Supplemental Materials and Methods

Cell lines

A20 lymphoma and 4T1 breast cancer cells were maintained at 37°C with 5% CO_2 in RPMI supplemented with 10% heat-inactivated FCS, 100 U/ml penicillin/streptomycin/ampicillin, and 50μM 2-mercaptoethanol. GFP-A20, mCherry-A20, and $B2m^{-/-}$GFP-A20 lymphoma cells were generated as previously described.(1) RAW264.7 (RAW) macrophage cells were a gift from Dr. Shu Hsia Chen, and were maintained at 37°C with 5% CO2 in DMEM with Glutamax (Gibco) with 10% heat-inactivated FCS and 100U/ml penicillin/streptomycin/ampicillin.

$TLR^{-/-}$ RAW were generated by CRISPR-Cas9 gene editing. Guide RNA targeting exon 3 of TLR2 (5'- GCTCGGCGATTTCAACCCCT-3'), exon 1 of TLR4 (5'-GTCCTAGCCAGGAGCCAGGG-3'), exon 3 of TLR7 (5-GCAGGAGCTCTGTCCTTGAG-3'), or exon 2 of TLR9 (5-GCTGGGCAGTCGGGGCACAG-3') were cloned into lentiCRISPRv2 (Addgene plasmid #52961) and transduced into RAW. After 1 week of 4ug/mL puromycin selection, surviving cells were single-cell sorted into 96-well plates. Viable clones that formed colonies were screened for TLR activity, using 2ug/mL Pam3CSK4, LPS, R848, and CpG (Invivogen). $TLR^{-/-}$ RAW cells were activated for 24hrs with TLR ligands; activation was measured as upregulation of CD40 by flow cytometry. A single clone from each generated $TLR^{-/-}$ cell line was selected based on lack of reactivity to respective TLR ligand while maintaining activity in non-targeted TLRs. An empty vector control cell line was generated by transduction with lentivirus encoding lentiCRISPRv2 plasmid and used as TLR-competent control (referred to as EV RAW).

Flt3L treatment *in vivo* and splenocyte isolation for murine phenotypic and functional assays

Balb/c WT, C57BL/6 WT, C57BL/6-$MyD88^{-/-}$, and C57BL/6-$TRIF^{-/-}$ mice were treated *in vivo* with intraperitoneal injection of 30ug Flt3L (Celldex) for 9 days, as previously described (1). On day 10, mice were sacrificed, spleens were dissected, and single cell suspensions were obtained by mechanical disruption and filtering through a 70μm cell strainer. Red blood cells were lysed using ACK buffer (Lonza). Flt3L-splenocytes, used as a DC source, were used fresh, or frozen in media containing 20% heat-inactivated FCS and 10% DMSO for later use. For a subset of experiments, $CD11c^+$ isolation was performed using magnetic separation with CD11c ultrapure microbeads (Miltenyi).

Multiplex bead assay (Luminex) for DC cytokine production

$CD11c^+$ cells isolated from Flt3L splenocytes were resuspended at $1x10^6$ cells/mL in RPMI and plated in 96-well plates. Following 24hr activation with synthetic TLRa or naPRRa, supernatants were collected and stored at -80°C until analysis. Samples were analyzed in duplicates by a 32-plex Luminex assay (Millipore). Morpheus software from the Broad Institute was used to generate heatmaps, with hierarchical clustering by k-means.

RT-qPCR

Flt3L splenocytes were plated at $1x10^6$ cells/200uL in 96-well plates. After 12hr activation with naPRRa or synthetic TLRa, RNA was extracted by RNeasy Mini Kit (Qiagen), and cDNA synthesized using SuperScript III First-Strand Synthesis SuperMix (Invitrogen). Quantitative RT-PCR was performed using PowerUP SYBR Green Master Mix (Applied Biosystems)

and primers listed in Supplemental Table III, and technical duplicates per sample were amplified on a BIO-RAD CFX384 Real-Time System, C1000 Touch Thermal Cycler. Results were quantified using the ΔΔCt method (normalized to 18s rRNA).

