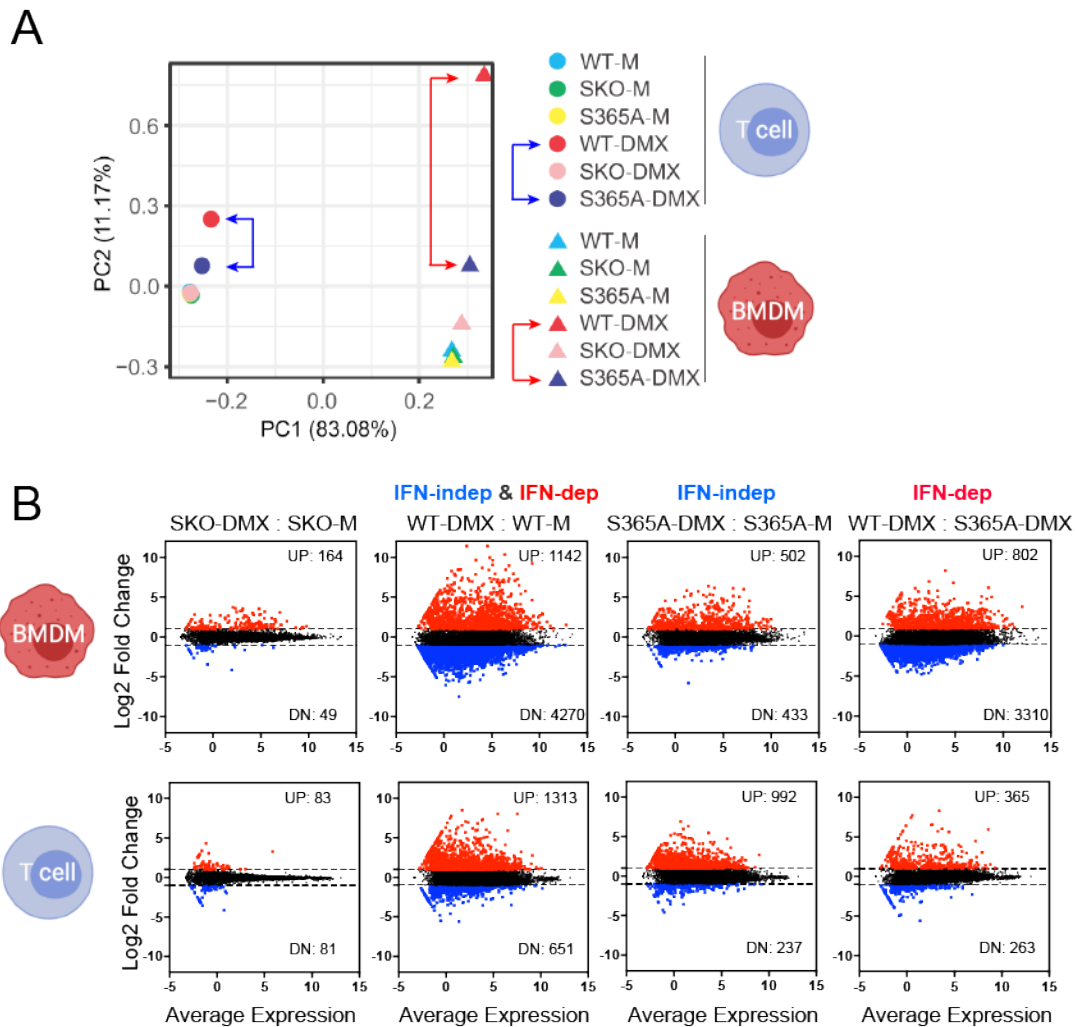


**Figure S1. Sting-S365A mutation does not block STING-mediated NFκB signalling and autophagy in BMDMs. Related to Figure 1.**

