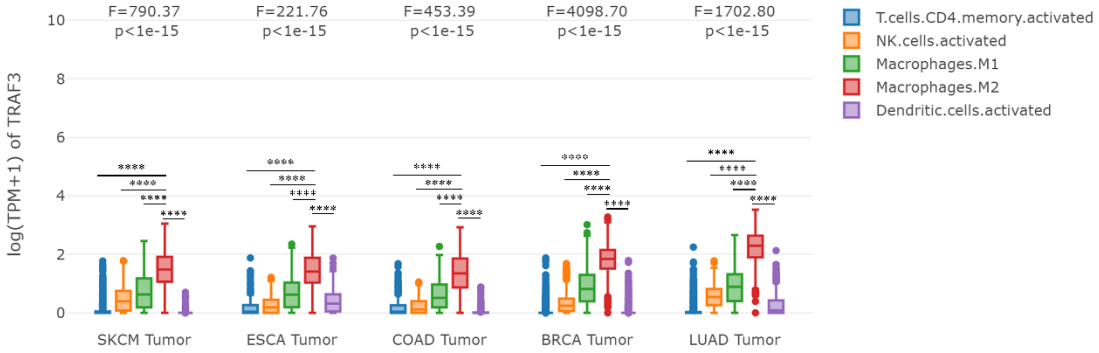
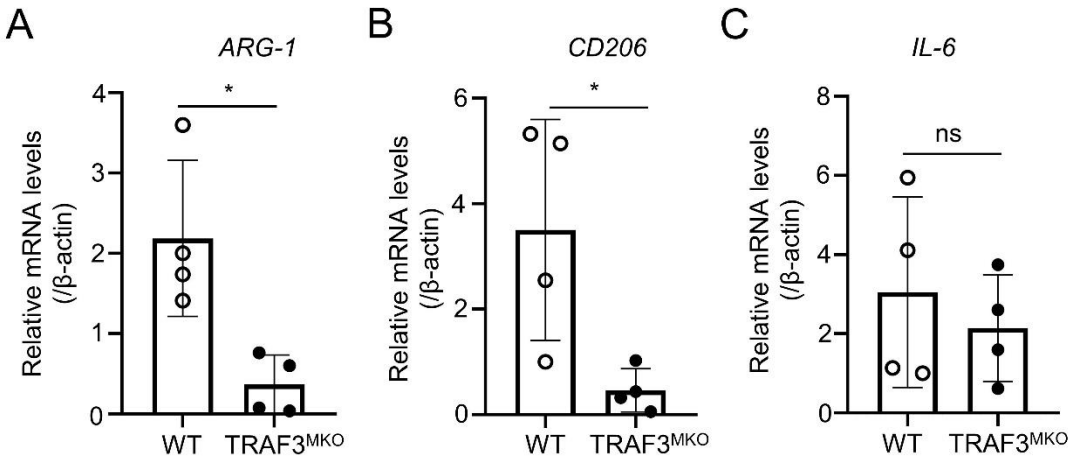
Figure S1



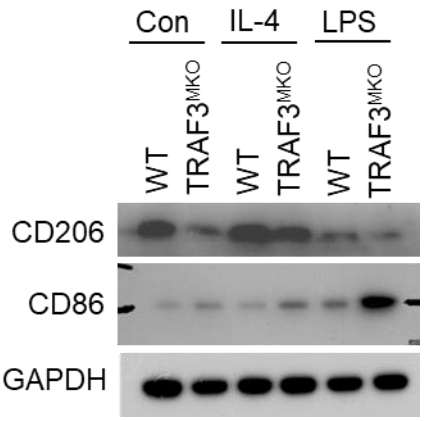

**Supplementary Figure S1. Cell type-level expression analysis of TRAF3 in tumor tissues.** Cell type expression levels of TRAF3 were analyzed using GEPIA2021 (http://gepia2021.cancer-pku.cn/) in the sub-datasets (indicated cancer types from TCGA). All the data are from TCGA (version 2016-09-01) expression database. The sample numbers of SKCM Tumor, ESCA Tumor, COAD Tumor, BRCA Tumor and LUAD Tumor datasets were 469, 182, 290, 1099 and 515, respectively. SKCM, Skin Cutaneous Melanoma; ESCA, Esophageal carcinoma; COAD, Colon adenocarcinoma; BRCA, Breast invasive carcinoma; LUAD, Lung adenocarcinoma. ****$p$<0.0001, compared with Macrophages M2 group.