OT-I ovalbumin cross-presentation assay

Flt3L splenocytes from C57BL/6 mice were resuspended at $1x10^6$ cells/mL in RPMI with 10ug/mL ovalbumin protein and plated at 200uL/well in a deep 96-well assay block plate (Corning). After 24hrs, synthetic TLRa or naPRRa were added to wells. After 24hrs of activation, spleen and LNs were removed from OT-I mice and processed as described above. OT-I cells were stained with CellTrace Violet (ThermoFisher) and labeled OT-I cells were then added at a Flt3L splenocyte:OT-I splenocyte ratio of 1:5. OT-1 activation was assessed by flow cytometry after 72hrs of co-culture, while proliferation was assessed after 96hrs.

RAW activation assay

WT and $TLR^{-/-}$RAW cells were plated at $5x10^4$ cells/well in DMEM in 96-well flat-bottom plates. After allowing cells to adhere overnight, 2ug/mL synthetic TLRa or 5% v/v naPRRa was added. Activation was assessed after 24hrs by flow cytometry.

RAW cross-presentation assay

WT and $TLR^{-/-}$RAW cells were plated in 96-well flat-bottom plates at $2.5x10^3$ cells/well. After 24hrs, 50uL $B2m^{-/-}$ or $B2m^{-/-}$GFP- XRT A20s (prepared as described above) or 50uL GFP peptide (1ug/mL) were added to the RAW cells, together with 1ug/mL synthetic TLRa or 5% v/v nPRRa. After 24hrs, CellTrace violet-stained JEDI anti-GFP CD8 T-cells, isolated using CD8 T-cell enrichment kit (Invitrogen), were added to each well at a density of $2.5x10^5$ cells per 100uL. JEDI anti-GFP CD8 T-cell activation was assessed by flow cytometry after 72hrs of co-culture.

Principal Component Analysis (PCA) and feature selection to generate predictive model of T-cell cytotoxicity

Phenotypic data of murine splenocytes and isolated DCs, acquired by spectral flow cytometry (MFI of costimulatory markers), RT-qPCR (ISG mRNA expression), and multiplex bead assay (cytokine production) were compiled, generating a dataset of 155 unique phenotypic observations induced by each synthetic PRRa and naPRRa. Feature selection was performed on this dataset, in order identify markers that correlated with priming of cytotoxic CD8 T-cell response by Spearman correlation with Benjamini-Hochberg False Discovery Rate correction for multiple hypothesis testing. A Spearman adjusted p value of < 0.01 was used as a cut-off to identify significant associations, generating a new dataset of 43 phenotypic markers that correlated with T-cell cytotoxicity. PCA was performed on both datasets. Principal Components (PC) were calculated using the prcomp function in R. The loading along PC1 was used as a summary metric to discriminate between putatively effective and ineffective naPRRa. Those candidates with PC1 loadings greater than Pneumovax23 in the 43 marker PCA were considered effective.

Immunofluorescence Imaging

Tumors were washed in PBS and incubated in PLP buffer (0.05M phosphate buffer containing 0.1M L-lysine [pH 7.4], 2mg/mL NaIO4, and 10mg/mL paraformaldehyde) overnight at 4°C. Tissue was equilibrated sequentially in 10%, 20%, and 30% sucrose solutions for 2hrs each before embedding in OCT (ThermoFisher) and rapidly frozen on dry ice, and then stored at -

Aleynick M, *et al. J Immunother Cancer* 2023; 11:e007198. doi: 10.1136/jitc-2023-007198

80°C. Frozen histological tumor samples were sectioned at 10uM with a cryostat. Sections were washed in PBS for 5min. Blocking was performed in the dark at RT, for 1hr, with PBS, 2% FBS, and 1% BSA (blocking buffer). Sections were incubated overnight in 10% blocking buffer at 4°C, with conjugated antibodies staining for GFP (Biolegend, AF488, clone FM264G, 1:200), CD11c (Biolegend, AF594, clone N418, 1:200) and CD8 (Biolegend, AF647, clone 53-6.7, 1:200). Nuclei were stained with 300nM DAPI (Invitrogen). Slides were mounted with Prolong Gold anti-fade reagent (Invitrogen) and left to dry overnight. Images were acquired using a Zeiss LSM780 confocal microscope. All images were obtained at 20x magnification. Fiji software was used for post-acquisition image processing and pixel intensity quantification.

