List of Supplemental Materials

Supplemental Methods

Multiplex Chemokine/Cytokine

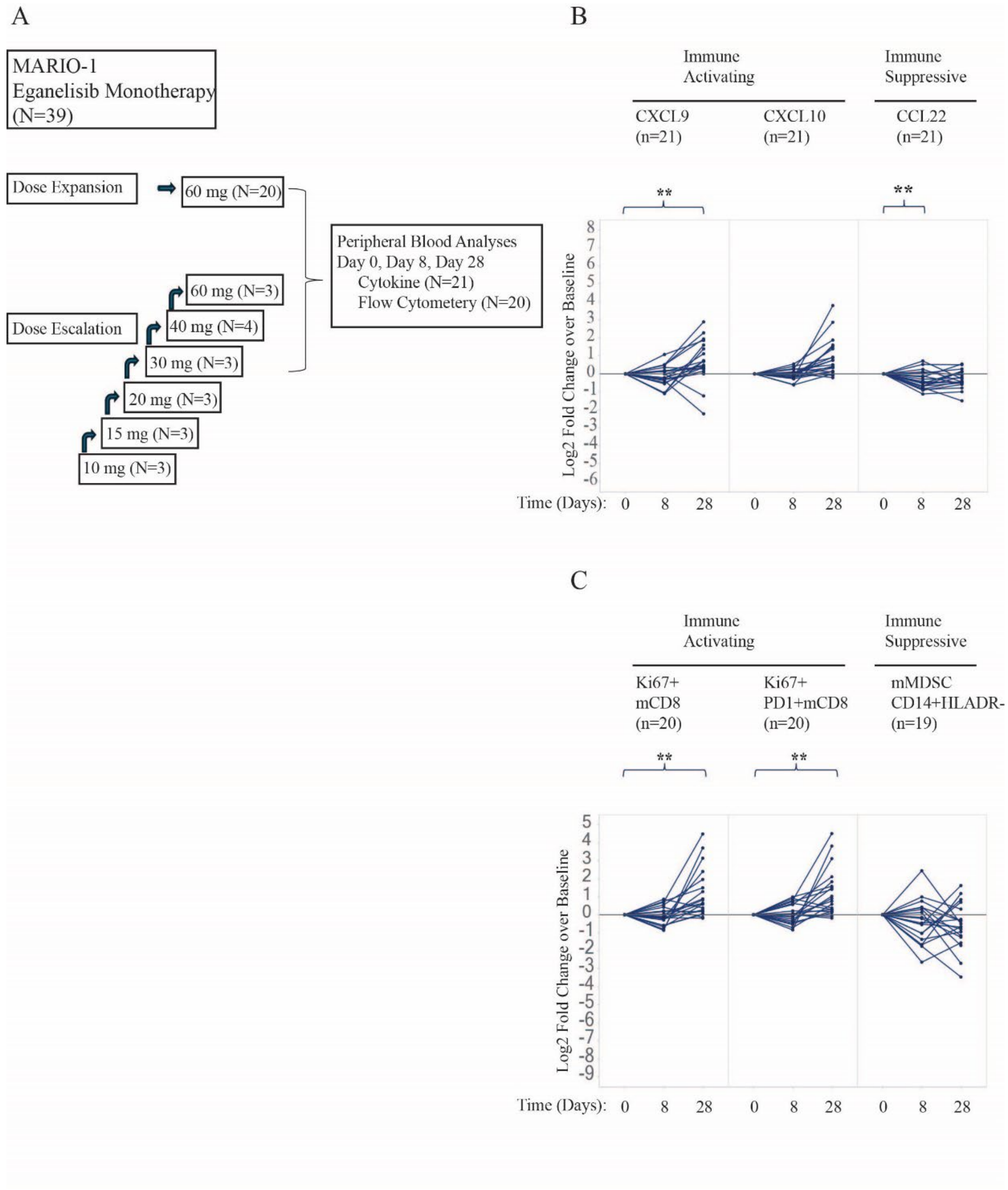
Multiplex protein analysis was performed by the multiplex core facility at The Forsyth Institute (Cambridge, MA, USA). Samples were thawed at 4°C prior to assay and kept on ice throughout the assay procedures. Manufacturers' protocols were followed for all panels, with a general protocol as follows. Assay plates (96-well) were loaded with assay buffer, standards, samples and beads and then covered and incubated on plate shaker (500 rpm) overnight at 4°C. After primary incubation, plates were washed twice and then detection antibody cocktail was added to all wells and incubated at room temperature for 1 hour on plate shaker. Next, streptavidin-phycoerythrin fluorescent reporter was added to all wells and incubated for 30 minutes at room temperature on plate shaker. Plates were washed twice, beads were resuspended in sheath fluid, placed on shaker for 5 minutes and then read on Bio-PlexR200 following manufacturers' specifications using Bio- Plex Manager software v 6.0. Values ≤ the lower limit of quantification (LLOQ) were set to the LLOQ for inclusion in the analysis. Changes in the concentration of cytokines in response to treatment were determined using One-Way Repeated Measures ANOVAs and Sidak *post hoc* contrasts . P-values were adjusted using Bonferroni corrections for multiple comparisons.

Flow Cytometry

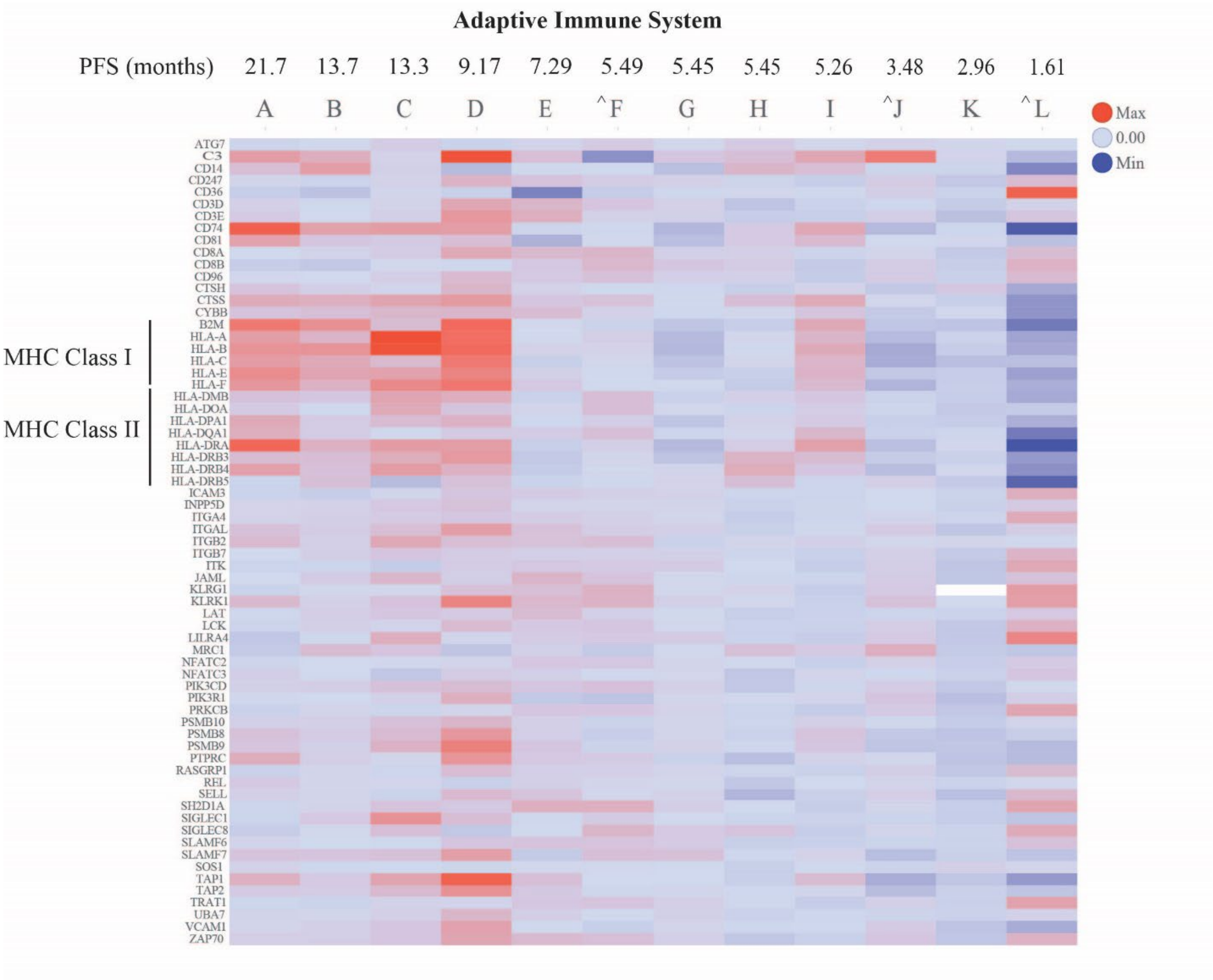
Flow cytometry analysis was performed by Cell Carta (Fremont, CA, USA) on whole blood samples collected in Streck Cyto-Chex™ tubes shipped and stored at room temperature. Myeloid cell analysis was performed on fresh samples processed within 4 days of sample collection and T-Cell analysis was performed on batched samples that were previously fixed (BD Phosflow lyse/fix) and frozen at -80^{0}C. Cells were processed and stained using a cocktail of fluorescent-labeled antibodies with a myeloid panel; (CD45 V500 (BD Biosciences catalog#624327), CD14 Pacific Blue (Biolegend catalog#325616), HLA-DR APC (Biolegend catalog#307610), CD15 Alexa700 (Biolegend 323026), CD66b PerCP-Cy5 (Biolegend 305108), CD11b PE-Cy7 (Biolegend 301322), CD33 PE (Biolegend 366608) and T-cell panel; (CD45 BUV805 (BD Biosciences catalog#612891), CD3 PE-Cy7 (Biolegend, 300420), CD4 BV480 (BD

