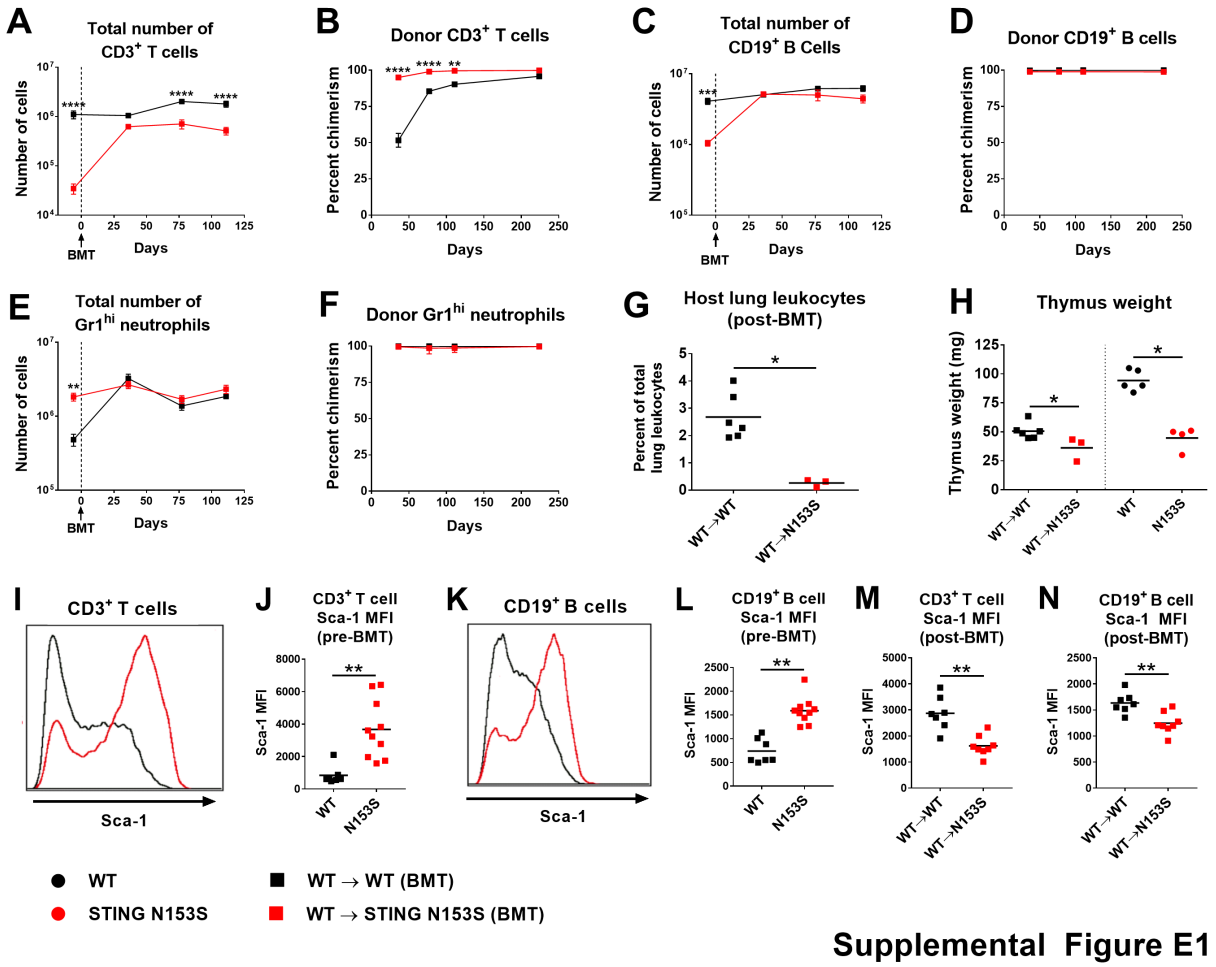
Epitope	*Clone*	*Manufacturer*
CD117	2B8	eBioscience
CD11b	M1/70	eBioscience, Biolegend
CD19	eBio1D3	eBioscience, Biolegend
CD3e	145-2C11, eBio500A2	eBioscience, Biolegend
CD4	GK1.5	eBioscience, Biolegend
CD45.1	A20	eBioscience, Biolegend
CD45.2	104	eBioscience, Biolegend
CD45R (B220)	RA3-6B2	eBioscience, Biolegend
CD8a	53-6.7	eBioscience, Biolegend
Ly6C	AL-21	Biolegend
Ly6G	1A8	Biolegend
NK1.1	PK136	eBioscience, Biolegend
Sca-1 (Ly-6A/E)	D7	eBioscience, Biolegend
Ter119	TER-119	eBioscience
CD44	IM7	eBioscience, Biolegend
CD25	PC61.5	eBioscience, Biolegend
F4/80	BM8	eBioscience, Biolegend

