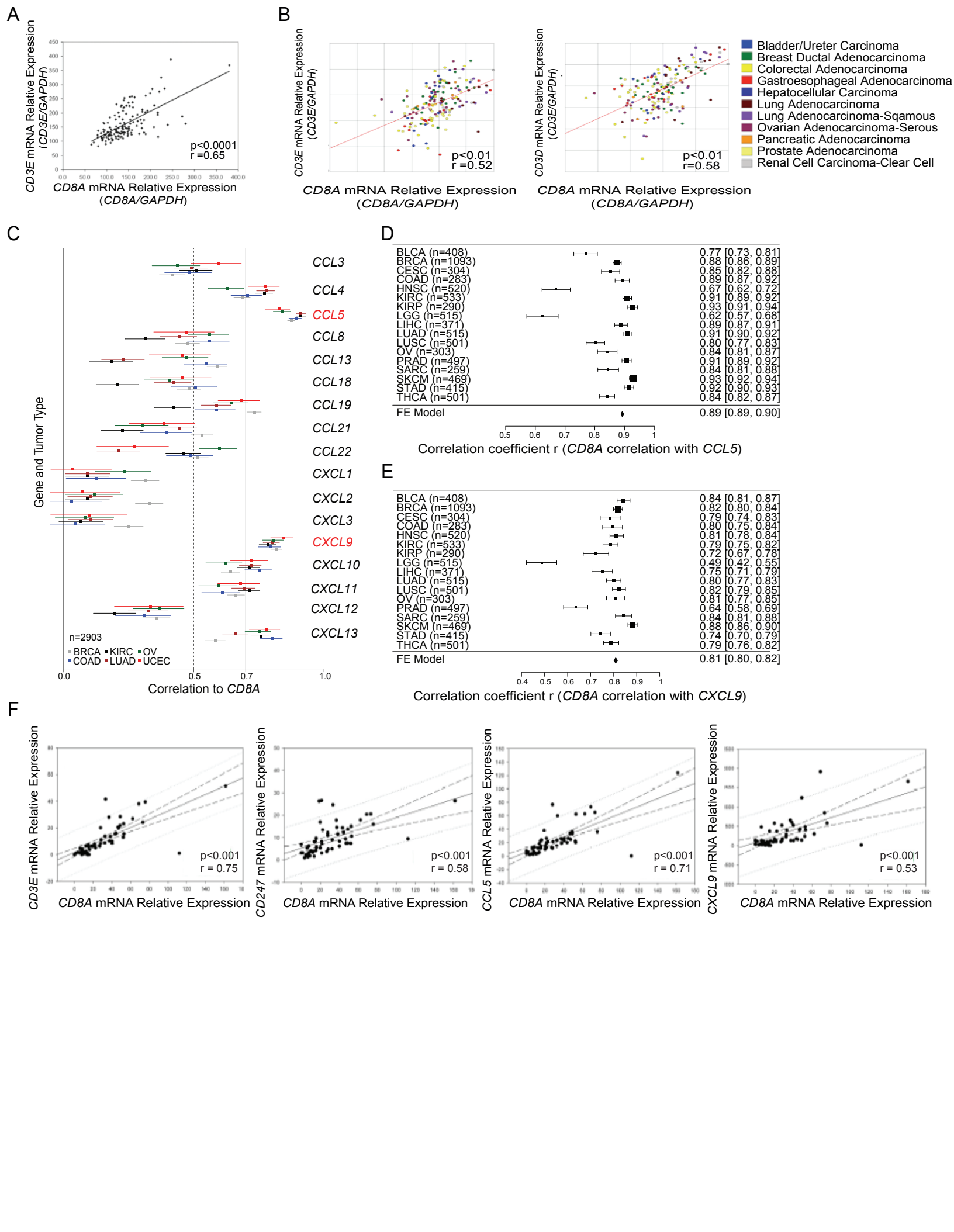
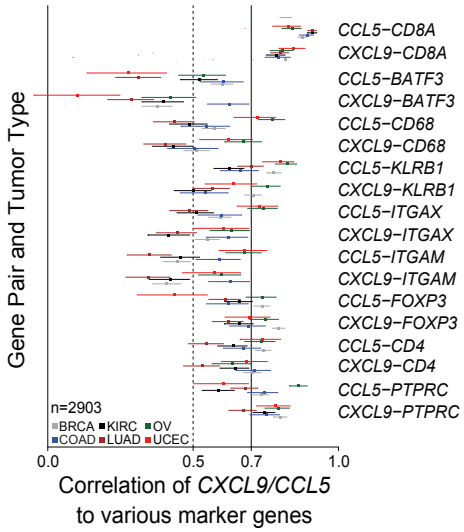

A
CD3E mRNA Relative Expression (CD3E/GAPDH)
CD8A mRNA Relative Expression (CD8A/GAPDH)
p<0.0001
r =0.65
B
CD3E mRNA Relative Expression (CD3E/GAPDH)
CD8A mRNA Relative Expression (CD8A/GAPDH)
p<0.01
r =0.52
CD3D mRNA Relative Expression (CD3E/GAPDH)
CD8A mRNA Relative Expression (CD8A/GAPDH)
p<0.01
r=0.58
Bladder/Ureter Carcinoma
Breast Ductal Adenocarcinoma
Colorectal Adenocarcinoma
Gastroesophageal Adenocarcinoma
Hepatocellular Carcinoma
Lung Adenocarcinoma
Lung Adenocarcinoma-Sqamous
Ovarian Adenocarcinoma-Serous
Pancreatic Adenocarcinoma
Prostate Adenocarcinoma
Renal Cell Carcinoma-Clear Cell
C
Gene and Tumor Type
CCL3
CCL4
CCL5
CCL8
CCL13
CCL18
CCL19
CCL21
CCL22
CXCL1
CXCL2
CXCL3
CXCL9
CXCL10
CXCL11
CXCL12
CXCL13
n=2903
BRCA KIRC OV
COAD LUAD UCEC
Correlation to CD8A
D
BLCA (n=408) 0.77 [0.73, 0.81]
BRCA (n=1093) 0.88 [0.86, 0.89]
CESC (n=304) 0.85 [0.82, 0.88]
COAD (n=283) 0.89 [0.87, 0.92]
HNSC (n=520) 0.67 [0.62, 0.72]
KIRC (n=533) 0.91 [0.89, 0.92]
KIRP (n=290) 0.93 [0.91, 0.94]
LGG (n=515) 0.62 [0.57, 0.68]
LIHC (n=371) 0.89 [0.87, 0.91]
LUAD (n=515) 0.91 [0.90, 0.92]
LUSC (n=501) 0.80 [0.77, 0.83]
OV (n=303) 0.84 [0.81, 0.87]
PRAD (n=497) 0.91 [0.89, 0.92]
SARC (n=259) 0.84 [0.81, 0.88]
SKCM (n=469) 0.93 [0.92, 0.94]
STAD (n=415) 0.92 [0.90, 0.93]
THCA (n=501) 0.84 [0.82, 0.87]
FE Model 0.89 [0.89, 0.90]
Correlation coefficient r (CD8A correlation with CCL5)
E
BLCA (n=408) 0.84 [0.81, 0.87]
BRCA (n=1093) 0.82 [0.80, 0.84]
CESC (n=304) 0.79 [0.74, 0.83]
COAD (n=283) 0.80 [0.75, 0.84]
HNSC (n=520) 0.81 [0.78, 0.84]
KIRC (n=533) 0.79 [0.75, 0.82]
KIRP (n=290) 0.72 [0.67, 0.78]
LGG (n=515) 0.49 [0.42, 0.55]
LIHC (n=371) 0.75 [0.71, 0.79]
LUAD (n=515) 0.80 [0.77, 0.83]
LUSC (n=501) 0.82 [0.79, 0.85]
OV (n=303) 0.81 [0.77, 0.85]
PRAD (n=497) 0.64 [0.58, 0.69]
SARC (n=259) 0.84 [0.81, 0.88]
SKCM (n=469) 0.88 [0.86, 0.90]
STAD (n=415) 0.74 [0.70, 0.79]
THCA (n=501) 0.79 [0.76, 0.82]
FE Model 0.81 [0.80, 0.82]
Correlation coefficient r (CD8A correlation with CXCL9)
F
CD3E mRNA Relative Expression
CD8A mRNA Relative Expression
p<0.001
r = 0.75
CD247 mRNA Relative Expression
CD8A mRNA Relative Expression
p<0.001
r = 0.58
CCL5 mRNA Relative Expression
CD8A mRNA Relative Expression
p<0.001
r = 0.71
CXCL9 mRNA Relative Expression
CD8A mRNA Relative Expression
p<0.001
r = 0.53

