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Table S1. Materials.

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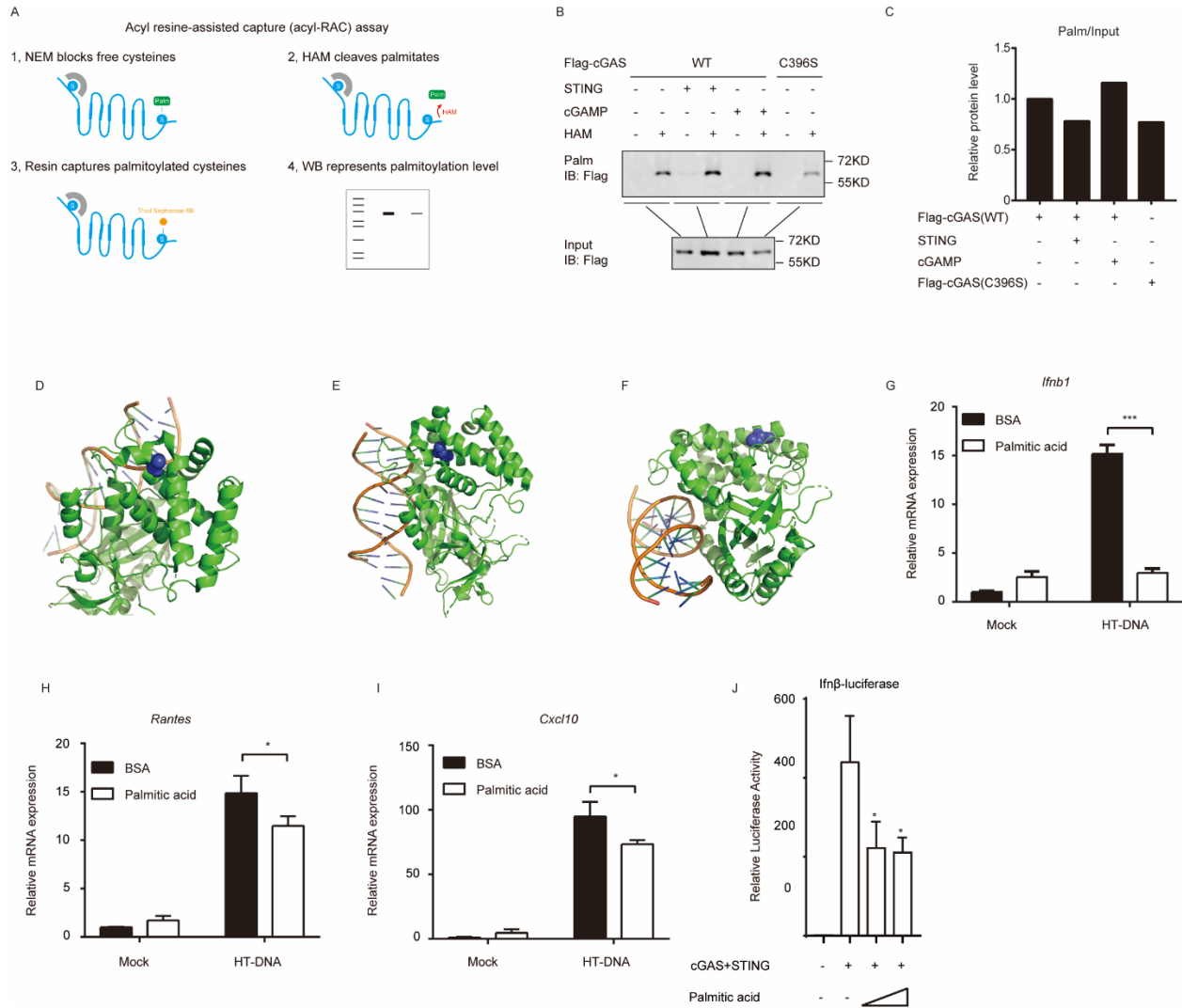


Figure S1. Palmitoylation of cGAS suppresses its activation.

(A) A schematic diagram showing the general process of the acyl resin-assisted capture (acyl-RAC) assay.

(B) Acyl-RAC assay of HEK293T cells transfected with Flag-cGAS and the indicated plasmids for 24 h or treated with cGAMP (1 μ g/ml) for 1 h.

(C) Quantification of palmitoylation levels of Flag-cGAS in (B)

(D to F) The positions of C405(D), C409(E) and C474(F) in the human cGAS-DNA complex. The blue sphere indicates cysteines and the yellow helix indicates DNA.

(G-I) L929 cells were treated with palmitic acid (0, 100 μ M, or 200 μ M) for 12 h and transfected with HT-DNA (2 μ g/mL) for 6 h before RT-qPCR analysis of Ifnb1 (G), Rantes (H) and Cxcl10 (I) expression. HT-DNA: herring testis DNA. BSA: Bovine serum albumin.

(J) HEK293T cells (5×10^5) were transfected with HA-cGAS (200 ng) and Flag-STING (200 ng) expression plasmids and treated with palmitic acid (0, 50 μ M, or 100 μ M) for 12 h before luciferase reporter assays were conducted.

Data information: Data are representative of at least two independent experiments; mean \pm SEM from triplicates of technical replicates, unpaired t test; *, $P < 0.01$. ***, $P < 0.001$.

