

Figure S1. Immune cell infiltration in The Cancer Genome Atlas-ovarian serous cystadenocarcinoma dataset estimated by the (A) quanTiseq and (B) MCP-counter algorithms.

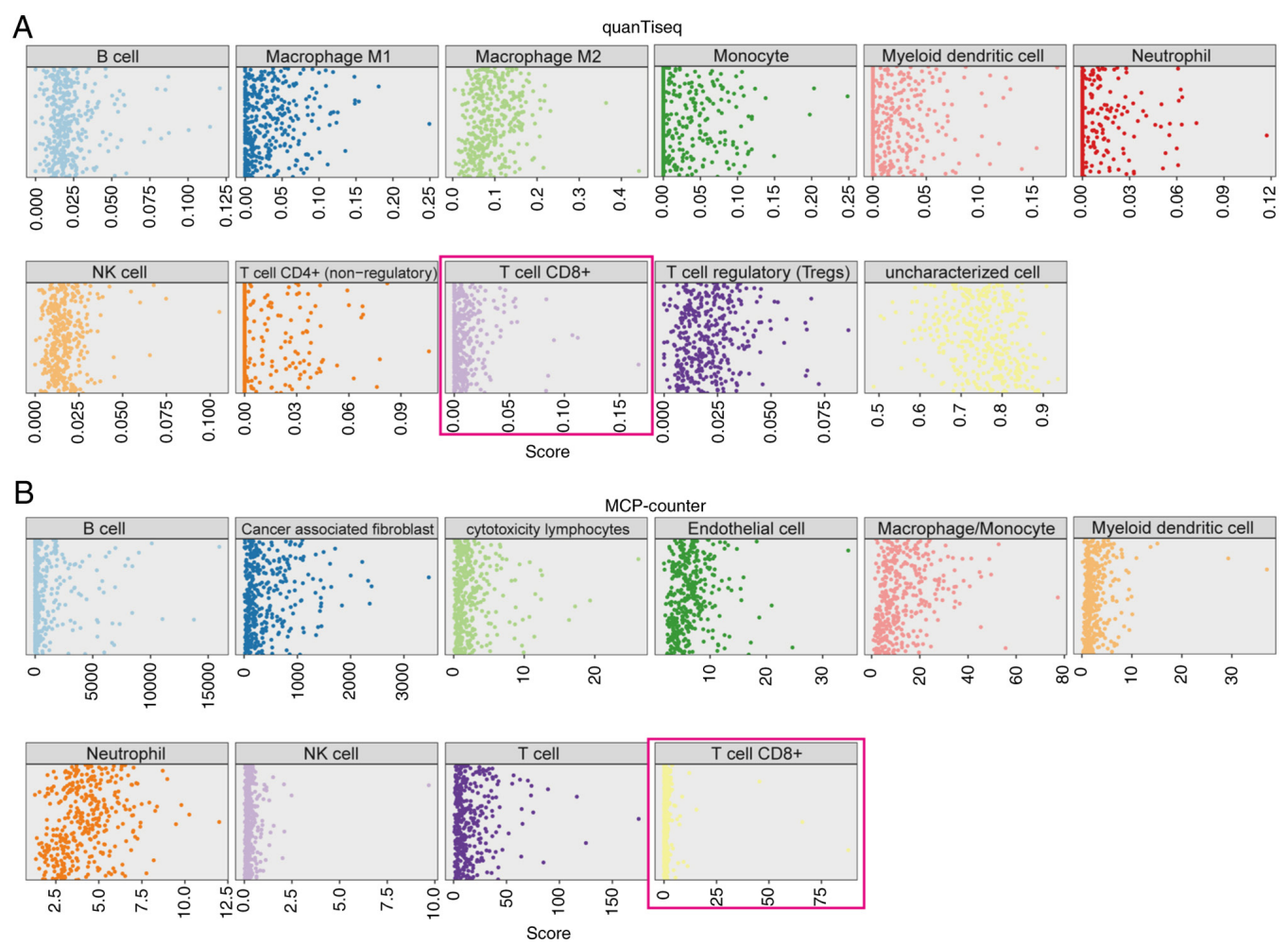


Figure S2. Spearman correlation plots of *CD8A* with CD8 T-cell score evaluated by the (A) quanTiseq or (B) MCP-counter algorithms in The Cancer Genome Atlas-ovarian serous cystadenocarcinoma dataset. Correlation coefficients (ρ) and P-values (Spearman rank test) are shown.