Figure S1 related to Figure 1

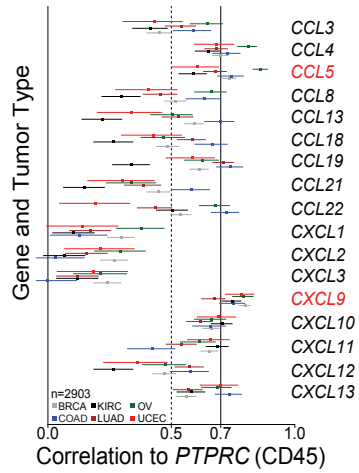
CD8$^+$ T-cell infiltration in tumors correlates with *CXCL9* and *CCL5* chemokine expression.

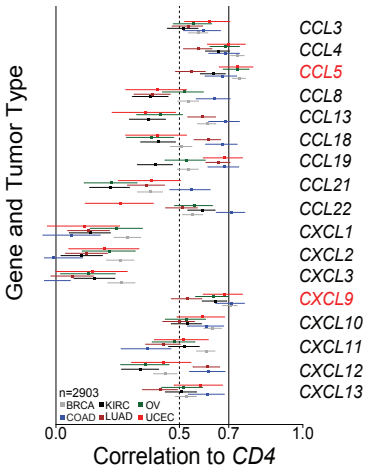
(A) Pearson correlation plots of *CD8A* with *CD3E* mRNA levels in ovarian cancer in microarray gene expression datasets. (**B**) Pearson correlation plots of *CD8A* and *CD3E* or *CD3D* mRNA levels in microarray gene data from different tumor types. (**C**) Correlation analyses of *CD8A* expression with that of genes of *CCL* and *CXCL* chemokines in the TCGA dataset. Average r (square) in a subset of 6 tumor types was plotted with 95% confidence intervals (CI) (lines) truncated on the left (n=2903). (**D-E**) Meta-analytical estimation of the correlation between expressions of *CD8A* with *CCL5* (**D**) or with *CXCL9* (**E**) for 17 tumor types (n=7777). Estimates (squares) are drawn in proportion to the standard errors. Lines indicate 95% CIs and diamond shows the pooled effect size at its center. TCGA abbreviations: BLCA (Bladder Urothelial Carcinoma), BRCA (Breast invasive carcinoma), CESC (Cervical squamous cell carcinoma and endocervical adenocarcinoma), COAD (Colon adenocarcinoma), HNSC (Head and Neck squamous cell carcinoma), KIRC (Kidney renal clear cell carcinoma), KIRP (Kidney renal papillary cell carcinoma), LGG (Brain Lower Grade Glioma), LIHC (Liver hepatocellular carcinoma), LUAD (Lung adenocarcinoma), LUSC (Lung squamous cell carcinoma), OV (Ovarian serous cystadenocarcinoma), PRAD (Prostate adenocarcinoma), SARC (Sarcoma), SKCM (Skin Cutaneous Melanoma), STAD (Stomach adenocarcinoma), THCA (Thyroid carcinoma). (**F**) Pearson correlation plots of *CD3E*, *CD247*, *CXCL9* and *CCL5* with *CD8A* quantified by qRT-PCR in an independent set of 57 stage III ovarian cancer specimens. Correlation coefficients (r) and p values are as displayed.

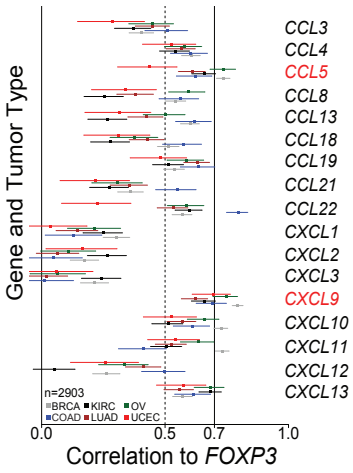
A

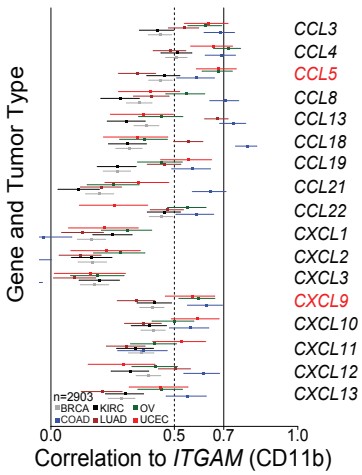

Gene Pair and Tumor Type
CCL5−CD8A
CXCL9−CD8A
CCL5−BATF3
CXCL9−BATF3
CCL5−CD68
CXCL9−CD68
CCL5−KLRB1
CXCL9−KLRB1
CCL5−ITGAX
CXCL9−ITGAX
CCL5−ITGAM
CXCL9−ITGAM
CCL5−FOXP3
CXCL9−FOXP3
CCL5−CD4
CXCL9−CD4
CCL5−PTPRC
CXCL9−PTPRC
n=2903
BRCA KIRC OV
COAD LUAD UCEC
0.0 0.5 0.7 1.0
Correlation of CXCL9/CCL5
to various marker genes