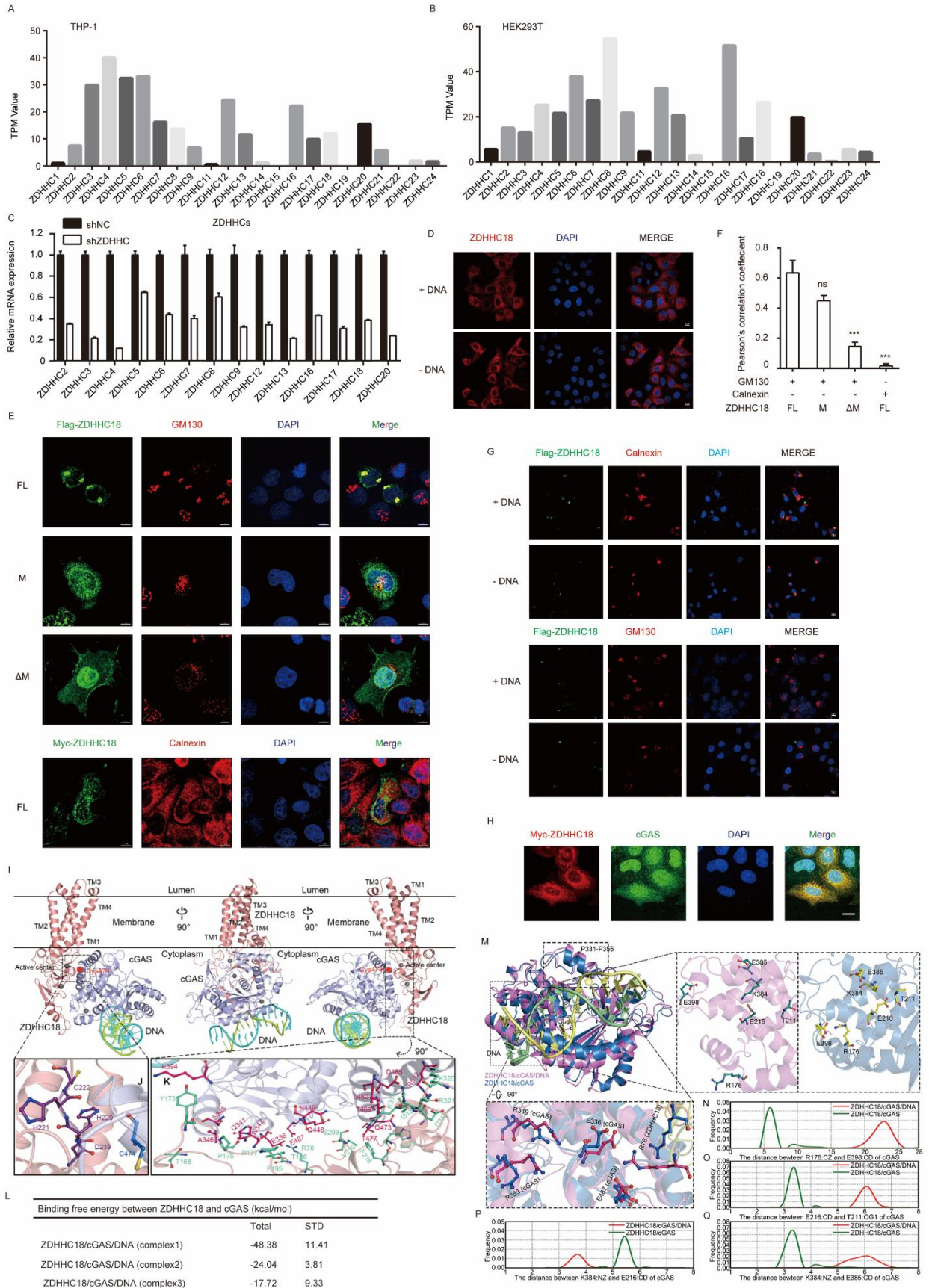


Figure S2. ZDHHC18 is a major acyltransferase for cGAS palmitoylation.

(A and B) Expression level of ZDHHCs in THP-1 cells (A) and HEK293T cells (B) according to The Human Protein Atlas (<https://www.proteinatlas.org/>). TPM: transcripts per million.

(C) The knockdown efficiency of individual ZDHHCs in HEK293T cells analyzed by RT-qPCR.

(D) Immunofluorescence analysis of endogenous ZDHHC18 in HeLa cells. Scale bars: 10 μm .

(E) Immunofluorescence analysis of Flag-ZDHHC18 (FL or truncated mutants) and GM130 or calnexin in HeLa cells. FL: full length. Scale bars: 7 μm .

(F) Colocalization (Pearson's correlation coefficient) of ZDHHC18 (FL or truncated mutants) and GM130 or calnexin in (E).

(G) Immunofluorescence analysis of stably overexpressed Flag-ZDHHC18 and GM130 or calnexin in HeLa cells with HT-DNA stimulation (or not). Scale bars: 10 μm .

(H) Immunofluorescence analysis of Myc-ZDHHC18 and endogenous cGAS in HeLa cells. Scale bars: 7 μm .

(I) Overall structure of the human ZDHHC18/cGAS/DNA complex. Cartoon representation of human ZDHHC18/cGAS/DNA complex. The ZDHHC18 is shown in salmon and the cGAS is highlighted with light blue, while two chains of DNA are limon and green, respectively. The three spheres represent the Zn^{2+} ions.

(J) Close-up of the ZDHHC18 active sites in (I). The ZDHHC motif is shown in firebrick sticks which surrounds C474 (skyblue stick) of cGAS.

(K) Close-up of the interaction face between ZDHHC18 and cGAS in (I). The key residues involved in the interaction are highlighted with pink sticks (cGAS) and limegreen sticks (ZDHHC18).

(L) Comparison of the binding free energy between ZDHHC18/cGAS/DNA complexes.

(M) Comparison of the structure of cGAS in different complexes. The cGAS proteins in ZDHHC18/cGAS/DNA and ZDHHC18/cGAS complexes are shown with pink cartoon and marine cartoon respectively.

(N-Q) Distribution frequency of the distance between R176:CZ and E398:CD (N), between E216:CD and T211:OG (O), between K384:NZ and E216:CD (P) and between K384:NZ and E385:CD (Q) in different complexes during the simulation in (M).

Data information: Data are representative of at least two independent experiments; mean \pm SEM from triplicates of technical replicates, unpaired t test; ns, not significant; ***, $P < 0.001$.

