

Supporting Information

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SI Materials and Methods

Viruses, Cell Culture, and Transfections. Sendai virus (Cantell strain; Charles River Laboratories) was used at a final concentration of 100 hemagglutinating units/mL. All cells were cultured at 37 °C in an atmosphere of 5% (vol/vol) CO₂. HEK 293T cells and Raw 264.7 cells were cultured in DMEM supplemented with 10% (vol/vol) cosmic calf serum with 100 U/mL penicillin and 100 µg/mL streptomycin. THP-1 cells were cultured in RPMI 1640 medium supplemented with 10% (vol/vol) FBS with 100 U/mL penicillin, 100 µg/mL streptomycin, and 0.05 mM 2-mercaptoethanol.

RNAi and Rescue with Transgenes. The lentiviral shRNA vector, pTY-shRNA-EF1a-puroR-2a-GFP-Flag, was provided by Dr. Yi Zhang (Harvard Medical School). The original vector was modified to pTY-shRNA-EF1a-GFP-IRES-puroR and pTY-shRNA-EF1a-GFP-IRES-hygroR by replacing the 2A peptide sequence with an IRES sequence and also by replacing a puromycin-resistant gene with a hygromycin-resistant gene. The shRNA sequences were cloned into the vectors with U6 promoter. RNAi-resistant cDNA sequences were cloned into the vectors to replace GFP. Lentiviral infection and establishment of stable cell lines were described previously (1). The shRNA sequences were as follows (only the sense strand is shown): human IRF5, 5'-GAG-GAAGAGCTGCAGAGGAT-3'; mouse IRF5, 5'-GCAGAGA-ATAACCCTGATTTA-3'; human IKKβ, 5'-GGGAGAACGAA-

GTGAAACT-3'; human IKKα, 5'-GTACCAGCATCGGGAAC-TT-3'; human NEMO, 5'-GGACAAGGCCTCTGTGAAA-3'; human TRAF6, 5'-GGAGAAACCTGTTGTGATT-3'.

Quantitative RT-PCR. Total cellular RNA was isolated using TRIzol. 0.1–1 µg total RNA was used for reverse transcription (RT) using iScript Kit (Bio-Rad). The resulting cDNA served as the template for quantitative RT-PCR analysis using iTaq Universal SYBR Green Supermix (Bio-Rad) and the ViiA7 Real-Time PCR System (Applied Biosystems). Primers for specific genes were as follows: human CXCL10, 5'-GTGGCATTCA-AGGAGTACCTC-3' and 5'-TGATGGCCTTCGATTCTGG-ATT-3'; human TNF-α, 5'-CCTCTCTCTAATCAGCCCTC-TG-3' and 5'-GAGGACCTGGGAGTAGATGAG-3'; human IFN-β, 5'-ACTGCAACCTTTTGAAGCCTTT-3' and 5'-TGG-AGAAGCACAACAGGAGAGC-3'; human GAPDH, 5'-ATG-ACATCAAGAAGGTGGTG-3' and 5'-CATACCAGGAAATG-AGCTTG-3'; human IL-12 p40, 5'-AAGGAGGCGAGGTTT-TAAGC-3' and 5'-AAGAGCCTCTGCTGCTTTT-3'; human IFIT3, 5'-TCAGAAGTCTAGTCACTTGGGG-3' and 5'-ACAC-CTTCGCCCTTTCATTTC-3'; human RSAD2, 5'-CAGCGT-CAACTATCACTTCACT-3' and 5'-AACTCTACTTTGCAGA-ACCTCAC-3'; human ISG15, 5'-CGCAGATCACCCAGAAGA-TCG-3' and 5'-TTCGTCGCATTTGTCCACCA-3'.

1. Tanaka Y, Chen ZJ (2012) STING specifies IRF3 phosphorylation by TBK1 in the cytosolic DNA signaling pathway. *Sci Signal* 5(214):ra20.