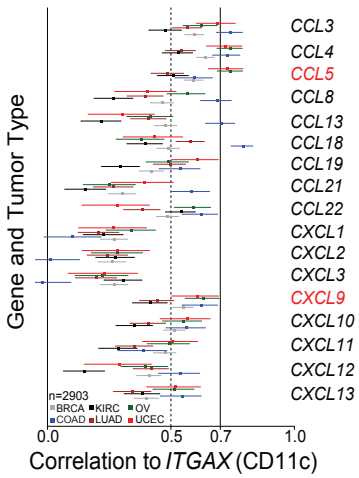
B

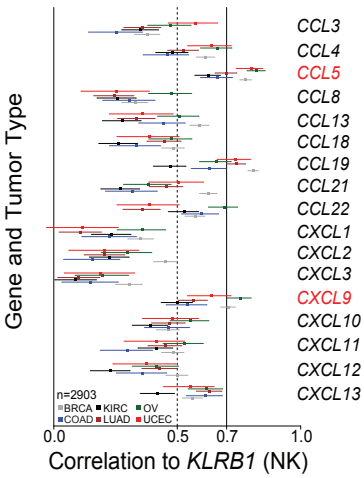

Gene and Tumor Type
CCL3
CCL4
CCL5
CCL8
CCL13
CCL18
CCL19
CCL21
CCL22
CXCL1
CXCL2
CXCL3
CXCL9
CXCL10
CXCL11
CXCL12
CXCL13
n=2903
BRCA KIRC OV
COAD LUAD UCEC
0.0 0.5 0.7 1.0
Correlation to PTPRC (CD45)

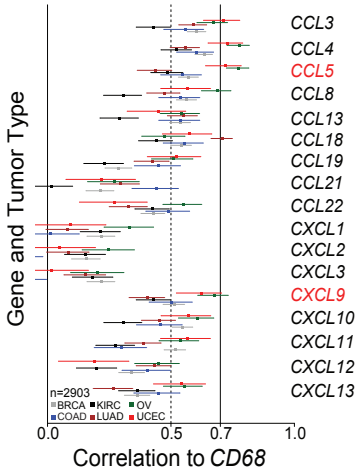

Gene and Tumor Type
CCL3
CCL4
CCL5
CCL8
CCL13
CCL18
CCL19
CCL21
CCL22
CXCL1
CXCL2
CXCL3
CXCL9
CXCL10
CXCL11
CXCL12
CXCL13
n=2903
BRCA KIRC OV
COAD LUAD UCEC
0.0 0.5 0.7 1.0
Correlation to CD4


Gene and Tumor Type
CCL3
CCL4
CCL5
CCL8
CCL13
CCL18
CCL19
CCL21
CCL22
CXCL1
CXCL2
CXCL3
CXCL9
CXCL10
CXCL11
CXCL12
CXCL13
n=2903
BRCA KIRC OV
COAD LUAD UCEC
0.0 0.5 0.7 1.0
Correlation to FOXP3


Gene and Tumor Type
CCL3
CCL4
CCL5
CCL8
CCL13
CCL18
CCL19
CCL21
CCL22
CXCL1
CXCL2
CXCL3
CXCL9
CXCL10
CXCL11
CXCL12
CXCL13
n=2903
BRCA KIRC OV
COAD LUAD UCEC
0.0 0.5 0.7 1.0
Correlation to ITGAM (CD11b)


Gene and Tumor Type
CCL3
CCL4
CCL5
CCL8
CCL13
CCL18
CCL19
CCL21
CCL22
CXCL1
CXCL2
CXCL3
CXCL9
CXCL10
CXCL11
CXCL12
CXCL13
n=2903
BRCA KIRC OV
COAD LUAD UCEC
0.0 0.5 0.7 1.0
Correlation to ITGAX (CD11c)


Gene and Tumor Type
CCL3
CCL4
CCL5
CCL8
CCL13
CCL18
CCL19
CCL21
CCL22
CXCL1
CXCL2
CXCL3
CXCL9
CXCL10
CXCL11
CXCL12
CXCL13
n=2903
BRCA KIRC OV
COAD LUAD UCEC
0.0 0.5 0.7 1.0
Correlation to KLRB1 (NK)


Gene and Tumor Type
CCL3
CCL4
CCL5
CCL8
CCL13
CCL18
CCL19
CCL21
CCL22
CXCL1
CXCL2
CXCL3
CXCL9
CXCL10
CXCL11
CXCL12
CXCL13
n=2903
BRCA KIRC OV
COAD LUAD UCEC
0.0 0.5 0.7 1.0
Correlation to CD68

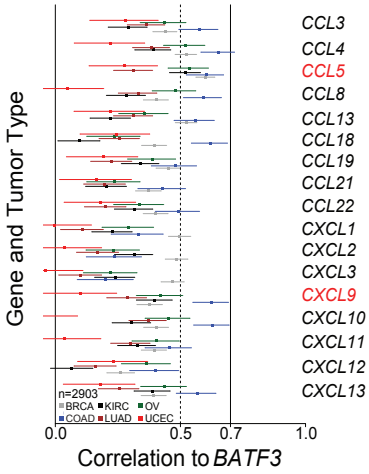

Gene and Tumor Type
CCL3
CCL4
CCL5
CCL8
CCL13
CCL18
CCL19
CCL21
CCL22
CXCL1
CXCL2
CXCL3
CXCL9
CXCL10
CXCL11
CXCL12
CXCL13
n=2903
BRCA KIRC OV
COAD LUAD UCEC
0.0 0.5 0.7 1.0
Correlation to BATF3

Figure S2 related to Figure 1

Correlation of *CXCL9* and *CCL5* chemokine expression with immune cell subset genes in solid tumors

(A) Correlation analyses of *CD8A, BATF3, CD68, KLRB1, ITGAX, ITGAM, FOXP3, CD4, PTPRC* and genes of the *CCL5* and *CXCL9* chemokines in the TCGA dataset. Average r (square) in a subset of 6 tumor types was plotted with 95% confidence CI (lines) truncated on the left (n=2903). (**B**) Correlation analyses of *BATF3, CD68, KLRB1, ITGAX, ITGAM, FOXP3, CD4, PTPRC* with CCL and CXCL chemokine genes in the same dataset. Average r (square) in a subset of 6 tumor types was plotted with 95%CI (lines) truncated on the left (n=2903).

