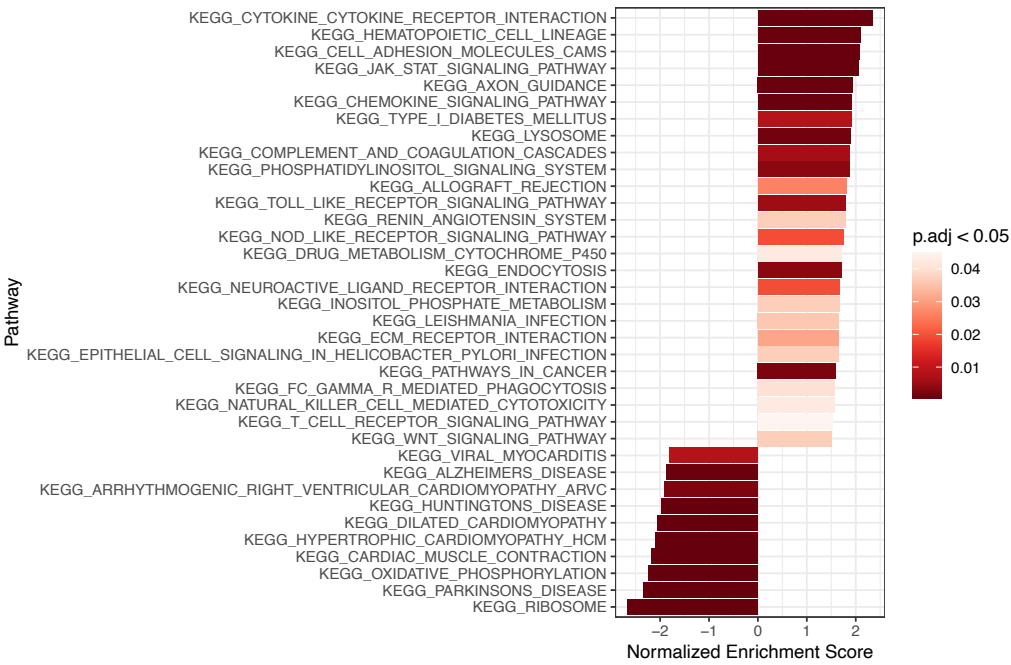


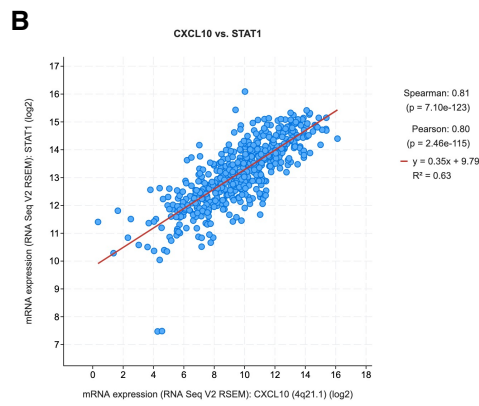
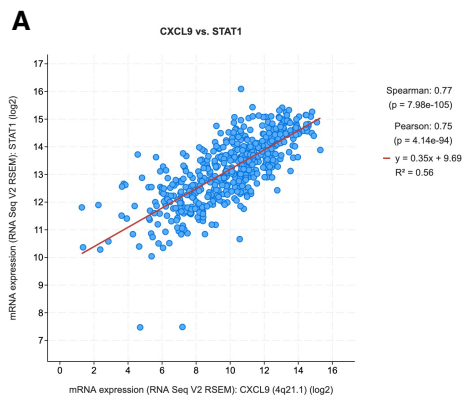
### KEGG Pathways, LY2

10Gy d3 vs. 0Gy ctrl



### SUPPLEMENTAL FIGURE 1 | KEGG Pathways for LY2 tumors 10Gy d3 versus 0Gy Ctrl

(A) Waterfall plot depicting all significant KEGG pathways for RNA-Seq expression data in LY2 tumors harvested 3 days post-RT (10Gy) versus 0Gy controls. Shaded by adjusted p value for multiple comparisons.



