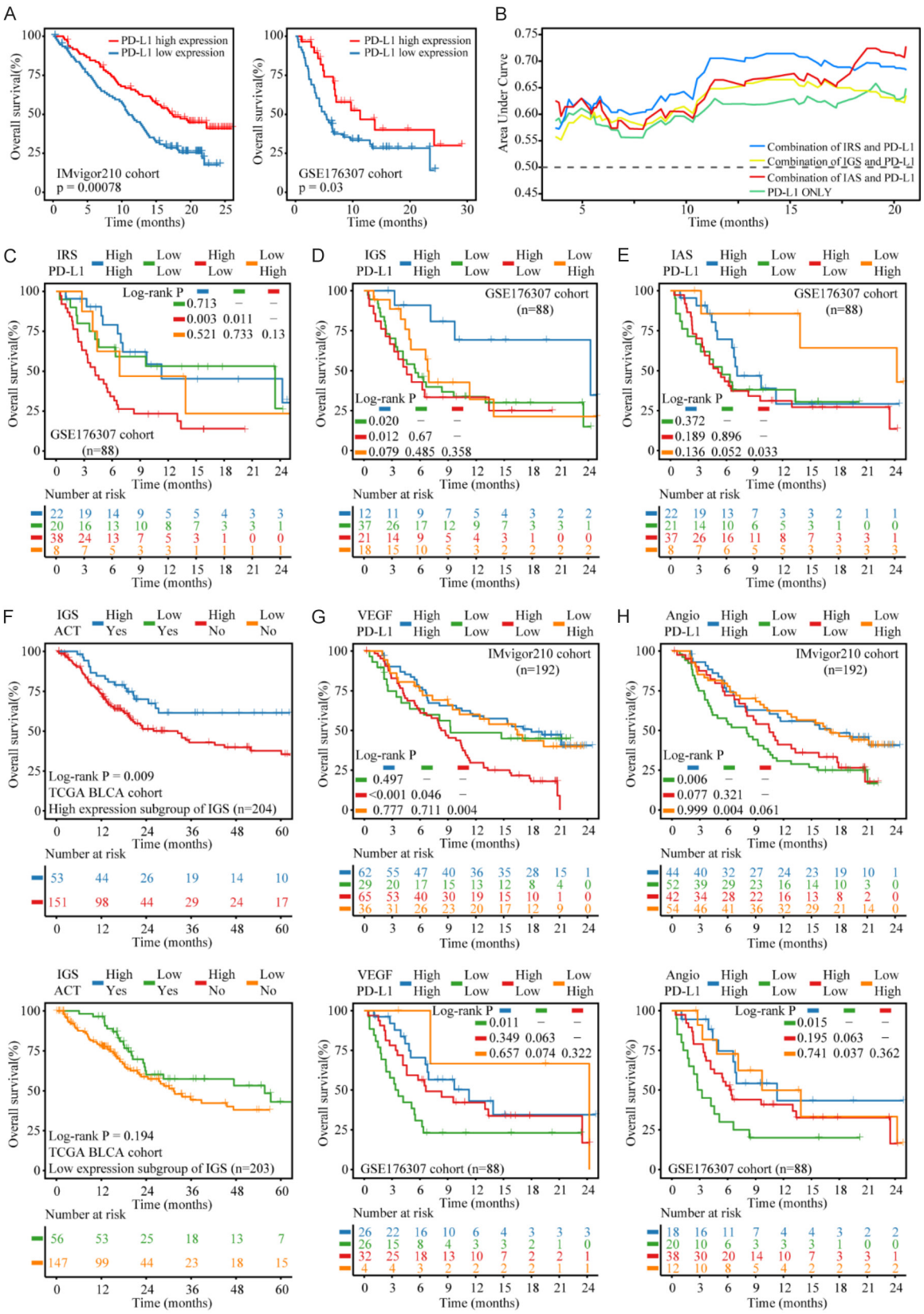

Figure S1. A. Kaplan-Meier analyses of OS in patients, according to PD-L1 mRNA expression values. Data were analyzed by log-rank test. B. Time-dependent receiver operating characteristic curve, the groups of blue line was de-

fined as IRS^{high}PD-L1^{high} and IRS^{low}PD-L1^{low} subgroups, yellow line was IGS^{high}PD-L1^{high} and IGS^{low}PD-L1^{low} subgroups, red line was IAS^{high}PD-L1^{low} and IAS^{low}PD-L1^{high} subgroups and green line used group that PD-L1 expression only. C-E. Kaplan-Meier survival curves of IRS/IGS/IAS and PD-L1 panel for OS of patients with ICBT from GSE176307 cohort. F. Kaplan-Meier analyses of OS, according to IGS expression level, top is patients with ACT and bottom is patients without ACT. G. Kaplan-Meier survival curves of VEGF pathway and PD-L1 panel for OS of patients with ICBT in IMvigor210 and GSE179306 cohort. H. Kaplan-Meier survival curves of 'Angiogenesis' signature and PD-L1 panel. OS, overall survival; PD-L1, programmed cell death ligand-1; IRS, ICBT RNA regulatory signature; IGS, ICBT genomic stability signature; IAS, ICBT angiogenesis signature; ACT, adjuvant chemotherapy; ICBT, immune checkpoint blockade therapy; BLCA, bladder urothelial carcinoma; TCGA, The Cancer Genome Atlas.