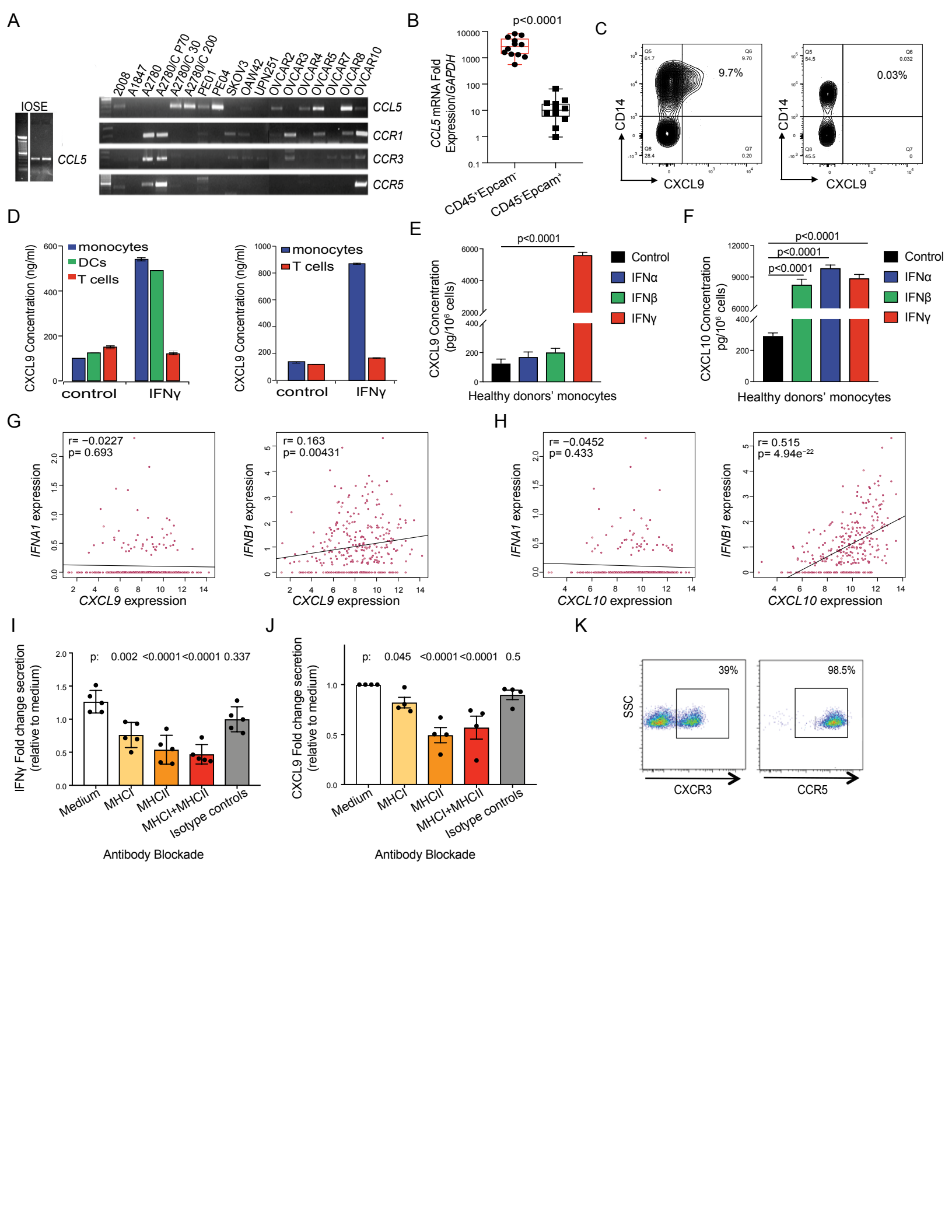
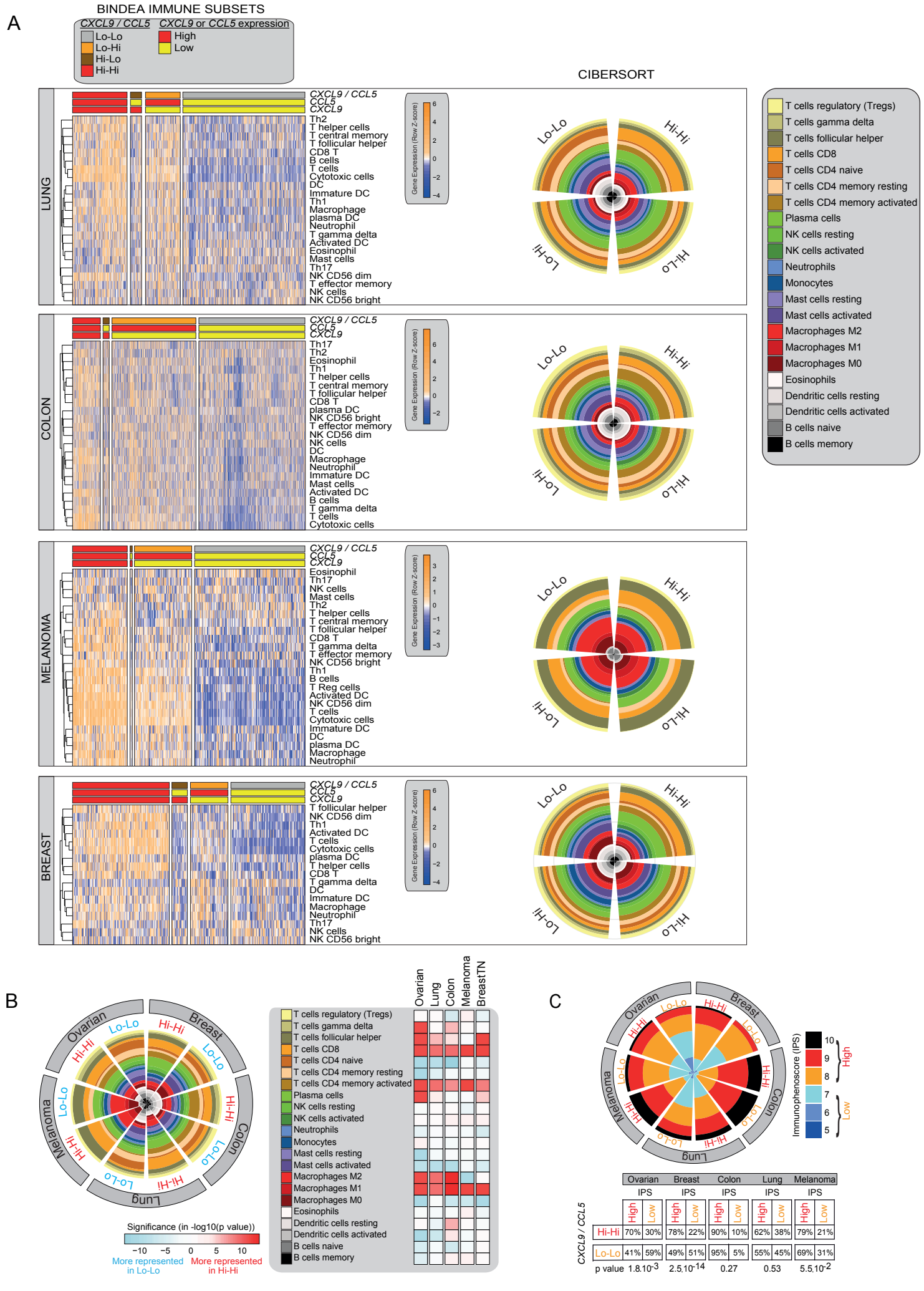

