

Supplementary Figure legends

Supplementary Figure S1. Integrated analysis of promoter methylation and protein expression of STING and cGAS in human melanoma cell lines. Methylation levels of *STING* (A) and *cGAS* (B) in 16 human melanoma cell lines were assessed by whole-genome methylation profiling using Illumina MethylationEPIC BeadChip microarray. Methylation levels for *STING* (18 probes) and *cGAS* (8 probes) are presented as β -values ranging from 0 to 1. Each melanoma cell line is presented by a unique marker. Colored lines below show the probes position in the gene, where TSS1500 (yellow) and TSS200 (purple) indicate 1500 and 200 base-pairs upstream of the transcription site, respectively. Column plots above represent the correlation (r) between the β -value in each probe and the protein expression (blue: negative correlation; red: positive correlation).

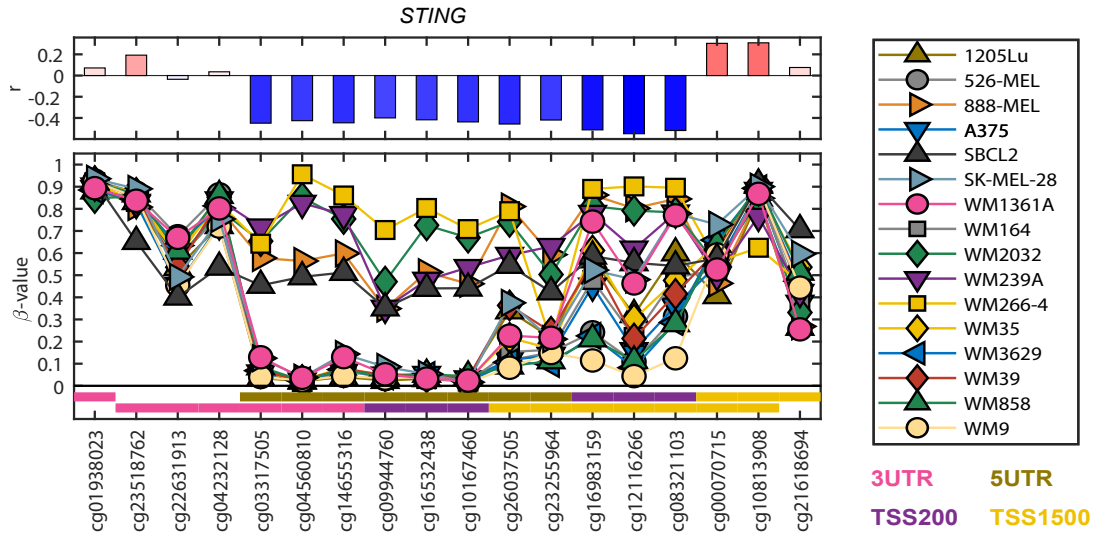
Supplementary Figure S2. Genetic depletion of DNMT1 and DNMT3B in WM1361A melanoma cell line results in re-expression of STING. Immunoblot analysis of STING, DNMT1 and DNMT3B expression in WM1361A melanoma cell line transfected with siRNA targeting DNMT1 (si-DNMT1), DNMT3B (si-DNMT3B) or control siRNA (si-Control) **(A)**. Ratio of total STING relative to β -actin in indicated cell lines quantified using ImageJ software **(B)**.

Supplementary Figure S3. CXCL10 and IFN- β expression in WM266-4, SBCL-2 and 888-MEL melanoma cell lines. WM266-4, SBCL-2 and 888-MEL with or without 5AZADC pretreatment were stimulated with 2'3'-cGAMP for 24 h. CXCL10 **(A)** and IFN- β **(B)** levels in cell culture supernatants were measured using ELISA. Data represent mean \pm SD for two or three biological replicates.