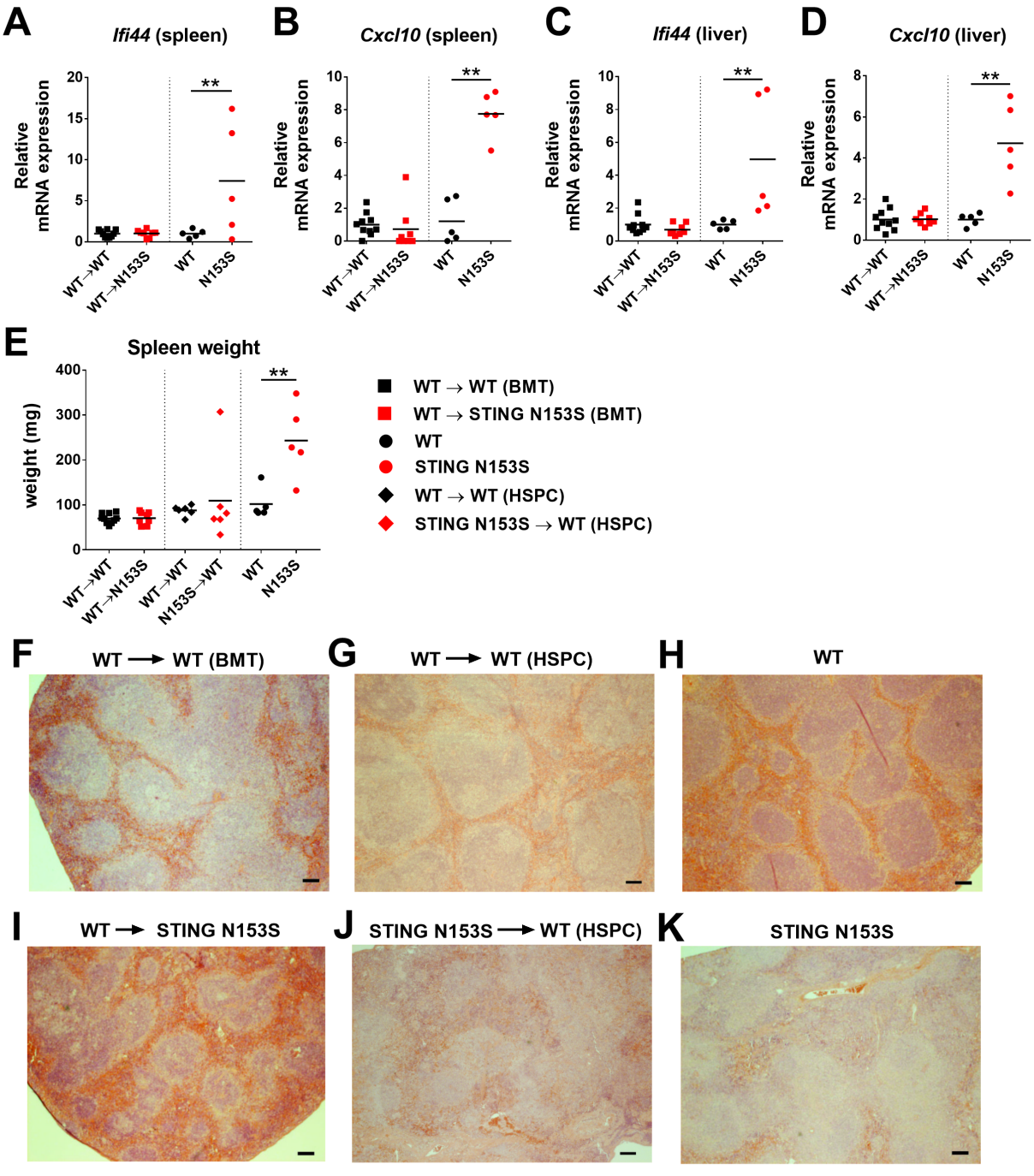
Table E1. Antibodies used in flow cytometry experiments.