Biosciences catalog#566104) , CD8 BV785 (Biolegend catalog#301046), CD45RA BUV395 (BD Biosciences catalog#624308), PD1 PE_Dazzle594 (Biolegend catalog#329940), CTLA-4 APC (Biolegend catalog#369612), and Ki67 Ax488 (BD Biosciences catalog#561165)), run on a flow cytometer (BD LSRII) and analyzed using Cell Engine software (CellCarta Montreal Canada). Cell populations were quantified as absolute cell counts or percent of parent. Monocytic MDSC's (mMDSC) and monocytes were defined as HLA-DR-CD14+CD45+CD11b+CD33+CD66b- CD15-and HLA-DR+CD14+CD45+CD11b+CD33+CD66b-CD15-, respectively. One-Way Repeated Measures ANOVAs and Sidak's *post hoc* contrasts were used to characterize changes in cell populations with treatment.

Supplemental Figures

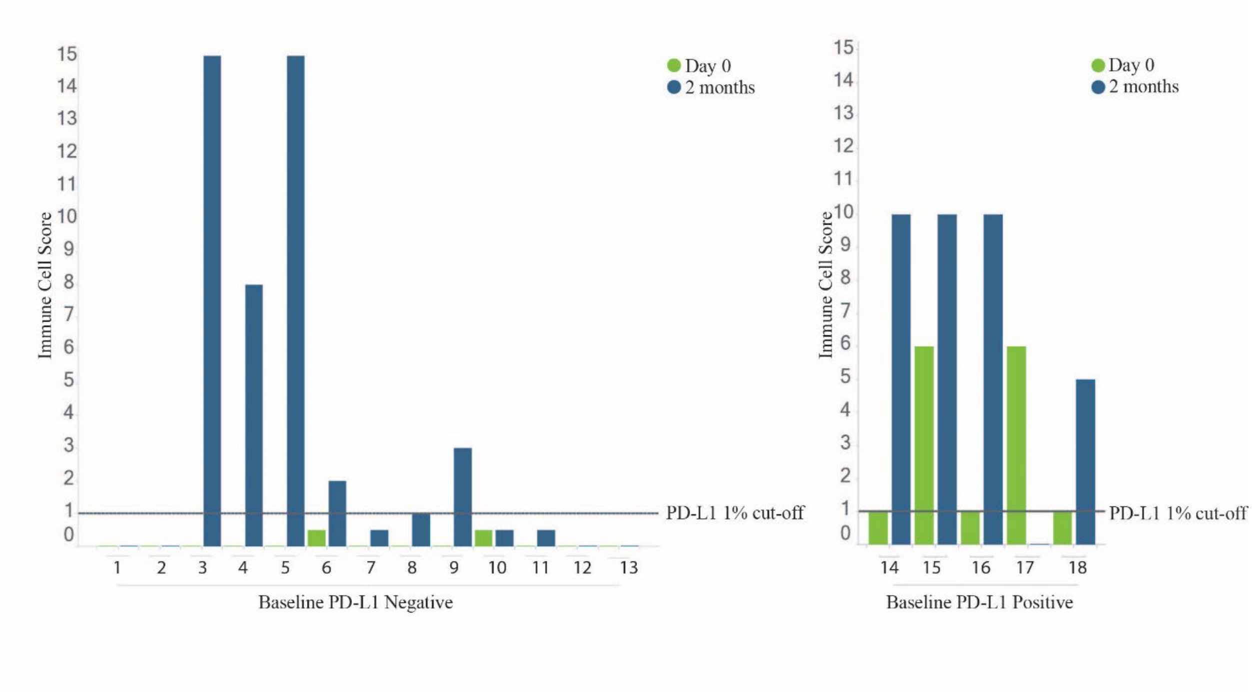


Supplemental Figure 1. Peripheral Blood analysis for Cytokines and Immune Cell Subsets from MARIO-1 solid tumor monotherapy. The flow chart shows the number of patients in each cohort of the study and the number of patients included in the analyses (A). Patients with a full set of Day 0, Day 8, and Day 28 samples are included in the analyses. Concentrations of cytokines were measured by Luminex and expressed as log2 fold change over baseline for indicated timepoints (B). Absolute cell counts for monocytic MDSCs (HLADR-CD14+CD11b+CD33+), proliferation of memory CD8 T-Cells (Ki67+ of CD45RA-CD8+), and proliferation of exhausted memory CD8 T-Cells (Ki67+ of PD1+CD45RA-CD8+ T-Cells) were measured by flow cytometry and expressed as log2fold change over baseline for indicated timepoints (C) One-way repeated measures ANOVA was performed to determine changes in cytokines and immune cell populations with treatment. For cytokine analysis, p-values were adjusted using Bonferonni correction for multiple comparisons *p<.05, **p<.01



Supplemental Figure 2. Individual Patient Analysis of Adaptive Immune System Pathway Genes within Leukocytes. Changes in gene expression for genes contributing to the core enrichment of the adaptive immune system identified in the group analysis (n=12) within CD45+

enriched regions were plotted as log2FC over baseline on an individual sample basis using heat maps. ^eganelisib hold with continued atezolizumab/nab-paclitaxel for 2 weeks prior to sample collection. mPFS (Recist v1.1) from April 14, 2023 datacut is indicated for each patient.



Baseline PD-L1 Negative **Baseline PD-L1 Positive**

Supplemental Figure 3. PD-L1 Immunohistochemistry in paired tumor biopsies. PD-L1 immune cell score was determined for baseline (Day0) and on-treatment (2months) biopsy samples using SP142 with ≥ 1% immune cell score cutoff for PD-L1 positive. Graphs are grouped according with baseline PD-L1 status with PD-L1 negative tumors on the left panel and PD-L1 positive tumors on the right panel. Numbers refer to individual patient paired biopsies.

Supplemental Tables

Supplemental Table 1. Individual Patient Clinical Data

Patient ID	*PFS (month)	Baseline PD-L1 Status	OT PD-L1 Status	Eganelisib Dose Hold	Atezolizumab Dose Hold	Nab-Paclitaxel Dose Hold	OT Biopsy Collection	Dose Hold (2week minimum)

								prior to OT Biopsy
A	21.7+	POS	POS	-	-	-	Day 65	
B	13.7+	NEG	NEG	-	-	-	Day 52	
C	13.3	NEG	POS	-	-	-	Day 49	
D	9.17+	NEG	POS	-	-	-	Day 63	
E	7.29	NEG	POS	-	-	-	Day 70	
F	5.49	POS	POS	Day 12-35, 39-56	Day 14-28	Day 14-28	Day 59	Eganelisib Only
G	5.45	NEG	POS	Day 15-28	Day 15-28	Day 15-28	Day 54	
H	5.45	NEG	NEG	Day 42-56	Day 42-56	-	Day 56	Eganelisib +Atezo
I	5.26	POS	POS	Day 54-63	Day 56-63	Day 56-63	Day 78	
J	3.48	POS	UNK	Day 28-50	-	-	Day 50	Eganelisib Only
K	2.96	NEG	NEG	-	-	-	Dau 54	
L	1.61	NEG	NEG	Day 28-69	-	Day 28-34	Day 69	Eganelisib Only

*Datacut April 14, 2023, + PFS ongoing at datacut, OT on-treatment

Supplemental Table 2. Top Differentially Expressed Genes Post Treatment within CD45+ Enriched Region

Top 50 Up-regulated genes (CD45+ Region)

measure	p.value	log2FC	n_patients
CXCL9	7.5E-07	0.99	12
C3	3.8E-07	0.85	12
CCL5	5.1E-07	0.60	12
CLU	1.7E-03	0.55	12
HLA-B	6.5E-06	0.55	12
KLRK1	2.2E-09	0.53	12
STAT1	3.9E-05	0.50	12
SERPINA1	1.1E-02	0.50	11
TRBC1/2	6.6E-04	0.49	12
CTSS	1.1E-02	0.45	12
HLA-F	4.7E-06	0.45	12
HLA-A	8.7E-04	0.43	12
CCL19	2.1E-04	0.40	12
NKG7	2.7E-07	0.40	12
B2M	2.6E-03	0.39	12
HLA-E	4.7E-05	0.38	12
IL2RB	1.1E-06	0.38	12
HLA-C	1.7E-03	0.38	12
TRAC	5.0E-03	0.37	12
GZMA	1.7E-06	0.37	12
ITGAL	2.3E-06	0.35	12
IL32	1.4E-03	0.33	12
GIMAP4	8.2E-06	0.32	12
A2M	2.1E-02	0.31	12
SERPING1	5.2E-03	0.31	12
ZAP70	2.2E-04	0.30	12