Figure S2



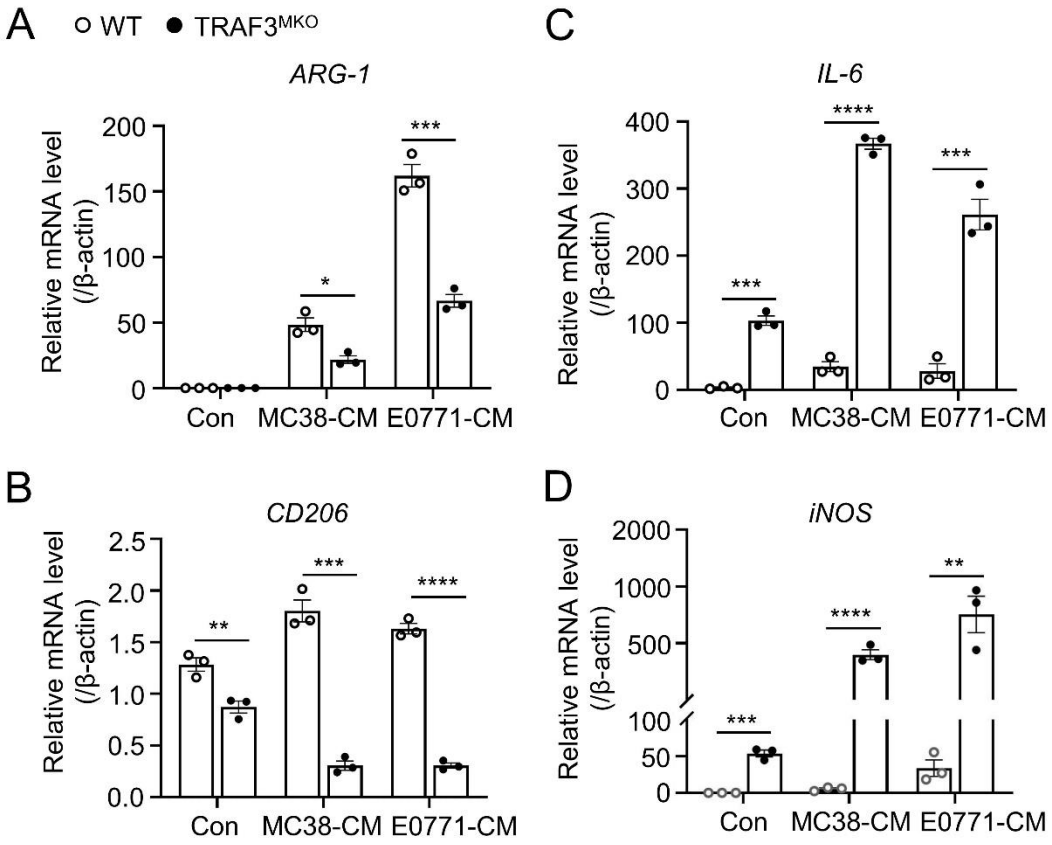

**Supplementary Figure S2. Macrophage polarization marker gene expression in TRAF3-deficient peripheral blood mononuclear cells (PBMCs).** PBMCs were obtained from WT and TRAF3MKO mice. Total RNA was extracted and qRT-PCR analysis of ARG-1, CD206 and IL-6 were performed. Bar graphs with error bars are represented as mean ± SD. $*p < 0.05$.