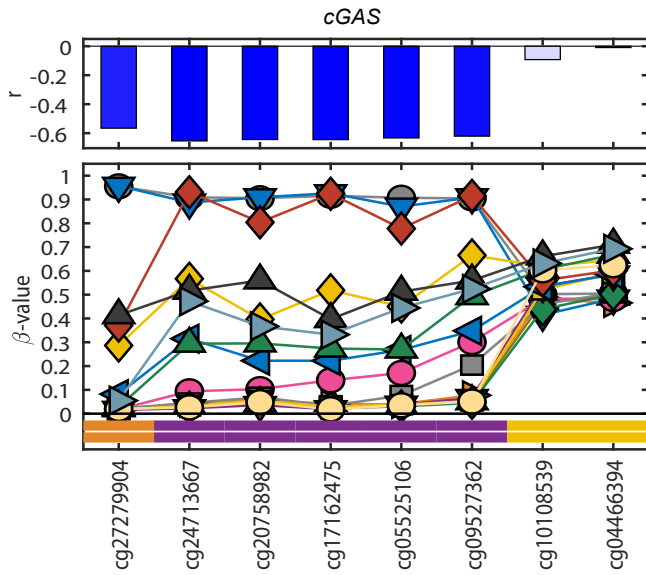
Supplementary Figure S4. Intact activation of STING signaling is required for dsDNA-induced upregulation of MHC class I. Representative histograms **(A)** and mean fluorescence intensity (MFI) **(B)** of HLA-A.B.C expression on 526-MEL cells (with or without 5AZADC pretreatment) following stimulation with dsDNA for 24 h. Data represent mean \pm SD for three biological replicates.

Supplementary Figure 1.

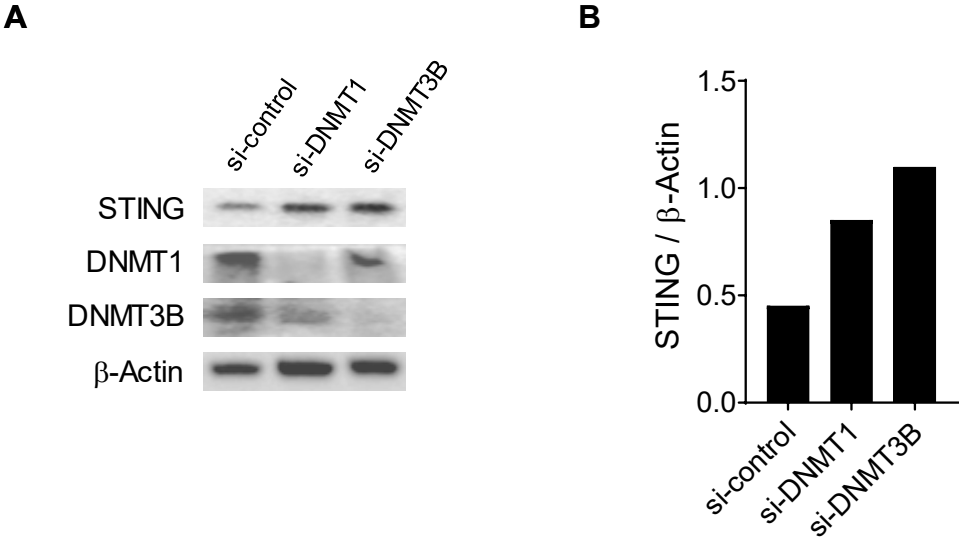
A



B

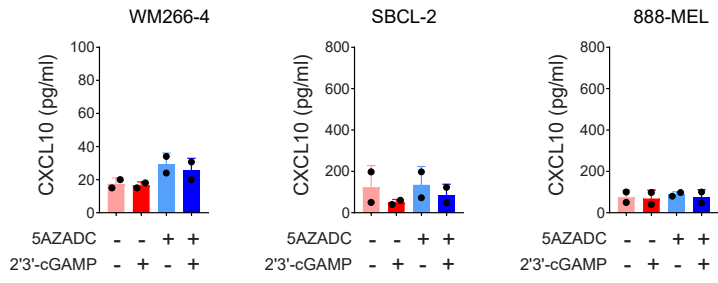


Supplementary Figure 2.

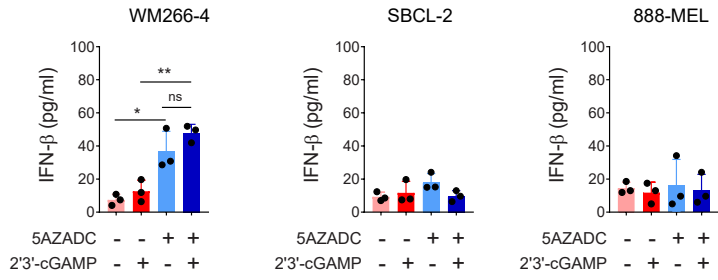


Supplementary Figure 3.

A



B



Supplementary Figure 4.

