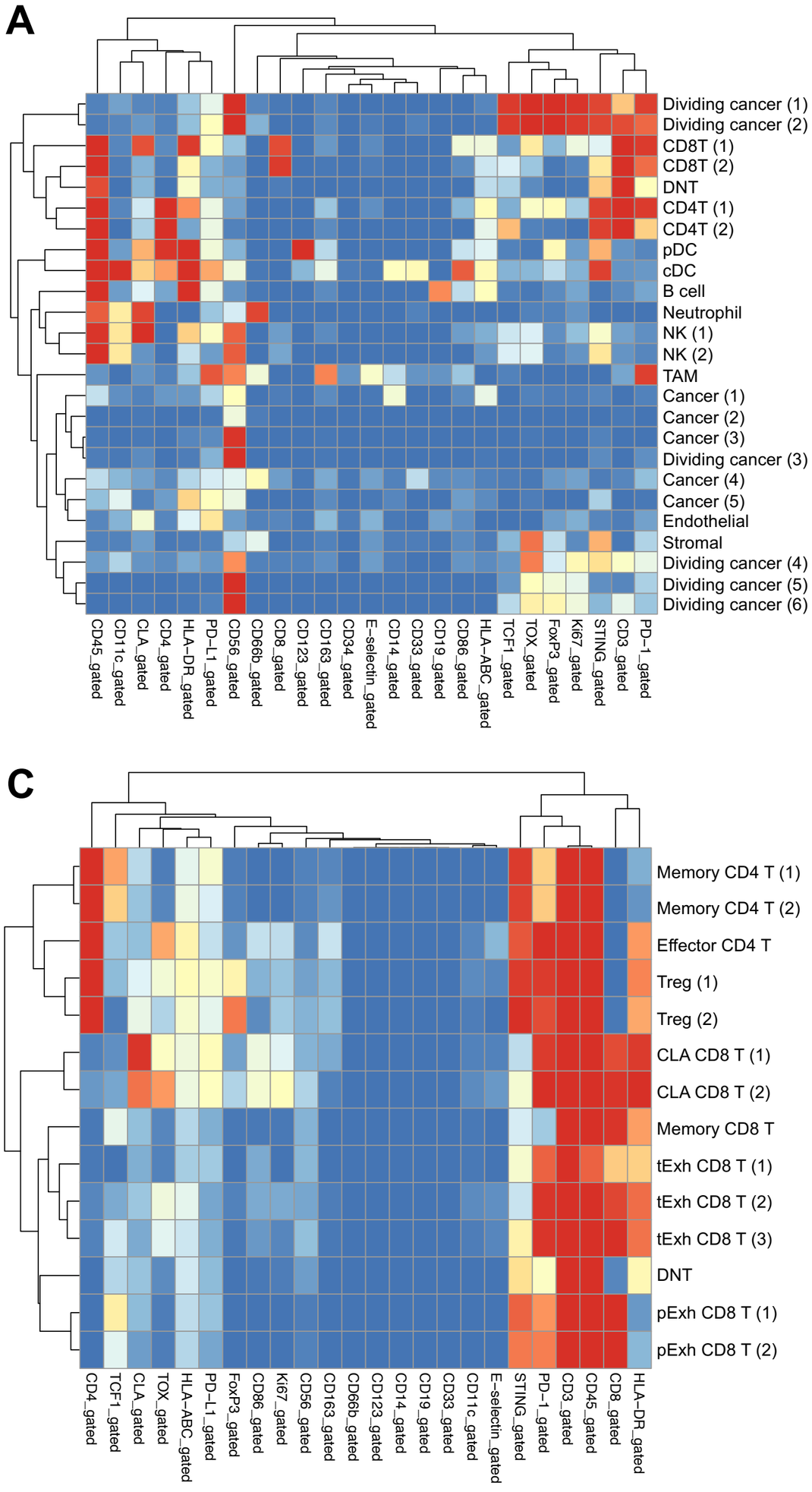

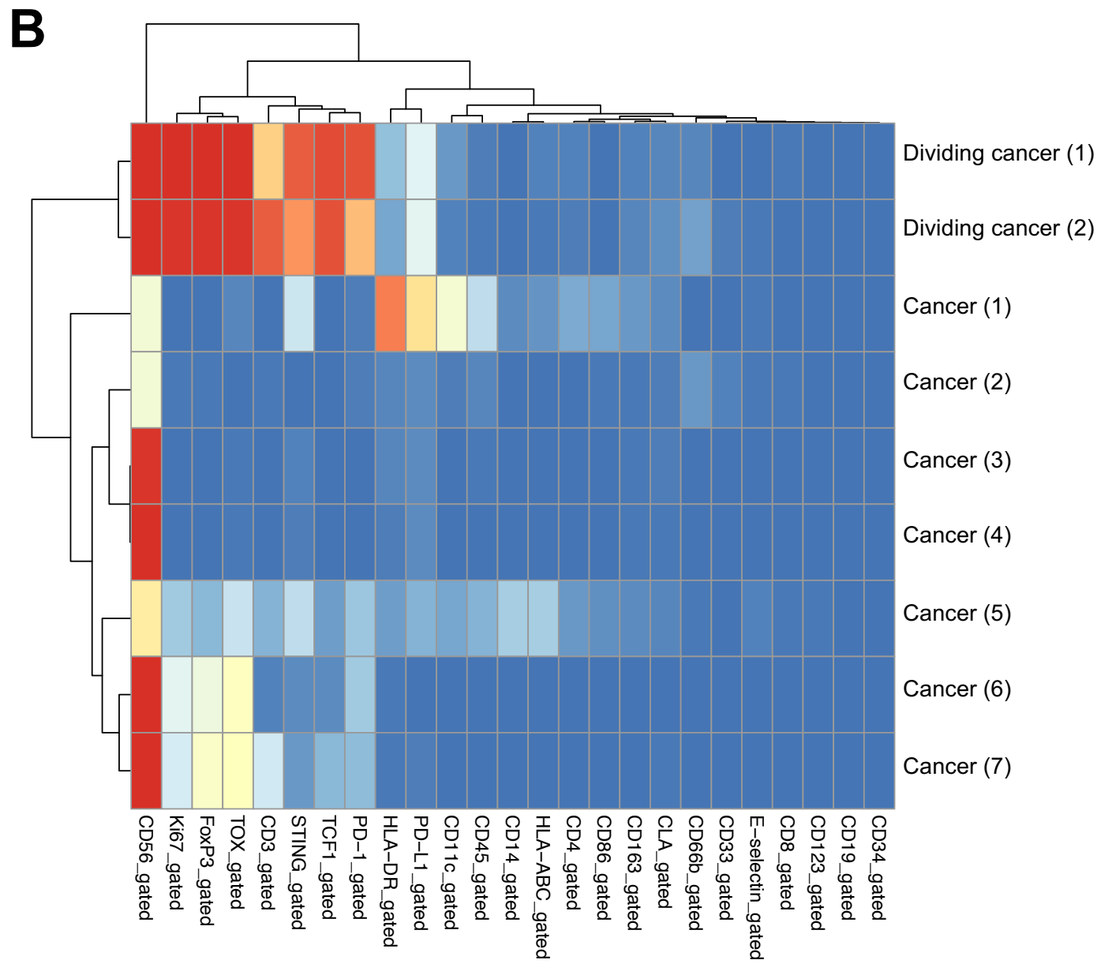

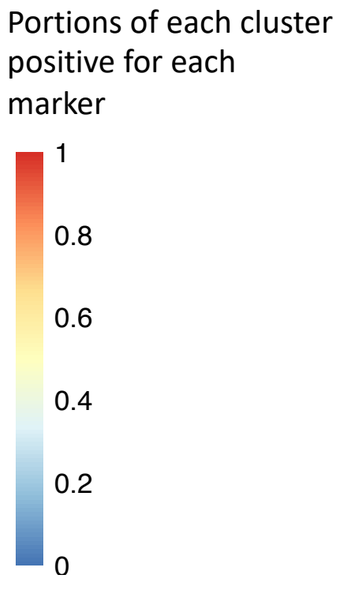

Supplemental Figure 3. Clustering and sub-clustering justification for flow cytometry data. Cells from pre or post-STING agonism were grouped into clusters using phenograph (see methods). Cluster identify was established by calculating mean proportion of cells positive for each protein. Heat map colored by portion of cells positive for each protein measured (x axis). Hierarchical clustering used to group cell populations (clusters) and markers.

A. Clustering of all live cells from flow cytometry data.
B. Cancer cells isolated *in silico* and reclustered for finer tuned identification.
C. T cells isolated *in silico* and reclustered for finer tuned identification.