Top 50 Down-regulated genes (CD45+ Region)

measure	p.value	log2FC	n_patients
FN1	6.9E-04	-0.65	12
COL5A1	5.6E-05	-0.60	12
TPM1	4.8E-07	-0.60	12
CALML5	5.9E-06	-0.52	11
SPP1	1.2E-02	-0.52	12
COL11A1	3.7E-06	-0.47	12
THBS1	8.3E-05	-0.46	12
COL5A2	1.2E-03	-0.45	12
IER3	8.1E-07	-0.41	12
MMP1	4.2E-06	-0.40	12
ACTA2	2.1E-04	-0.40	12
PLAUR	3.9E-06	-0.38	12
MCAM	2.1E-08	-0.38	12
MMP9	4.4E-02	-0.37	12
INHBA	2.8E-06	-0.32	12
FLNB	5.4E-06	-0.32	12
OLFML2B	5.8E-07	-0.32	12
VCAN	1.1E-02	-0.31	12
NOTCH3	2.6E-05	-0.30	12
FLNA	1.8E-03	-0.29	12
DSC3	1.6E-04	-0.29	12
ANLN	1.1E-06	-0.29	12
HEY1	3.4E-03	-0.16	12
SPRED1	1.5E-02	-0.16	12
DDIT4	2.5E-02	-0.16	12
EIF4EBP1	1.3E-03	-0.16	12

CTSW	7.9E-06	0.30	12
IL7R	1.3E-02	0.30	12
CD8A	5.5E-05	0.30	12
GZMK	2.8E-05	0.29	12
NLRC5	1.2E-05	0.29	12
TRDC	1.2E-05	0.28	12
PTPRC	1.5E-03	0.28	12
GBP1	4.2E-04	0.28	12
TARP/TRGC1/2	6.6E-05	0.27	12
CD2	2.3E-03	0.27	12
SSX1	2.3E-02	0.27	12
IL2RG	2.4E-04	0.26	12
JAML	1.6E-05	0.26	12
SH2D1A	3.1E-05	0.26	12
CXCL13	6.9E-03	0.25	12
CD37	9.3E-04	0.25	12
CXCL11	4.7E-04	0.25	12
ITGB2	2.5E-02	0.25	12
ADGRE5	3.3E-06	0.24	12
CD3E	2.6E-03	0.24	12
PIK3CD	4.5E-05	0.24	12
XCL1/2	1.8E-05	0.24	12
LCP1	2.1E-02	0.24	12
SELL	7.9E-04	0.24	11

CACNG4	1.8E-02	-0.16	9
FOS	3.4E-02	-0.15	12
MAP3K8	6.0E-04	-0.15	12
CXCL8	3.9E-02	-0.15	12
MFGE8	2.2E-02	-0.15	11
SOCS3	1.2E-02	-0.15	12
PLOD2	1.1E-02	-0.15	12
AKAP1	1.2E-02	-0.15	12
BCAT1	2.5E-02	-0.15	12
CACNB3	1.2E-02	-0.15	12
TCF7L1	5.7E-03	-0.15	12
IRAK1	1.6E-03	-0.15	12
SLC39A6	1.9E-03	-0.14	12
FGFR1	2.7E-02	-0.14	12
PBX1	8.5E-03	-0.14	12
RUNX1	4.5E-03	-0.14	12
MAPK9	1.2E-03	-0.14	12
ITPK1	2.9E-02	-0.14	12
CD276	1.6E-02	-0.14	12
FGFR3	1.1E-02	-0.14	9
DUSP6	9.8E-03	-0.14	12
FOSL1	8.1E-03	-0.14	12
ETV1	3.8E-03	-0.14	12
CXADR	1.6E-02	-0.14	12

Supplemental Table 3. Individual Patient Pathway Analysis Post Treatment within CD45+ Enriched Region

Patient ID	Reactome Pathway ID	Description	NES	pvalue
A	R-HSA-1280218	Adaptive Immune System	2.06	4.24E-08
B	R-HSA-1280218	Adaptive Immune System	1.72	6.43E-05
C	R-HSA-1280218	Adaptive Immune System	2.04	1.09E-08
D	R-HSA-1280218	Adaptive Immune System	2.11	2.16E-09
E	R-HSA-1280218	Adaptive Immune System	1.11	2.56E-01
F	R-HSA-1280218	Adaptive Immune System	1.40	6.92E-03
G	R-HSA-1280218	Adaptive Immune System	-1.47	6.71E-03
H	R-HSA-1280218	Adaptive Immune System	-1.26	5.90E-03
I	R-HSA-1280218	Adaptive Immune System	1.41	1.81E-02
J	R-HSA-1280218	Adaptive Immune System	-1.28	3.94E-02
K	R-HSA-1280218	Adaptive Immune System	-1.01	4.68E-01
L	R-HSA-1280218	Adaptive Immune System	-1.69	6.17E-05
A	R-HSA-877300	Interferon gamma signaling	2.46	8.84E-09
B	R-HSA-877300	Interferon gamma signaling	1.89	3.00E-04
C	R-HSA-877300	Interferon gamma signaling	2.63	2.42E-10
D	R-HSA-877300	Interferon gamma signaling	2.62	1.42E-10
E	R-HSA-877300	Interferon gamma signaling	1.13	2.82E-01
F	R-HSA-877300	Interferon gamma signaling	0.69	9.41E-01

G	R-HSA-877300	Interferon gamma signaling	-1.26	1.93E-01
H	R-HSA-877300	Interferon gamma signaling	0.80	7.91E-01
I	R-HSA-877300	Interferon gamma signaling	2.10	2.45E-05
J	R-HSA-877300	Interferon gamma signaling	-1.88	5.92E-04
K	R-HSA-877300	Interferon gamma signaling	-1.68	7.93E-03
L	R-HSA-877300	Interferon gamma signaling	-2.93	4.31E-11
A	R-HSA-913531	Interferon Signaling	2.36	3.19E-08
B	R-HSA-913531	Interferon Signaling	1.86	2.68E-04
C	R-HSA-913531	Interferon Signaling	2.36	3.06E-08
D	R-HSA-913531	Interferon Signaling	2.85	1.94E-16
E	R-HSA-913531	Interferon Signaling	1.02	4.17E-01
F	R-HSA-913531	Interferon Signaling	-1.21	1.90E-01
G	R-HSA-913531	Interferon Signaling	-1.37	9.29E-02
H	R-HSA-913531	Interferon Signaling	-1.58	1.57E-03
I	R-HSA-913531	Interferon Signaling	1.90	3.16E-04
J	R-HSA-913531	Interferon Signaling	-2.40	2.14E-09
K	R-HSA-913531	Interferon Signaling	-1.64	3.60E-03
L	R-HSA-913531	Interferon Signaling	-3.04	1.80E-14
A	R-HSA-983169	Class I MHC mediated antigen processing & presentation	2.16	5.86E-06
B	R-HSA-983169	Class I MHC mediated antigen processing & presentation	1.92	3.98E-05
C	R-HSA-983169	Class I MHC mediated antigen processing & presentation	2.11	3.70E-06
D	R-HSA-983169	Class I MHC mediated antigen processing & presentation	1.90	2.36E-04
E	R-HSA-983169	Class I MHC mediated antigen processing & presentation	-0.83	7.76E-01
F	R-HSA-983169	Class I MHC mediated antigen processing & presentation	-0.96	5.36E-01
G	R-HSA-983169	Class I MHC mediated antigen processing & presentation	-1.51	4.45E-02
H	R-HSA-983169	Class I MHC mediated antigen processing & presentation	-0.69	9.41E-01
I	R-HSA-983169	Class I MHC mediated antigen processing & presentation	2.25	2.84E-07
J	R-HSA-983169	Class I MHC mediated antigen processing & presentation	-1.96	3.48E-05
K	R-HSA-983169	Class I MHC mediated antigen processing & presentation	-1.09	3.28E-01
L	R-HSA-983169	Class I MHC mediated antigen processing & presentation	-1.65	5.94E-03
A	R-HSA-2132295	MHC class II antigen presentation	2.22	2.25E-06
B	R-HSA-2132295	MHC class II antigen presentation	1.89	8.55E-04
C	R-HSA-2132295	MHC class II antigen presentation	2.06	9.67E-05
D	R-HSA-2132295	MHC class II antigen presentation	1.71	5.25E-03
E	R-HSA-2132295	MHC class II antigen presentation	-1.01	4.43E-01
F	R-HSA-2132295	MHC class II antigen presentation	1.28	1.51E-01
G	R-HSA-2132295	MHC class II antigen presentation	-1.48	7.79E-02
H	R-HSA-2132295	MHC class II antigen presentation	1.39	7.93E-02
I	R-HSA-2132295	MHC class II antigen presentation	2.01	2.10E-04
J	R-HSA-2132295	MHC class II antigen presentation	-1.42	8.25E-02
K	R-HSA-2132295	MHC class II antigen presentation	-0.64	9.21E-01
L	R-HSA-2132295	MHC class II antigen presentation	-2.70	3.55E-08
A	R-HSA-1236975	Antigen processing-Cross presentation	2.29	1.52E-06
B	R-HSA-1236975	Antigen processing-Cross presentation	2.01	3.10E-05
C	R-HSA-1236975	Antigen processing-Cross presentation	2.26	1.78E-06
D	R-HSA-1236975	Antigen processing-Cross presentation	2.04	6.83E-05
E	R-HSA-1236975	Antigen processing-Cross presentation	0.82	7.74E-01
F	R-HSA-1236975	Antigen processing-Cross presentation	-0.90	5.96E-01