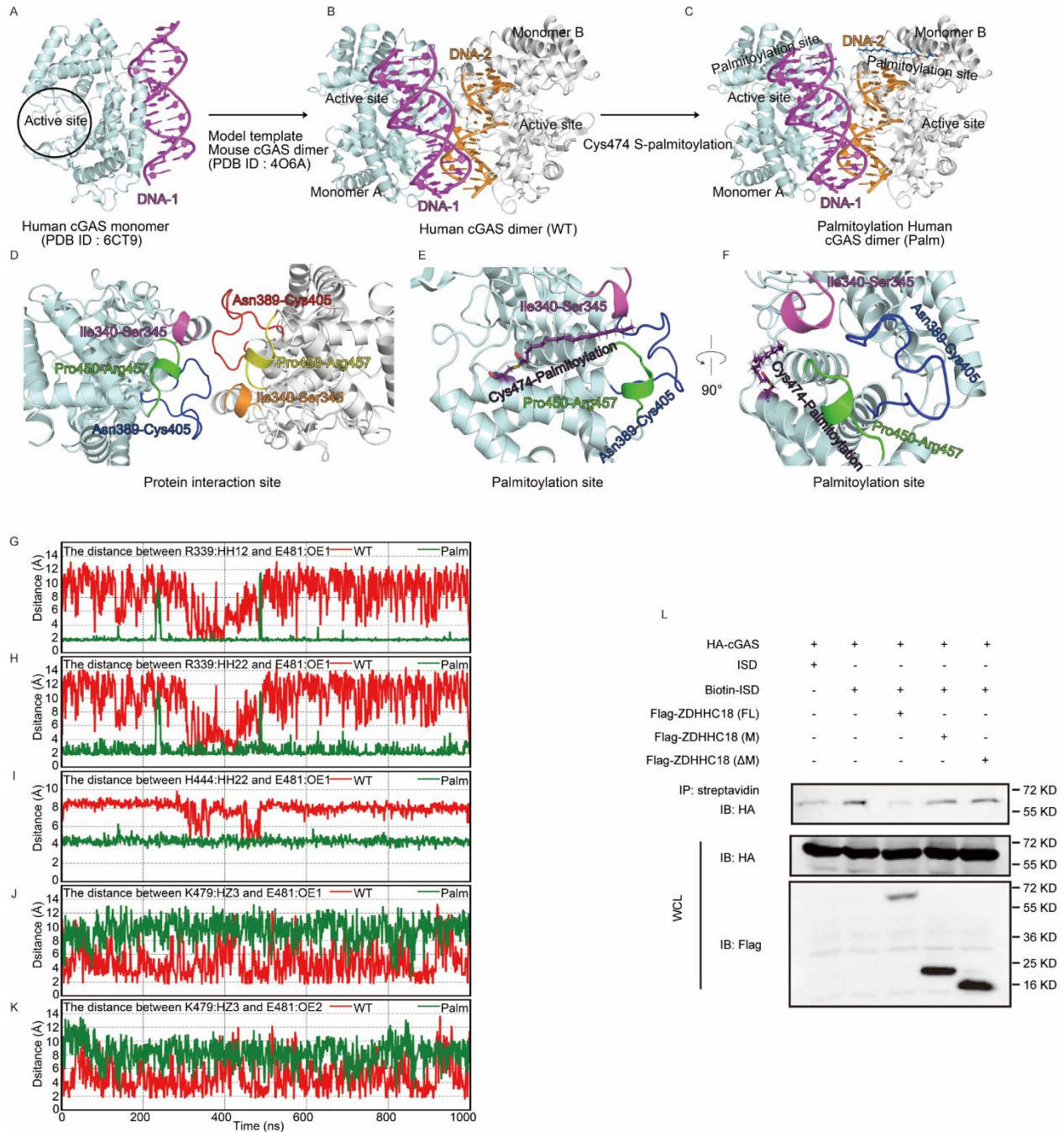


Figure S3. Palmitoylation inhibits DNA binding to cGAS.

(A) Structure of the functionally active human cGAS-DNA 1:1 complex (PDB ID: 6CT9).

(B) The human cGAS-DNA 2:2 complex was constructed by SWISS MODEL based on the mouse cGAS-DNA 2:2 complex (PDB ID: 4O6A). Monomer A and monomer B in the dimer are displayed as cartoons and colored pale cyan and white, respectively. DNA-1 and DNA-2 are colored magenta and orange, respectively.

(C) Human cGAS-DNA 2:2 complex in the palmitoylation state. The S-palmitoylated C474 residues in monomer A and monomer B are shown as sticks and colored fire brick and deep teal, respectively.

(D) The interaction locations of monomer A and monomer B. I340-S345, N389-C405 and P450-R457 are the key residues involved in the interaction between monomer A and monomer B.

(E and F) The location of the S-palmitoylation C474 site in monomer A.

(G-K) Evolution of the distance between R339:HH12 and E481:OE1 (G), R339:HH22 and E481:OE1, (H), H444:HH22 and E481:OE1 (I), K479:HZ3 and E481:OE1 (J), and K479:HZ3 and E481:OE2 (K) of the WT and palmitoylated cGAS proteins over time.

(L) HEK293T cells (1×10^6) were transfected with HA-cGAS and Flag-ZDHHC18 (FL or truncated mutants) expression plasmids. Biotin-conjugated ISD was transfected into cells 6 h before harvesting. Lysates were coprecipitated with streptavidin beads and then assessed by immunoblot analysis as shown.

Data information: FL: full length; WCL: whole cell lysate; IP: immunoprecipitation.