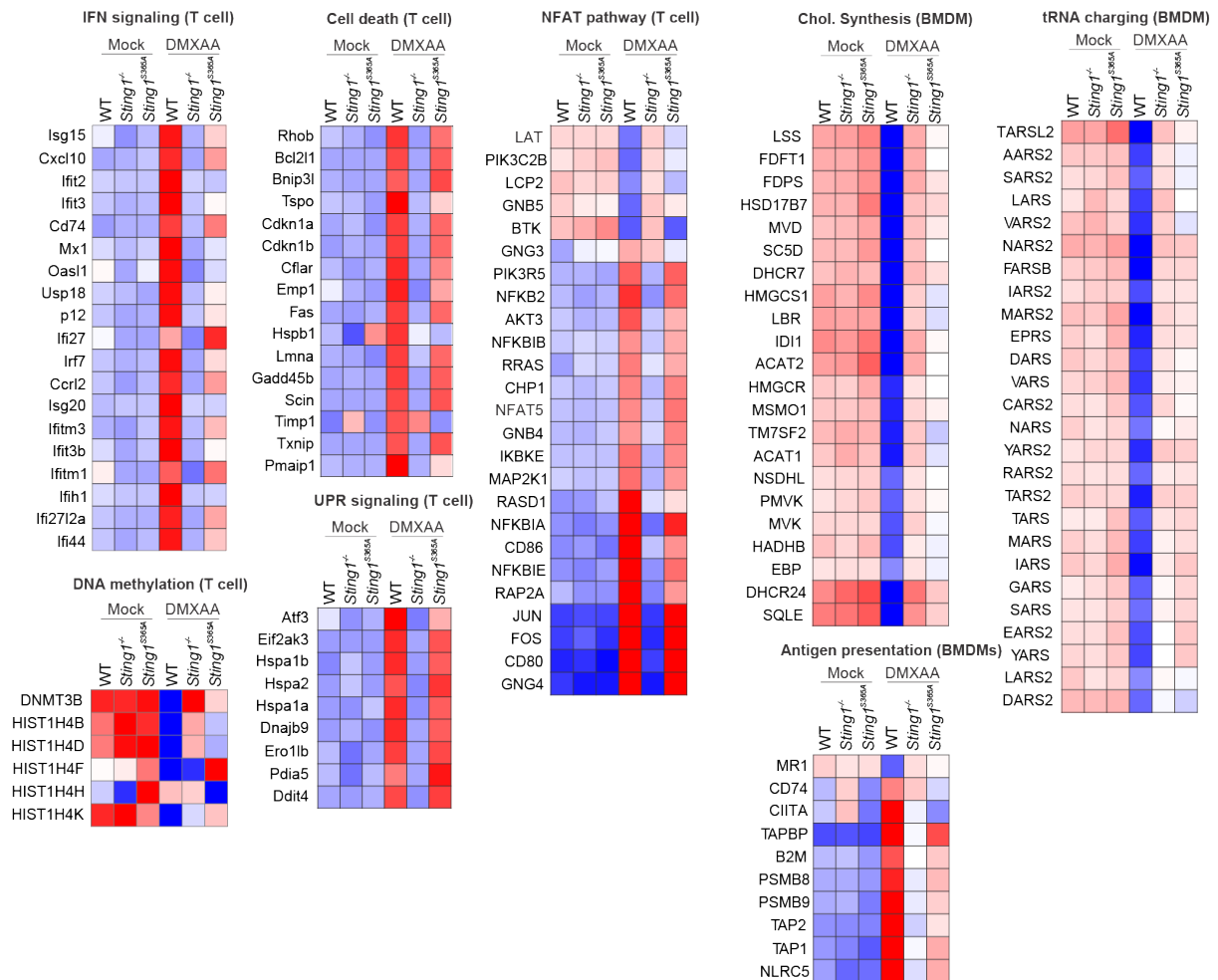
WT, *Sting1*<sup>-/-</sup> or *Sting1*<sup>S365A/S365A</sup> (*Sting1*<sup>S365A</sup>) BMDMs were treated with mock or DMXAA (10 μg/ml) for 6 h. NFκB pathway and autophagy activation were measured by Western blot with indicated antibodies.



