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**Supplementary Data**

**Transcriptome profiling highlights regulated biological processes and type III interferon antiviral responses upon Crimean-Congo hemorrhagic fever virus infection**

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Table S1. Details of the up-regulated DEGs.

Table S2. Details of the down-regulated DEGs.

Table S3. Primers for RT-qPCR used in this study.

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| --- | --- | --- |
| **Genes** | **Sequence ( 5'- 3')** |  **Orientation** |
| IFNλ1-qF | ACAGGAGCTAGCGAGCTTC |  Forward |
| IFNλ1-qR | ACCTGGAGAAGCCTCAGGT |  Reverse |
| IFNλ2/3-qF | CACACCCTGCACCATATCC |  Forward |
| IFNλ2/3-qR | GGTTGAAGGTGACAGAGGC |  Reverse |
| HSPA5-qF | ATGCCGCCAAGAACCAGCTCAC |  Forward |
| HSPA5-qR | CTTGATGTCCTGCTGCACAGACG |  Reverse |
| XBP1-qF | CAGAGTAGCAGCTCAGACTGCC |  Forward |
| XBP1-qR | CATCCATCCCCAAGCGCTGT |  Reverse |
| IFITM1-qF | GGAGGAACATGAGGTGGCTGTG |  Forward |
| IFITM1-qR | GACTTCACGGAGTAGGCGAATGC |  Reverse |
| IFIT1-qF | CCTCCTTGGGTTCGTCTACA |  Forward |
| IFIT1-qR | GGCTGATATCTGGGTGCCTA |  Reverse |
| OAS1-qF | CATCCGCCTAGTCAAGCACTG |  Forward |
| OAS1-qR | CACCACCCAAGTTTCCTGTAG |  Reverse |
| ISG15-qF | CACCGTGTTCATGAATCTGC |  Forward |
| ISG15-qR | CTTTATTTCCGGCCCTTGAT |  Reverse |
| MxA-qF | CTACACACCGTGACGGATATG |  Forward |
| MxA-qR | CGAGCTGGACTGGAAAGCCC |  Reverse |
| GAPDH-qF | ACCACAGTCCATGCCATCAC |  Forward |
| GAPDH-qR | TCCACCACCCTGTTGCTGTA |  Reverse |
| IFNβ-qF | CACTACAGCTCTTTCCATGA |  Forward |
| IFNβ-qR | AGCCAGTGCTAGATGAATCT |  Reverse |
| CCHFVS-qF | TCGCCGATTACCAACAGGCTG |  Forward |
| CCHFVS-qR | CCTGCACCACTCCACATGTTC |  Reverse |
| CCHFVM-qF | CCGAGTATCACTATATTGAGTGCATC |  Forward |
| CCHFVM-qR | GGAGCTGATGTGACCATTGTGTC |  Reverse |
| CCHFVL-qF | CAAGAGGAGCCTGAGGCTAAG |  Forward |
| CCHFVL-qR | CTTCAAACTGTGGCAGTATTCTAAG |  Reverse |



Figure S1. Top 15 significantly enriched pathways of DEGs. The x-axis indicates the rich factor and the y-axis indicates the pathway terms. Rich factor is the ratio of the DEGs identified upon CCHFV infection to all genes noted in the corresponding pathway term. A greater rich factor indicates higher intensiveness.



Figure S2. RT-qPCR analyses of CCHFV induction of representative host genes in different human cell types. Human cells including A549 (**A**), HUVEC (**B**), and Huh7 (**C**) were treated as HEK293 in Figure 7B, followed by RT-qPCR analyses. Dotted lines indicate the ordinate value 1 (i.e., 2-fold induction) for reference.