

Supplementary information, Fig. S8

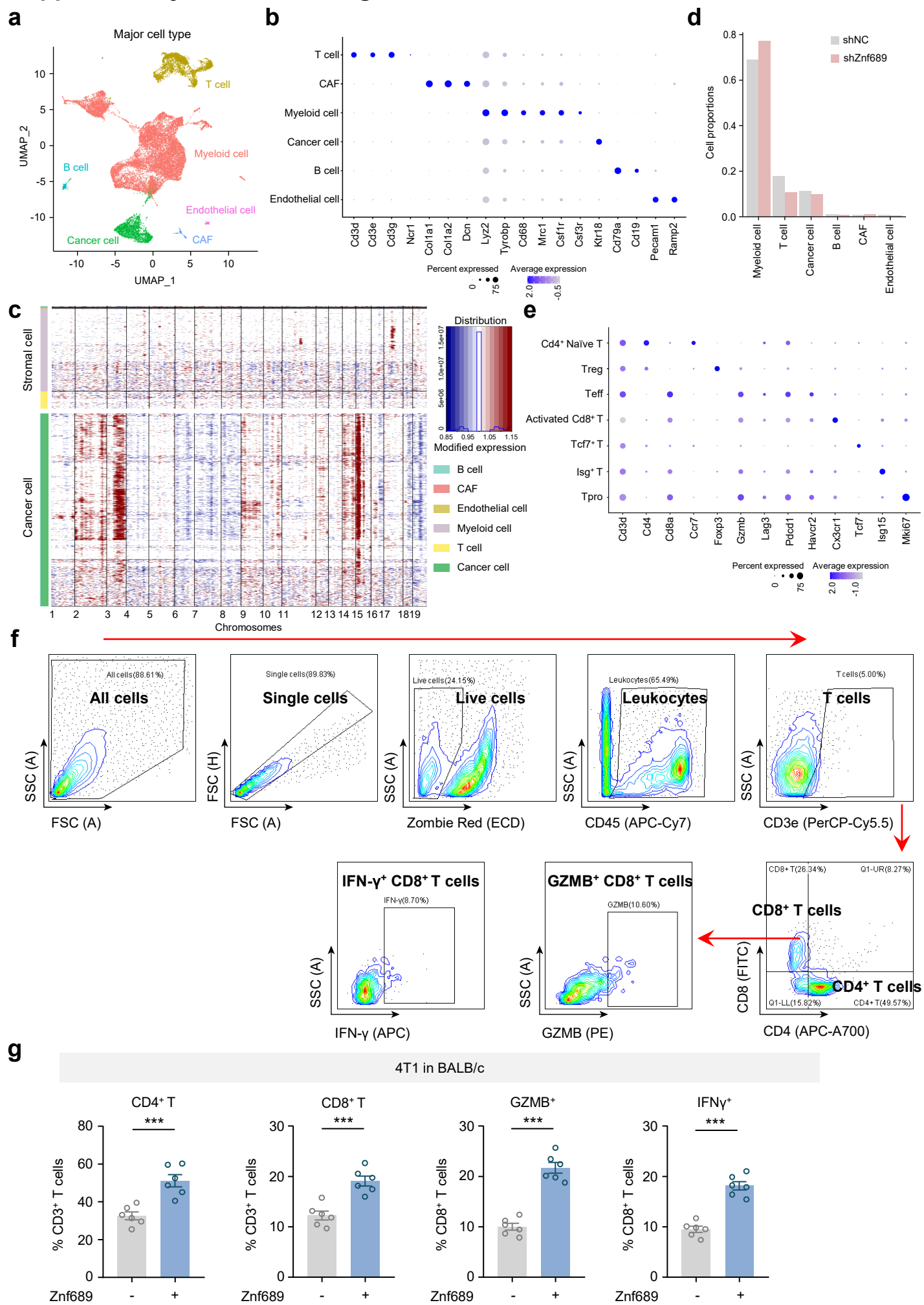


Fig. S8 ZNF689 deficiency promotes immune escape in TNBC.

a UMAP plot of 25,701 cells acquired from 4T1 tumors. Cells and clusters are color coded by the major cell types found. **b** Bubble plots of the marker genes expressed in the major cell types. Dot color reflects the expression level and dot size represents the percent of cells expressing marker genes in different cell types. **c** CNV profile in cancer versus stromal cells assessed using InferCNV based on scRNA-seq. **d** The distribution of major cell types between shNC and shZnf689 tumors. **e** Bubble plots of the marker genes expressed in the T-cell subtypes. Dot color reflects the expression level and dot size represents the percent of cells expressing marker genes in different cell subtypes. **f** Gating strategy for flow cytometry analysis of live cells (Zombie red), leucocytes (CD45⁺), T cells (CD45⁺CD3e⁺), CD4⁺ T cells (CD45⁺CD3e⁺CD4⁺), CD8⁺ T cells (CD45⁺CD3e⁺CD8a⁺), GZMB⁺ CD8⁺ T cells (CD45⁺CD3e⁺CD8a⁺GZMB⁺) and IFN- γ ⁺ CD8⁺ T cells (CD45⁺CD3e⁺CD8a⁺IFN- γ ⁺). The numbers in the graphs indicate the percentages of cells. Plots of data from one representative tumor are shown. **g** Primary tumors of 4T1 cells overexpressing Znf689 in BALB/c mice were harvested for flow cytometry to determine the percentages of CD4⁺ T cells among CD3⁺ T cells, CD8⁺ T cells among CD3⁺ T cells, GZMB⁺ cells among CD8⁺ T cells, and IFN- γ ⁺ cells among CD8⁺ T cells (n = 6). P values were determined using two-tailed unpaired Student's t tests. ***p < 0.001.