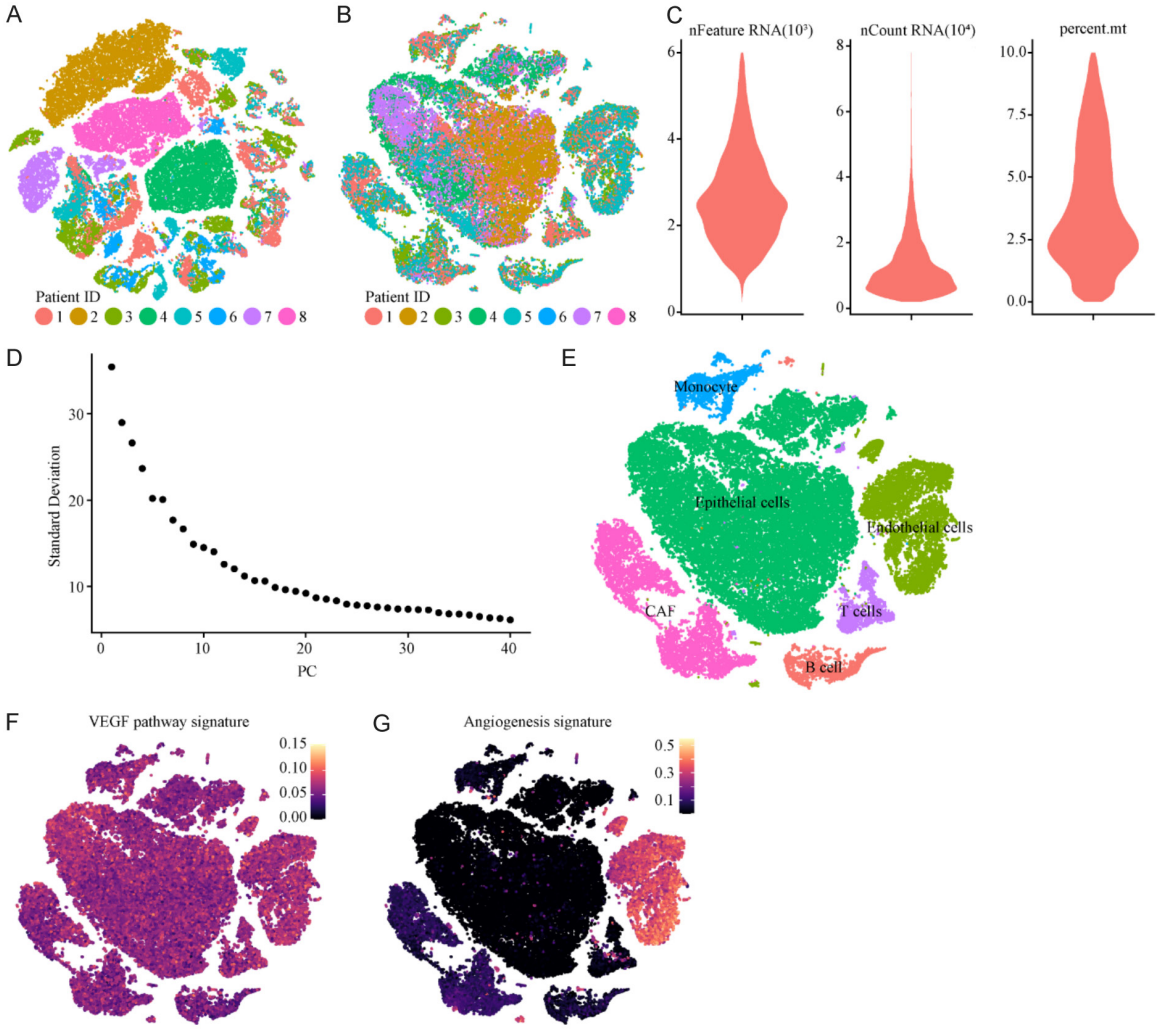

Figure S2. (A-E) Quality control of single cell sequencing data. (A) Significant batch effect among patients. (B) Removing batch effect between batches with 3000 variable features. (C) Violin plot shows number of features (nfeature RNA), number of genes (nCounts RNA) detected and percent of mitochondrial derived transcripts (percent.mt) per single cell after quality control. (D) Scree plot show top 40 principle components of principle component analysis. Top 30 principle components were used in downstream analysis. (E) tSNE plot of single cells profiled in the colored by major cell types in preliminary identification. (F and G) tSNE plot of the expression pattern of VEGF pathway (F) and 'Angiogenesis' (G) signature in the single cells profiled.