

Supplementary Figure. A. Difference in frequency of CD8+ staining by IHC in control or PIK3CA H1047R tumors treated with PD-1 blockade, quantification of Figure 2A. B. tSNE projection of scRNA-seq profiles from CD45⁺ tumor infiltrating immune cells from control or PIK3CA H1047R MC38 tumors, colored by tumor of origin in tSNE. C. Gene expression matrix from single-cell RNA-seq experiment characterizing expression of lineage-defining genes in cell clusters. D. Frequency of indicated immune cell types by flow cytometry from control or PIK3CA H1047R MC38 tumors on day 14. E. Correlation of *MYC* and *HRAS* and mRNA levels with *CCR2* mRNA levels in indicated cancers. Volcano plot showing the Spearman's correlation and estimated significance from RNA-seq data across TCGA cancer types calculated by TIMER (Tumor Immune Estimation Resource) and adjusted for tumor purity[27]. Each dot represents a cancer type in TCGA; red dots indicate significant correlations ($P < 0.05$). F. *Ccl2* transcript abundance measured by qPCR in control and PIK3CA H1047R MC38 cells after transfection with sgRNA targeting *Ccl2*. Data are mean \pm s.d. G. *Ccl2* protein abundance in cell supernatant measured by ELISA in control and PIK3CA H1047R MC38 cells after transfection with sgRNA targeting *Ccl2* or control guide. Data are mean \pm s.d. H. Frequency of Ccr2^{hi} myeloid cells in control and PIK3CA H1047R MC38 tumors after transfection with sgRNA targeting *Ccl2* or control guide.