Primer	*PrimerBank ID*	*Sequence*
cxcl10-for	10946576a1	CCAAGTGCTGCCGTCATTTTC
cxcl10-rev	10946576a1	GGCTCGCAGGGATGATTTCAA
ifi44-for	19527086a1	AACTGACTGCTCGCAATAATGT
ifi44-rev	19527086a1	GTAACACAGCAATGCCTCTTGT
hprt-for	7305155a1	TCAGTCAACGGGGGACATAAA
hprt-rev	7305155a1	GGGGCTGTACTGCTTAACCAG
rpl13a-for	334688867c2	AGCCTACCAGAAAGTTTGCTTAC
rpl13a-rev	334688867c2	GCTTCTTCTTCCGATAGTGCATC
eef2-for	237858599c1	CCGACTCCCTTGTGTGCAA
eef2-rev	237858599c1	AGTTCAGGTCGTTCTCAGAGAG

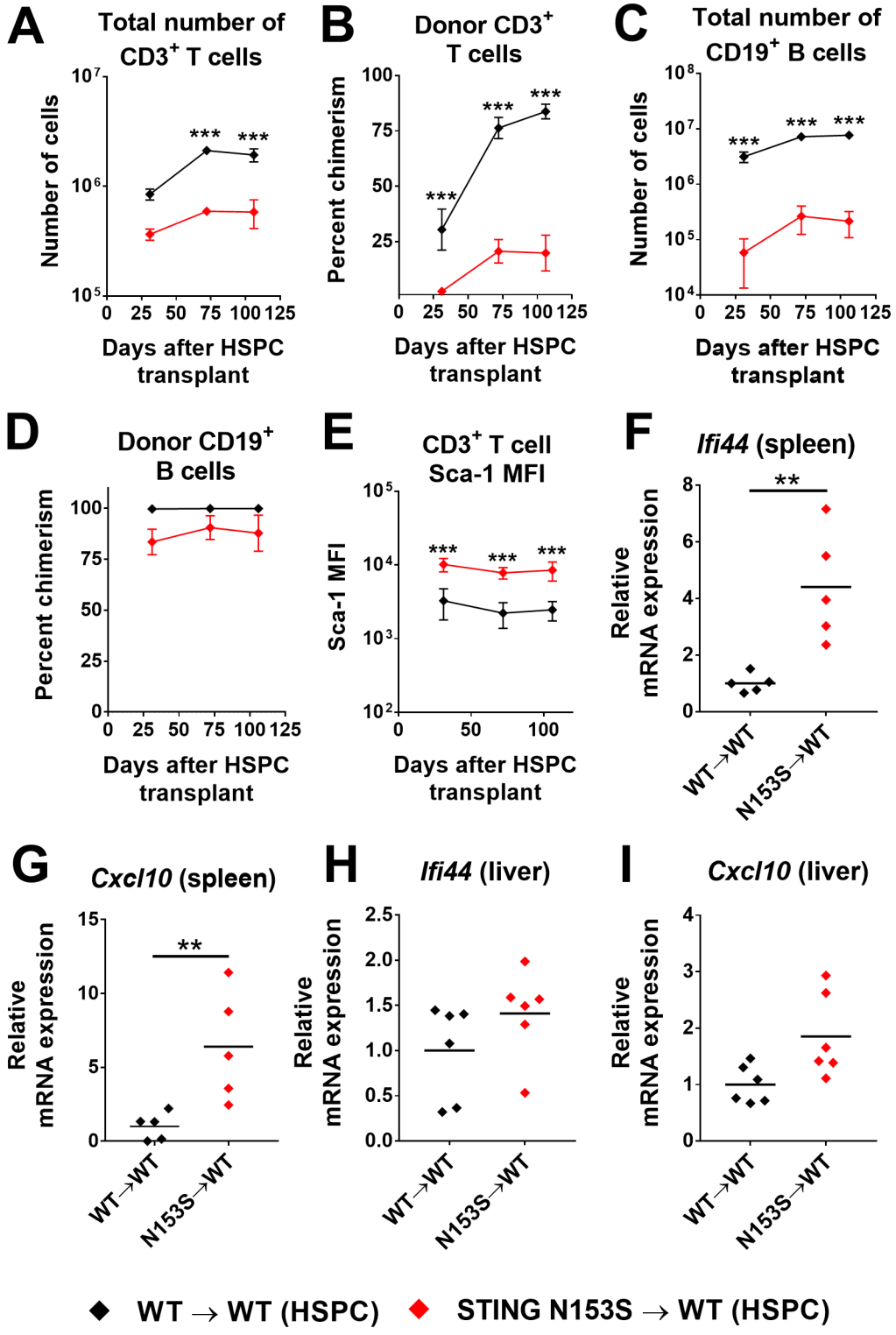
Table E2. Primers used in qRT-PCR experiments.