**C** TCGA HNSCC CXCL9 correlates

Correlated Gene	Cytoband	Spearman's Correlation	p-Value	q-Value ▲
CXCL10	4q21.1	0.859	2.59e-153	<b>5.22e-149</b>
IDO1	8p11.21	0.837	1.51e-138	<b>1.52e-134</b>
GBP4	1p22.2	0.834	2.97e-136	<b>2.00e-132</b>
CXCR2P1	2q35	0.825	3.88e-131	<b>1.96e-127</b>
IFNG	12q15	0.825	5.32e-131	<b>2.15e-127</b>
GBP5	1p22.2	0.821	6.46e-129	<b>2.17e-125</b>
CXCL11	4q21.1	0.817	1.15e-126	<b>3.32e-123</b>
CD8A	2p11.2	0.815	2.72e-125	<b>6.86e-122</b>
GBP1	1p22.2	0.809	2.37e-122	<b>5.31e-119</b>
SLA2	20q11.23	0.799	9.04e-117	<b>1.83e-113</b>
IL12RB1	19p13.11	0.791	4.52e-113	<b>8.31e-110</b>
FASLG	1q24.3	0.788	2.11e-111	<b>3.55e-108</b>
SIRPG	20p13	0.780	5.96e-108	<b>9.26e-105</b>
PDCD1	2q37.3	0.778	3.41e-107	<b>4.65e-104</b>
APOL6	22q12.3	0.778	3.45e-107	<b>4.65e-104</b>
GZMB	14q12	0.778	5.08e-107	<b>6.42e-104</b>
TIGIT	3q13.31	0.777	1.21e-106	<b>1.43e-103</b>
IL18BP	11q13.4	0.775	1.02e-105	<b>1.14e-102</b>
CITA	16p13.13	0.775	1.07e-105	<b>1.14e-102</b>
CXCR6	3p21.31	0.774	3.01e-105	<b>3.04e-102</b>
<b>STAT1</b>	<b>2q32.2</b>	<b>0.773</b>	<b>7.98e-105</b>	<b>7.67e-102</b>
TBX21	17q21.32	0.772	3.07e-104	<b>2.82e-101</b>
CXCR3	Xq13.1	0.770	2.24e-103	<b>1.96e-100</b>
JAKMIP1	4p16.1	0.769	2.68e-103	<b>2.26e-100</b>
NRG7	19q13.41	0.769	4.93e-103	<b>3.98e-100</b>

**D** TCGA HNSCC CXCL10 correlates

Correlated Gene	Cytoband	Spearman's Correlation	p-Value	q-Value ▲
CXCL11	4q21.1	0.947	1.27e-257	<b>2.57e-253</b>
CXCL9	4q21.1	0.859	2.59e-153	<b>2.61e-149</b>
GBP1	1p22.2	0.858	1.13e-152	<b>7.61e-149</b>
TAP1	6p21.32	0.834	1.49e-136	<b>7.51e-133</b>
IDO1	8p11.21	0.830	1.19e-133	<b>4.80e-130</b>
GBP4	1p22.2	0.811	2.76e-123	<b>9.30e-120</b>
<b>STAT1</b>	<b>2q32.2</b>	<b>0.810</b>	<b>7.10e-123</b>	<b>2.05e-119</b>
GBP5	1p22.2	0.810	2.25e-122	<b>5.68e-119</b>
IRF1	5q31.1	0.809	7.25e-122	<b>1.63e-118</b>
TRIM22	11p15.4	0.800	2.22e-117	<b>4.48e-114</b>
APOL3	22q12.3	0.798	1.09e-116	<b>2.01e-113</b>
ETV7	6p21.31	0.798	1.41e-116	<b>2.29e-113</b>
IFNG	12q15	0.798	1.47e-116	<b>2.29e-113</b>
LAP3	4p15.32	0.796	2.15e-115	<b>3.10e-112</b>
GZMB	14q12	0.780	3.69e-108	<b>4.95e-105</b>
BATF2	11q13.1	0.780	7.97e-108	<b>9.83e-105</b>
CXCR2P1	2q35	0.780	8.27e-108	<b>9.83e-105</b>
LAG3	12p13.31	0.779	2.23e-107	<b>2.50e-104</b>
LGALS17A	19q13.2	0.776	4.14e-106	<b>4.40e-103</b>
PSMB9	6p21.32	0.774	2.75e-105	<b>2.78e-102</b>
APOL6	22q12.3	0.767	4.41e-102	<b>4.24e-99</b>
UBE2L6	11q12.1	0.760	2.07e-99	<b>1.90e-96</b>
WARS	14q32.2	0.748	1.43e-94	<b>1.26e-91</b>
IL12RB1	19p13.11	0.748	1.93e-94	<b>1.62e-91</b>
EPST11	13q14.11	0.747	2.92e-94	<b>2.36e-91</b>