Figure S3



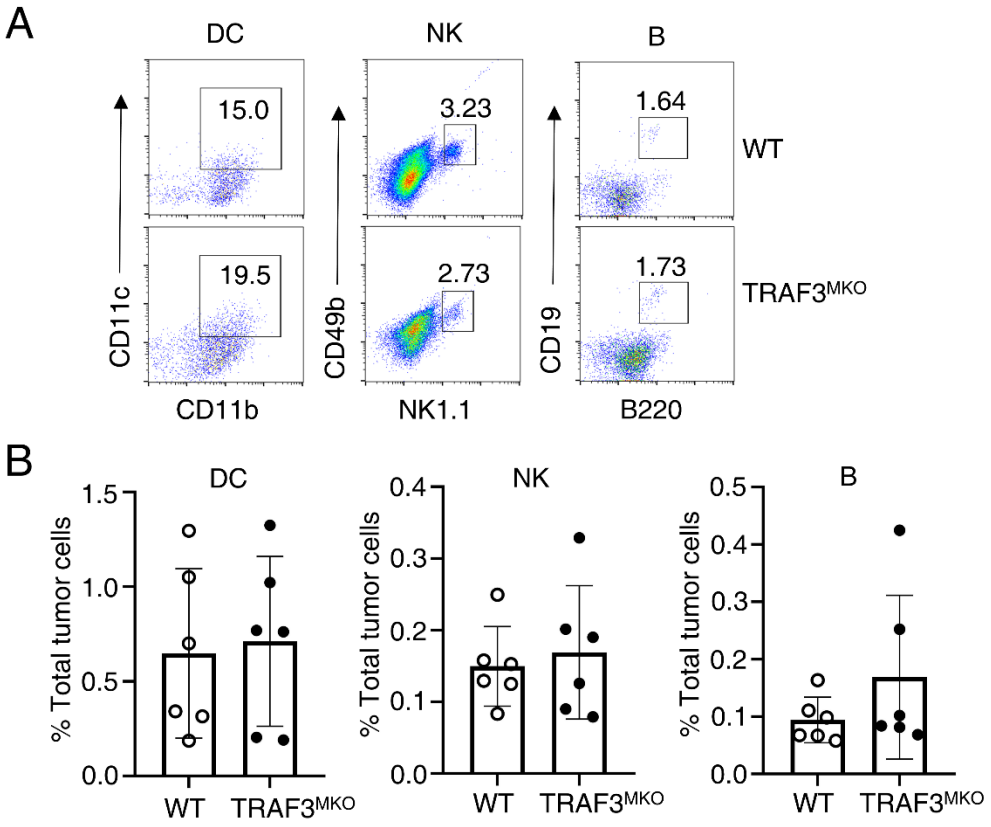

**Supplementary Figure S3. CD206 and CD86 expression in IL-4 and LPS induced WT and TRAF3$^{MKO}$ BMDMs.** BMDMs from WT and TRAF3$^{MKO}$ mice were treated with IL-4 (10 ng/mL) or LPS (1 μg/mL) for 48 h. Total cell lysates was extracted and CD206 and CD86 protein levels were detected by immunoblotting.

Figure S4




**Supplementary Figure S4. TRAF3 deficiency suppressed tumor induced M2 TAM polarization. A-D,** BMDMs were co-cultured with MC38 or E0771 conditional media (MC38-CM, E0771-CM) for 48 h. Total RNA was extracted and qRT-PCR ananlysis of ARG-1 (A), CD206 (B), IL-6 (C) and iNOS (D) was performed. Bar graphs with error bars are represented as mean ± SD. Each panel is a representative experiment of at least three independent biological replicates. $**p < 0.01$, $***p < 0.001$, $****p < 0.0001$.

Figure S5




**Supplementary Figure S5. TRAF3 regulates immune cell infiltration in B16 tumor model.** Flow cytometric analysis of immune cells (CD45+) infiltrated to day 21 tumor tissues. A, Frequency of tumor infiltrated DCs (CD3-CD11b+CD11c+), NK cells (CD3-NK1.1+CD49b+) and B cells (CD3-CD19+B220+). B, Summary of flow cytometry data of (A) based on multiple mice, showing the frequency of the indicated cell populations within total tumor cells. Data are represented as mean ± SD. Each panel is a representative experiment of at least three independent biological replicates.