G	R-HSA-1236975	Antigen processing-Cross presentation	-1.69	1.34E-02
H	R-HSA-1236975	Antigen processing-Cross presentation	0.68	9.26E-01
I	R-HSA-1236975	Antigen processing-Cross presentation	2.46	4.09E-09
J	R-HSA-1236975	Antigen processing-Cross presentation	-2.09	2.19E-05
K	R-HSA-1236975	Antigen processing-Cross presentation	-1.13	2.93E-01
L	R-HSA-1236975	Antigen processing-Cross presentation	-1.84	2.37E-03
A	R-HSA-202403	TCR signaling	2.14	2.27E-05
B	R-HSA-202403	TCR signaling	1.41	6.37E-02
C	R-HSA-202403	TCR signaling	1.47	2.52E-02
D	R-HSA-202403	TCR signaling	1.96	2.48E-04
E	R-HSA-202403	TCR signaling	0.95	5.42E-01
F	R-HSA-202403	TCR signaling	1.07	3.23E-01
G	R-HSA-202403	TCR signaling	-1.40	8.95E-02
H	R-HSA-202403	TCR signaling	-1.58	7.34E-03
I	R-HSA-202403	TCR signaling	1.39	7.97E-02
J	R-HSA-202403	TCR signaling	-1.19	1.99E-01
K	R-HSA-202403	TCR signaling	-1.37	8.65E-02
L	R-HSA-202403	TCR signaling	-1.94	4.36E-04
A	R-HSA-380108	Chemokine receptors bind chemokines	1.48	6.03E-02
B	R-HSA-380108	Chemokine receptors bind chemokines	1.54	3.76E-02
C	R-HSA-380108	Chemokine receptors bind chemokines	1.35	9.41E-02
D	R-HSA-380108	Chemokine receptors bind chemokines	1.53	1.87E-02
E	R-HSA-380108	Chemokine receptors bind chemokines	2.16	7.14E-06
F	R-HSA-380108	Chemokine receptors bind chemokines	1.31	1.34E-01
G	R-HSA-380108	Chemokine receptors bind chemokines	1.94	1.21E-03
H	R-HSA-380108	Chemokine receptors bind chemokines	0.98	4.93E-01
I	R-HSA-380108	Chemokine receptors bind chemokines	0.99	4.75E-01
J	R-HSA-380108	Chemokine receptors bind chemokines	0.92	5.49E-01
K	R-HSA-380108	Chemokine receptors bind chemokines	-1.98	1.35E-04
L	R-HSA-380108	Chemokine receptors bind chemokines	-1.32	1.18E-01
A	R-HSA-1474244	Extracellular matrix organization	1.00	4.82E-01
B	R-HSA-1474244	Extracellular matrix organization	1.43	4.74E-02
C	R-HSA-1474244	Extracellular matrix organization	-1.03	3.91E-01
D	R-HSA-1474244	Extracellular matrix organization	1.26	9.63E-02
E	R-HSA-1474244	Extracellular matrix organization	-2.46	1.02E-10
F	R-HSA-1474244	Extracellular matrix organization	-0.94	5.61E-01
G	R-HSA-1474244	Extracellular matrix organization	-2.27	3.01E-08
H	R-HSA-1474244	Extracellular matrix organization	1.56	2.86E-03
I	R-HSA-1474244	Extracellular matrix organization	0.96	5.56E-01
J	R-HSA-1474244	Extracellular matrix organization	1.04	3.86E-01
K	R-HSA-1474244	Extracellular matrix organization	2.87	1.03E-12
L	R-HSA-1474244	Extracellular matrix organization	-2.05	3.73E-05

Supplemental Table 4. Top Differentially Expressed Genes Post Treatment within CD45+ Enriched Region Grouped by Baseline PD-L1 Status

Top 50 Up-Regulated Genes PD-L1 Positive (CD45+)			
measure	p.value	LOG2FC	n
SERPINA1	2.5E-08	1.87	11
CXCL9	9.6E-08	1.56	12
C3	2.3E-03	0.73	12
A2M	3.5E-04	0.71	12
SMC1B	3.5E-02	0.70	3
APOC2	7.7E-04	0.70	11
CTSS	1.5E-02	0.70	12
CD244	1.7E-02	0.66	3
AMBP	1.0E-03	0.65	11
CCL5	7.2E-04	0.59	12
CXCR6	2.8E-02	0.56	3
HLA-DQA1	8.4E-03	0.56	12
CCRL2	3.8E-02	0.54	3
KLRK1	1.9E-04	0.53	12
HLA-DMA	2.2E-02	0.51	12
IGFBP3	1.0E-03	0.50	12
B2M	1.7E-02	0.49	12
TRBC1/2	4.2E-02	0.49	12
APOB	5.0E-03	0.48	11
CD63	1.9E-02	0.48	12
NKG7	5.6E-05	0.48	12
ADH1A/B/C	5.3E-03	0.48	11
GPX1	2.0E-02	0.46	12
ADH4	1.8E-02	0.44	12
TRDC	2.8E-05	0.44	12
ITGAX	3.4E-02	0.44	12
GZMA	2.9E-04	0.43	12
PTPRC	4.8E-03	0.43	12
ITGB2	2.3E-02	0.43	12
HLA-E	4.2E-03	0.43	12
SGK1	1.0E-02	0.42	12
LCP1	1.5E-02	0.41	12
TUBB	8.1E-03	0.41	12
TARP/TRGC1/2	1.3E-04	0.40	12
CD81	1.1E-02	0.39	12
HLA-DPA1	8.9E-03	0.39	12
TTR	1.7E-02	0.38	12
CCL19	2.5E-02	0.38	12

Top 50 Down-Regulated Genes PD-L1 Positive (CD45+)			
measure	p.value	LOG2FC	n
IL1RAP	2.9E-02	-0.77	3
IFI6	2.2E-03	-0.63	12
C4B	4.1E-03	-0.59	12
DSC3	3.1E-05	-0.47	12
MX1	1.5E-04	-0.47	12
ISG15	3.7E-02	-0.42	12
EYA1	7.5E-05	-0.40	12
RSAD2	1.8E-03	-0.39	12
DSP	5.3E-03	-0.39	12
CT45A1	2.3E-02	-0.37	12
IFIT3	1.4E-03	-0.37	12
KRT5	2.9E-03	-0.35	12
OLR1	4.8E-02	-0.35	12
PHGDH	1.6E-03	-0.35	12
OAS3	1.0E-02	-0.32	12
LTF	1.1E-02	-0.32	12
MYCT1	1.7E-03	-0.31	12
PLA2G2A	1.2E-02	-0.30	12
DKK1	3.4E-04	-0.30	9
FGF6	1.5E-04	-0.30	9
PTCRA	1.6E-02	-0.28	12
OAS2	2.4E-03	-0.27	12
CDH3	2.3E-02	-0.27	12
CCL13	3.5E-03	-0.26	9
FST	2.6E-02	-0.26	12
CASP12	8.0E-03	-0.26	12
REN	5.6E-03	-0.26	9
CACNG4	1.4E-02	-0.26	9
SRD5A2	3.0E-02	-0.26	12
EIF2AK2	1.4E-03	-0.24	12
HERC6	1.4E-03	-0.24	12
RIN1	1.1E-02	-0.24	9
PPP3R2	1.7E-02	-0.24	12
EFNA5	2.8E-03	-0.24	12
MME	1.8E-02	-0.24	12
RAD51	1.4E-04	-0.24	9
CD79A	4.7E-02	-0.23	12
NOG	1.2E-03	-0.23	9

APOA1	4.7E-02	0.36	11
PFKFB3	1.1E-03	0.36	12
ITGAL	2.2E-03	0.35	12
CXCL12	1.4E-02	0.34	12
PIK3CD	3.4E-04	0.33	12
IL10RA	6.9E-03	0.33	12
CD44	2.8E-02	0.33	12
ZAP70	1.4E-02	0.33	12
NLRC5	2.7E-03	0.32	12
GIMAP4	6.2E-03	0.32	12
CD84	2.3E-02	0.32	12
HLA-F	3.6E-02	0.32	12

TNN	3.1E-03	-0.23	9
BLK	8.5E-03	-0.23	9
EDN1	1.3E-02	-0.22	12
CREB3L3	4.0E-02	-0.22	12
PDK1	3.1E-02	-0.22	12
OAS1	2.3E-02	-0.22	12
RET	1.6E-02	-0.21	9
SYCP1	1.6E-02	-0.21	12
NFIL3	2.2E-03	-0.21	12
OASL	7.9E-03	-0.21	12
HNF1A	3.0E-03	-0.21	9
PRDM1	1.2E-02	-0.21	12