A
IOSE
CCL5
2008
A1847
A2780
A2780/C P70
A2780/C 30
A2780/C 200
PE01
PE04
SKOV3
OAW42
UPN251
OVCAR2
OVCAR3
OVCAR4
OVCAR5
OVCAR7
OVCAR8
OVCAR10
CCL5
CCR1
CCR3
CCR5
B
p<0.0001
CCL5 mRNA Fold Expression/GAPDH
CD45+Epcam-
CD45-Epcam+
C
9.7%
0.03%
CD14
CXCL9
D
monocytes
DCs
T cells
CXCL9 Concentration (ng/ml)
control
IFNγ
E
p<0.0001
CXCL9 Concentration (pg/10^6 cells)
Control
IFNα
IFNβ
IFNγ
Healthy donors' monocytes
F
p<0.0001
p<0.0001
p<0.0001
CXCL10 Concentration pg/10^6 cells)
Healthy donors' monocytes
G
r= −0.0227
p= 0.693
r= 0.163
p= 0.00431
IFNA1 expression
IFNB1 expression
CXCL9 expression
H
r= −0.0452
p= 0.433
r= 0.515
p= 4.94e-22
CXCL10 expression
I
p: 0.002 <0.0001 <0.0001 0.337
IFNγ Fold change secretion (relative to medium)
Medium
MHCI
MHCII
MHCI+MHCII
Isotype controls
Antibody Blockade
J
p: 0.045 <0.0001 <0.0001 0.5
CXCL9 Fold change secretion (relative to medium)
Antibody Blockade
K
39%
98.5%
SSC
CXCR3
CCR5

Figure S3 related to Figures 2, 3 and 4

Characterization of CCL5, CXCL9 and CXCL10 in ovarian cancer

(**A)** *CCL5*, *CCR1, CCR3* and *CCR5* mRNA detection by RT-PCR in 18 ovarian cancer and normal epithelial IOSE cell lines. (**B**) Relative *CCL5* mRNA quantification by qPCR in FACS-sorted $Epcam^{+}CD45^{-}$ ovarian cancer cells and FACS-sorted $Epcam^{-}CD45^{+}$tumor infiltrating leukocytes. Boxplots represent 25th and 75th percentiles with midline indicating the median; whiskers extend to the lowest/highest values. P value was calculated with unpaired student T test. (**C**) Representative FACS dot plots of CXCL9 expression in $CD14^{+}$ monocytes from EOC (**left**) and PBMCs (**right**). (**D**) Quantification of CXCL9 secretion (ELISA) of rested and IFNγ activated monocytes, dendritic cells and T cells from healthy donors (**left**) and EOC patients (**right**). (**E, F**) Cytokine bead array (CBA) quantification of CXCL9 (**E**) and CXCL10 (**F**) secretion in healthy donors' blood monocytes 72 hr post stimulation with IFNα, IFNβ or IFNγ (40 ng/ml). P values were calculated with multiple T tests. (**G, H)** Pearson correlation plots of *IFNA1* and *IFNB1* with *CXCL9* (**G***)* or *CXCL10* (**H**) in ovarian cancer TCGA. R and p values are shown in each plot. (**I, J**) Relative quantification of IFNγ (**I**) and CXCL9 (**J**) secretion in mixed tumor co-cultures in the presence of MHC I and/or MCH II blocking or control isotype antibodies. Shown p values were calculated with T tests comparing each condition to medium only (n=4). (**K**) Representative FACS dot plots of CXCR3 and CCR5 expression in autologous donor $CD8^{+}$ cells transduced with HLA-A^{*}02-restricted NY-ESO-1 TCR. All bar-graph data are presented as mean ± SEM.



CXCL9 / CCL5	Ovarian IPS High	Ovarian IPS Low	Breast IPS High	Breast IPS Low	Colon IPS High	Colon IPS Low	Lung IPS High	Lung IPS Low	Melanoma IPS High	Melanoma IPS Low
Hi-Hi	70%	30%	78%	22%	90%	10%	62%	38%	79%	21%
Lo-Lo	41%	59%	49%	51%	95%	5%	55%	45%	69%	31%

Figure S4 related to Figure 5

Immune landscape of triple negative breast cancer, colon cancer, lung cancer and melanoma.

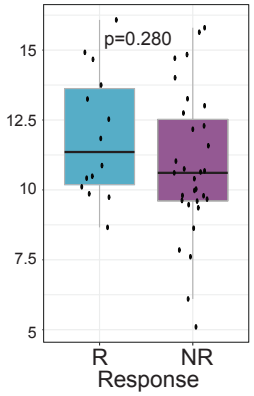
(**A**) This figure is associated with Figure 5C and 5D and shows the equivalent panel for lung adenocarcinoma, triple-negative breast cancer, colorectal cancer and melanoma. **Left**: Heatmaps show scoring of immune gene signatures as described by Bindea et al according to *CCL5/CXCL9* chemokine expression subgroups. **Right**: Pie charts show the relative immune subset proportions computed by the CIBERSORT algorithm according to chemokine subgroups. (**B**) **Left**: Relative pie chart representation of immune component proportions as computed by the CIBERSORT algorithm and averaged over the $CXCL9^{hi}CCL5^{hi}$ (Hi-Hi) and $CXCL9^{lo}CCL5^{lo}$ (Lo-Lo) tumors from the five cancer types. **Right**: Heatmap displaying the significance level of the differences in immune subsets between Hi-Hi and Lo-Lo tumors for each cancer type (ANOVA followed by Tukey test) and the directionality of the difference (red: over-representation in Hi-Hi, light blue over-representation in Lo-Lo). (**C**) **Top**: Pie chart representation showing the proportion of patients with different immunophenoscores (McDonough et al.) according to their *CXCL9/CCL5* subgroups (Hi-Hi versus Lo-Lo) and cancer type. Patients were categorized into high IPS (IPS 8 to 10) and low IPS (IPS 5 to 7). **Bottom**: results of Fisher's exact tests for differences in IPS proportions between the Hi-Hi and Lo-Lo groups.