Supplemental Figure E1

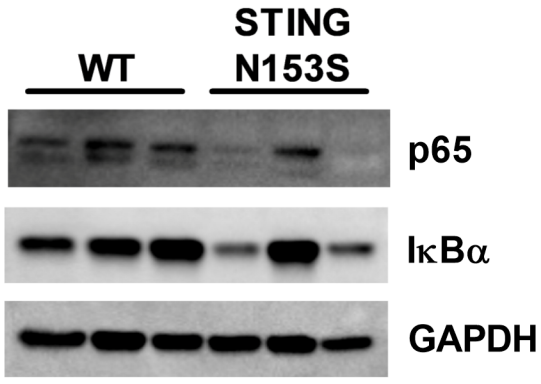


Supplemental Figure E2

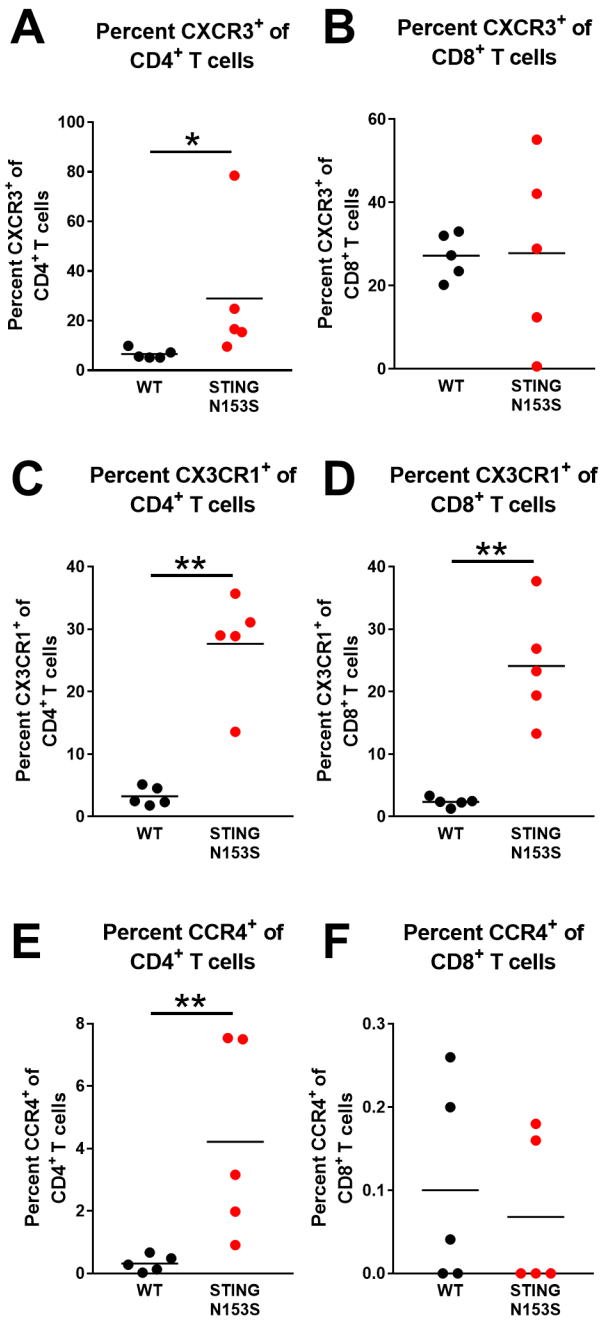


Supplemental Figure E3

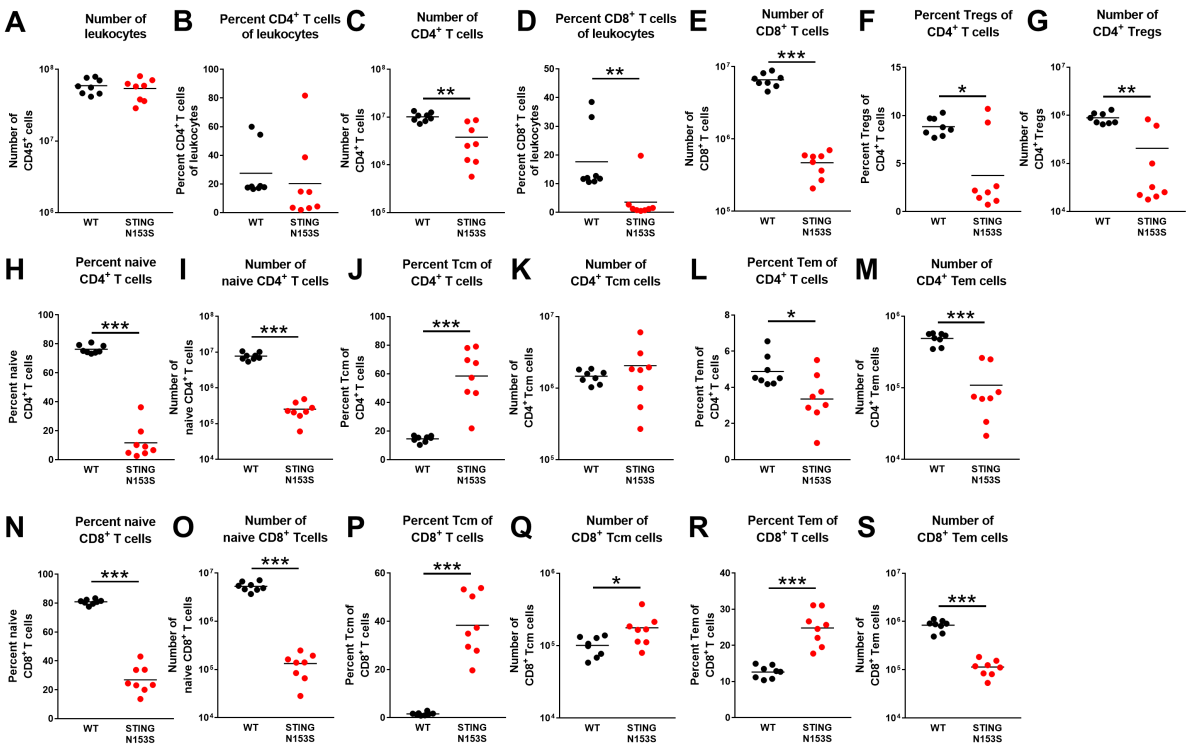
A



Supplemental Figure E4



Supplemental Figure E5



Supplemental Figure E6

ONLINE REPOSITORY

STING-associated lung disease in mice relies primarily on T cells but not type I interferon

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FIGURE LEGENDS

FIG E1. Mixed chimerism after WT bone marrow transplantation (BMT). 9-13 week-old adult WT and STING N153S mice were lethally irradiated and followed by transplantation of WT bone marrow. **A-F,** Peripheral blood was longitudinally analyzed for total numbers of $CD3^+$ T cells (A), donor $CD3^+$ T cells (B), total number of $CD19^+$ T cells (C), donor $CD19^+$ B cells (D), total number of $CD11b^+$ $Gr\text{-}1^{hi}$ neutrophils (E) and donor neutrophils. Data in (A-F) represent the mean ± SEM of n = 6-10 samples. **G,** Total number of $CD45.2^+$ leukocytes in the lung of WT and STING N153S recipient mice as quantitated by flow cytometry 224 days after transplantation. **H,** Thymus weight of transplanted WT and STING N153S mice as well as age-matched non-transplanted WT and STING N153S control animals. **I,** Representative histogram showing Sca-1 expression on $CD3^+$ splenocytes of non-transplanted WT and STING N153S mice. **J,** MFI of Sca-1 expression on $CD3^+$ T cells before BMT. **K,** Representative histogram showing Sca-1 expression on $CD3^+$ splenocytes of non-transplanted WT and STING N153S mice. **L,** MFI of Sca-1 expression on $CD19^+$ B cells before BMT. **M,** MFI of Sca-1 expression on $CD3^+$ T cells after BMT. **N,** MFI of Sca-1 expression on $CD19^+$ B cells after BMT. with n = 3 - 6 mice per group. Data in (A-F) were analyzed by 2-way ANOVA. **, $P < 0.01$; ***, $P < 0.001$; ****, $P < 0.0001$. Data in (G-N) were analyzed by Mann-Whitney test. *, $P < 0.05$; **, $P < 0.01$.

