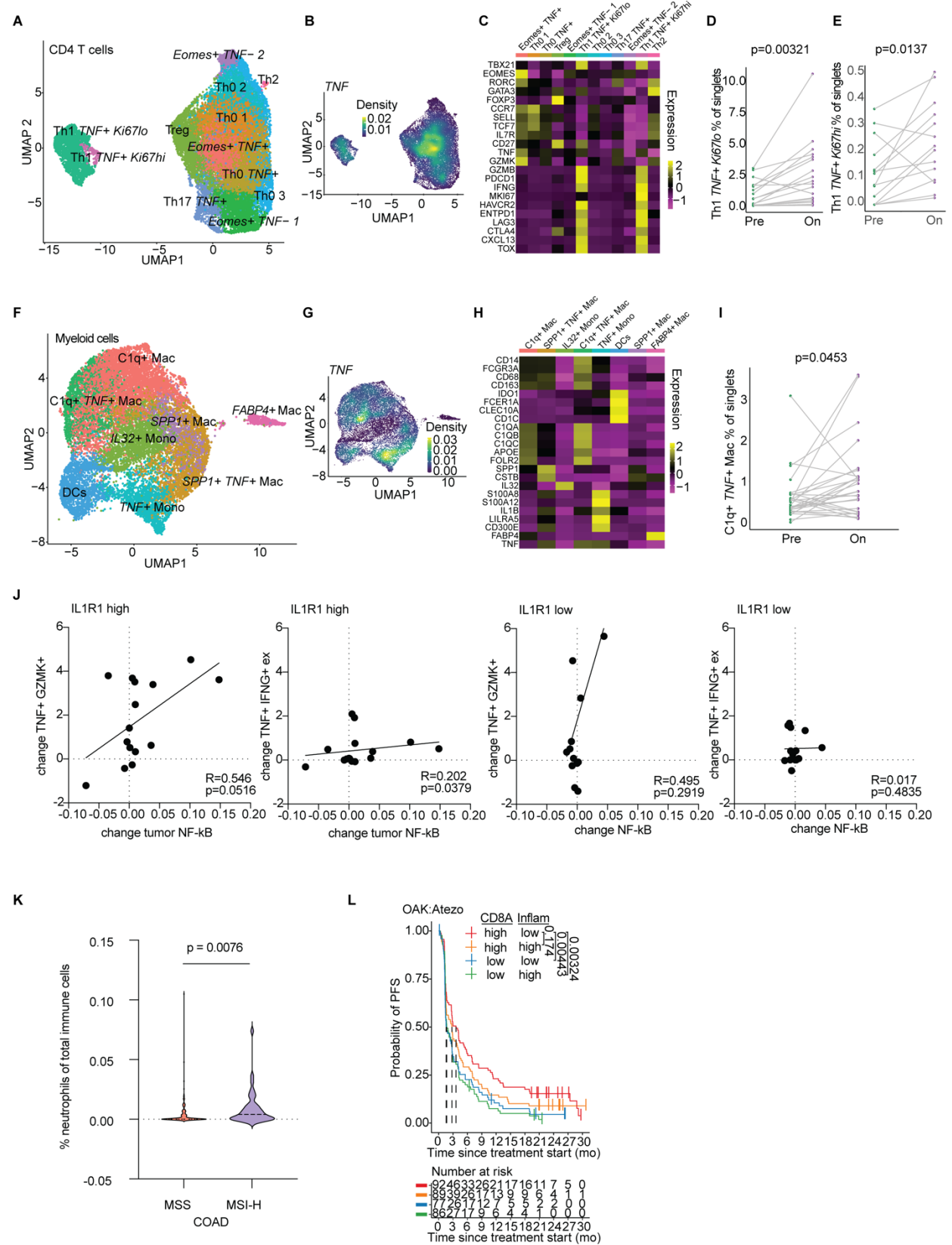


Figure S13



Supplementary Figure S13.

A, UMAP of 24,468 CD4 T cells from the BIOKEY study (EGAS00001004809), color coded by CD4 T cell phenotype. **B**, UMAP cell density plot for *TNF* expressing cells. **C**, Heatmap of genes defining CD4 T cell clusters. **D and E**, Percent of cells in indicated cluster out of singlet cells in tumor for pre vs. on-treatment samples for each patient. P values by two-tailed matched-pairs t test. **F**, UMAP of 16,485 myeloid cells from the BIOKEY study (EGAS00001004809), color coded by myeloid cell phenotype. **G**, UMAP cell density plot for *TNF* expressing myeloid cells. **H**, Heatmap for genes defining myeloid cell clusters. **I**, Percent of cells in the C1q+ *TNF*+ Macrophage cluster out of singlet cells in tumor for pre vs. on-treatment samples for each patient. P value by two-tailed matched-pairs t test. **J**, Spearman correlation analysis between the changes in indicated cluster frequencies vs. changes in tumor NF-kB score before and after ICI treatment, stratified by *IL1R1* high and *IL1R1* low status. **K**, Violin plots of neutrophil quantification by CIBERTSORTx from MSS and MSI-H COAD patients in TCGA. P value by two-tailed Mann-Whitney test. **L**, Kaplan-Meier curves of patients in the OAK trial (NCT02008227) for progression-free survival (PFS), stratified by *CD8A* status and inflammation gene score status (“inflam”). P values by log-rank test.