ISV *ex vivo* T-cell profiling assays

GFP-A20 tumors were inoculated and ISV performed as described above. On day 11 after irradiation, tumors and draining LNs were harvested, homogenized, and passed through a 70mm cell strainer. Tumor cell suspensions were depleted of tumor cells by CD19 nanobead magnetic separation (Mojosort, BioLegend). Tumor and LN cells were either stained immediately or plated with 1ug/mL GFP peptide and Brefeldin for 6hrs prior to staining and analysis by spectral flow cytometry.

Exome and RNA sequencing and alignment

Next-generation sequencing and data processing of A20 cells was performed as previously described.(2) Total DNA and RNA were purified using DNeasy Blood and Tissue Kit (QIAGEN) and RNAeasy Mini Kit (QIAGEN) from triplicate cultures of A20 lymphoma cells. SureSelectXT mouse exon kit (Agilent) was used for exome capture. Exome capture libraries were then paired-ended sequenced using an Illumina HiSeq 4000 and the HiSeq 4000 sequencing Kit (200 cycles). 50M exome reads were sequenced per sample. Barcoded mRNA-seq cDNA libraries were generated using the Illumina TruSeq V2 kit and 500ng total RNA per sample. All libraries were sequenced on an Illumina HiSeq4000 with 30M reads sequenced per sample.

DNA and RNA sequencing data was analyzed using HTSeqGenie(3) in BioConductor.(4) Reads with low nucleotide qualities (70% of bases with quality <23), matches to adapter sequences, and RNA reads matching to rRNA were removed.(5) Remaining reads were aligned to the mouse reference genome (GRCm38.p5) using GSNAP(6) (v. '2013-10-10-v2'), allowing up to 2 mismatches per 75 bases. The DNA alignment parameters were: '-M 2 -n 10 -B 2 -i 1 –pairmax-dna=1000 –terminal-threshold=1000 –gmap-mode=none –clip-overlap' and RNA alignment parameters were: '-M 2 -n 10 -B 2 -i 1 -N 1 -w 200000 -E 1 –pairmax-rna=200000 –clip-overlap.'

Variant Calling and Annotation

The union of Lofreq 2.1.2(7) and Strelka1.0.14(8) SNV calls were used to call somatic variants, and only Strelka1 indel calls. Indel qualities were assigned to alignments using 'lofreq indelqual –dindel,'and somatic mutations called using 'lofreq somatic' with the '–call-indels' option. Strelka-based somatic mutations were called using strelka_config_bwa_default.ini, with 'isSkipDepthFilters = 1' instead of 'isSkipDepthFilters = 0.' modified in settings.

Somatic mutations were annotated using the Ensembl 90 Variant Effect Predictor (VEP)(9) on GENCODE M15-basic(5) based gene models. Novel and potentially expressed sequence downstream of frameshift indels, as well as downstream of stop loss mutations, were identified using the downstream plugin (EMBL-EBI, n.d.) in VEP. Nonsynonymous mutations were

identified by only retaining mutations whose consequences were: frameshift_variant, stop_lost, stop_gained, start_lost, initiator_codon_variant, inframe_insertion, inframe_deletion, missense_variant, coding_sequence_variant, or protein_altering_variant.

Neoantigen Prediction

The R package VariantTools 1.20.0(10) tallyVariants function and gmapR 1.20.1(11) were used to tally RNA-seq alignments for identified mutations in the exome data to identify expressed mutations. RNA reads that had mapping quality >= 23 were tallied. Each mutation's neoantigen potetional was predicted by specifying A20 cell MHC-I genotype and assigning the optimal MHC-neoepitope pair across all MHC-I alleles and 8- to 11-mer peptides containing the mutation. A20 MHC-I genotype was assumed identical to BALB/c; 'H-2-Kd,' 'H-2-Dd,' and 'H-2-Ld.' Each MHC-neoepitope pair was scored based on MHC-allele-specific percentile rank of the neoepitope's IC50 score, as predicted by the NetMHCpan4.0(12) 'rank' method (via IEDB 2.19).(13)

14-25-mer peptides were synthesized and purified using the PepPower Peptide Synthesis Platform (GenScript), with peptide quality assessed by mass spectrometry and HPLC to ensure >75% purity. Solubility of individual peptides were tested ty identify adequate solvents.