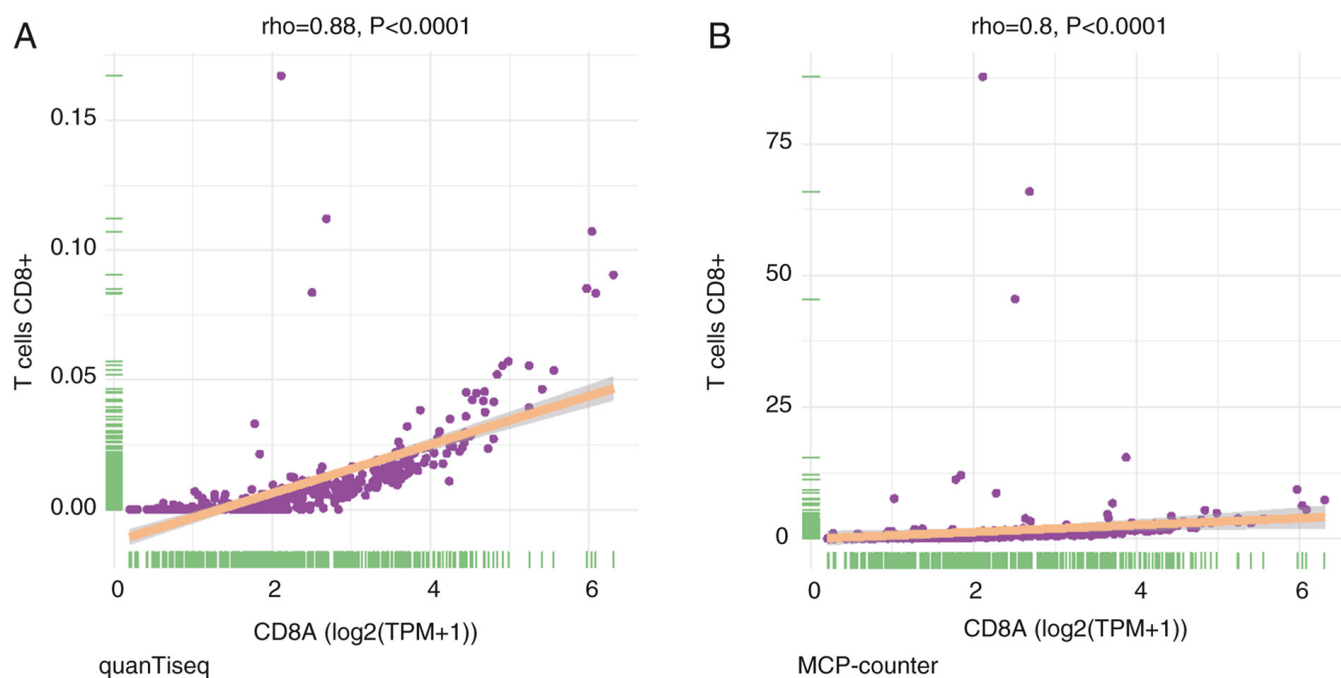


Figure S3. Relationship between *STAT4* and (A) age and (B) clinical stage of patients with ovarian serous adenocarcinoma. Unpaired Student's t-test was used for comparisons between two groups, one-way ANOVA with Tukey's post hoc test was used for comparisons between multiple groups. TCGA, The Cancer Genome Atlas; *STAT4*, signal transducer and activator of transcription 4.