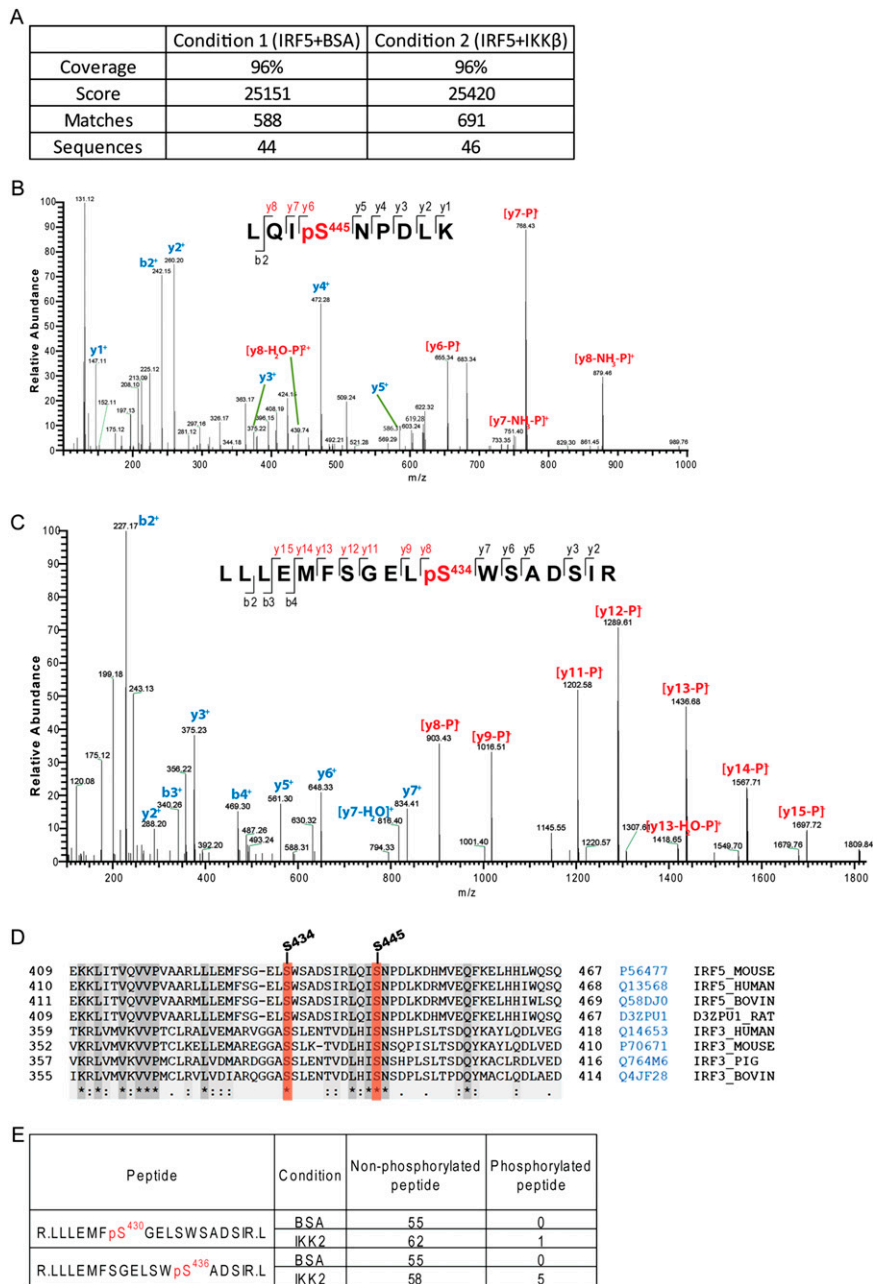


Fig. S2. Identification of IRF5 phosphorylation sites by mass spectrometry and functional analyses. (A) Summary of mass spectrometry data indicating the coverage of the IRF5 protein and the total numbers of peptide sequences in the experiment described in Fig. 3 B and C. The data were analyzed by Mascot (Matrix Science). (B) Tandem mass (MS2) spectrum after HCD fragmentation of the ion with $m/z = 554.28$ ($z = 2^+$), indicating S445 phosphorylation. (C) MS2 spectrum after HCD fragmentation of the ion with $m/z = 1,067.50$ ($z = 2^+$), indicating S434 phosphorylation. (D) Sequence alignment of the C-termini of IRF5 and IRF3 from different species as indicated. Conserved serine residues in IRF5 and IRF3, including S434 and S445 of mouse IRF5, are highlighted. (E) IRF5 protein incubated with IKK β or BSA was analyzed by tandem mass spectrometry as described in Fig. 3 A and B. The total numbers of the indicated phosphorylated and nonphosphorylated peptides are shown.