Top 50 Up-Regulated Genes PD-L1 Negative (CD45+)			
measure	p.value	LOG2FC	n
C3	1.9E-04	1.06	12
CLU	2.7E-03	0.80	12
WIF1	1.1E-03	0.77	3
ZIC2	8.4E-03	0.57	3
CDKN2B	3.1E-02	0.52	3
KLRK1	1.4E-05	0.46	12
CCL5	1.0E-02	0.44	12
SSX1	2.4E-03	0.44	12
HLA-B	6.3E-03	0.43	12
STAT1	3.5E-02	0.43	12
CALML3	4.6E-02	0.38	3
CCL19	1.1E-02	0.38	12
HLA-F	1.0E-02	0.37	12
IL2RB	1.5E-03	0.33	12
KRT14	5.4E-05	0.33	12
CACNB2	4.4E-02	0.32	3
CD8A	4.4E-04	0.32	12
CCL13	5.8E-05	0.32	9
SH2D1A	7.7E-05	0.31	12
CXCL11	2.4E-03	0.31	12
CD2	1.3E-02	0.30	12
FASLG	9.7E-06	0.29	9
CTSW	1.0E-03	0.28	12
OAS2	6.5E-04	0.27	12
ITGAL	7.0E-03	0.27	12
XCL1/2	3.0E-04	0.26	12

Top 50 Down-Regulated Genes PD-L1 Negative (CD45+)			
measure	p.value	LOG2FC	n
FN1	8.3E-05	-0.70	12
COL5A1	2.1E-07	-0.69	12
TPM1	1.1E-07	-0.66	12
CALML5	1.2E-05	-0.56	11
IGFBP3	1.9E-05	-0.55	12
IER3	1.5E-08	-0.52	12
COL3A1	2.3E-03	-0.49	12
MCAM	5.8E-09	-0.48	12
COL5A2	7.1E-05	-0.47	12
COL11A1	6.4E-06	-0.47	12
THBS1	2.5E-04	-0.47	12
MMP1	1.9E-06	-0.46	12
CSF1R	9.8E-03	-0.46	12
COL1A1	7.7E-03	-0.43	12
MMP9	4.3E-02	-0.42	12
PLAUR	3.2E-06	-0.41	12
FLNA	2.3E-05	-0.40	12
ACTA2	6.0E-04	-0.39	12
OLFML2B	5.6E-09	-0.39	12
THY1	1.2E-04	-0.39	12
LRP1	4.3E-03	-0.35	12
ENG	9.3E-04	-0.35	12
FLNB	2.4E-05	-0.34	12
INHBA	1.9E-05	-0.33	12
PDCD1LG2	1.8E-02	-0.33	3
NRP1	7.8E-05	-0.33	12

GZMA	7.8E-03	0.26	12
NKG7	1.2E-02	0.26	12
IFIT3	3.8E-02	0.26	12
FGFR2	6.0E-03	0.26	12
GZMK	4.5E-03	0.26	12
EGR2	5.1E-04	0.25	12
PRF1	1.2E-03	0.25	12
EOMES	2.9E-03	0.25	12
SFRP1	5.2E-03	0.24	12
GNLY	4.7E-02	0.24	12
LTF	3.7E-02	0.24	12
SELL	2.2E-02	0.24	11
IDO1	4.4E-02	0.23	12
KLRG1	4.5E-03	0.23	12
GPT	8.1E-03	0.22	12
IL11RA	1.1E-04	0.22	12
IL2RG	3.3E-02	0.22	12
HERC6	1.4E-03	0.21	12
GIMAP4	3.2E-02	0.21	12
FGFR4	2.5E-02	0.21	12
CD3D	2.9E-02	0.21	12
ZAP70	4.1E-02	0.21	12
RORA	4.9E-03	0.21	12
CD38	2.2E-03	0.21	12

ITGA5	1.3E-06	-0.33	12
NOTCH3	2.8E-05	-0.33	12
CST2	8.4E-04	-0.32	9
KRT7	2.2E-03	-0.32	12
TPM4	2.2E-04	-0.32	12
VEGFA	6.1E-04	-0.32	12
ACTB	3.9E-04	-0.32	12
VCAN	3.6E-03	-0.32	12
S100A9	1.9E-02	-0.31	12
ITGAV	3.2E-05	-0.31	12
PLAU	2.9E-03	-0.31	12
PDGFRB	2.9E-04	-0.30	12
FPR3	3.3E-02	-0.29	12
RHOB	3.2E-02	-0.29	12
ANLN	2.3E-04	-0.28	12
C5AR1	1.4E-02	-0.28	9
ITGB1	2.8E-03	-0.27	12
HSPB1	7.0E-03	-0.27	12
LAIR1	1.9E-02	-0.27	12
MMP3	1.9E-03	-0.27	9
IFITM2	5.0E-03	-0.26	12
UBE2C	6.1E-03	-0.26	12
H3C10	4.4E-02	-0.26	12
JUNB	4.5E-03	-0.26	12

Supplemental Table 5. Differential Gene Expression at Baseline within CD45+ Enriched Region Grouped by Baseline PD-L1 Status

Top 50 Genes Associated with Baseline PD-L1 Negative (CD45+ Region)			
measure	p.value	LOG2FC	n_patients
COL1A1	1.52E-06	-2.29	12
COL1A2	1.19E-03	-2.22	12
COL3A1	5.17E-06	-2.14	12
COL6A3	9.25E-03	-1.94	12
SFRP2	6.43E-03	-1.79	12
COL5A2	3.22E-04	-1.48	12
COL5A1	1.01E-04	-1.43	12
VCAN	2.83E-03	-1.29	12
FN1	2.06E-02	-1.16	12
SFRP4	2.89E-03	-1.13	12
TPM4	1.15E-02	-0.93	12

Top 50 Genes Associated with Baseline PD-L1 Positive (CD45+ Region)			
measure	p.value	LOG2FC	n_patients
C4B	6.47E-03	1.95	12
CRP	1.40E-02	1.18	12
LBP	3.53E-02	1.11	12
IFI6	4.64E-02	1.04	12
C8B	4.52E-03	1.01	12
PCK1	1.43E-02	0.97	12
MX1	2.43E-02	0.86	12
IFIT3	1.50E-03	0.85	12
ARG1	8.53E-03	0.83	12
C9	2.20E-02	0.81	12
MASP2	3.33E-02	0.72	12

PKM	1.59E-02	-0.89	12
THY1	1.03E-03	-0.85	12
ALDOA	4.06E-02	-0.82	12
CD9	2.39E-02	-0.82	12
FLNA	1.73E-02	-0.82	12
CD44	3.40E-02	-0.80	12
SERPINH1	3.10E-04	-0.78	12
COL11A1	7.35E-03	-0.77	12
COMP	4.41E-02	-0.77	12
TPM1	1.82E-02	-0.74	12
ANXA1	1.34E-02	-0.73	12
PLAU	1.48E-03	-0.68	12
THBS1	9.51E-03	-0.67	12
PDGFRB	2.26E-04	-0.67	12
KRT7	8.44E-03	-0.64	12
CD99	1.60E-02	-0.62	12
LRP1	4.38E-02	-0.60	12
IER3	5.48E-03	-0.59	12
CSF1R	2.14E-02	-0.59	12
COLEC12	6.64E-03	-0.59	12
OLFML2B	1.44E-03	-0.58	12
RUNX1	3.07E-03	-0.58	12
CTNNB1	4.16E-02	-0.57	12
PLAUR	4.62E-04	-0.57	12
FAP	2.93E-03	-0.56	12
FGFR1	7.72E-03	-0.55	12
GAS1	6.32E-03	-0.52	12
ACTA2	3.46E-02	-0.51	12
NOTCH3	1.67E-02	-0.51	12
FZD1	4.33E-03	-0.50	12
ITGAV	2.16E-03	-0.50	12
DAB2	1.79E-03	-0.48	12
ITGA5	9.24E-04	-0.46	12
CD55	2.58E-02	-0.46	12
SBNO2	4.40E-03	-0.43	12
PFKFB3	3.96E-06	-0.41	12
INHBA	4.81E-02	-0.40	12
CAPN2	8.61E-03	-0.40	12
IFNGR2	3.52E-02	-0.39	12