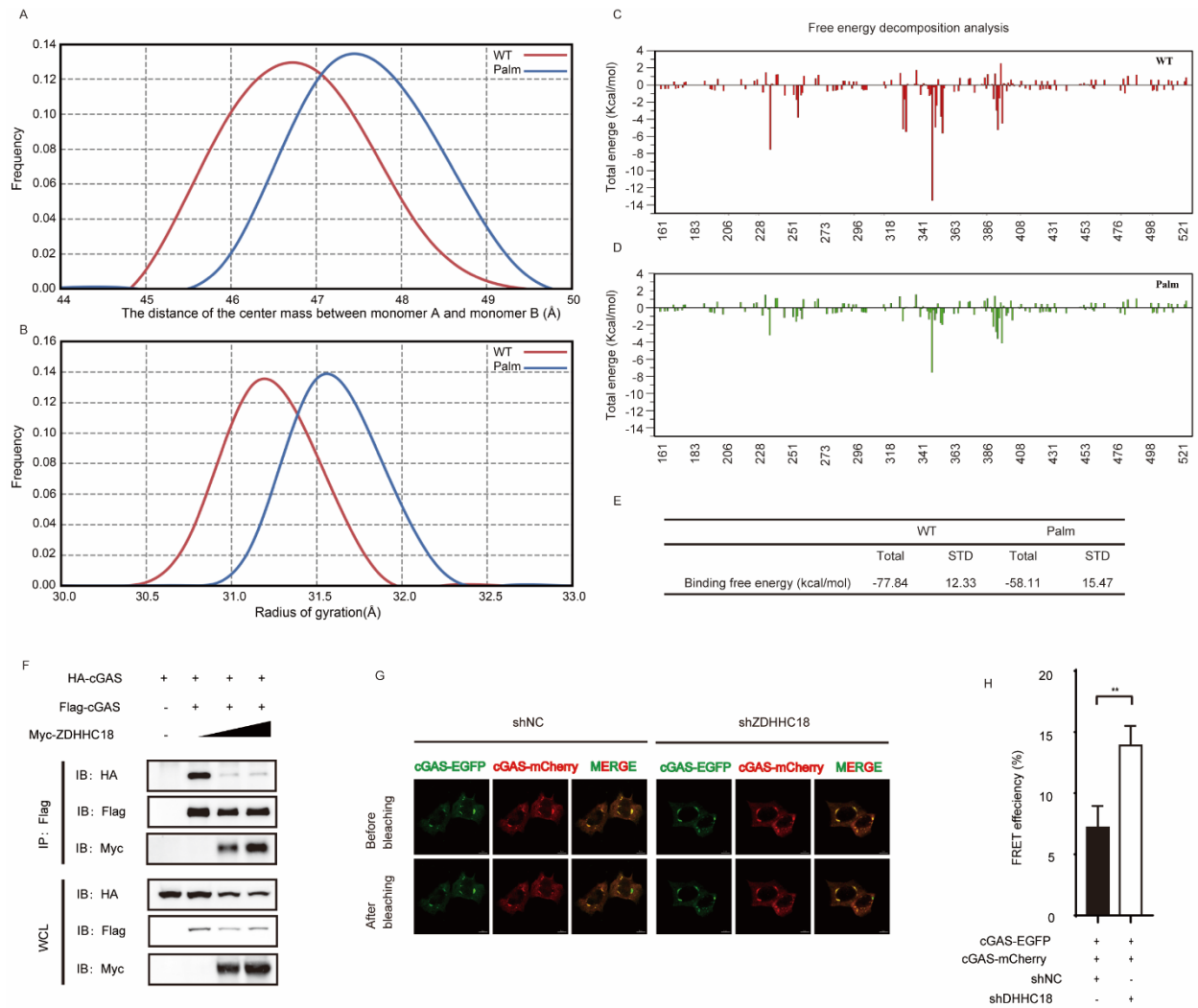


Figure S4. Palmitoylation dampens cGAS dimerization.

(A) Distribution frequency of the distance between the center masses of monomer A and monomer B in the human cGAS-DNA 2:2 complex in the resting and palmitoylation states during the simulation.

(B) Distribution frequency of the radius of gyration (Rg) of the human cGAS-DNA 2:2 complex in the resting and palmitoylation states during the simulation.

(C and D) Comparison of the per-residue binding energy decomposition to the binding affinity between complex I and complex II in the human cGAS-DNA 2:2 complex in the resting (C) and palmitoylation (D) states.

(E) The MM-GBSA results for the human cGAS-DNA 2:2 complex in the resting and palmitoylation states.

(F) Immunoprecipitation (with an anti-Flag antibody) and immunoblot analysis of HEK293T cells transfected with plasmids encoding Flag-cGAS (2 μ g), HA-cGAS (2 μ g), and Myc-ZDHHC18 (0, 1, or 2 μ g) for 24 h. WCL: whole cell lysate; IP: immunoprecipitation.

(G) FRET assay of HeLa cells transfected with cGAS-EGFP and cGAS-mCherry expression plasmids for 24 h after transfection with the indicated shRNA. Scale bar: 8 μ m.

(H) FRET efficiency of cGAS-GFP and cGAS-mCherry in (G).

Data information: Data are representative of at least two independent experiments; mean \pm SEM from triplicates of technical replicates, unpaired t test; nc: negative control; **, $P < 0.005$.

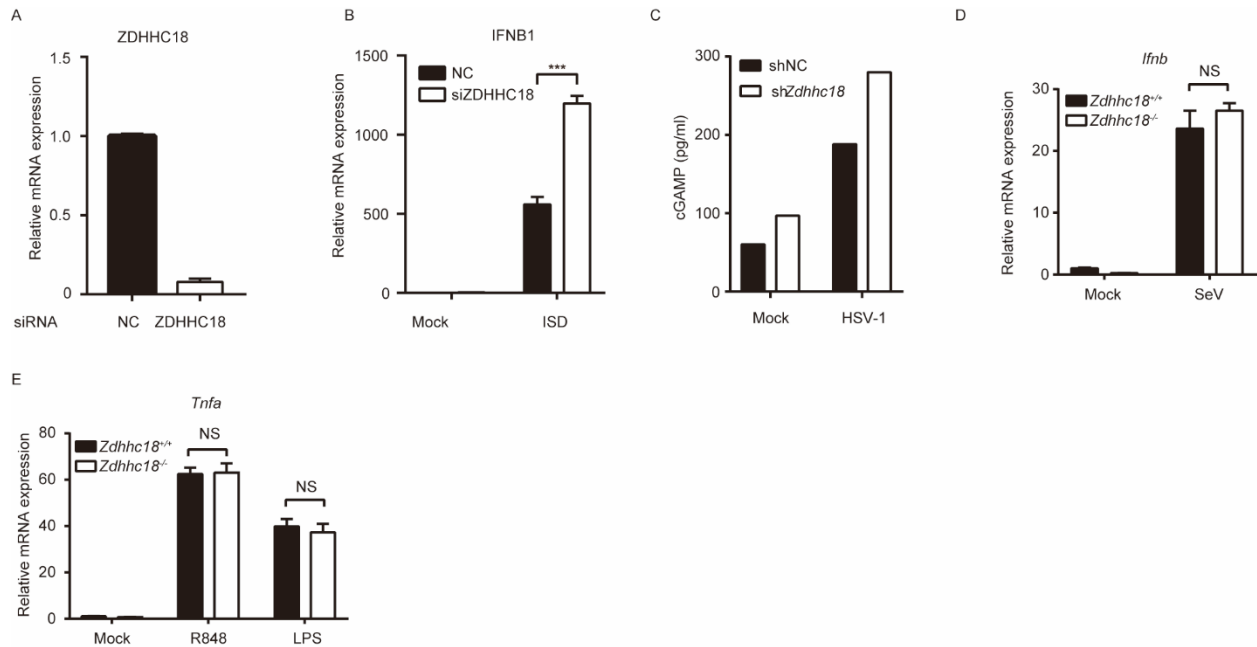


Figure S5. ZDHHC18 negatively regulates cGAS activation.

