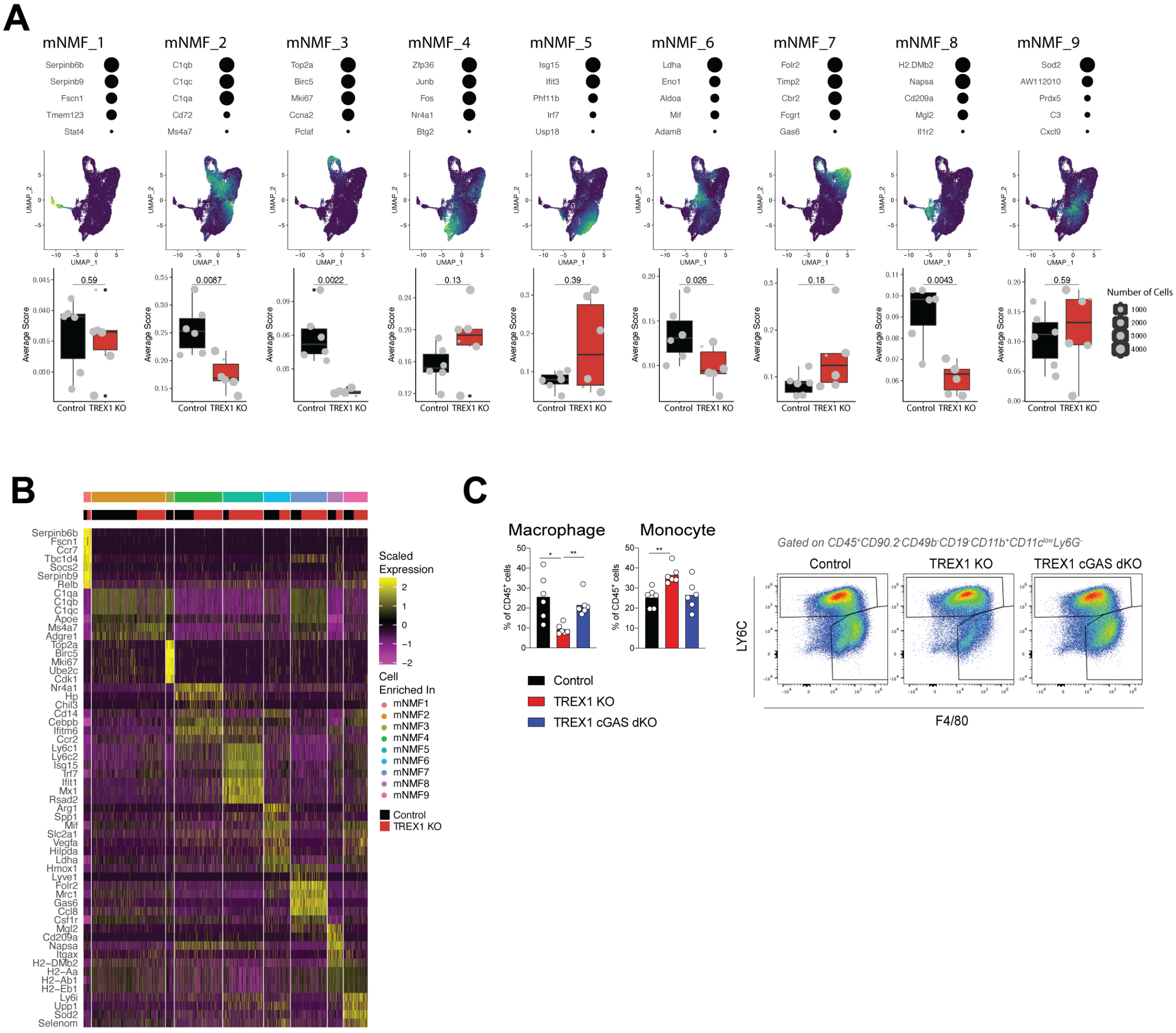

Supplementary Figure 5. TREX1 loss remodels an immunosuppressive myeloid tumor microenvironment

A. NMF programs from monocytes, macrophages and cDC2s (mNMF, Supplementary Table 1). The top five genes contributing to each program are listed with dots sized according to their relative contribution to the NMF program. UMAPs show scaled program scores for the given NMF program from low (blue) to high (yellow). Box plots display the NMF scores averaged by animal (grey points). Size of the points represents the number of cells for each animal. Wilcox rank-sum test. **B.** Heatmap of selected genes related to the myeloid NMF programs. Cells are ordered according to the NMF program with the highest score for the cell, then by tumor genotype. **C.** Bar graphs and representative flow cytometry plots showing monocyte and macrophage proportions in CT26 tumors. Circles represent individual animals. Bars represent the mean. One-way ANOVA (n=6 per group). *P < 0.05 and **P < 0.01.