Table S4 related to Figure 5: Gene sets I, II and III show the genes that were common in 5, 4 and 3 cancer types, respectively.

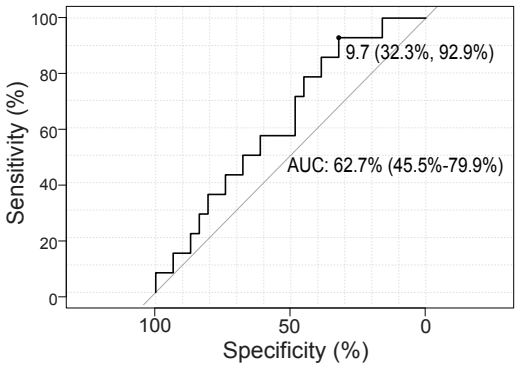
Hi-Hi genes expressed in 5/5 tumor types	Hi-Hi genes expressed in 4/5 tumor types	Hi-Hi genes expressed in 3/5 tumor types
CCL5	*C1QB*	*C1QA*
CD2	*CCL5*	*C1QB*
CD247	*CD2*	*CCL5*
CD3E	*CD247*	*CD2*
CD4	*CD3D*	*CD247*
CD53	*CD3E*	*CD3D*
CD86	*CD3G*	*CD3E*
CD8A	*CD4*	*CD3G*
CXCL9	*CD53*	*CD4*
DOCK2	*CD86*	*CD53*
GBP2	*CD8A*	*CD86*
GZMK	*CD96*	*CD8A*
IL10RA	*CORO1A*	*CD96*
IL2RB	*CXCL9*	*CECR1*
IRF1	*CYBB*	*CORO1A*
LAPTM5	*DOCK2*	*CXCL10*
LCP1	*EVI2B*	*CXCL9*
PTPRC	*GBP1*	*CYBB*
SLC7A7	*GBP2*	*CYTIP*
STAT1	*GZMA*	*DOCK2*
TNFRSF9	*GZMH*	*EVI2B*
	GZMK	*FASLG*
	HCLS1	*GBP1*
	IFNG	*GBP2*
	IGSF6	*GZMA*
	IL10RA	*GZMH*
	IL18RAP	*GZMK*
	IL2RB	*HCLS1*
	IRF1	*HLA.DMB*
	ITGB2	*HLA.DOB*
	KLRD1	*HLA.DPA1*
	LAG3	*HLA.DRA*
	LAPTM5	*ICOS*
	LCP1	*IDO1*
	LILRB4	*IFNG*
	MYO1F	*IGSF6*
	NKG7	*IL10RA*
	PRF1	*IL18RAP*
	PTPN22	*IL2RB*

	PTPRC	*IRF1*
	SH2D1A	*ITGB2*
	SLC7A7	*KLRD1*
	SRGN	*LAG3*
	STAT1	*LAPTM5*
	TNFRSF9	*LCP1*
	TRAF3IP3	*LILRB4*
		MYO1F
		NCKAP1L
		NKG7
		PRF1
		PTPN22
		PTPRC
		SH2D1A
		SLA
		SLC7A7
		SRGN
		STAT1
		TNFRSF9
		TRAF3IP3
		TRAT1

A


p=0.280
15
12.5
10
7.5
5
R
NR
Response

B


9.7 (32.3%, 92.9%)
AUC: 62.7% (45.5%-79.9%)
Sensitivity (%)
Specificity (%)
100
80
60
40
20
0
100
50
0

C

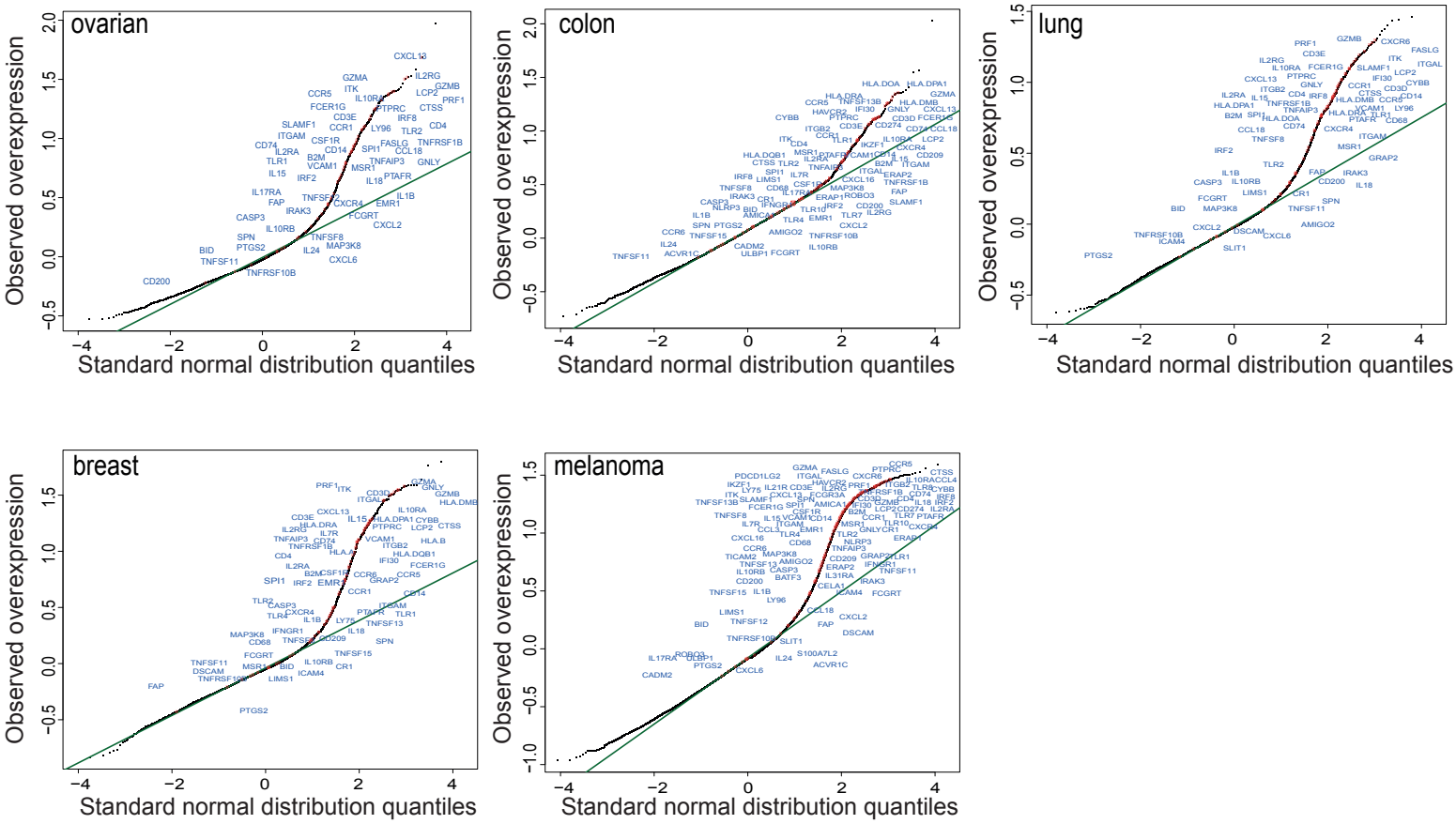
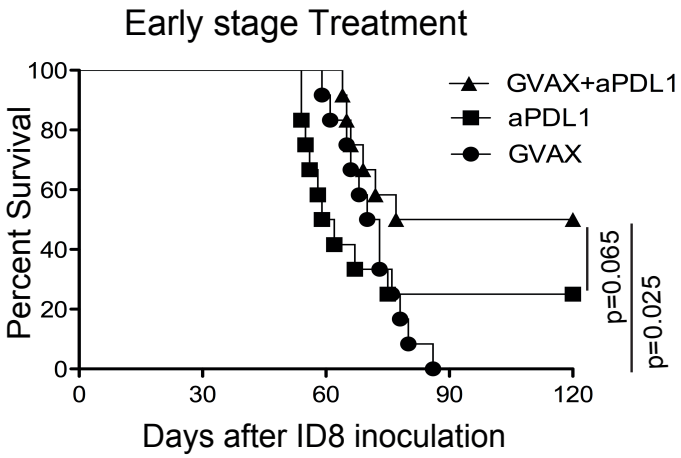

