

Figure S1. The relationship between the three PPI networks. (A) The PPI network of all DEGs in meta-analysis consists of 275 nodes and 2,038 edges. (B) PPI network extracted from (A) by Degree Centrality consists of 56 nodes and 644 edges. (C) The PPI network extracted from (B) by MCODE consists of 32 nodes and 446 edges. PPI, protein-protein interaction; dEGs, differentially expressed genes.

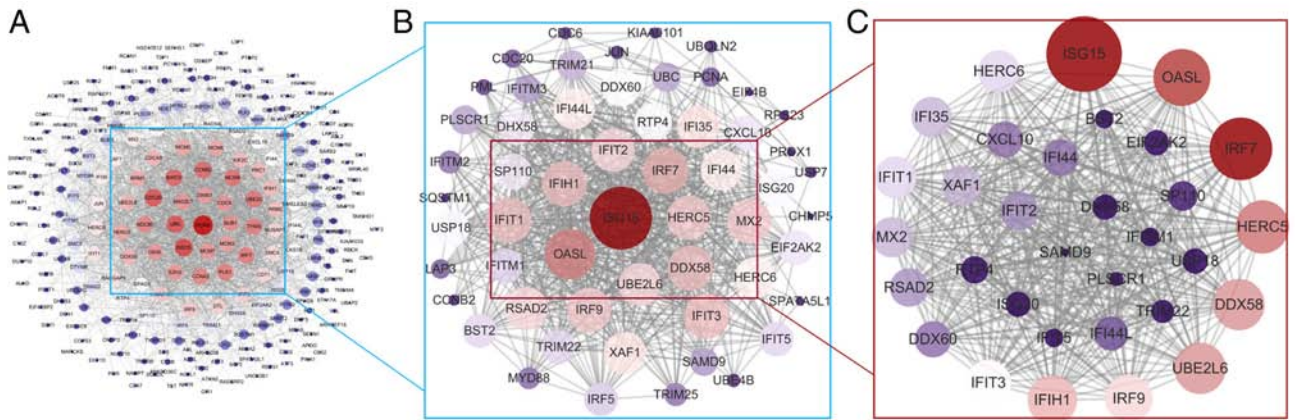


Table SI. Sequences of primers used.

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ISG15	Forward: 5'-CGCAGATCACCCAGAAGATCG-3' Reverse: 5'-TTCGTCCGATTTGTCCACCA-3'
OASL	Forward: 5'-AAGGTAGTCAAGGTGGGCTC-3' Reverse: 5'-CTCCTGGAAGCTGTGGAAAC-3'
IRF7	Forward: 5'-GCTGGACGTGACCATCATGTA-3' Reverse: 5'-GGGCCGTATAGGAACGTGC-3'
DDX58	Forward: 5'-TGCGAATCAGATCCCAGTGTA-3' Reverse: 5'-TGCCTGTA ACTCTATACCCATGT-3'
$\beta$ -actin	Forward: 5'-CCTGGCACCCAGCACAAT-3' Reverse: 5'-GCCGATCCACACGGAGTACT-3'

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ISG15, interferon-stimulated gene 15; OASL, 2'-5-oligoadenylate synthetase like; IRF7, interferon regulatory factor 7; DDX58, DExD/H-box helicase 58.

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Table SII. Thermocycling conditions for reverse transcription-quantitative PCR.

Step	Temperature (°C)	Reaction time (sec)	Number of cycles
Initial denaturation	95	30	1
Denaturation	95	10	40
Annealing	60	30	
Elongation	95	15	
Final extension	60	60	1
	95	15	