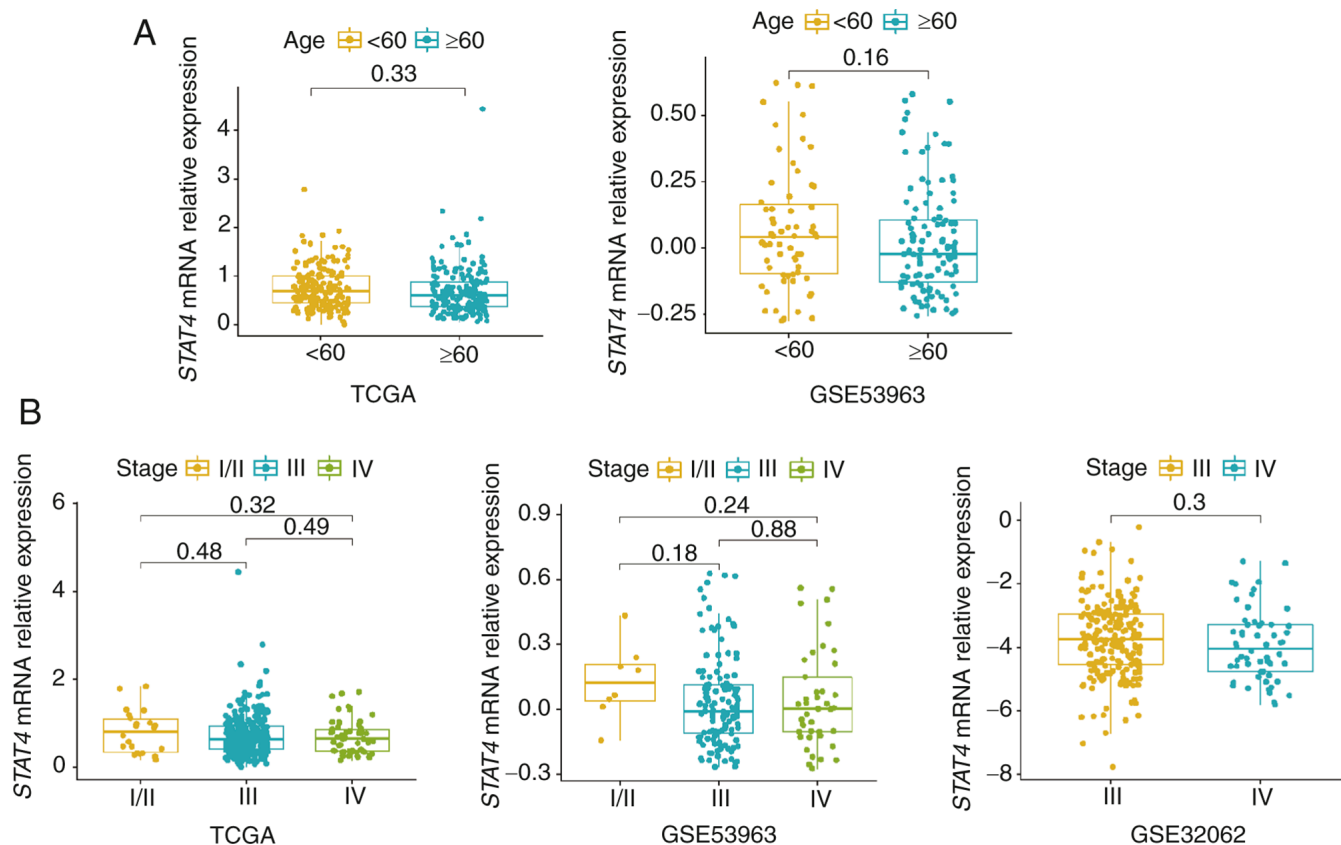


Figure S4. Enrichment plots of GSEA. The enrichment analysis of (A) ‘leukocyte mediated immunity’ and (B) ‘positive regulation of cytokine production’ Gene Ontology Biological Process terms was performed using GSEA. The enrichment analysis of (C) ‘Cytokine-cytokine receptor interaction’ and (D) ‘Chemokine signaling pathway’ Kyoto Encyclopedia of Genes and Genomes pathways was conducted using GSEA. GSEA, Gene Set Enrichment Analysis.