CYP4A11/22	1.16E-02	0.70	12
ADH6	2.89E-02	0.70	12
GBP1	5.89E-03	0.67	12
C8A	1.28E-02	0.66	12
GBP4	3.85E-03	0.66	12
HSD11B1	6.26E-03	0.65	12
TDO2	3.06E-02	0.65	12
APOL6	2.69E-02	0.65	12
LEPR	3.54E-02	0.65	12
CYP8B1	4.79E-02	0.61	12
CFI	1.99E-02	0.61	12
F12	3.15E-02	0.60	12
IFIT2	2.10E-03	0.60	12
OAS1	1.99E-02	0.59	12
C6	2.11E-02	0.59	12
RORC	1.82E-02	0.57	12
SRD5A2	5.00E-02	0.57	12
LTF	8.91E-03	0.56	12
CCL21	6.93E-03	0.56	11
C5	4.27E-02	0.51	12
OAS2	1.62E-02	0.51	12
CREB3L3	2.24E-02	0.50	12
IFIH1	4.50E-03	0.49	12
CXCL11	1.37E-02	0.49	12
IDO1	3.28E-02	0.49	12
RSAD2	3.67E-04	0.46	12
ST6GAL1	1.41E-03	0.46	12
HERC6	2.28E-02	0.45	12
HHEX	9.36E-03	0.45	12
ASL	2.52E-02	0.44	12
CCL13	3.08E-02	0.44	9
PCK2	3.26E-02	0.43	12
MGMT	3.04E-02	0.43	12
PHGDH	4.71E-03	0.43	12
PARP9	9.80E-03	0.43	12
PSAT1	3.66E-02	0.40	12
IFI35	2.65E-03	0.38	12
PSMB8	4.66E-02	0.38	12
FSTL3	3.69E-02	0.37	12

Supplemental Table 6. Top Differentially Expressed Genes Post Treatment within CD68+ Enriched Region

Up-regulated genes (CD68+ Region)			
measure	p.value	LOG2FC	n_patients
CLU	4.4E-02	1.25	11
KLRK1	2.5E-02	0.37	12
SGK1	1.6E-02	0.35	12
CFD	5.0E-02	0.34	12
NKG7	1.2E-02	0.34	12
ITGAL	5.6E-03	0.31	12
IL2RB	1.5E-02	0.25	12
PIK3CD	2.5E-02	0.24	12
GZMA	3.5E-02	0.24	12
CD38	2.9E-02	0.22	12
TMEM140	9.4E-03	0.21	12
TARP/TRGC1/2	3.4E-02	0.21	12
G6PD	3.2E-02	0.20	12
CD59	4.7E-02	0.18	12
ATG7	1.1E-02	0.17	12
FZD7	4.0E-02	0.17	12
NR3C1	1.2E-02	0.14	12
REL	4.1E-02	0.13	11
UBA7	4.7E-02	0.10	12

Down-regulated genes (CD68+ Region)			
measure	p.value	LOG2FC	n_patients
PLAUR	1.7E-02	-0.54	12
SLC11A1	3.4E-02	-0.53	12
ITGA5	2.3E-02	-0.43	12
MERTK	2.6E-02	-0.38	12
COL11A1	2.0E-02	-0.32	11
FLNB	1.1E-02	-0.30	12
NRP1	3.9E-02	-0.30	12
THBD	2.4E-02	-0.29	12
HIF1A	1.3E-02	-0.28	11
CKLF	2.2E-02	-0.28	12
PLAU	4.0E-02	-0.27	11
TNFAIP6	3.7E-02	-0.27	12
MCAM	2.4E-02	-0.26	12
BCAT1	1.5E-02	-0.21	12
PLAT	1.1E-02	-0.20	12
EIF4EBP1	3.8E-02	-0.17	12
MAPKAPK2	2.3E-02	-0.15	12
KMT2C	1.9E-02	-0.09	12

Supplemental Table 7. Individual Patient Pathway Analysis Post Treatment within CD68+ Enriched Region

Patient ID	Reactome Pathway ID	Description	NES	pvalue
A	R-HSA-1236975	Antigen processing-Cross presentation	2.24	3.32E-07
B	R-HSA-1236975	Antigen processing-Cross presentation	1.42	3.61E-02
C	R-HSA-1236975	Antigen processing-Cross presentation	1.92	6.19E-04
D	R-HSA-1236975	Antigen processing-Cross presentation	2.05	9.36E-05
E	R-HSA-1236975	Antigen processing-Cross presentation	-1.39	7.17E-02
F	R-HSA-1236975	Antigen processing-Cross presentation	0.87	7.24E-01
G	R-HSA-1236975	Antigen processing-Cross presentation	-1.61	3.76E-02
H	R-HSA-1236975	Antigen processing-Cross presentation	-1.38	3.05E-02
I	R-HSA-1236975	Antigen processing-Cross presentation	2.53	7.51E-10
J	R-HSA-1236975	Antigen processing-Cross presentation	-2.67	2.43E-08
K	R-HSA-1236975	Antigen processing-Cross presentation	1.84	9.26E-03
L	R-HSA-1236975	Antigen processing-Cross presentation	-1.90	8.57E-04
A	R-HSA-983169	Class I MHC mediated antigen processing & presentation	2.12	1.80E-06
B	R-HSA-983169	Class I MHC mediated antigen processing & presentation	1.34	7.48E-02

C	R-HSA-983169	Class I MHC mediated antigen processing & presentation	1.81	5.66E-04
D	R-HSA-983169	Class I MHC mediated antigen processing & presentation	1.83	7.24E-04
E	R-HSA-983169	Class I MHC mediated antigen processing & presentation	-1.13	2.45E-01
F	R-HSA-983169	Class I MHC mediated antigen processing & presentation	0.62	9.92E-01
G	R-HSA-983169	Class I MHC mediated antigen processing & presentation	-1.46	6.53E-02
H	R-HSA-983169	Class I MHC mediated antigen processing & presentation	-1.03	2.58E-01
I	R-HSA-983169	Class I MHC mediated antigen processing & presentation	2.33	1.82E-08
J	R-HSA-983169	Class I MHC mediated antigen processing & presentation	-2.26	8.02E-06
K	R-HSA-983169	Class I MHC mediated antigen processing & presentation	1.37	8.70E-02
L	R-HSA-983169	Class I MHC mediated antigen processing & presentation	-1.81	9.65E-04
A	R-HSA-1236974	ER-Phagosome pathway	2.20	4.13E-07
B	R-HSA-1236974	ER-Phagosome pathway	1.44	4.39E-02
C	R-HSA-1236974	ER-Phagosome pathway	1.79	4.45E-03
D	R-HSA-1236974	ER-Phagosome pathway	2.05	3.29E-04
E	R-HSA-1236974	ER-Phagosome pathway	-0.96	5.10E-01
F	R-HSA-1236974	ER-Phagosome pathway	-0.61	9.52E-01
G	R-HSA-1236974	ER-Phagosome pathway	-1.57	5.25E-02
H	R-HSA-1236974	ER-Phagosome pathway	-1.32	4.95E-02
I	R-HSA-1236974	ER-Phagosome pathway	2.37	2.48E-07
J	R-HSA-1236974	ER-Phagosome pathway	-2.22	7.10E-05
K	R-HSA-1236974	ER-Phagosome pathway	1.64	4.87E-02
L	R-HSA-1236974	ER-Phagosome pathway	-2.18	1.39E-05
A	R-HSA-1474244	Extracellular matrix organization	0.99	5.04E-01
B	R-HSA-1474244	Extracellular matrix organization	-1.58	2.17E-03
C	R-HSA-1474244	Extracellular matrix organization	-1.24	1.31E-01
D	R-HSA-1474244	Extracellular matrix organization	-0.92	6.13E-01
E	R-HSA-1474244	Extracellular matrix organization	-2.17	1.84E-07
F	R-HSA-1474244	Extracellular matrix organization	-1.27	1.31E-01
G	R-HSA-1474244	Extracellular matrix organization	-2.43	1.60E-10
H	R-HSA-1474244	Extracellular matrix organization	1.28	7.15E-02
I	R-HSA-1474244	Extracellular matrix organization	1.29	9.86E-02
J	R-HSA-1474244	Extracellular matrix organization	-1.84	3.26E-04
K	R-HSA-1474244	Extracellular matrix organization	2.64	8.14E-10
L	R-HSA-1474244	Extracellular matrix organization	1.40	5.63E-02
A	R-HSA-877300	Interferon gamma signaling	2.35	7.31E-09
B	R-HSA-877300	Interferon gamma signaling	1.26	1.43E-01
C	R-HSA-877300	Interferon gamma signaling	2.46	8.20E-08
D	R-HSA-877300	Interferon gamma signaling	2.66	6.25E-10
E	R-HSA-877300	Interferon gamma signaling	-0.84	7.21E-01
F	R-HSA-877300	Interferon gamma signaling	1.07	3.27E-01
G	R-HSA-877300	Interferon gamma signaling	-1.68	1.86E-02
H	R-HSA-877300	Interferon gamma signaling	-1.89	1.40E-04
I	R-HSA-877300	Interferon gamma signaling	2.35	1.06E-07
J	R-HSA-877300	Interferon gamma signaling	-3.31	1.14E-13
K	R-HSA-877300	Interferon gamma signaling	-1.05	3.67E-01
L	R-HSA-877300	Interferon gamma signaling	-1.86	1.09E-03
A	R-HSA-913531	Interferon Signaling	2.25	5.57E-08
B	R-HSA-913531	Interferon Signaling	1.16	2.32E-01
C	R-HSA-913531	Interferon Signaling	2.17	8.77E-07
D	R-HSA-913531	Interferon Signaling	3.11	1.44E-18