ovarian
colon
lung
breast
melanoma
Observed overexpression
Standard normal distribution quantiles

Figure S5 related to Figure 5

Co-expression of *CCL5* and *CXCL9* does not correlate to CTLA-4 response

(**A**) 21-gene chemokine signature score for pre-treatment samples are shown for responders (R) and non-responders (NR) from the the Ipilimumab-Nivolumab sequential treatment arm of Checkmate 064. Boxplots represent 25th and 75th percentiles with midline indicating the median; whiskers extend to the lowest/highest values. Points show values for individual subjects. Statistical comparison is based on one-sided Wilcoxon rank sum tests. (**B**) ROC plot for 21-gene signature score vs. response in the Ipilimumab-Nivolumab sequential treatment arm of Checkmate 064. (**C**) Position of the genes considered as upregulated under CTLA-4 and PD-1 therapy by Chen et al (Chen et al., 2016) in the Q-Q plot showing the sorted log-fold expression levels of the comparison of the Hi-Hi and Lo-Lo groups in ovarian, colon, lung, triple-negative breast cancer and melanoma. Departure from the green line Q-Q line indicates effects stronger than expected.


Early stage Treatment
Percent Survival
100
80
60
40
20
0
0
30
60
90
120
Days after ID8 inoculation
GVAX+aPDL1
aPDL1
GVAX
p=0.065
p=0.025

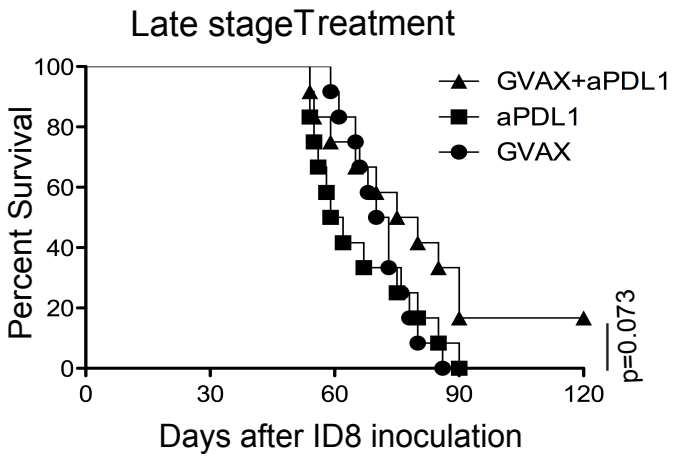

Late stageTreatment
Percent Survival
100
80
60
40
20
0
0
30
60
90
120
Days after ID8 inoculation
GVAX+aPDL1
aPDL1
GVAX
p=0.073

Figure S6 related to Figure 6

Kaplan-Meier curves showing survival of mice with intraperitoneal ID8 tumors treated at early (**left**) or late (**right**) stages with irradiated ID8-GVAX (expressing murine GM-CSF) and/or anti-PD-L1 antibody.