FIG E2. WT bone marrow transplantation (BMT) reduces ISG expression and improves splenic architecture in STING N153S mice. **A-D,** ISG expression levels in spleens and livers of indicated groups of mice were assessed by qRT-PCR and reported as the fold change relative to the average of 3 housekeeping genes (*hprt1*, *rpl13a*, and *eef2*). Data represent the mean of n = 5-10 tissues per group. Results were analyzed by Mann-Whitney test. *, $P < 0.05$; **, $P < 0.01$. **E,** Weights of spleen from irradiated WT and STING N153S recipients of WT bone marrow, WT recipients of either STING N153S or WT HSPCs and WT and STING N153S non-irradiated control animals. **F-K,** Representative images of

H&E-stained spleen sections of indicated genotypes. Scale bar = 200 μm. Data represent the mean of n = 5-10 mice.

FIG E3. STING N153S HSPC transplantation into WT mice causes ISG upregulation. Flow cytometric characterization of PBMCs and tissue expression of ISGs in WT mice transplanted with WT and STING N153S HSPCs. **A-E,** Peripheral blood was longitudinally examined for total numbers of $CD3^+$ T cells (A), donor $CD3^+$ T cells (B), total number of $CD19^+$ B cells (C), donor $CD19^+$ B cells (D), and Sca-1 MFI on $CD3^+$ T cells (E). Data in (A-E) represent mean ± SEM of two independent experiments and were analyzed by two-way ANOVA test. n = 6 mice per group. ***, $P < 0.001$. **F-I,** ISG expression levels in spleens and livers of indicated groups of mice were assessed by qRT-PCR and reported as the fold change relative to the average of 3 housekeeping genes (*hprt1*, *rpl13a*, and *eef2*). Results were analyzed by Mann-Whitney test. n = 6 per group. **, $P < 0.01$.

FIG E4. NF-κB activation in the lungs of WT and STING N153S mice. Western blot analysis from WT and STING N153S lung homogenates taken from n = 3 mice per genotype for p65, IκBα, and housekeeping control GAPDH protein expression in lung homogenate from age-matched 13-17 week-old WT and STING N153S mice. Results are representative of 7 biological replicates analyzed in 2 independent experiments.

FIG E5. Chemokine receptor expression on $CD4^+$ and $CD8^+$ splenic T cells WT and STING N153S spleens were harvested for flow cytometric characterization of chemokine receptors on $CD4^+$ and $CD8^+$ T cells. **A-F,** Percent positivity of CXCR3 (A,B), CX3CR1 (C,D), and CCR4 (E,F) on $CD4^+$ and $CD8^+$ splenic T cells.Data in (A-F) represent mean of two independent experiments and were analyzed by Mann-Whitney test. n = 5 mice per group. *, $P < 0.05$; **, $P < 0.01$.

FIG E6. T cell subset analysis in WT and STING N153S mice. Splenocytes from 4-month-old WT and STING N153S mice were harvested and T cell subsets examined by flow cytometry. **A,** Total number of $CD45^+$ cells. **B-C**, Percent and number of $CD4^+$ T cells. **D-E**, Percent and number of $CD8^+$ T cells. **F-G**, Percent and number of $CD25^+$ $Foxp3^+$ $CD4^+$ T cells. **H-I**, Percent and number of $CD44^{lo}$ $CD62L^{hi}$ naïve $CD4^+$ T cells. **J-K**, Percent and number of $CD44^{hi}$ $CD62L^{hi}$ $CD4^+$ central memory T cells (Tcm). **L-M**, Percent and number of $CD44^{hi}$ $CD62L^{lo}$ $CD4^+$ effector memory T cells (Tem). **N-O**, Percent and number of $CD44^{lo}$ $CD62L^{hi}$ $CD8^+$ naïve T cells. **P-Q**, Percent and number of $CD44^{hi}$ $CD62L^{hi}$ $CD8^+$ Tcm cells. **R-S**, Percent and number of $CD44^{hi}$ $CD62L^{lo}$ $CD8^+$ Tem cells. Data in A-S represent the mean of $n = 8$ mice per genotype from two independent experiments. Data were analyzed by Mann-Whitney test. *, $P < 0.05$; **, $P < 0.01$.