

Supplementary material

Tabel S1. Primer sequencing in this study.

| lncRNA | Forward primer(5'-3') | Reverse primer(3'-5') |
|-----------------------|------------------------------|------------------------------|
| <i>XR_001471472.2</i> | CCGGGCCTGCACTCTTGATA | GCAAATCCACACGGCCTGAC |
| <i>XR_003077657.1</i> | GATAAGGCGGTAACAACCTC | ATAGGAAGCCACTCACAAA |
| <i>XR_212291.3</i> | CTCTCCTGCTGAGCAAGCCATTG | TCCCTGGATGAAGACCCGTTCTG |
| <i>XR_001466777.2</i> | TGGCATAATGGCTGAACAGGGAAG | GCACTACTCTGGGCAACCTTGG |
| <i>XR_001466502.2</i> | GGTAGGAAGATATAGGAGAGCATGC | CTTGTGGGATAGAGAGATTCACTGG |
| <i>MSTRG.17928.1</i> | GAGCTGGAATTCACTGGTAGATACC | GGGAGGAGGAGCAAATCTATAGAAG |

Figure legends

Figure S1 Screening of LncRNAs. (A) The distribution of reads length for lncRNAs; (B) The exons length distribution of lncRNAs and mRNAs.

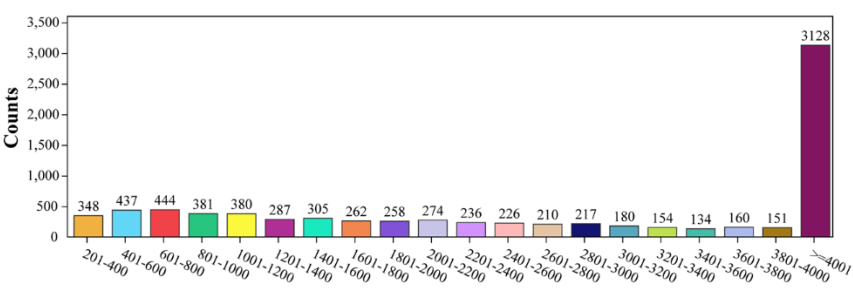
Figure S2 Sample relationship analysis. (A) The PCA of lncRNA. (B) The Pearson correlation heat map between lncRNA.

Figure S3 Weighted gene co-expression network analysis (A) The Power value curve; (B) Module gene correlation analysis.

Figure S4 (A) The Functional enrichment analysis of the cis-regulation lncRNAs. A. the top 20 significantly changed biological process terms of mRNAs; B Top 20 significantly changed pathways associated with mRNAs.

Figure S1

A



B

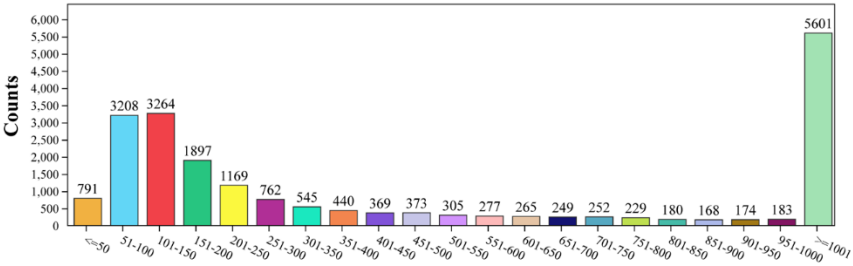


Figure S2

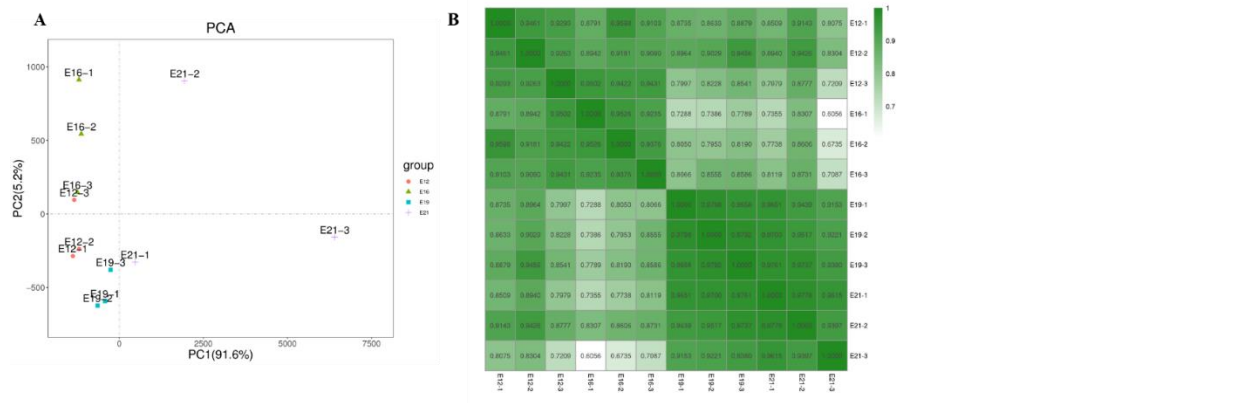


Figure S3

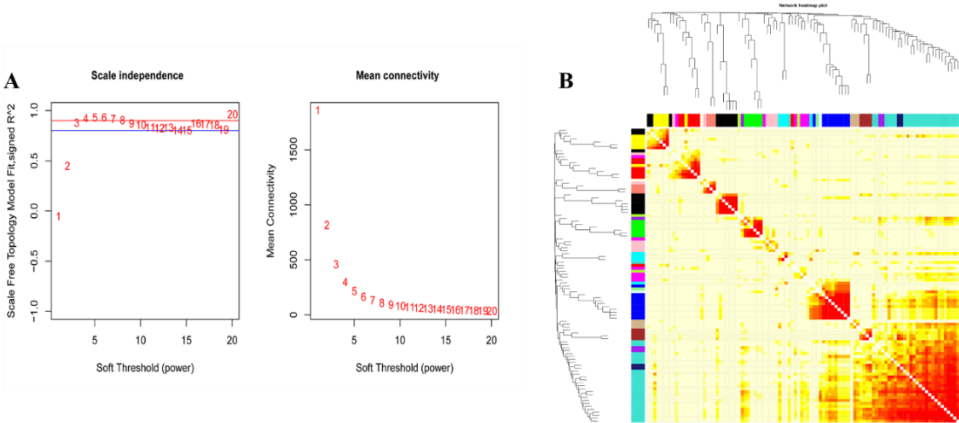


Figure S4

