

## Electronic Supplementary Material

## Expression Profile and Function Analysis of Long Non-Coding RNAs in the Infection of Coxsackievirus B3

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Fig S1. The whole lncRNA-mRNA correlation network. The red color indicates up-regulation while the blue color indicates down-regulation. The solid lines mean positive correlation and the dashed line mean negative correlation.

Table S1. Primers used for qPCR

lncRNA/mRNA/viralRNA	Forward primer (5'-3')	Reverse primer (5'-3')
RNASEK	AGATGGCTTGGTCACTATTCCC	GCTGACTTGCTCGTAAAGGTTGT
RP11-893F2.6	GAGGAAGTATTTAGCAAGGGTGAA	TGCTGTAGGATTCTTTGTGGA
XLOC_001188	CTCCACCCTCCAGCCAAACT	CAGACTCACCAACTTAGAAGCACA
RP11-715J22.4	CGGGATTTTGGTTTGGGTAA	CAATAAGGACAGATGGAGCCTCT
OR6W1P	GTTCCAGGTTCTGCTGTTTGC	GGTGAGTGAAGGCGGGAATC
SNHG6	TCTGCTTCGTTACCTCAAGTG	TCTGCTTCGTTACCTCAAGTG
XLOC_012858	GCACAGTGTACAATGCCTCT	CCTTGCTTTATGGGTGGTTTA
RP11-20G13.3	CAGCCACAGCGACAGCAG	CCTATTTTCATACCGTAGGCAAAT
Human NFAT5	GAAGTGGACATTGAAGGCACT	CTGGCTTCGACATCAGCATT
CVB3 genome	ATCAAGTTGCGTGCTGTG	TGCGAAATGAAAGGAGTGT
GAPDH	AATCCCATCACCATCTTCCA	TGGACTCCACGACGTACTCA

Table S2. Raw data for the expression profile of differentially expressed lncRNAs. V: CVB3-infected cells; N: sham-infected control cells.

Table S3. Raw data for the expression profile of differentially expressed mRNAs. V: CVB3-infected cells; N: sham-infected control cells.

Table S4. Raw data from the lncRNA-mRNA correlation analysis.

Table S5. The list of predicted pathways related to the differentially expressed lncRNAs.

Table S6. The correlation degrees of differentially expressed lncRNAs and pathways.