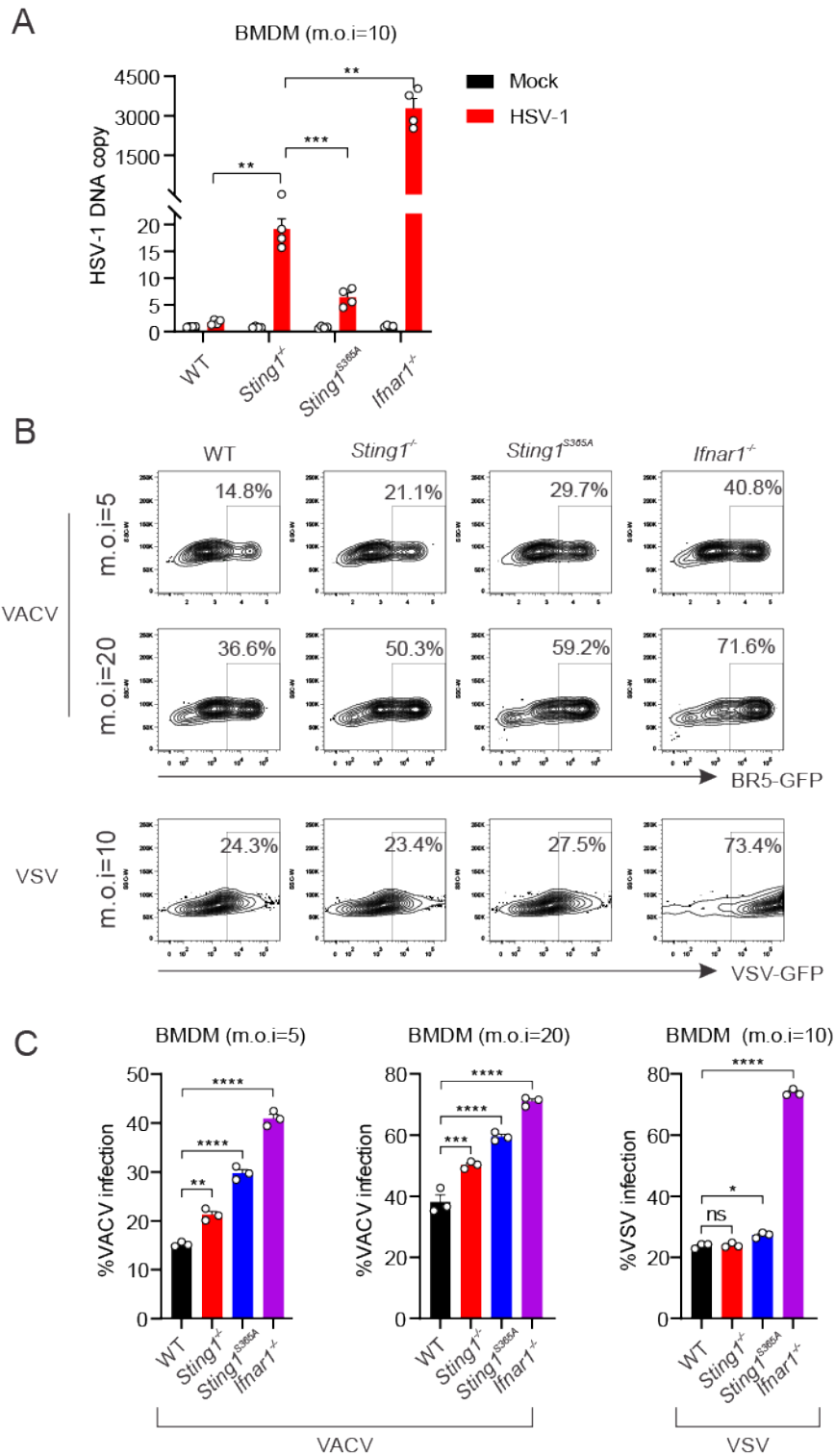
**Figure S2. Transcriptomic discovery of IFN-dependent and IFN-independent activities of STING. Related to Figure 2.**

