

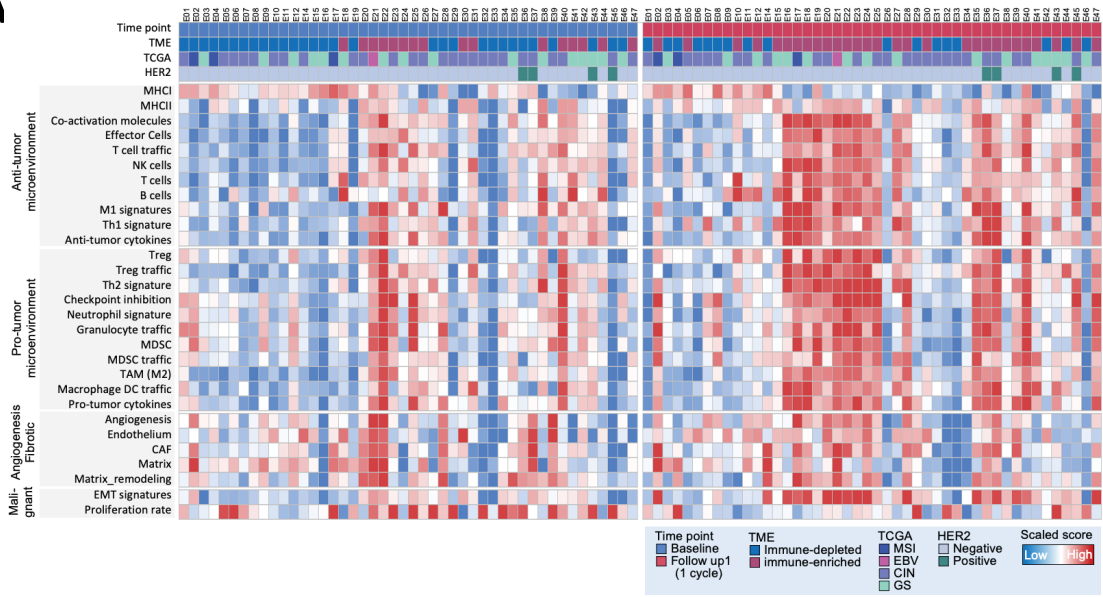
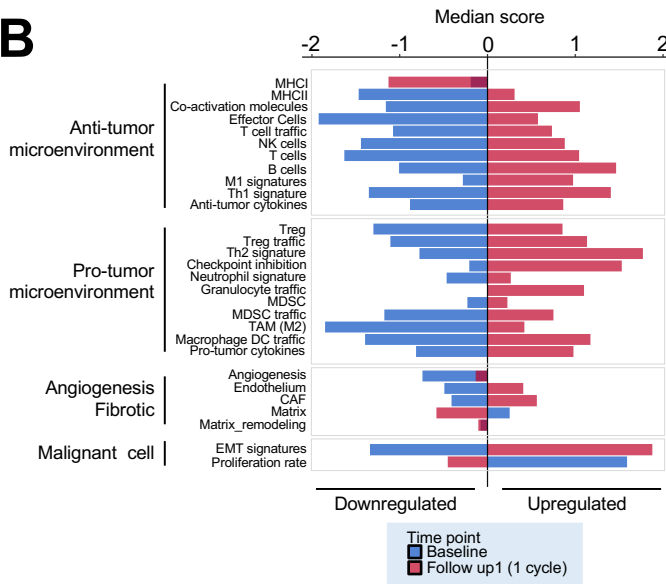
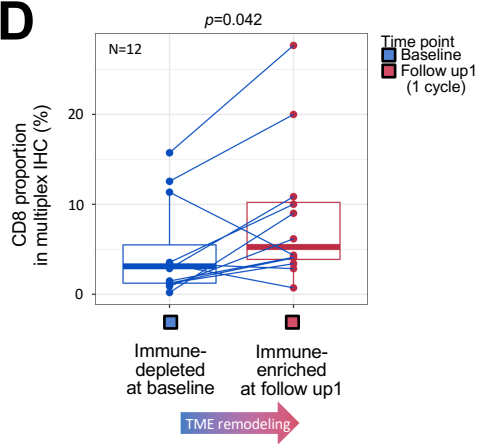
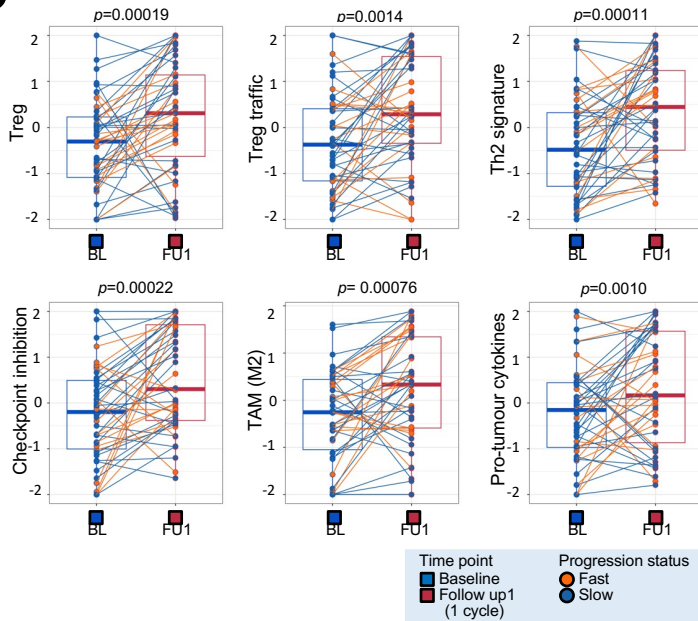
A**B****D****C**

Figure S3. (A) Enrichment of gene expression signatures for TME subtypes using bulk RNA-sequencing data for all patient samples at baseline and after chemotherapy (follow-up 1; FU1). (B) Pathway enrichment analysis on differentially expressed genes comparing bulk RNA-seq profiles for samples obtained pre-treatment (baseline) and samples obtained after 1 cycle of chemotherapy (FU1). (C) Plots demonstrating change in immune related gene signatures (Treg, Treg trafficking, Th2, immune checkpoints, M2 macrophages, pro-tumorigenic cytokines) after chemotherapy treatment. Lines connect samples obtained from the same patient. Statistical comparison performed using a Wilcoxon signed-rank test. (D) Quantification of CD8⁺ cell abundance using immunohistochemistry (IHC) at baseline and after chemotherapy (FU1) in 12 patient samples. Statistical comparison performed using a Wilcoxon signed-rank test.