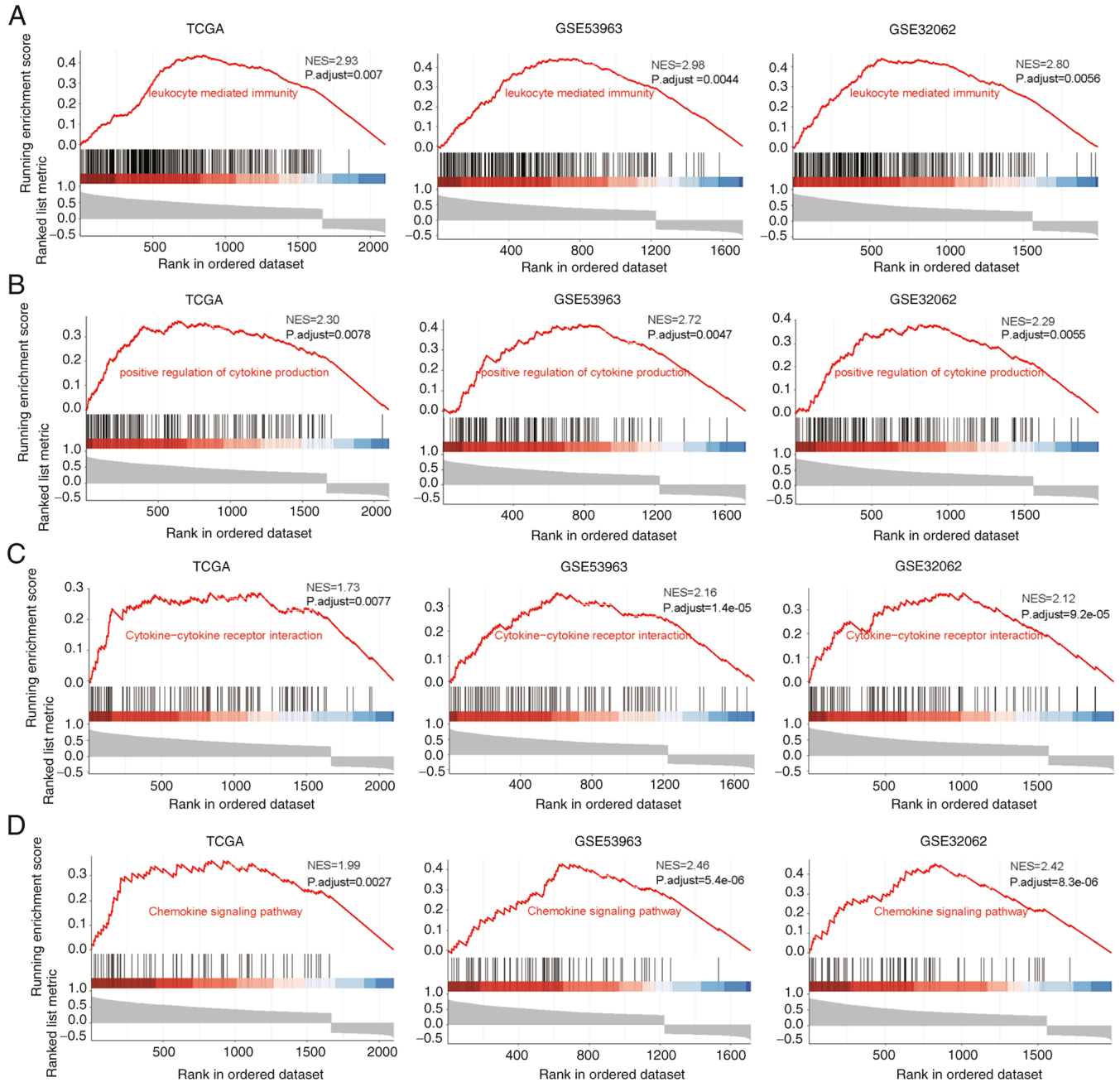


Figure S5. Spearman correlation plots of *CCL5* with CD8 T cells evaluated by the (A) quanTiseq and (B) MCP-counter algorithms in The Cancer Genome Atlas-ovarian serous cystadenocarcinoma dataset. (C) Spearman correlation plots of *CCL5* with *CD8A* quantified by reverse transcription-quantitative PCR in an independent set of 16 ovarian serous adenocarcinoma specimens. Correlation coefficients (ρ) and P-values (Spearman rank test) are displayed. *CCL5*, CC chemokine ligand 5.

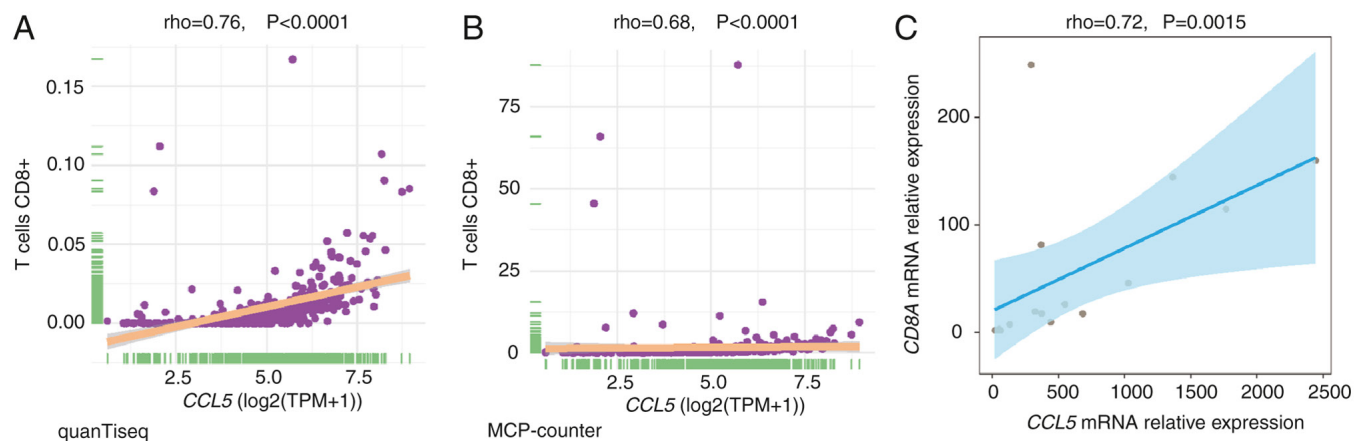


Figure S6. (A) *STAT4* and (B) *CCL5* expression levels in four ovarian cancer cell lines were detected by RT-qPCR. (C) *CCL5* levels were measured by ELISA. Verification of *STAT4* expression by (D) western blotting and (E) RT-qPCR in OVCAR8 cells transfected with siRNA. * $P < 0.05$, ** $P \leq 0.01$, one-way ANOVA with Tukey's post hoc test. GAPDH was used as a loading control. Effect of knockdown of *STAT4* in OVCAR8 cells on (F) *CCL5* mRNA expression levels and (G) secretion levels. *STAT4*, signal transducer and activator of transcription 4; *CCL5*, CC chemokine ligand 5; RT-qPCR, reverse transcription-quantitative PCR; si, small interfering; NC, negative control.