**(A)** Principal component analysis (PCA) showing transcriptomic landscape of WT, *Sting1*<sup>-/-</sup> (SKO), and *Sting1*<sup>S365A</sup> (S365A) BMDMs or T cells after mock or DMXAA stimulation.

**(B)** MA plots of differentially expressed genes (DEGs) in paired groups. The plot visualizes the differences between measurements taken in a pair of samples, by transforming the data onto M (log ratio) and A (mean average) scales, then plotting these values. Sample pair names are showing on top. UP, up-regulated genes; DN, Down-regulated gene. See **STAR Method** for more details.



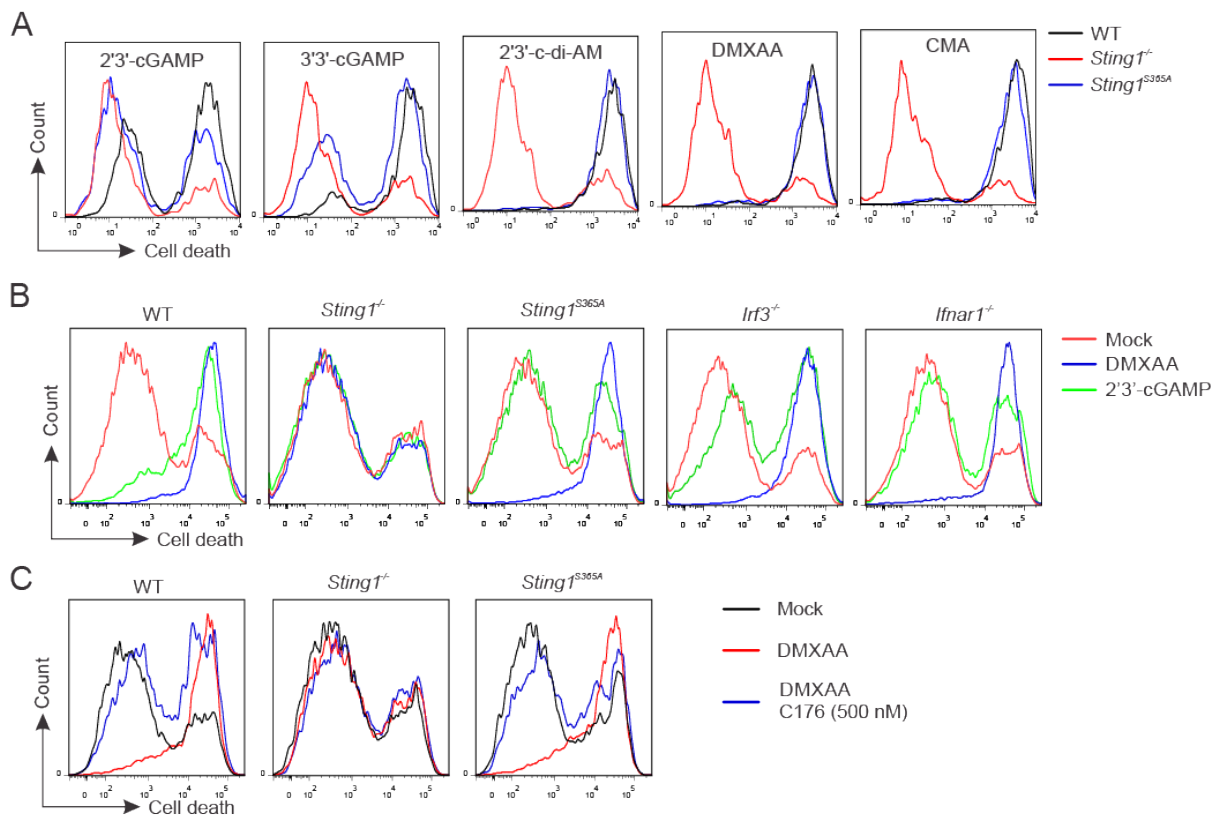
**Figure S3. Selected IFN-dependent and IFN-independent pathways altered by STING activation. Related to Figure 2.** Heatmaps showing previously known and unknown pathways altered by STING activation in BMDMs or T cells. Data from RNA-seq and pathway analysis in Figure 2.