ISV T-cell neoantigen-reactivity assays

For initial screening, 14-25-mer peptides were grouped into pools containing 10-11 peptides and pulsed onto CD11c+ DCs isolated from splenocytes of Flt3L treated mice, at 20ug/mL. GFP-peptide, non-pulsed, and DMSO-treated DCs were used as controls (non-pulsed DCs shown as controls in figures as they did not differ from DMSO-treated DCs). After overnight pulse, DCs were co-cultured with tumor and TdLN cell suspensions from B/P/R-ISV-treated mice, prepared as described above. T-cell activation was assessed after 24hrs by flow cytometry.

Supplementary Figure Legends

Supplementary Figure 1: Flt3L increases DC numbers and potentiates their activation. (a) Bar graphs showing MFI fold change of costimulatory marker expression on cDC subsets and pDCs from patient PBMCs, as defined by viSNE clustering in Fig 1a. Statistical significance between "No PRRa" and the different conditions was calculated by two-way ANOVA with Dunnett's multiple comparison test. (b) Costimulatory marker expression on DC, B cells, and macrophages measured by flow cytometry. Statistical significance between "No PRRa" and the different conditions was calculated by two-way ANOVA with Dunnett's multiple comparison test. (c) Quantification of murine splenic DCs pre- and post-Flt3L treatment by spectral flow cytometry. Statistical significance was calculated using t test with Welch's correction. (d) DC costimulatory molecule expression measured by flow cytometry. Statistical significance was calculated using one-way ANOVA and Holm-Sidak test. (e) Bar graphs showing MFI fold change of costimulatory marker expression on cDC subsets and pDCs from murine splenocytes, as defined by viSNE clustering in Fig 1b. Statistical significance between "No PRRa" and the different conditions was calculated by two-way ANOVA with Dunnett's multiple comparison test.

Supplementary Figure 2: naPRRa-activated DCs prime patient T-cells. (a) PBMCs from Flt3L-treated patients were treated with naPRRa and SEB. T-cell activation was measured by flow cytometry, representative scatter plots and bar graphs quantifying activation are shown. Statistical significance was calculated by two-way ANOVA with Tukey's multiple comparison test.

Supplementary Figure 3: naPRRa-activated DCs cross-prime OT-I T-cells. Splenocytes from Flt3L-treated mice were isolated, pulsed with ovalbumin protein, activated with synthetic PRRa or naPRRa, and co-cultured with OT-I cells. OT-I CD8 TC activation was measured as (a) production of IFNγ, (b) proliferation, and (c) upregulation of CD69. Statistical significance was calculated against "No PRRa" condition by one-way ANOVA with Dunnett's multiple comparison test.

Supplementary Figure 4: naPRRa-activated DCs cross-present tumor-derived antigen to T-cells. (a) Histograms depicting proliferation of cross-primed anti-GFP CD8 T-cells, quantified in adjacent graph. DC can effectively cross-present tumor-derived GFP to anti-GFP CD8 T-cells; cross-priming can be potentiated by activation of DCs with synthetic PRRa or naPRRa. Statistical significance was calculated by one-way ANOVA with Tukey's multiple comparison test.