(A and B) THP-1 cells were transfected with scrambled siRNA or ZDHHC18 siRNA (cocktail) for 48 h and then transfected with HT-DNA (2 μ g/mL) for the indicated times before RT-qPCR analysis of IFNB1 expression. The knockdown efficiency of ZDHHC18 is shown in A. ISD: IFN-stimulatory DNA.

(C) ZDHHC18 stably knockdown L929 cells were infected with HSV-1 (MOI:5). After six hours, the cGAMP concentration was tested using LC-MS/MS.

(D-E) MEFs (*Zdhhc18*^{+/+} or *Zdhhc18*^{-/-}) were infected with SeV (1:500) (D) or R848 (100 ng/ml) and LPS (100 ng/ml) (E). After six hours, the expression of interferon alpha and TNF beta were analyzed by RT-qPCR.

Data information: Data are representative of at least two independent experiments; mean \pm SEM from triplicates of technical replicates, unpaired t test; nc: negative control; ***, $P < 0.001$; NS; no significance.

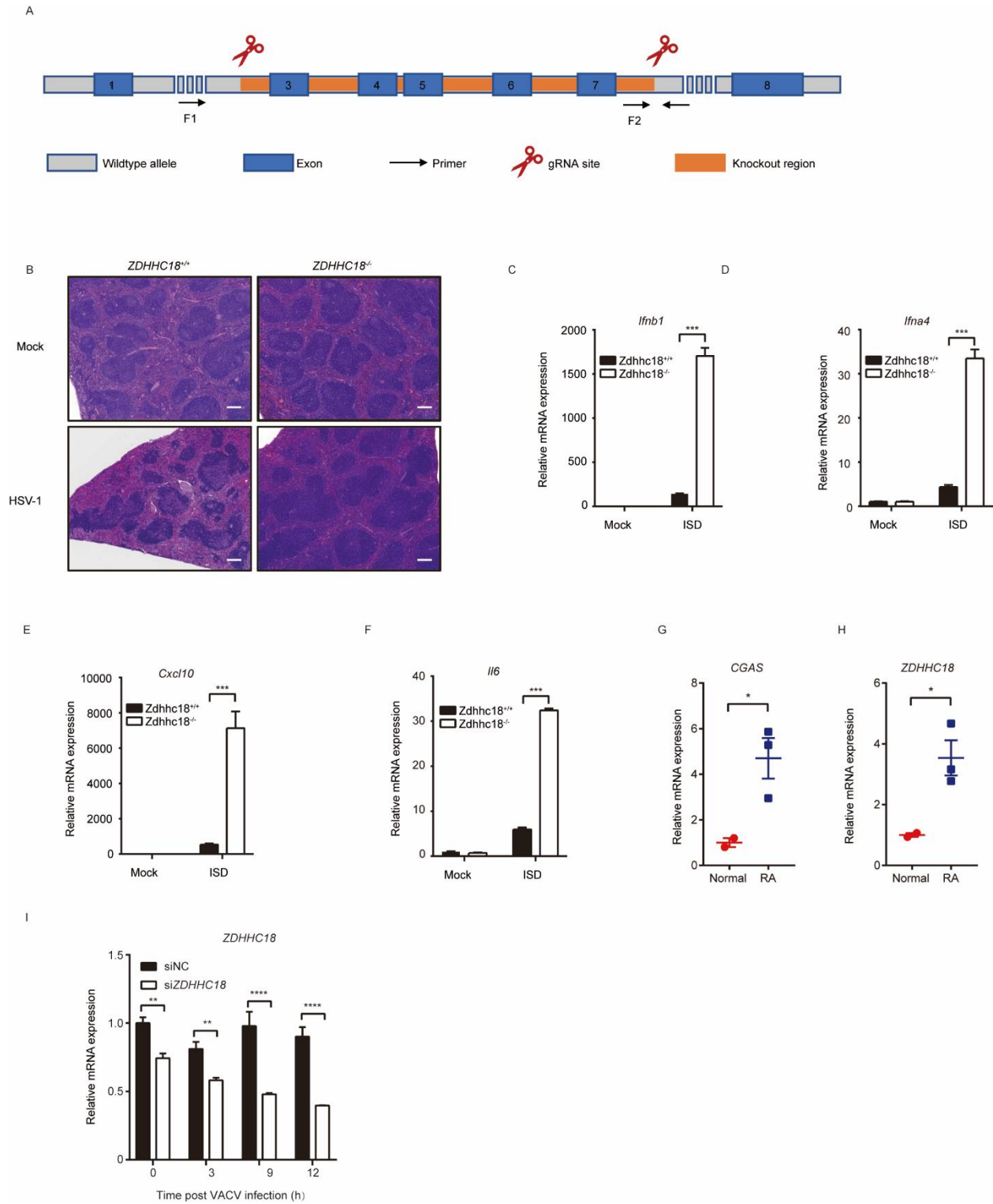


Figure S6. *Zdhhc18* deficiency promotes antiviral activity against DNA viruses in mice.

(A) Schematic presentation of the knockout strategy.

(B) Representative photomicrographs of spleen tissue H&E-stained sections from mice (*Zdhhc18*^{+/+} or *Zdhhc18*^{-/-}) intravenously injected with HSV-1-FS (5×10^7 PFU per mouse) or not after 2 days. PFU: plaque-forming units. H&E staining: hematoxylin-eosin staining. Scale bars: 200 μ m.

(C-F) BMDMs (*Zdhhc18*^{+/+} or *Zdhhc18*^{-/-}) were transfected with ISD (2 μ g/ml) for 8 h before RT-qPCR analysis for the expression of *Ifnb1* (C), *Ifna4* (D), *Cxcl10* (E) and *Il6* (F).