**Figure S4. *Sting1*<sup>S365A/S365A</sup> restricts HSV-1 but not Vaccinia virus infection in BMDMs. Related to Figure 3.**

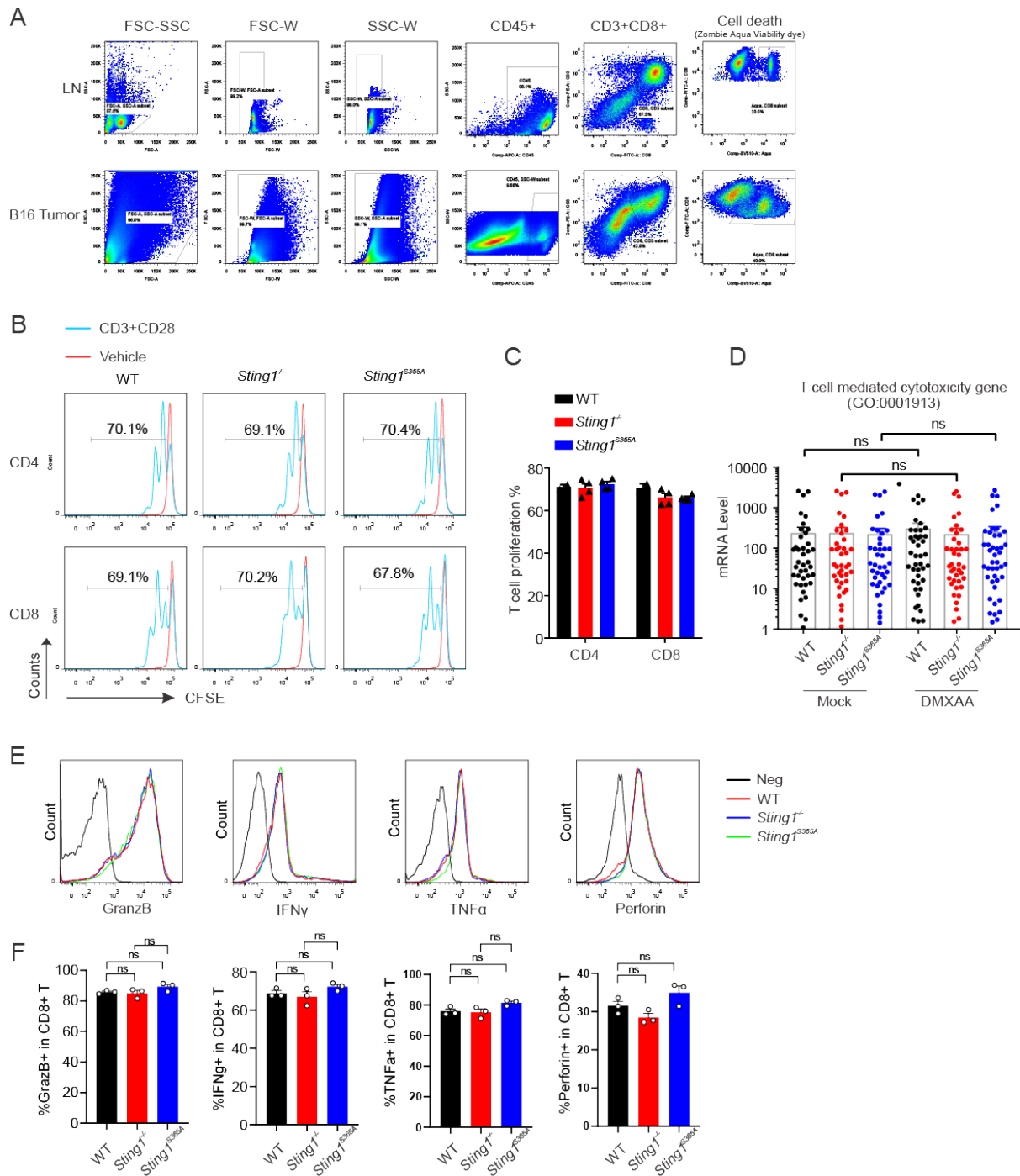
**(A)** HSV-1 infection of BMDMs. WT, *Sting1*<sup>-/-</sup>, *Sting1*<sup>S365A/S365A</sup> (*Sting1*<sup>S365A</sup>) or *Ifnar1*<sup>-/-</sup> BMDMs were infected with HSV-1 (m.o.i.=10) for 24 hours. HSV-1 DNA copy was quantified by qPCR.