Supplementary Figure 5: Identifying unique activation profiles of naPRRa. (a) Scree plot showing variance explained by each PC calculated in Fig 3a. (b) Table of top phenotypic metrics and their loadings influencing the two plotted PCs, PC1 and PC2. (c) CRISPR-cas9 was used to delete individual TLRs from RAW cells. Heatmap of $TLR^{-/-}$ RAW macrophage CD40 expression, illustrating that $TLR^{-/-}$ RAW cells are unable to respond to specific TLR ligands. (d, e) WT and $TLR^{-/-}$ RAW cells were activated with vaccine naPRRa, and flow cytometry was used to compare CD40 upregulation in WT vs $TLR7^{-/-}$ (d) and $TLR9^{-/-}$ (e)

Supplementary Figure 6: Rational combination identifies the naPRRa triplet B/P/R that promotes anti-tumor immunity. (a) Feature selection was performed, identifying 43 phenotypic markers that significantly correlated with DC priming of cytotoxic T-cells using a Spearman correlation p-value cutoff of <0.01. (b) Scree plot showing variance explained by each PC. (c) Table of top phenotypic metrics and their loadings influencing the two plotted PCs, PC1 and PC2. (d) Equation to determine vaccine efficacy based on positioning along PC1 from 43 phenotypic observations that correlate with TC cytotoxicity.

Supplementary Figure 7: The naPRRa triplet B/P/R that promotes anti-tumor immunity in ISV against 4T1 mammary carcinoma. (a) Schema of murine pre-clinical 4T1 ISV model. 4T1 tumor-bearing mice were treated i.t. with Flt3L. Tumors were then locally irradiated (XRT), and naPRRa or saline was injected i.t. Mice were monitored for tumor growth (b). (c) Schema of pre-immunization model. Mice were pre-immunized with saline or B/P/R triplet in the left subiliac area; one week later, GFP-A20 lymphoma tumors were inoculated in the right flank. GFP-A20 tumor-bearing mice were treated i.t. with Flt3L. Tumors were then locally irradiated, and B/P/R or saline was injected i.t. Mice were monitored for tumor growth (d). Statistical significance was calculated by two-way ANOVA with Dunnett's multiple comparison test, n=10-14 mice per group.

Supplemental Table I. Pathogen vaccines used as naPRRa

Vaccine Name	Pathogen	Vaccine Type	Manufacturer
TICE BCG	*M. tuberculosis*	Live attenuated	Merck & Co.
M-M-R II	Measles virus Mumps virus Rubella virus	Live attenuated	Merck & Co.
Zostavax	Varicella zoster virus	Live attenuated	Merck & Co.
RotaTeq	*Rotavirus*	Live attenuated	Merck & Co.
Fluvirin	Influenza virus Types A and B	Inactivated	Seqirus Vaccines
Havrix	Hepatitis A virus	Inactivated	GlaxoSmithKline
Rabavert	Rabies virus	Inactivated	GlaxoSmithKline
IPOL	Poliovirus types 1, 2, 3	Inactivated	Sanofi Pasteur
Pneumovax23	*S. pneumoniae*	Subunit	Merck & Co.
Typhim Vi	*S. enterica* serovar Typhi	Subunit	Sanofi Pasteur
Menveo	*N. meningitidis*	Protein conjugated subunit	Novartis AG
PedvaxHIB	*H. Influenzae* type b	Protein conjugated subunit	Merck & Co.
Pentacel	*C. diphtheriae* *C. tetani* *B. pertussis* Poliovirus *H. influenzae* type b	Protein conjugated subunit, Inactivated	Sanofi Pasteur
Prevnar13	*S. pneumoniae*	Protein conjugated subunit, Alum adjuvant	Pfizer
Engerix-B	Hepatitis B virus	Subunit, Alum adjuvant	GlaxoSmithKline
Infanrix	*C. diphtheriae* *C. tetani* *B. Pertussis*	Subunit, Alum adjuvant	GlaxoSmithKline
Gardasil	Human Papillomavirus	Subunit, Alum adjuvant	Merck & Co.
Tenivac	*C. diphtheriae* *C. tetani*	Subunit, Alum adjuvant	Sanofi Pasteur
Pediarix	*C. diphtheriae* *C. tetani* *B. Pertussis* Hepatitis B virus Poliovirus	Subunit, Inactivated, Alum Adjuvant	GlaxoSmithKline