**SUPPLEMENTAL FIGURE 2 | TCGA HNSCC STAT1, CXCL9, CXCL10**

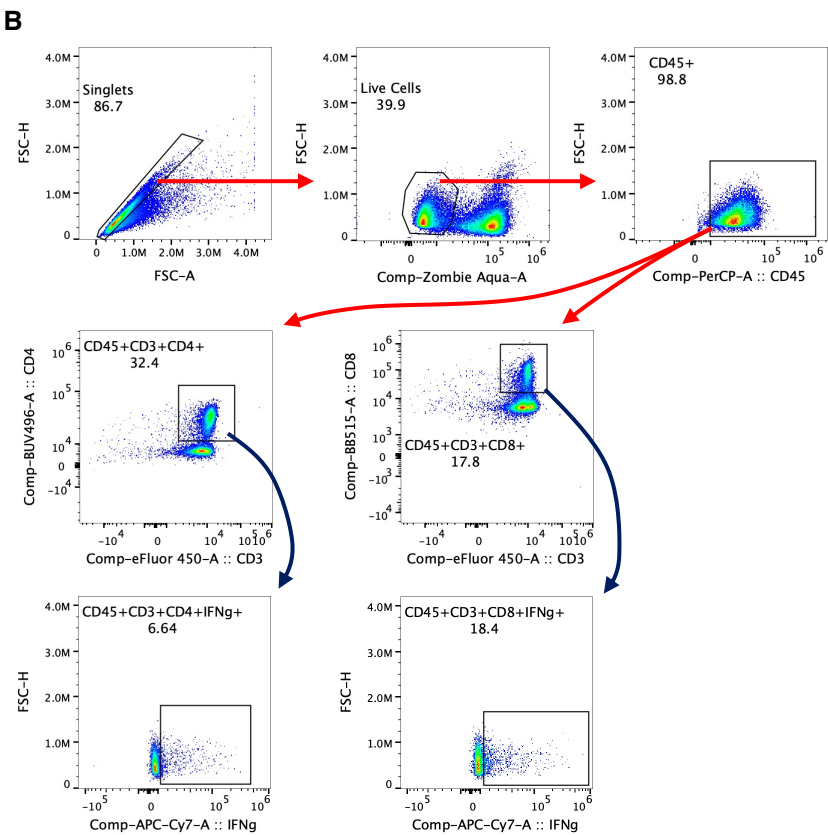
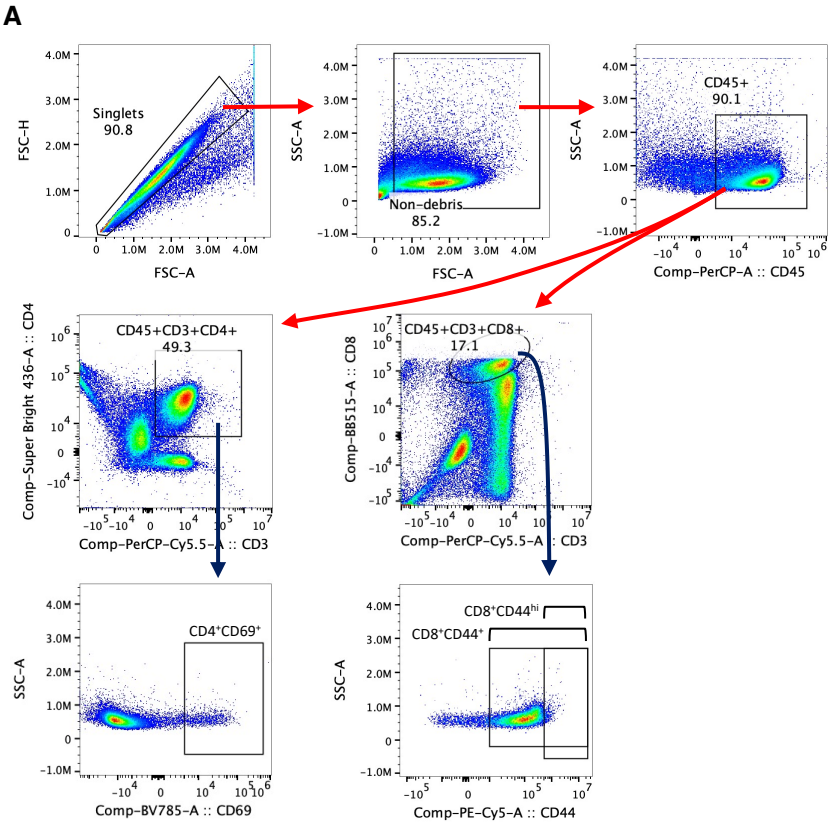
(A) Correlation of gene expression between CXCL9 and STAT1 and (B) correlation of gene expression between CXCL10 and STAT1. (C) Top correlates of CXCL9 and (D) CXCL10, with most highly correlated STAT family member indicated. Taken from cBioportal.

