Assay for patient-specific monitoring and treatment for ovarian cancer

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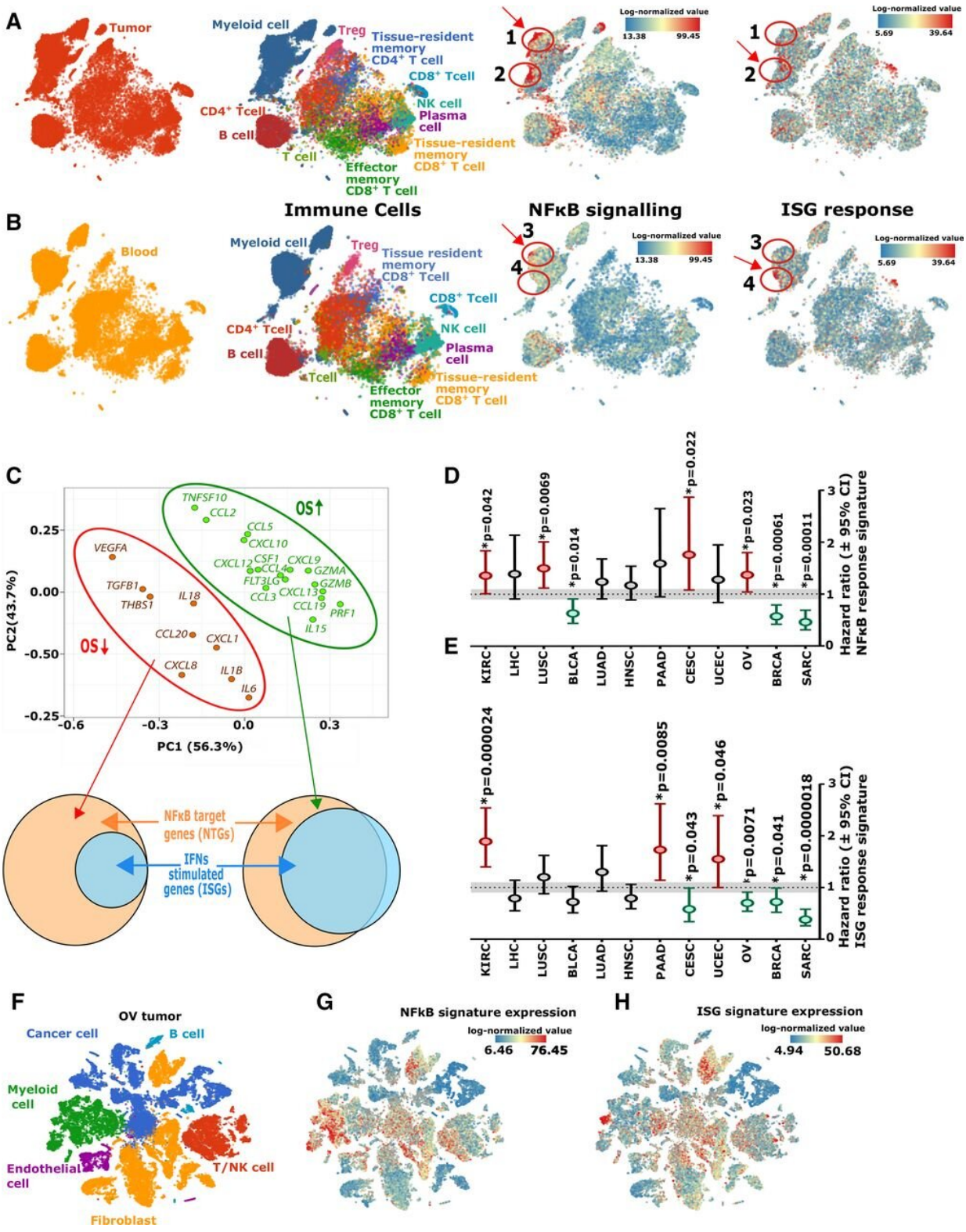

Figure 1. Interrogation of the tumor derived bulk-RNAseq or tumor/blood single-cell (sc)-RNAseq data of patients with cancer. (A,B) The t-distributed stochastic

neighbor embedding (tSNE) visualizations of indicated immune cell types, from scRNAseq data from patients with renal cell and large cell neuroendocrine carcinoma (n=4 patients in total) (derived from GSE139555) isolated from tumor tissue (A) or peripheral blood (B). These immune cells were further colored for NFκB and IFN/ISG response gene-signature levels. Herein, the arrows highlight main immune populations with overlaps between tumor and blood for these signatures, and the circles indicate different myeloid cell subsets. (C) PCA analyses of median expression for each gene across cancer types (from online supplemental figure S5A) and median HR values (from online supplemental figure S5B). Venn diagram represents the portion of NFκB and ISGs in each cluster. (D,E) Visualization of the hazard ratio (HR) ±95% confidence interval (CI) for the impact of expression of NFκB signaling gene signature (D) or ISG signaling gene signature (E), for the indicated TCGA cancer datasets wherein the signature expression cut-off for binary (high vs low expression) patient stratification was based on best-performing threshold principle for OS of indicated TCGA patients with cancer (LIHC, n=371; PAAD, n=177; LUSC, n=501; LUAD, n=513; HNSC, n=500; CESC, n=304; BLCA, n=405; UCEC, n=543; OV, n=374; SARC, n=259; BRCA; n=1090; KIRC; n=530) (Mantel-Cox test, *p