Supplemental Table II. Antibodies used for flow cytometry

Marker	**Fluorophore**	**Clone**	**Company**	**Species**
CD11c	FITC	B-ly6	BD	anti-human
CD123	Brilliant Violet 650	6H6	Biolegend	anti-human
CD14	Brilliant Violet 570	M5E2	Biolegend	anti-human
CD141	Brilliant Violet 605	M80	Biolegend	anti-human

CD16	Alexa Fluor 700	3G8	Biolegend	anti-human
CD19	Pacific Blue	4G7	Biolegend	anti-human
CD19	PerCP-Cy5.5	HIB19	Biolegend	anti-human
CD1c	PerCP-eFluor 710	L161	Biolegend	anti-human
CD25	Brilliant Violet 785	M-A251	Biolegend	anti-human
CD3	PE-Cy5	UCHT1	Biolegend	anti-human
CD4	Alexa Fluor 700	RPA-T4	Biolegend	anti-human
CD40	Brilliant Violet 711	5C3	Biolegend	anti-human
CD56	PerCP-Cy5.5	5.1H11	Biolegend	anti-human
CD8	Brilliant Violet 650	RPA-T8	Biolegend	anti-human
CD80	Brilliant Violet 421	2D10	Biolegend	anti-human
CD83	Alexa Fluor 647	HB15e	Biolegend	anti-human
CD86	PE-Dazzle594	IT2.2	Biolegend	anti-human
HLA-ABC	Brilliant Violet 510	W6/32	Biolegend	anti-human
HLA-DR	PE-Cy7	L243	Biolegend	anti-human
IFNγ	PE	4S.B3	Biolegend	anti-human
PD-1	Brilliant Violet 711	EH12.2H7	Biolegend	anti-human
PD-L1	PE	29E.2A3	Biolegend	anti-human
TNF	Alexa Fluor 647	MAb11	Biolegend	anti-human
(CD197) CCR7	Brilliant Violet 421	4B12	Biolegend	anti-mouse
B220	BUV496	RA-3-6B2	Biolegend	anti-mouse
B220	APC	RA-3-6B2	Biolegend	anti-mouse
B220	Brilliant Violet 711	RA-3-6B2	Biolegend	anti-mouse
CCR7	PE-Cy5	4B12	Biolegend	anti-mouse
CD11c	PE-Cy7	HL3	Biolegend	anti-mouse
CD11c	Alexa Fluor 532	N418	ThermoFisher	anti-mouse
CD11c	Alexa Fluor 700	N418	Biolegend	anti-mouse
CD127	APC-eFluor 780	A7R34	ThermoFisher	anti-mouse
CD132	PE	TUGm2	Biolegend	anti-mouse
CD16.2	Pacific Blue	9-E9	Biolegend	anti-mouse
CD169	PE-Dazzle594	3D6.112	Biolegend	anti-mouse
CD223 (Lag3)	PE	C9B7W	Biolegend	anti-mouse
CD25	Brilliant Violet 785	PC61	Biolegend	anti-mouse
CD25	Brilliant Violet 650	PC61	Biolegend	anti-mouse
CD3	PerCP-Cy5.5	145-2C11	Biolegend	anti-mouse
CD317	Brilliant Violet 605	927	Biolegend	anti-mouse
CD4	FITC	RM4-5	Biolegend	anti-mouse
CD4	Brilliant Violet 650	RM4-5	Biolegend	anti-mouse
CD4	Brilliant Violet 785	RM4-5	Biolegend	anti-mouse
CD4	Alexa Fluor 700	RM4-5	Biolegend	anti-mouse
CD40	APC	3/23	Biolegend	anti-mouse
CD44	PE-Cy5	IM7	Biolegend	anti-mouse
CD45.1	Alexa Fluor 700	A20	Biolegend	anti-mouse

