

FU1 (post-chemotherapy) co-varying programs

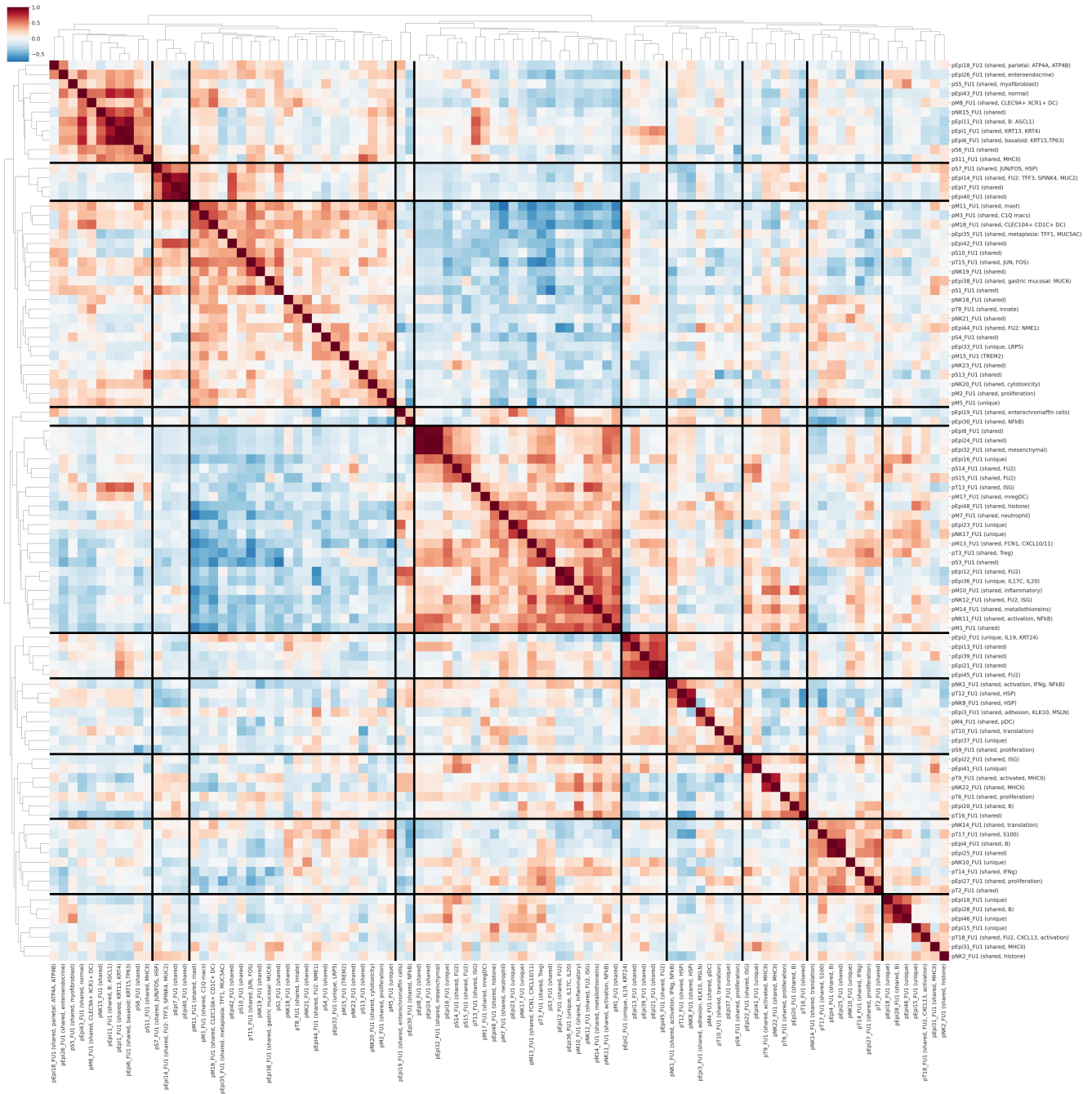


Figure S16. Heatmap showing pairwise correlation of gene program activities across all patient samples post-chemotherapy (FU1) using the 90th percentile of patient-level program activity in epithelial, myeloid, T, NK and stromal cells. Hierarchical clustering was performed to identify clusters of co-varying proteins.