E	R-HSA-913531	Interferon Signaling	-1.16	2.02E-01
F	R-HSA-913531	Interferon Signaling	-0.79	8.16E-01
G	R-HSA-913531	Interferon Signaling	-1.46	5.93E-02
H	R-HSA-913531	Interferon Signaling	-1.58	4.08E-04
I	R-HSA-913531	Interferon Signaling	2.03	1.05E-05
J	R-HSA-913531	Interferon Signaling	-3.27	4.72E-16
K	R-HSA-913531	Interferon Signaling	1.22	1.57E-01
L	R-HSA-913531	Interferon Signaling	-2.45	3.59E-10
A	R-HSA-6785807	Interleukin-4 and Interleukin-13 signaling	1.12	3.19E-01
B	R-HSA-6785807	Interleukin-4 and Interleukin-13 signaling	1.01	4.70E-01
C	R-HSA-6785807	Interleukin-4 and Interleukin-13 signaling	-1.17	2.05E-01
D	R-HSA-6785807	Interleukin-4 and Interleukin-13 signaling	-1.54	5.71E-03
E	R-HSA-6785807	Interleukin-4 and Interleukin-13 signaling	-1.61	5.33E-03
F	R-HSA-6785807	Interleukin-4 and Interleukin-13 signaling	-1.17	2.30E-01
G	R-HSA-6785807	Interleukin-4 and Interleukin-13 signaling	-1.86	4.15E-04
H	R-HSA-6785807	Interleukin-4 and Interleukin-13 signaling	0.98	5.50E-01
I	R-HSA-6785807	Interleukin-4 and Interleukin-13 signaling	1.31	1.02E-01
J	R-HSA-6785807	Interleukin-4 and Interleukin-13 signaling	-1.85	4.65E-04
K	R-HSA-6785807	Interleukin-4 and Interleukin-13 signaling	1.52	2.46E-02
L	R-HSA-6785807	Interleukin-4 and Interleukin-13 signaling	-0.76	8.79E-01
A	R-HSA-2132295	MHC class II antigen presentation	2.24	8.49E-08
B	R-HSA-2132295	MHC class II antigen presentation	1.13	3.31E-01
C	R-HSA-2132295	MHC class II antigen presentation	1.84	3.57E-03
D	R-HSA-2132295	MHC class II antigen presentation	1.78	1.09E-02
E	R-HSA-2132295	MHC class II antigen presentation	-1.23	2.17E-01
F	R-HSA-2132295	MHC class II antigen presentation	1.85	1.49E-03
G	R-HSA-2132295	MHC class II antigen presentation	-1.79	9.66E-03
H	R-HSA-2132295	MHC class II antigen presentation	-1.21	2.29E-01
I	R-HSA-2132295	MHC class II antigen presentation	2.19	7.76E-06
J	R-HSA-2132295	MHC class II antigen presentation	-2.86	2.24E-08
K	R-HSA-2132295	MHC class II antigen presentation	1.38	1.39E-01
L	R-HSA-2132295	MHC class II antigen presentation	-1.50	5.71E-02
A	R-HSA-194138	Signaling by VEGF	1.09	3.59E-01
B	R-HSA-194138	Signaling by VEGF	-0.80	8.45E-01
C	R-HSA-194138	Signaling by VEGF	-1.38	7.84E-02
D	R-HSA-194138	Signaling by VEGF	-0.68	9.37E-01
E	R-HSA-194138	Signaling by VEGF	-1.18	2.19E-01
F	R-HSA-194138	Signaling by VEGF	-0.44	9.97E-01
G	R-HSA-194138	Signaling by VEGF	-1.71	7.42E-03
H	R-HSA-194138	Signaling by VEGF	0.85	7.51E-01
I	R-HSA-194138	Signaling by VEGF	1.34	9.21E-02
J	R-HSA-194138	Signaling by VEGF	-0.66	9.55E-01
K	R-HSA-194138	Signaling by VEGF	1.22	1.91E-01
L	R-HSA-194138	Signaling by VEGF	-0.96	5.28E-01

Supplemental Table 8. Individual Patient Analysis of Interferon Gamma Signaling Pathway Genes Post Treatment within CD68+ Enriched Region

Patient ID	measure	p.value	LOG2FC

Patient ID	measure	p.value	LOG2FC

A	B2M	3.72E-04	2.15
B	B2M	2.84E-01	0.82
C	B2M	7.26E-01	0.09
D	B2M	3.34E-02	1.64
E	B2M	9.32E-01	-0.03
F	B2M	4.19E-01	0.24
G	B2M	4.13E-01	-0.50
H	B2M	4.26E-02	-0.78
I	B2M	6.63E-05	1.08
J	B2M	4.96E-01	-0.22
K	B2M	8.28E-01	0.23
L	B2M	1.82E-06	-3.23
A	GBP1	9.93E-03	0.56
B	GBP1	2.41E-01	0.13
C	GBP1	5.73E-02	0.62
D	GBP1	4.30E-02	1.18
E	GBP1	1.63E-01	1.09
F	GBP1	4.39E-01	-0.37
G	GBP1	3.33E-02	0.35
H	GBP1	8.87E-01	-0.04
I	GBP1	1.88E-03	0.65
J	GBP1	4.36E-03	-0.46
K	GBP1	1.04E-01	-0.48
L	GBP1	4.58E-02	-1.16
A	GBP2	2.03E-01	0.06
B	GBP2	5.83E-02	0.36
C	GBP2	8.02E-03	0.67
D	GBP2	4.31E-02	0.47
E	GBP2	1.10E-01	-0.31
F	GBP2	4.73E-02	0.21
G	GBP2	3.75E-01	-0.06
H	GBP2	3.80E-04	-0.28
I	GBP2	3.21E-01	-0.14
J	GBP2	3.48E-01	0.06
K	GBP2	5.77E-02	-0.43
L	GBP2	3.05E-01	0.34
A	HLA-C	3.22E-05	1.32
B	HLA-C	4.61E-02	0.70
C	HLA-C	7.33E-01	0.06
D	HLA-C	3.63E-02	1.46
E	HLA-C	4.54E-01	-0.38
F	HLA-C	1.97E-01	0.39
G	HLA-C	2.53E-01	-0.60
H	HLA-C	1.96E-01	-0.41
I	HLA-C	1.70E-03	0.80
J	HLA-C	3.18E-02	-0.66
K	HLA-C	9.14E-01	0.04
L	HLA-C	1.10E-02	-0.99

A	GBP4	5.84E-03	0.41
B	GBP4	8.27E-01	-0.03
C	GBP4	2.39E-02	0.32
D	GBP4	3.17E-02	0.80
E	GBP4	4.20E-01	0.30
F	GBP4	6.69E-01	-0.10
G	GBP4	1.50E-02	0.28
H	GBP4	7.06E-01	-0.08
I	GBP4	3.93E-02	0.21
J	GBP4	8.93E-01	-0.01
K	GBP4	2.09E-01	-0.23
L	GBP4	2.83E-01	-0.33
A	HLA-A	2.81E-04	1.33
B	HLA-A	8.27E-01	0.11
C	HLA-A	1.26E-03	2.04
D	HLA-A	2.22E-02	1.49
E	HLA-A	6.28E-01	-0.25
F	HLA-A	2.47E-01	0.45
G	HLA-A	3.04E-02	-0.84
H	HLA-A	2.24E-01	-0.34
I	HLA-A	1.45E-03	0.74
J	HLA-A	9.49E-02	-0.42
K	HLA-A	4.21E-01	0.71
L	HLA-A	4.94E-05	-2.25
A	HLA-B	8.91E-05	1.62
B	HLA-B	1.40E-01	1.02
C	HLA-B	9.60E-04	1.91
D	HLA-B	2.38E-02	1.51
E	HLA-B	8.94E-01	-0.06
F	HLA-B	2.56E-01	0.40
G	HLA-B	5.15E-02	-0.94
H	HLA-B	1.16E-01	-0.41
I	HLA-B	1.59E-04	0.90
J	HLA-B	1.70E-02	-0.83
K	HLA-B	4.55E-01	0.63
L	HLA-B	1.56E-05	-2.17
A	HLA-DRA	1.11E-03	2.16
B	HLA-DRA	6.28E-01	0.35
C	HLA-DRA	5.26E-02	0.69
D	HLA-DRA	1.25E-01	0.78
E	HLA-DRA	5.36E-01	-0.33
F	HLA-DRA	8.24E-02	0.63
G	HLA-DRA	3.19E-01	-0.71
H	HLA-DRA	9.14E-01	-0.03
I	HLA-DRA	9.18E-05	1.23
J	HLA-DRA	1.89E-01	-0.42
K	HLA-DRA	6.68E-01	0.44
L	HLA-DRA	5.43E-09	-4.87

