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Electronic Supplementary Material

Dynamic Host Immune and Transcriptomic Responses to Respiratory Syncytial Virus Infection in a Vaccination-Challenge Mouse Model

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Supplementary Materials

Table S1 Total 5582 differentially expressed genes.

Table S2 The differentially expressed genes in each time point.

Table S3 The clusters of differentially expressed genes in PBS-treated and/or UV-RSV vaccinated group.

Table S4 Gene ontology (GO) and Kyoto encyclopedia of genes and genomes (KEGG) enrichment analysis of clustered differentially expressed genes.

Table S5 The differentially expressed genes within conserved high influential modules.

Table S6 Gene ontology (GO) and Kyoto encyclopedia of genes and genomes (KEGG) enrichment analysis of conserved high influential modules.

Table S7 Primers used for RT-qPCR validation

Gene	Forward primer (5′-3′)	Reverse sequence (5′-3′)
Col4a1	AGGAACGACTACTCTTACTG	CACTGCGGAATCTGAATG
Col5a1	ATGTTGCCTACCGAGTC	TTGTCAGGATGGAGAAGTC
Col5a2	GGACACTATGATGAGAAC	CTGACTACTGAGAGACTT
Col6a1	CTGGTGAAGGAGAACTAT	GAGGAGAATGTGATTGGA
Cxcr2	CGTCCTTGTCTTCCT	ATCTCCGTAGCATTCA
Ptafr	ACCTCGTAGTGTCATTAG	CCTCTTCAGTTCCTATCA
Fprl	GTGTCTTCCTGATTGC	ACGATGATTACCTTCTTG
Lilrb4a	TGAAGATGGACTGGAA	CCGATGAGGATGAGAA
GAPDH	AGGTCGGTGTGAACGGATTTG	TGTAGACCATGTAGTTGAGGTCA

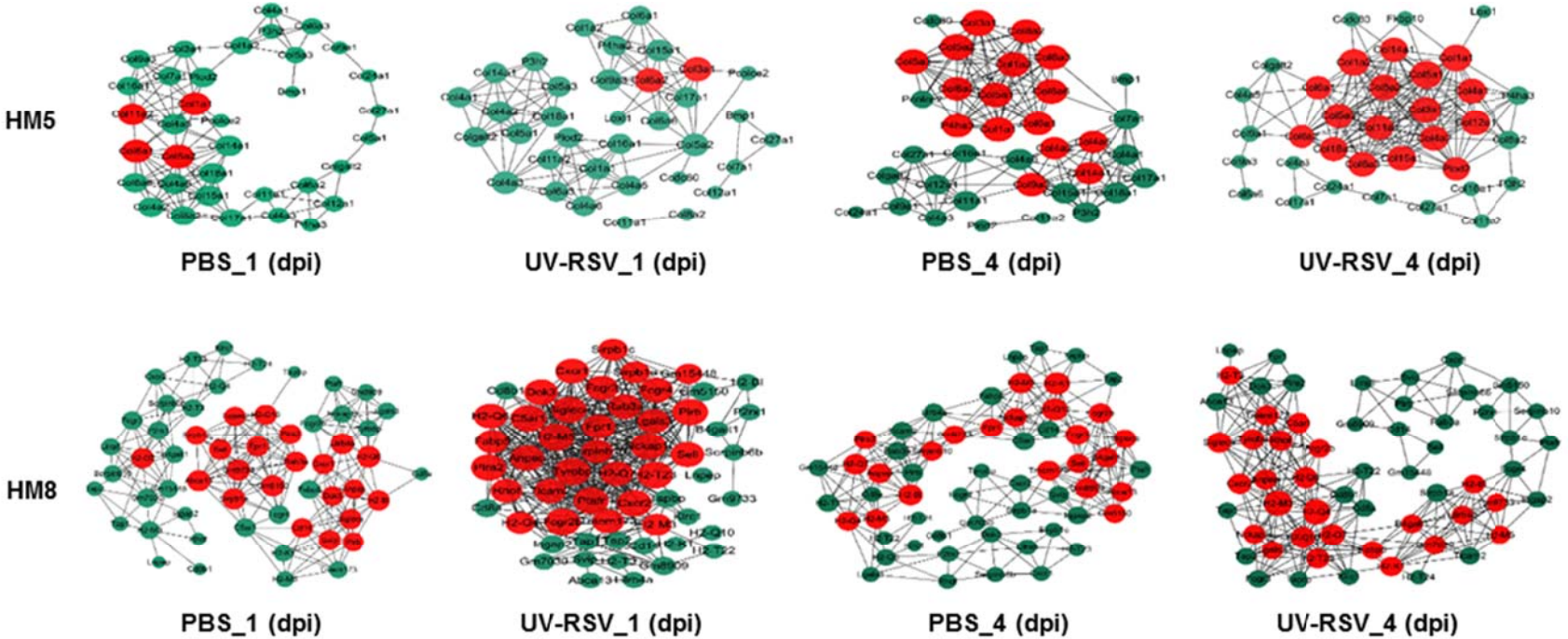

Fig. S1 Dynamic regulatory networks of HM5 and HM8. Dynamic networks were constructed by integrating gene expression data into PPI data, and the corresponding modules were identified using ClusterONE algorithm (Nepusz *et al.* 2012) and a model-based framework (Li *et al.* 2015). Genes with a connectivity
degree of $\geqslant$ 10 were defined as hub genes (red).