HGNC symbols	MGI symbols
IFI27	Ifi27
IRF7	Irf7
USP18	Usp18
BST2	Bst2
CXCL10	Cxcl10
DDX60	Ddx60
HERC6	Herc6
HLA-B	
HLA-G	
IFI35	Ifi35
IFI44	Ifi44
IFI44L	Ifi44l
IFIT1	Ifit1
IFIT3	Ifit3
ISG15	Isg15
LGALS3BP	Lgals3bp
LY6E	Ly6e
MX1	Mx2
MX2	Mx1
OAS3	Oas3
OASL	Oasl1
PLSCR1	Plscr1
STAT1	Stat1
TRIM14	Trim14
HSD17B1	Hsd17b1
OAS1	Oas1a
CA2	Car2
CCNA1	Ccna1
CXCL1	Cxcl1
GALC	Galc
IFI6	
IFITM1	Ifitm1
LAMP3	Lamp3
MCL1	Mcl1
ROBO1	Robo1
SLC6A15	Slc6a15
THBS1	Thbs1
TIMP3	Timp3

### SUPPLEMENTAL FIGURE 3

Manually curated list of predicted orthologous equivalents in mouse of the human gene signature used in Figure 3D.

Cancer Immunology, Immunotherapy (submitted in 2021) - Michael Knitz et al.



**SUPPLEMENTAL FIGURE 4**

Representative flow cytometry gating used for manually gated populations depicted in Figure 4E and 4J. (A) Gating strategy used for events collected from tumor-draining lymph nodes from mice bearing LY2 STAT1 KO tumors or LY2 PX458 Ctrl tumors. (B) Gating strategy used for events collected from tumor-draining lymph nodes from mice bearing MOC2 STAT1 KO tumors or MOC2 PX458 Ctrl tumors.