(G-H) PBMCs from two healthy people and three RA patients were analyzed by RT-qPCR for the expression of cGAS and ZDHHC18.

(I) PBMCs from healthy people were transfected with scrambled siRNA or ZDHHC18 siRNA (cocktail) for 48 h and then infected with VACV (1:200) for the indicated time before RT-qPCR analysis of ZDHHC18 expression.

Data information: Data are representative of at least two independent experiments; mean \pm SEM from triplicates of technical replicates, unpaired t test; nc: negative control; *, P<0.05; **, P<0.01; ***, P<0.001; ****, P<0.0001.

Table S1. Materials.

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Antibodies		
cGAS (D3O8O) (mouse specific)	Cell Signaling Tech	31659S
cGAS (D1D3G)	Cell Signaling Tech	15102S
ZDHHC18	Abcam	ab154790
STING/TMEM173	Proteintech	19851-1-AP
p-STING (S365) (D8F4W)	Cell Signaling Tech	72971S
IRF3 (D6I4C)	Cell Signaling Tech	11904S
p-IRF3 (S396) (4D4G)	Cell Signaling Tech	4947S
p-I κ B α (Ser32)	Bioss	bsm-52169S
Anti-Flag tag pAb	MBL	PM020
Anti-Myc tag pAb	MBL	562
Anti-HA tag pAb	MBL	561
Rabbit IgG (DA1E) Isotype Control	Cell Signaling Tech	3900S
GAPDH (14C10)	Cell Signaling Tech	2118S
Calnexin	Abcam	ab22595
Rab7 (D95F2)	Cell Signaling Tech	9367T
EEA1 (C45B10)	Cell Signaling Tech	3288T
Alexa Fluor 488 goat anti-mouse IgG (H+L)	Invitrogen	A11001
Alexa Fluor 488 goat anti-rabbit IgG (H+L)	Invitrogen	A11034
Alexa Fluor 568 goat anti-mouse IgG (H+L)	Invitrogen	A11031
Alexa Fluor 568 goat anti-rabbit IgG (H+L)	Invitrogen	A11011
Bacterial and virus strains		
HSV-1	Zhengfan Jiang's laboratory	N/A
HSV-1 F strain	Zhengfan Jiang's laboratory	N/A
GFP-HSV-1	Zhengfan Jiang's laboratory	N/A
Chemicals, peptides, and recombinant proteins		
Protease Inhibitor Cocktail	Thermo Fisher Scientific	Cat#78430
Phosphatase inhibitor	Thermo Fisher Scientific	Cat#A32957
HT-DNA	Sigma	Cat#D6898
Palmitic acid	Sigma	Cat#P5585
2-Bromopalmitate	Sigma	Cat#238422
NEM	Sigma	Cat#04260
Hydroxylamine	Beyotime	Cat#ST093
Palmostatin B	Merck	Cat#178501
NBD-palmitoyl-CoA	Avanti	Cat#810705
IRDye 800 CW Azide Infrared Dye	LI-COR	Cat#929-60000
17-ODYA	Cayman	Cat#90270
M-CSF, mouse	Sigma	Cat#SRP3221
PMA	Sigma	Cat#P1585
Anti-Myc Magnetic Beads	Bimake	Cat#B26301
Anti-Flag M2 Magnetic Beads	Sigma	Cat#M8823
Anti-Flag affinity gel	Bimake	Cat#B23102
Passive lysis buffer	Promega	Cat#E194A

Luciferase Assay Reagent	Promega	Cat#E1483
TRIzol Reagent	Invitrogen	Cat#15596018
Streptavidin Sepharose-R Beads	Cell Signaling Tech	Cat#3419S
Pierce RIPA Buffer	Thermo Fisher Scientific	Cat#89900
Protein A/G Plus-Agarose	Santa Cruz	Cat#sc-2003
cGAMP	Sigma	Cat#SML1299
DAPI	Beyotime	Cat#C1006
Fluoromount™ Aqueous Mounting Medium	Sigma	Cat#F4680
Crystal Violet Staining Solution	Beyotime	Cat#C0121
Critical commercial assays		
Lipofectamine 3000 Transfection Kit	Invitrogen	Cat#2145954
iScript cDNA synthesis kit	Bio-Rad	Cat#1706691
iTaq Universal SYBR Green Supermix	Bio-Rad	Cat#172521
Pierce BCA Protein Assay Kit	Thermo Fisher Scientific	Cat#23225
Mouse IFN Beta ELISA Kit	Abcam	Cat#252363
Fast Mutagenesis System	Transgen	Cat#FM111
pEASY-Uni Seamless Cloning and Assembly Kit	Transgen	Cat#CU101
SuperSignal™ West Pico PLUS Substrate Kit	Thermo Fisher Scientific	Cat#34578
2'3'-cGAMP ELISA Kit	Cayman	501700
Experimental models: Cell lines		
HEK293T	ATCC	Cat#CRL-3216
HeLa	NICR (National Infrastructure of Cell Line Resource)	N/A
RAW264.7	NICR	N/A
L929	NICR	N/A
Vero	NICR	N/A
THP-1	NICR	N/A
Experimental models: Organisms/strains		
<i>Zdhhc18</i> ^{-/-} mice	Cyagen Biosciences	N/A
C57BL/6 mice	Jackson Laboratory	JAX: 000664
Oligonucleotides		
(FITC-, Biotin-) ISD (45 bp): TACAGATCTACTAGTGATCTATGACTGATCTGTACAT GATCTACA	This paper	N/A
siRNA targeting sequence: ZDHHC18 #1: CCGGCCUCUUCUUCGUCUU	This paper	N/A
siRNA targeting sequence: ZDHHC18 #2: GCGCUCAGGGAAGCAACUU	This paper	N/A
siRNA targeting sequence: ZDHHC18 #3: CCAAGCCUGAUGCCAGCAU	This paper	N/A
Scrambled (control): UUCUCCGAACGUGUCACGU	This paper	N/A
Recombinant DNA		
IFN-Beta pGL3	Addgene	#102597
pCMV3-IRF3-Flag	Sino Biological	#HG12007-CF
pCMV-3Tag (Flag)	Agilent Technologies	#240195
pCMV-3Tag (Myc)	Agilent Technologies	#240196
pLKO.1	Addgene	#10878
pMD2.G	Addgene	#12259