**(B-C)** Vaccinia virus (VACV) and Vesicular stomatitis virus (VSV) infection of BMDMs. WT, *Sting1*<sup>-/-</sup>, *Sting1*<sup>S365A/S365A</sup> (*Sting1*<sup>S365A</sup>) or *Ifnar1*<sup>-/-</sup> BMDMs were infected with VACV or VSV at indicated m.o.i. for 12 h. Then, cells were fixed and analysed by FACS. Representative FACS plots are shown in **B** and quantitation of viral infection are shown in **C**. Data are representative from at least two independent experiments.



**Figure S5. STING agonists show differential dependency on S365/IFN in inducing T cell death. Related to Figure 4.**

Representative FACS plots corresponding to data in **Figure 4, A** for **Figure 4B-F**; **B** for **Figure 4G**; **C** for **Figure 4H**.



**Figure S6. WT, *Sting1*<sup>-/-</sup> and *Sting1*<sup>S365A/S365A</sup> T cells show similar proliferation and cytotoxicity in vitro. Related to Figure 5.**

(A) Gating strategy of T cell death FACS analysis in B16 tumour and draining lymph node.

(B,C) Proliferation analysis of WT, *Sting1*<sup>-/-</sup> and *Sting1*<sup>S365A/S365A</sup> CD4<sup>+</sup> and CD8<sup>+</sup> T cells.

Splenic T cells were labelled with CFSE and treated with vehicle or  $\alpha$ -CD3/CD28 antibodies for 3 days. Cell proliferation was analysed by FACS and quantified by CFSE dilution. Representative FACS plots (B) and quantitation (C) are shown.

(D) T cell-mediated cytotoxicity (GO term: 0001913) mRNA expression. Data from RNA-seq dataset. Each dot represents a different gene. ns, not significant. Two-way ANOVA test.

(E) T cell-mediated cytotoxicity (GO term: 0001913) mRNA expression. Data from RNA-seq dataset. Each dot represents a different gene. ns, not significant. Two-way ANOVA test.

(F) T cell-mediated cytotoxicity (GO term: 0001913) mRNA expression. Data from RNA-seq dataset. Each dot represents a different gene. ns, not significant. Two-way ANOVA test.

**(E,F)** Cytotoxicity of primary CD8<sup>+</sup> T cells. CD8<sup>+</sup> T cell were isolated from spleen and stimulated with  $\alpha$ -CD3/CD28 antibodies for 2 days followed by intracellular staining of Granzym B (GranzB), IFN $\gamma$ , TNF $\alpha$  and Perforin. Representative FACS plots **(E)** and quantitation **(F)** are shown.

Data are reprehensive of at least two independent experiments.