A	HLA-DPA1	1.02E-03	1.12
B	HLA-DPA1	7.99E-01	-0.10
C	HLA-DPA1	2.35E-01	0.33
D	HLA-DPA1	2.21E-01	0.43
E	HLA-DPA1	8.24E-01	-0.11
F	HLA-DPA1	5.17E-02	0.52
G	HLA-DPA1	2.63E-01	-0.46
H	HLA-DPA1	1.84E-01	-0.20
I	HLA-DPA1	3.50E-03	0.46
J	HLA-DPA1	3.54E-01	-0.15
K	HLA-DPA1	7.20E-01	-0.24
L	HLA-DPA1	1.17E-03	-1.29
A	HLA-DQA1	2.41E-03	1.05
B	HLA-DQA1	6.14E-01	0.28
C	HLA-DQA1	1.65E-01	-0.24
D	HLA-DQA1	6.87E-01	0.11
E	HLA-DQA1	7.33E-01	0.20
F	HLA-DQA1	4.78E-02	0.71
G	HLA-DQA1	7.58E-01	-0.13
H	HLA-DQA1	2.17E-01	-0.18
I	HLA-DQA1	2.47E-03	1.05
J	HLA-DQA1	1.23E-01	-0.23
K	HLA-DQA1	8.39E-01	0.16
L	HLA-DQA1	1.15E-05	-2.80
A	HLA-E	6.42E-05	1.56
B	HLA-E	2.49E-01	0.84
C	HLA-E	1.09E-02	0.73
D	HLA-E	7.28E-02	1.13
E	HLA-E	7.09E-01	0.08
F	HLA-E	4.62E-01	0.15
G	HLA-E	3.11E-01	-0.48
H	HLA-E	8.42E-02	-0.50
I	HLA-E	3.95E-04	0.73
J	HLA-E	2.74E-01	-0.23
K	HLA-E	5.17E-01	0.45
L	HLA-E	2.96E-07	-2.36
A	HLA-F	9.25E-05	1.45
B	HLA-F	1.70E-01	0.46
C	HLA-F	3.55E-03	0.97
D	HLA-F	1.43E-02	1.45
E	HLA-F	7.57E-01	-0.14
F	HLA-F	5.47E-01	0.20
G	HLA-F	9.52E-01	0.03
H	HLA-F	8.60E-03	-0.71
I	HLA-F	7.51E-03	0.71
J	HLA-F	1.95E-02	-0.66
K	HLA-F	2.62E-01	0.59
L	HLA-F	1.18E-05	-1.90

A	HLA-DRB3	1.51E-02	0.74
B	HLA-DRB3	7.52E-01	0.21
C	HLA-DRB3	6.22E-02	0.47
D	HLA-DRB3	8.45E-02	0.84
E	HLA-DRB3	2.85E-01	-0.51
F	HLA-DRB3	3.17E-01	0.44
G	HLA-DRB3	2.35E-01	-0.69
H	HLA-DRB3	2.54E-01	0.54
I	HLA-DRB3	2.13E-03	0.71
J	HLA-DRB3	2.11E-01	-0.29
K	HLA-DRB3	9.63E-01	-0.04
L	HLA-DRB3	3.46E-05	-1.50
A	HLA-DRB4	1.19E-03	1.18
B	HLA-DRB4	9.97E-01	0.00
C	HLA-DRB4	2.90E-02	0.76
D	HLA-DRB4	5.49E-01	0.31
E	HLA-DRB4	3.93E-01	-0.44
F	HLA-DRB4	1.86E-01	0.53
G	HLA-DRB4	9.51E-01	0.03
H	HLA-DRB4	2.39E-01	0.52
I	HLA-DRB4	6.88E-03	0.49
J	HLA-DRB4	4.20E-02	-0.67
K	HLA-DRB4	3.90E-01	0.57
L	HLA-DRB4	8.14E-05	-2.02
A	IRF2	1.01E-01	0.11
B	IRF2	4.06E-01	0.18
C	IRF2	8.74E-02	0.29
D	IRF2	3.76E-01	0.30
E	IRF2	4.09E-01	0.23
F	IRF2	3.67E-01	0.20
G	IRF2	6.00E-02	0.20
H	IRF2	4.87E-01	-0.10
I	IRF2	3.50E-01	0.12
J	IRF2	9.63E-01	-0.01
K	IRF2	7.58E-02	-0.46
L	IRF2	2.48E-01	0.17
A	IRF7	2.40E-02	0.41
B	IRF7	2.21E-01	0.92
C	IRF7	2.52E-01	-0.37
D	IRF7	8.13E-02	1.15
E	IRF7	3.08E-01	-0.53
F	IRF7	1.26E-01	-0.68
G	IRF7	5.30E-01	-0.14
H	IRF7	5.86E-03	-1.38
I	IRF7	8.24E-01	0.07
J	IRF7	2.04E-01	-0.30
K	IRF7	5.28E-01	0.54
L	IRF7	6.35E-01	-0.13

A	IRF1	3.80E-01	0.06
B	IRF1	3.20E-01	0.24
C	IRF1	1.39E-01	0.32
D	IRF1	4.34E-01	0.24
E	IRF1	4.78E-01	-0.18
F	IRF1	2.46E-01	0.26
G	IRF1	1.99E-01	0.19
H	IRF1	3.62E-01	-0.12
I	IRF1	3.48E-01	-0.07
J	IRF1	5.43E-03	0.18
K	IRF1	1.88E-02	-0.53
L	IRF1	2.82E-01	0.35
A	OAS2	3.91E-02	-0.19
B	OAS2	5.79E-01	0.16
C	OAS2	9.16E-01	-0.02
D	OAS2	5.24E-02	0.85
E	OAS2	1.95E-01	0.34
F	OAS2	3.99E-01	-0.27
G	OAS2	8.72E-01	0.02
H	OAS2	3.69E-02	0.67
I	OAS2	7.08E-01	-0.05
J	OAS2	8.62E-03	-0.55
K	OAS2	2.79E-01	0.28
L	OAS2	5.20E-01	-0.16
A	OAS3	3.57E-01	-0.14
B	OAS3	5.98E-01	0.24
C	OAS3	5.81E-01	0.28
D	OAS3	3.38E-02	1.45
E	OAS3	4.62E-01	-0.35
F	OAS3	1.79E-01	-0.52
G	OAS3	8.05E-02	0.13
H	OAS3	2.92E-01	0.13
I	OAS3	2.78E-01	-0.15
J	OAS3	1.20E-01	-0.28
K	OAS3	5.71E-01	0.23
L	OAS3	1.25E-01	-0.44
A	PML	1.49E-02	-0.12
B	PML	1.30E-01	0.37
C	PML	4.60E-02	0.29
D	PML	7.09E-02	0.37
E	PML	4.21E-01	0.16
F	PML	3.70E-01	0.31
G	PML	6.05E-01	-0.05
H	PML	4.21E-02	0.72
I	PML	2.36E-03	-0.29
J	PML	6.01E-01	-0.07
K	PML	3.33E-01	-0.21
L	PML	3.65E-01	0.17

A	IRF9	4.17E-01	0.05
B	IRF9	4.84E-01	0.15
C	IRF9	1.99E-01	0.17
D	IRF9	4.87E-02	0.46
E	IRF9	8.60E-01	-0.03
F	IRF9	5.33E-01	0.08
G	IRF9	2.79E-01	0.13
H	IRF9	4.24E-01	0.07
I	IRF9	6.92E-02	0.27
J	IRF9	3.43E-01	-0.12
K	IRF9	3.45E-01	0.28
L	IRF9	7.72E-03	-0.61
A	SOCS1	7.63E-01	-0.02
B	SOCS1	7.59E-02	0.37
C	SOCS1	8.42E-01	0.02
D	SOCS1	8.50E-01	0.11
E	SOCS1	4.49E-01	-0.32
F	SOCS1	3.64E-01	-0.38
G	SOCS1	2.30E-01	0.21
H	SOCS1	1.50E-01	0.22
I	SOCS1	9.65E-01	0.01
J	SOCS1	2.64E-01	0.17
K	SOCS1	8.17E-02	-0.53
L	SOCS1	2.08E-03	1.27
A	SOCS3	1.19E-01	-0.14
B	SOCS3	5.52E-02	0.74
C	SOCS3	1.19E-01	-0.20
D	SOCS3	2.91E-03	-0.71
E	SOCS3	3.25E-03	0.75
F	SOCS3	8.54E-02	-0.50
G	SOCS3	8.88E-01	-0.02
H	SOCS3	1.78E-01	0.24
I	SOCS3	3.29E-01	0.20
J	SOCS3	3.19E-01	0.16
K	SOCS3	6.73E-02	-0.52
L	SOCS3	2.77E-03	-0.93
A	STAT1	5.80E-04	1.57
B	STAT1	6.07E-01	0.20
C	STAT1	5.91E-02	1.20
D	STAT1	4.12E-02	2.05
E	STAT1	5.80E-01	0.43
F	STAT1	8.84E-01	0.06
G	STAT1	2.60E-01	0.48
H	STAT1	2.75E-01	-0.43
I	STAT1	9.57E-03	0.69
J	STAT1	2.36E-02	-0.56
K	STAT1	6.09E-01	0.21
L	STAT1	1.69E-04	-2.41

A	TRIM21	9.02E-02	-0.12
B	TRIM21	9.71E-01	0.00
C	TRIM21	4.50E-02	0.16
D	TRIM21	8.71E-01	0.04
E	TRIM21	3.23E-01	0.28
F	TRIM21	1.64E-01	0.21
G	TRIM21	2.79E-01	0.10
H	TRIM21	1.22E-02	0.67
I	TRIM21	7.64E-01	-0.03
J	TRIM21	9.33E-03	0.18
K	TRIM21	2.71E-02	-0.63
L	TRIM21	1.61E-01	0.54