Electronic Supplementary Material

The long non-coding RNA expression profile of Coxsackievirus A16 infected RD cells identified by RNA-seq

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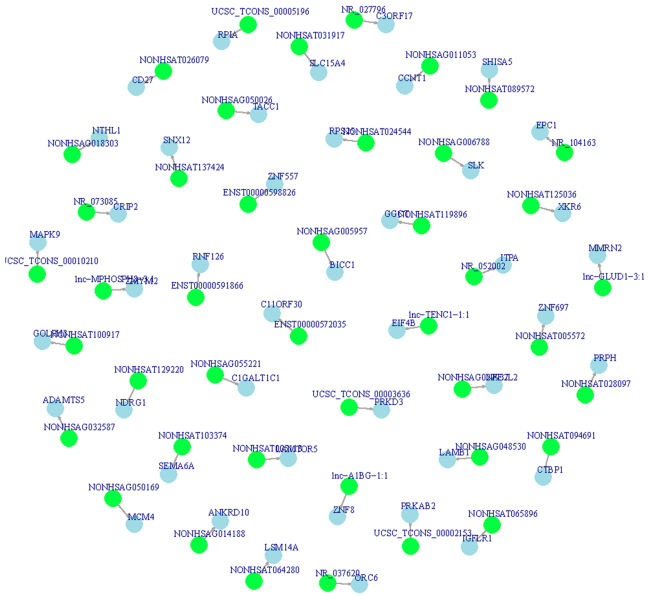
A LncRNA *cis*-acting regulatory network



B LncRNA *trans*-acting regulatory network

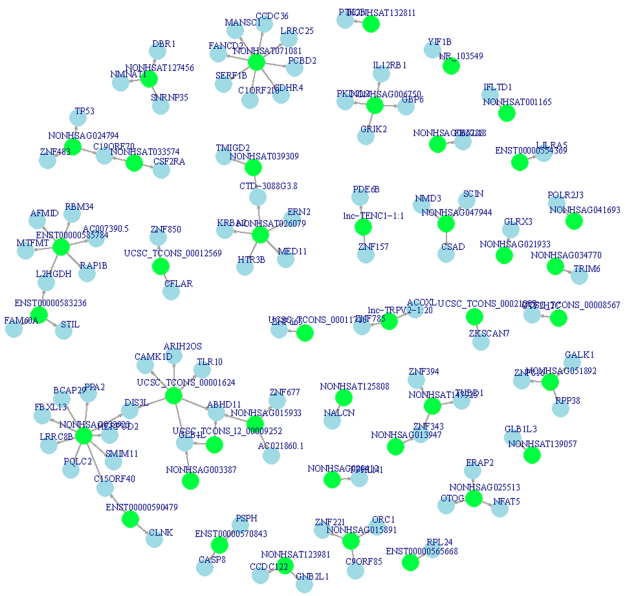


Figure S1. *Cis*-acting and *trans*-acting regulatory network. (A) *Cis*-acting regulatory network; (B) *Trans*-acting regulatory network. Red circles represent lncRNAs and blue circles represent mRNA.

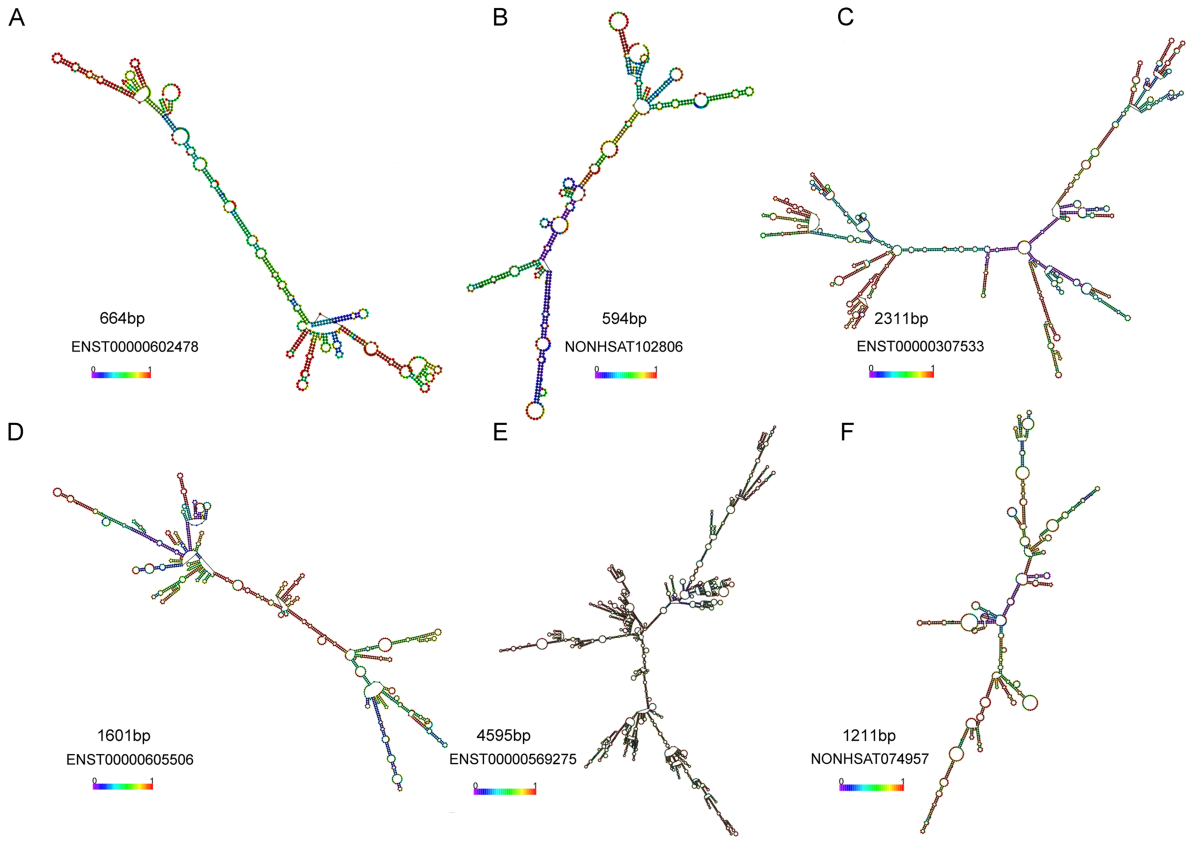


Figure S2. The secondary structures prediction of lncRNAs were performed using RNAfold software. (A–C) RNA secondary structure of three upregulated lncRNAs. (D–F) RNA secondary structure of three downregulated lncRNAs. The second structures are minimal free energy structures. Base pairing probabilities have been color coded using a scale from 0 (blue) to 1 (red).

Table S1. The 1970 differentially expressed lncRNAs expressed in RD cells after CVA16 infection

Table S2. The 6416 differentially expressed mRNAs expressed in RD cells after CVA16 infection

Table S3. *Cis*-acting lncRNA-mRNA co-expression network

Table S4. *Tran*-acting lncRNA-mRNA co-expression network