CD49b	Brilliant Violet 421	DX5	Biolegend	anti-mouse
CD49b	Alexa Fluor 647	DX5	Biolegend	anti-mouse
CD49b	PerCP-Cy5.5	DX5	Biolegend	anti-mouse
CD62L	Brilliant Violet 570	MEL-14	Biolegend	anti-mouse
CD69	PE	H1.2F3	Biolegend	anti-mouse
CD69	Alexa Fluor 647	H1.2F3	Biolegend	anti-mouse
CD69	Brilliant Violet 510	H1.2F3	Biolegend	anti-mouse
CD8	Pacific Orange	5H10	BD	anti-mouse
CD8	APC	53-6.7	Biolegend	anti-mouse
CD8	PerCP-Cy5.5	53-6.7	Biolegend	anti-mouse
CD8	Brilliant Violet 480	53-6.7	Biolegend	anti-mouse
CD80	PE	16-10A1	Biolegend	anti-mouse
CD80	PE-Cy7	16-10A1	Biolegend	anti-mouse
CD86	Alexa Fluor 700	GL-1	Biolegend	anti-mouse
CD86	Brilliant Violet 480	PO3	BD	anti-mouse
CD8	Brilliant Violet 711	53-6.7	Biolegend	anti-mouse
CTLA-4	PE-Dazzle594	UC10-4B9	Biolegend	anti-mouse
CXCR3	Brilliant Violet 650	CXCR3-173	Biolegend	anti-mouse
F4/80	PerCP-Cy5.5	BM8	Biolegend	anti-mouse
F4/80	Brilliant Violet 510	BM8	Biolegend	anti-mouse
FoxP3	Alexa Fluor 647	MF-14	Biolegend	anti-mouse
Galectin-9	PerCP-eFluor 710	RG9-35	ThermoFisher	anti-mouse
Granzyme B	Pacific Blue	QA16A02	Biolegend	anti-mouse
H-2kd	PerCP-Cy5.5	SF1-1.1	Biolegend	anti-mouse
I-Ad	FITC	39-10-8	BD	anti-mouse
IFNγ	PE	XMG1.2	Biolegend	anti-mouse
Ki67	PerCP-eFluor 710	SolA15	Invitrogen	anti-mouse
KLRG1	Brilliant Violet 711	2F1	Biolegend	anti-mouse
Ly6A/E Sca-1	Alexa Fluor 700	D7	Biolegend	anti-mouse
Ly6C	PerCP-Cy5.5	HK1.4	Biolegend	anti-mouse
Ly6C	Brilliant Violet 570	HK1.4	Biolegend	anti-mouse
Ly6G	PerCP-Cy5.5	1A8	Biolegend	anti-mouse
PD-1	Brilliant Violet 605	29F.1A12	Biolegend	anti-mouse
PD-L1	Brilliant Violet 711	MIH5	Biolegend	anti-mouse
MHC-Ib Qa-2	Alexa Fluor 647	695H1-9-9	Biolegend	anti-mouse
TCRβ	Brilliant Violet 421	H57-597	Biolegend	anti-mouse
TCRβ	PE-Cy7	H57-597	Biolegend	anti-mouse
Tim3	PE-Dazzle594	B8.2C12	Biolegend	anti-mouse
TNF	APC	MP6-XT22	Biolegend	anti-mouse
TNF	Brilliant Violet 711	MP6-XT22	Biolegend	anti-mouse
XCR1	Brilliant Violet 510	ZET	Biolegend	anti-mouse
XCR1	Brilliant Violet 650	ZET	Biolegend	anti-mouse
B220	PerCP-Cy5.5	RA-3-6B2	Biolegend	anti-mouse/anti-human

B220	Brilliant Violet 750	RA-3-6B2	Biolegend	anti-mouse/anti-human
CD11b	APC-Cy7	M1/70	BD	anti-mouse/anti-human
CD11b	APC	M1/70	Biolegend	anti-mouse/anti-human
CD11b	Brilliant Violet 510	M1/70	BD	anti-mouse/anti-human
Tbet	Brilliant Violet 785	4B10	Biolegend	anti-mouse/anti-human

Supplemental Table III. RT- qPCR Primer Sequences (5' to 3' end)

Gene	Forward primer	Reverse primer	Species
ISG-15	GGTGTCCGTGACTAACTCCAT	TGGAAAGGGTAAGACCGTCCT	Mouse
IRF7	GAGACTGGCTATTGGGGGAG	GACCGAAATGCTTCCAGGG	Mouse

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