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**Supplementary Data**

**Integrated interactome and transcriptome analysis reveals key host factors critical for SARS-CoV-2 infection**

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**Figure S1.** Prediction of upstream TFs that regulate the co-expression network. The ENCODE ChIP-seq library was chosen as the resource, with FET *P*-value < 0.05.

**Figure S2.** *In vitro* confirmation of key host factors. (**A**) Western blot analysis of lysates immunoprecipitated (IP) for Flag from HEK293T cells co-transfected with HA-tagged human IFITM1, TNFAIP2 and DDX60 expression plasmids and Flag-tagged SARS-CoV-2 viral proteins M, Orf7b, NSP4, Orf3, NSP1 and Orf8 expression plasmids. Western blot results are representative of three independent experiments. (**B**)Time-series expression of key host factors after SARS-CoV-2 infection. (**C**) qRT-PCR validation of key host factors expression. The label “mock” indicates mock samples at 0 hpi. The labels from 0 to 24 h represent infected samples at the indicated time points. Statistical significance is tested using *t*-test. "\*" denotes significant difference and "ns" for no significance. The error bars represent mean ± SD. \**P* < 0.05, \*\**P* < 0.01, \*\*\**P* < 0.001 and \*\*\*\**P* < 0.0001.

(Please see separate excel files for supplementary Tables)

Table S1. Primers for RT-qPCR.

Table S2. Level 1: direct SARS-CoV-2-human PPIs

Table S3. Cellular component enrichment of SIPs for each viral protein.

Table S4. Biological process enrichment of SIPs for each viral protein.

Table S5. Detalis of transcriptomics data used for RRA

Table S6. GO and KEGG analysis of CLCGs.

Table S7. List of 35 core genes.Table S8. TFs predicted to regulate the co-expression network.