psPAX2	Addgene	#12260
pEF-TBK1-Flag	Dr. Zhengfan Jiang	N/A
pET28b-His-sumo-cGAS	Dr. Conggang Zhang	N/A
pTY-EGFP-cGAS	Dr. Conggang Zhang	N/A
pEF-HA-cGAS	This manuscript	N/A
pCMV-Flag-cGAS	This manuscript	N/A
pCDNA3.1-STING-Flag	This manuscript	N/A
pCMV-Myc-cGAS	This manuscript	N/A
pCMV-Flag-ZDHHC18	This manuscript	N/A
pCMV-Myc-ZDHHC18	This manuscript	N/A
pCMV-HA-ZDHHC18	This manuscript	N/A
pCMV-Myc-ZDHHC18 (CS)	This manuscript	N/A
pCMV-Flag-cGAS (1-160)	This manuscript	N/A
pCMV-Flag-cGAS (161-522)	This manuscript	N/A
pCMV-Flag-ZDHHC18 (M)	This manuscript	N/A
pCMV-Flag-ZDHHC18 (deltaM)	This manuscript	N/A
pLKO.1-shZDHHC2	This manuscript	N/A
pLKO.1-shZDHHC3	This manuscript	N/A
pLKO.1-shZDHHC4	This manuscript	N/A
pLKO.1-shZDHHC5	This manuscript	N/A
pLKO.1-shZDHHC6	This manuscript	N/A
pLKO.1-shZDHHC7	This manuscript	N/A
pLKO.1-shZDHHC8	This manuscript	N/A
pLKO.1-shZDHHC9	This manuscript	N/A
pLKO.1-shZDHHC12	This manuscript	N/A
pLKO.1-shZDHHC13	This manuscript	N/A
pLKO.1-shZDHHC16	This manuscript	N/A
pLKO.1-shZDHHC17	This manuscript	N/A
pLKO.1-shZDHHC18	This manuscript	N/A
pLKO.1-shZDHHC20	This manuscript	N/A
pLKO.1-shmZDHHC18	This manuscript	N/A
Software and algorithms		
GraphPad Prism 7	https://www.graphpad.com/	N/A
Adobe Illustrator CC	https://www.adobe.com/products/illustrator.html	N/A
NIS-Elements Viewer 5.21	https://www.microscope.healthcare.nikon.com	N/A
ImageJ 1.53c	https://imagej.nih.gov	N/A
PyMOL 2.2.0	https://pymol.org	N/A
Imaris 9.6.0	Imaris.oxinst.com	N/A
CaseViewer 2.2	https://www.3dhistech.com	N/A

Table S2. Target sequences of shRNAs.

shRNA	Sequences (5' to 3')
hZDHHc2-sh-F	CCGGGTATGAGCAATCCTGCATTAACCTCGAGTTAATGCAGGATTGCTCATACTT TTTTG
hZDHHc2-sh-R	AATTCAAAAAAGTATGAGCAATCCTGCATTAACCTCGAGTTAATGCAGGATTGCT CATACT
hZDHHc3-sh-F	CCGGCCAGAAGTACTTCGTCCTGTTCTCGAGAACAGGACGAAGTACTTCTGGTT TTTTG
hZDHHc3-sh-R	AATTCAAAAAACCAGAAGTACTTCGTCCTGTTCTCGAGAACAGGACGAAGTACT TCTGGT
hZDHHc4-sh-F	CCGGGAGGTGCTCTACTTGTGATTTCTCGAGAAATCACAAGTAGAGCACCTCTT TTTG
hZDHHc4-sh-R	AATTCAAAAAAGAGGTGCTCTACTTGTGATTTCTCGAGAAATCACAAGTAGAGCA CCTC
hZDHHc5-sh-F	CCGGCGATGTCTTACAGCAGCCAAACTCGAGTTTGGCTGCTGTAAGACATCGTT TTTTG
hZDHHc5-sh-R	AATTCAAAAAACGATGTCTTACAGCAGCCAAACTCGAGTTTGGCTGCTGTAAGA CATCG
hZDHHc6-sh-F	CCGGGGTTTACGATACTGGTTATATCTCGAGATATAACCAGTATCGTAAACCTT TTTTG
hZDHHc6-sh-R	AATTcAAAAAAGGTTTACGATACTGGTTATATCTCGAGATATAACCAGTATCGTAA ACC
hZDHHc7-sh-F	CCGGACTGCCCGTGGGTGAACAATTCTCGAGAATTGTTCAACCCACGGGCAGTTT TTTTG
hZDHHc7-sh-R	AATTcAAAAAACTGCCCGTGGGTGAACAATTCTCGAGAATTGTTCAACCCACGGG CAGT
hZDHHc8-sh-F	CCGGCACCTGCCATGTACAAGTTTACTCGAGTAAACTTGTACATGGCAGGTGTT TTTTG
hZDHHc8-sh-R	AATTcAAAAAACACCTGCCATGTACAAGTTTACTCGAGTAAACTTGTACATGGCA GGTG
hZDHHc9-sh-F	CCGGGAGGAACTACCGCTACTTCTACTCGAGTAGAAGTAGCGGTAGTTCCTCTT TTTTG
hZDHHc9-sh-R	AATTcAAAAAAGAGGAACTACCGCTACTTCTACTCGAGTAGAAGTAGCGGTAGT TCCTC
hZDHHc12-sh-F	CCGGATGGACCCTGGCTACGTGAATCTCGAGATTCACGTAGCCAGGGTCCATT TTTTG
hZDHHc12-sh-R	AATTcAAAAAATGGACCCTGGCTACGTGAATCTCGAGATTCACGTAGCCAGGGT CCAT
hZDHHc13-sh-F	CCGGCTCATGTTATCAGCTCACAAACTCGAGTTTGTGAGCTGATAACATGAGTT TTTTG
hZDHHc13-sh-R	AATTcAAAAAACTCATGTTATCAGCTCACAAACTCGAGTTTGTGAGCTGATAACA TGAG
hZDHHc16-sh-F	CCGGGAAAGACACAATGTGGAGAAACTCGAGTTTCTCCACATTGTGTCTTTCTT TTTTG
hZDHHc16-sh-R	AATTcAAAAAAGAAAGACACAATGTGGAGAAACTCGAGTTTCTCCACATTGTGT CTTTT
hZDHHc17-sh-F	CCGGGCAGGGAATACCACAGTCATTCTCGAGAATGACTGTGGTATTCCCTGCTT TTTTG
hZDHHc17-sh-R	AATTcAAAAAAGCAGGGAATACCACAGTCATTCTCGAGAATGACTGTGGTATTCC CCTGC
hZDHHc18-sh-F	CCGGGTTTATTCTCTCCCTCTCATTCTCGAGAATGAGAGGGAGAGAATAAACTT TTTTG