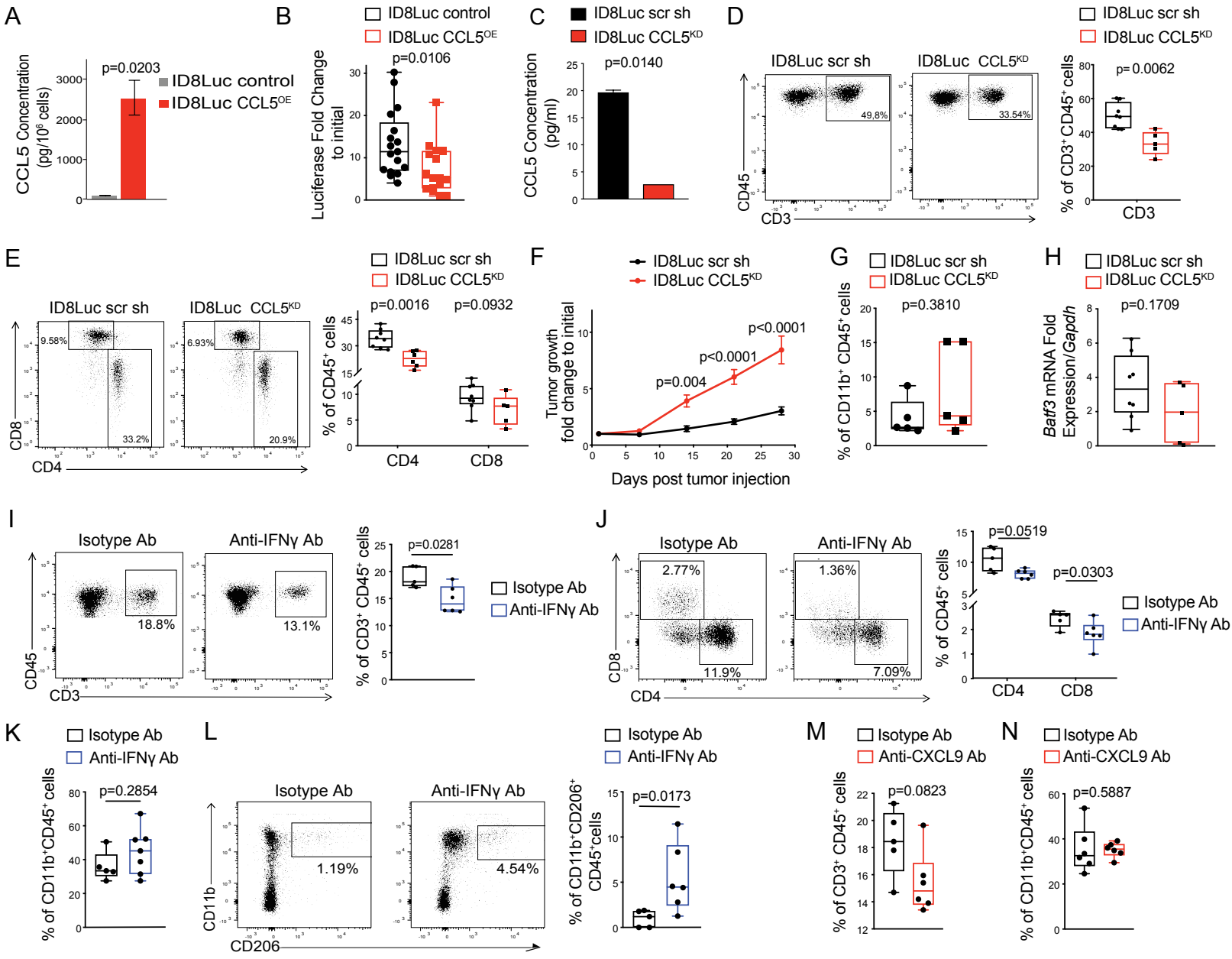

A
CCL5 Concentration (pg/10^6 cells)
p=0.0203
ID8Luc control
ID8Luc CCL5OE
B
ID8Luc control
ID8Luc CCL5OE
Luciferase Fold Change to initial
p=0.0106
C
ID8Luc scr sh
ID8Luc CCL5KD
CCL5 Concentration (pg/ml)
p=0.0140
D
ID8Luc scr sh
ID8Luc CCL5KD
CD45
CD3
49.8%
33.54%
% of CD3+ CD45+ cells
p= 0.0062
E
ID8Luc scr sh
ID8Luc CCL5KD
CD8
CD4
9.58%
33.2%
6.93%
20.9%
% of CD45+ cells
p=0.0016
p=0.0932
CD4
CD8
F
ID8Luc scr sh
ID8Luc CCL5KD
Tumor growth fold change to initial
p<0.0001
p<0.0001
p=0.004
Days post tumor injection
G
ID8Luc scr sh
ID8Luc CCL5KD
% of CD11b+ CD45+ cells
p=0.3810
H
ID8Luc scr sh
ID8Luc CCL5KD
Baf3 mRNA Fold Expression/Gapdh
p=0.1709
I
Isotype Ab
Anti-IFNγ Ab
CD45
CD3
18.8%
13.1%
% of CD3+ CD45+ cells
p=0.0281
Isotype Ab
Anti-IFNγ Ab
J
Isotype Ab
Anti-IFNγ Ab
CD8
CD4
2.77%
11.9%
1.36%
7.09%
% of CD45+ cells
p=0.0519
p=0.0303
CD4
CD8
Isotype Ab
Anti-IFNγ Ab
K
Isotype Ab
Anti-IFNγ Ab
% of CD11b+CD45+ cells
p=0.2854
L
Isotype Ab
Anti-IFNγ Ab
CD11b
CD206
1.19%
4.54%
% of CD11b+CD206+ CD45+cells
p=0.0173
M
Isotype Ab
Anti-CXCL9 Ab
% of CD3+ CD45+ cells
p=0.0823
N
Isotype Ab
Anti-CXCL9 Ab
% of CD11b+CD45+ cells
p=0.5887

Figure S7 related to Figure 7

Tumor-intrinsic CCL5 defines tumor immunoreactivity and enables monocyte-derived and IFNγ-induced *CXCL9* expression *in vivo*

(**A**) CBA analysis of CCL5 in cell-free supernatants of ID8Luc CCL5^{OE} and ID8Luc control cells cell lines. The concentration (pg/ml) was normalized to cell number and is represented as mean ± SD (n=2). P value was calculated with unpaired T test. (**B**) Comparison of endpoint tumor growth volumes in mice injected with ID8Luc CCL5^{OE} or ID8Luc control cells as detected bioluminescence imaging of tumor luciferase expression. P value was calculated with unpaired T test. (**C**) CBA analysis of CCL5 in cell-free supernatants of ID8Luc scr sh or ID8Luc CCL5^{KD} cell lines. The concentration (pg/ml) was normalized to cell number and is represented as mean ± SD (n=2). P value were calculated with unpaired T test. **(D, E**) Representative FACS dot plots and quantification of CD3$^+$ (**D**), CD4$^+$ and CD8$^+$ TILs (**E**) in ID8Luc scr sh or ID8Luc CCL5^{KD} tumors. (**F**) Intraperitoneal tumor growth kinetics of ID8Luc scr sh or ID8Luc CCL5^{KD} tumors as detected by bioluminescence imaging. Data presented as mean ± SEM. P values were calculated with Two-way Anova T tests. (**G**) FACS quantification of CD11b$^+$ TAMs in ID8Luc scr sh or ID8Luc CCL5^{KD} tumors. P value was calculated with Mann-Whitney test (**H**) Relative mRNA quantification of *Batf3* in ID8Luc scr sh or ID8Luc CCL5^{KD} tumors. P value was calculated with Mann-Whitney test. (**I, J**) Representative FACS dot plots and quantification of CD3$^+$ (**I**), CD4$^+$ and CD8$^+$ (**J**) TILs in ID8Luc CCL5^{OE} intraperitoneal tumors after treatment with IFNγ blockade or isotype control antibodies. P values were calculated with Mann-Whitney test. (**K**) FACs quantification of CD11b$^+$ cells in the above tumors. P value was calculated with Mann-Whitney test. (**L**) Representative FACS dot plots and quantification of CD11b$^+$CD206$^+$ TAMs in the above tumors. P value was calculated with Mann-Whitney test. (**M, N**) FACS quantification of CD3$^+$ TILs (**M**) and CD11b$^+$ TAMs (**N**) in ID8Luc CCL5^{OE} tumors after treatment with CXCL9 neutralizing or isotype control antibodies. P values were calculated with Mann-Whitney test.

All boxplots represent 25th and 75th percentiles with midline indicating the median; whiskers extend to the lowest/highest values.