**Supplementary Figure 1: anti-PD-1 and anti-CTLA-4 synergistically induce CXCL9 and CXCL10 expression and leads to enhanced anti-tumor responses**

**A)** C57BL/6 mice were injected s.c. with 5 x 105 AT-3ovacells and allowed to establish for 14 days before dual treatment with anti-PD-1and/or anti-CTLA4 (P+C), or 2A3 isotype control (ISO). **B)** Expression of chemokine receptors following dual PD-1 and CTLA-4 blockade relative to isotype treated mice at day 7 post therapy as determined by nanostring. Data shown is average fold induction from 3 mice per group. **C)** Production of chemokines from tumor supernatants generated as per **Figure 1**. Some data points in **C)** are also shown in **Figure 1** for ISO and P+C conditions. n = 6 mice per group (\* P<0.05, one way ANOVA).

**Supplementary Figure 2: Expression of CXCR3 ligands (CXCL9/10/11) correlates with survival in urothelial carcinoma patients treated with anti-PD-L1 therapy**

**A)** Differential gene expression analysis in melanoma patients pre and post therapy with nivolumab (103 samples from 61 patients). **B)** Kaplan-Meiercurves showing overall survival of 348 urothelial carcinoma patients treated with anti-PD-L1 therapy (ImVigor210 trial) stratified by high and low expression of indicated chemokines. Survival curves were compared with the log-rank test. **C)** Differential gene expression analysis of responders and non-responders in ImVigor210 trial (n = 348, Pre-therapy unadjusted p values plotted with adjusted p value < 0.05 indicated in purple). **D)** Correlation between expression of indicated chemokines and gene expression based cytotoxic T cell score (ImVigor210 trial). **E)** C57BL/6 mice were injectedwith 5 x 105AT-3ovatumorssub-cutaneously and on days 7, 11, 15 and 19 mice were treated with anti-PD-1(200µg/mouse) and, where indicated, anti-CXCR3 (200µg/mouse). Data is represented as the mean ± SEM of 6 mice per group (\*\*\*\* P<0.0001, one way ANOVA).

**Supplementary Figure 3 Expression of CXCR3 ligands (CXCL9/10/11) correlates with survival in patients treated with standard-of-care therapies**

Patients from the **A)** Triple negative breast cancers from the METABRIC cohort (n= 279 with survival data) and **B)** melanoma cases from TCGA (n = 295 with survival data) were stratified based upon expression of indicated chemokines and correlations with overall survival determined. Survival curves were compared with the log-rank test. **C).** Correlation between indicated chemokines/chemokine receptors and cytotoxic T cell score within the TCGA melanoma cohort (n = 441). Correlation tested with Pearson’s product moment correlation coefficient.

**Supplementary Figure 4: Modulation of intratumoral T cell activation/infiltration by of CXCR3 blockade.**

C57BL/6 mice were injected s.c. with 5 x 105 AT-3ovacells and allowed to establish for 14 days before dual treatment with anti-PD-1and anti-CTLA-4 (P+C) or 2A3 isotype control (ISO). Tumor infiltrating lymphocytes were analyzed by flow cytometry at day 21 (day 7 post treatment) **A)** Number of CD8+ T cells per mg of tissue. **B)** Percent of NK1.1+ cells expressing IFNγ and TNFα. **C)** Expression of tbet within CD8+ and CD4+foxp3- cells. **A-C)** Data representative of 1-2 experiments with n =8-12 mice per group.  **D)** 1 x 105AT-3ova cells were plated for 16 hours and then cocultured with activated OT-I T cells at a 1:1 ratio for 6 hours in the presence or absence of anti-CXCR3 (50 µg/ml). Supernatants were taken and analysed for and IFNγ and TNFα levels.

**Supplementary Figure 5: IFNγ and TNFα synergistically enhance CXCL9 and CXCL10 production from AT-3ovatumor cells**

4 x 105 AT-3ovatumor cells were stimulated with IFNγ and/or TNFα at indicated concentrations (ng/ml) for 18 hours. Expression of CXCL9 and CXCL10 was determined by qRT-PCR, relative to expression GAPDH (**A**), or by cytometirc bead array (**B**). Data is presented as mean ± SD of triplicates from a representative experiment. (**C**) 1.5x105 AT-3ova dim cells were stimulated with 10 ng/ml IFNγ and 10 ng/ml TNFα for 18 hours. CXCL9, CXCL10 and actin expression were determined by Western blot.

Data shown is represented as the mean ± SD of triplicate qRT-PCRs from cells pooled from n = 4 mice per group.

**Supplementary Figure 6: Analysis of intratumoural myeloid cell populations following dual PD-1/CTLA-4 combination therapy.**

**A)** C57BL/6 mice were injected s.c. with 5 x 105 AT-3ovacells and allowed to establish for 14 days before dual treatment with anti-PD-1and anti-CTLA4 (P+C) or 2A3 isotype control (ISO). Tumor infiltrating lymphocytes were FACS sorted by flow cytometry at day 21 (day 7 post treatment) and expression of CXCL9 and CXCL10 mRNA determined by qRT-PCR as per **Figure 4**. **B**) Gating of CD11b+Ly6CintCD11c+ (Mo/Mac) cells. **C)** Percentage of Mo/Mac from viable CD45.2+ cells and **D**) their expression of MHCII and CD64 relative to total CD45+ population after P+C treatment. **E)** Percentage of CD103+ DCs from viable CD45+ cells. Data shown is mean ± SEM of 6 mice per group from a representative experiment of n = 3. **F)** Representative flow cytometry gating and co-expression of CXCL9 and CD103 or F4/80. **G)** Expression of CXCL9 in TCRβ‑B220+ B cells following treatment with 2A3 (ISO) or anti-PD-1 and anti-CTLA-4 (P+C). Data is from concatenated samples from n = 4-6 mice and is shown relative to Mo/Macs. **H)** Proportion of MHCII+ F4/80+ cells following anti-F4/80 treatment. Data shown is from 4 concatenated samples.

**Supplementary Figure 7: Macrophages are the major source of CXCL9, CXCL10 and CXCL11 in melanoma and Head and Neck cancer patient cohorts and a chemokine producing macrophage signature is associated with favorable response to immunotherapy**

**A-B)** Violin plots of chemokine expression across subpopulations from single cell RNASeq of immune infiltrate in **A**) cohort of metastatic melanoma (n = 4861 cells from 32 patients, Jerby-Arnon *et al.*) or **B)** Puram *et al* cohort of head and neck cancer patients, n = 2801 cells from 18 patients, tumour infiltrating immune cells only. Dots represent cells. **C)** Macrophage gene signature in non-responder and responder patients from Sade-Feldmann *et al.* study.