1 RT-qPCR primers

| Gene | 5'-3' |
|-----------------------|-------------------------|
| <i>LncRNA-NEAT1-F</i> | CGCATTGTGTGTCTGGTTCA |
| <i>LncRNA-NEAT1-R</i> | CTGCCACACGAAACCTTAC |
| <i>TNFRSF1B-F</i> | TGAAACATCAGACGTGGTGTG |
| <i>TNFRSF1B-R</i> | TGCAAATATCCGTGGATGAAGTC |
| <i>IL8-F</i> | ACTGAGAGTGATTGAGAGTGGAC |
| <i>IL8-R</i> | AACCCTCTGCACCCAGTTTTTC |
| <i>MCP1-F</i> | CAGCCAGATGCAATCAATGCC |
| <i>MCP1-R</i> | TGGAATCCTGAACCCACTTCT |
| <i>β-actin-F</i> | ACCCTGAAGTACCCCATCGAG |
| <i>β-actin-R</i> | AGCACAGCCTGGATAGCAAC |
| <i>18S-F</i> | CAGCCACCCGAGATTGAGCA |
| <i>18S-R</i> | TAGTAGCGACGGGCGGTGTG |

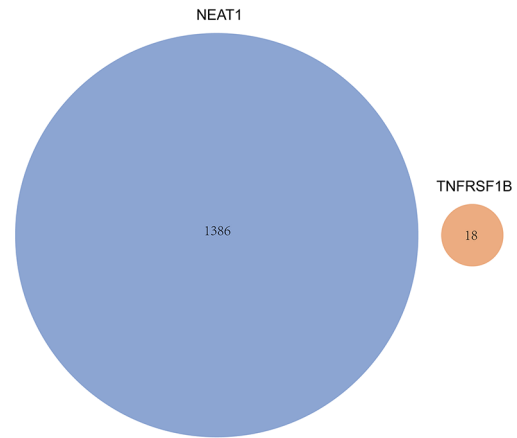


Figure S2 There were no overlaps between the downstream candidate miRNAs of NEAT1 and the upstream regulatory miRNA of TNFRSF1B.

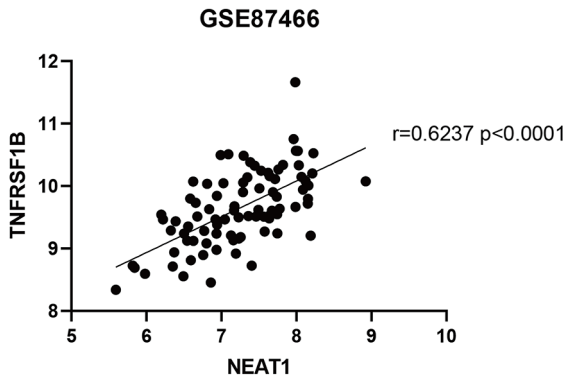


Figure S1 Pearson correlation analysis was performed between NEAT1 and TNFRSF1B and showed that NEAT1 and TNFRSF1B are positively correlated.