hZDHHc18 -sh-R	AATTcAAAAAAGTTTATTCTCTCCCTCTCATTCTCGAGAATGAGAGGGAGAGAAT AAAC
hZDHHc20 -sh-F	CCGGGAAGTGGCTCAAATCAACCTTCTCGAGAAGGTTGATTTGAGCCACTTCTT TTTTG
hZDHHc20 -sh-R	AATTcAAAAAAGAAGTGGCTCAAATCAACCTTCTCGAGAAGGTTGATTTGAGCC ACTTC
mZDHHc1 8-sh-F	CCGGCCTGACAACCTAACGAAGATATCTCGAGATATCTTCGTTAGTTGTCAGGTT TTTTG
mZDHHc1 8-sh-R	aattcaaaaaCCTGACAACCTAACGAAGATATCTCGAGATATCTTCGTTAGTTGTCAGG

Table S3. Primers for Quantitative PCR.

qPCR Primers	Sequences (5' to 3')
<i>GAPDH-F</i>	ATGACATCAAGAAGGTGGTG
<i>GAPDH-R</i>	CATACCAGGAAATGAGCTTG
<i>ZDHHC18-F</i>	ACCGGCCTCTTCTTCGTCT
<i>ZDHHC18-R</i>	AACTGCCTGTGTTGTCGATCT
<i>cGAS-F</i>	AAGAAGGCCTGCGCATTCAA
<i>cGAS-R</i>	CCGCCATGTTTCTTCTTGGA
<i>IFN-β-F</i>	CATTACCTGAAGGCCAAGGA
<i>IFN-β-R</i>	CAATTGTCCAGTCCCAGAGG
<i>CXCL10-F</i>	TGGCATTCAAGGAGTACCTC
<i>CXCL10-R</i>	TTGTAGCAATGATCTCAACACG
<i>HSV-1 UL30-F</i>	CATCACCAGCCGGAGAGGGAC
<i>HSV-1 UL30-R</i>	GGGCCAGGCGCTTGTGGTGTA
<i>mActin-F</i>	TGACGTTGACATCCGTAAAGACC
<i>mActin-R</i>	AAGGGTGTAACACGCAGCTCA
<i>mZD18-F</i>	TCAACGGGCAGACAGTGAAAC
<i>mZD18-R</i>	GAAGCGGTAGTTCCTCTCC
<i>mCgas-F</i>	ACCGGACAAGCTAAAGAAGGTGCT
<i>mCgas-R</i>	GCAGCAGGCGTCCACAACCTTAT
<i>mIfn-β-F</i>	ATGGTGGTCCGAGCAGAGAT
<i>mIfn-β-R</i>	CCACCACTCATTCTGAGGCA
<i>mIfn-α4-F</i>	ACCCACAGCCCAGAGAGTGACC
<i>mIfn-α4-R</i>	AGGCCCTCTTGTTCCTGAGGT
<i>mIl6-F</i>	GAGGATACTCCCAACAGACC
<i>mIl6-R</i>	AAGTGCATCATCGTTGTTTCATACA
<i>mCxcl10-F</i>	GCCGTCATTTTCTGCCTCA
<i>mCxcl10-R</i>	CGTCCTTGCGAGAGGGATC
<i>mCcl5-F</i>	GACACCACTCCCTGCTGCTT
<i>mCcl5-R</i>	ACACTTGGCGGTTTCCTTCG
<i>ZDHHC2-F</i>	AACACTGGCGAACAAGTTGTG
<i>ZDHHC2-R</i>	AGATGGGAAGATCCTTGGCTG
<i>ZDHHC3-F</i>	CCACTCCGAAACATTGAGCG
<i>ZDHHC3-R</i>	CCACAGCCGTCACGGATAAA
<i>ZDHHC4-F</i>	TGATGGGTCTTGTCTTATCTGC
<i>ZDHHC4-R</i>	AGGTGTGGTTTCTCGTATGGAA
<i>ZDHHC5-F</i>	CACCTGCCGCTTTTACCGT
<i>ZDHHC5-R</i>	CGGCGACCAATACAGTTATTCAC
<i>ZDHHC6-F</i>	ATGGGTACGTTCTGTTCCGTT
<i>ZDHHC6-R</i>	AAGGGCCAATACCACAACACA
<i>ZDHHC7-F</i>	CTGACCGGGTCTGGTTCATC

<i>ZDHHC7-R</i>	CATGACGAAAGTCACCACGAA
<i>ZDHHC8-F</i>	CTGTTCCCGTCTACAATGGCA
<i>ZDHHC8-R</i>	GACCTGGATACCTCGCACAT
<i>ZDHHC9-F</i>	CCCAGGCAGGAACACCTTTT
<i>ZDHHC9-R</i>	CCGAGGAATCACTCCAGGG
<i>ZDHHC12-F</i>	GTGCTGACCTGGGGAATCAC
<i>ZDHHC12-R</i>	CTGCACATTCACGTAGCCA
<i>ZDHHC13-F</i>	ACCCCACTCTTATTGATGGAGA
<i>ZDHHC13-R</i>	TGTCTGCCCATTTACATCTGTC
<i>ZDHHC16-F</i>	ACTCCGGGGTCTAGTACAGC
<i>ZDHHC16-R</i>	CCAGCGGATCACGTTGTCT
<i>ZDHHC17-F</i>	TGAACCTCTTGGACGGAAAAC
<i>ZDHHC17-R</i>	TGCTTCCACCAATTCTCGACA
<i>ZDHHC20-F</i>	TTCGTGGTTCGTCTGGTCCTA
<i>ZDHHC20-R</i>	AGGTAAACAACGGTCTTTCCATT