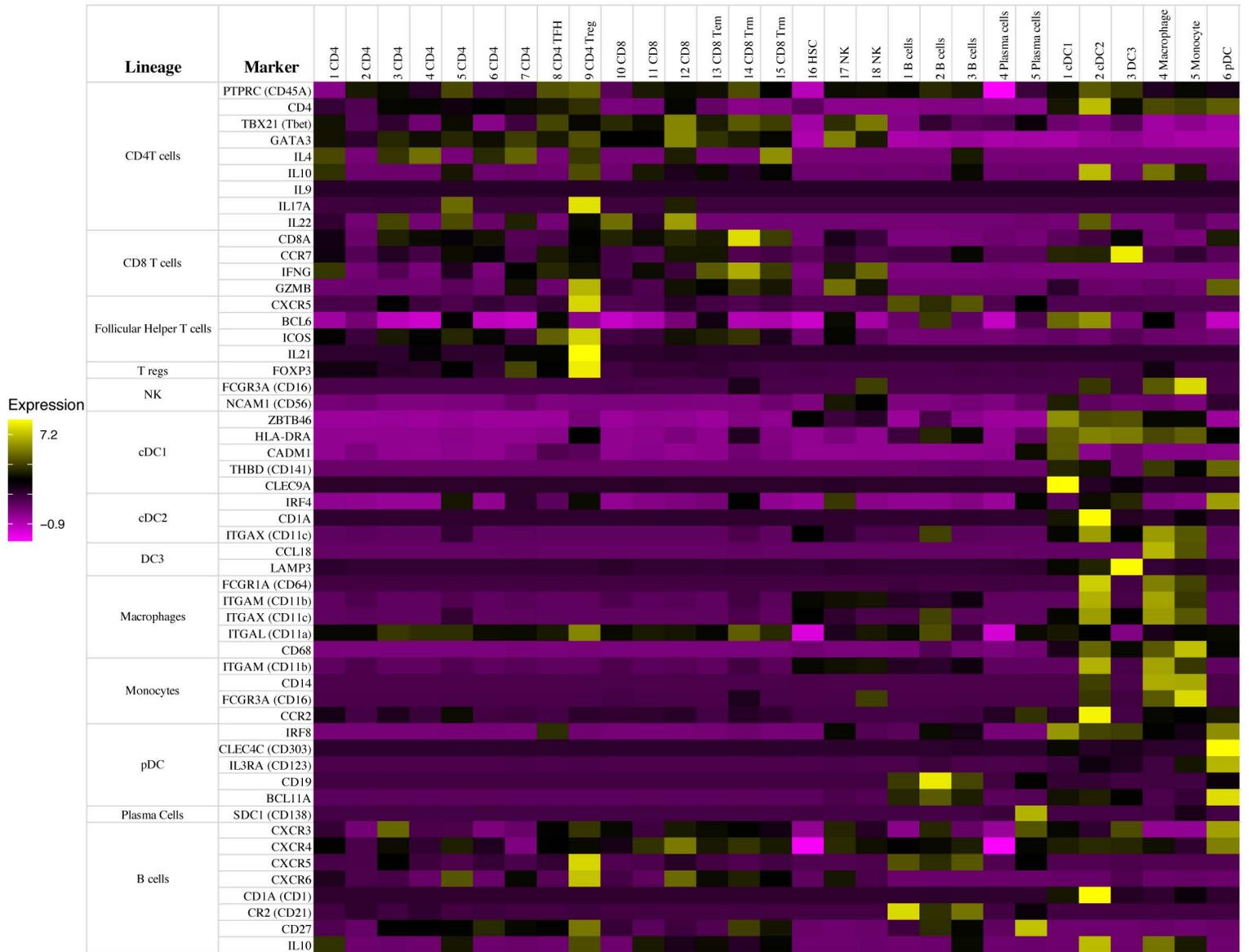
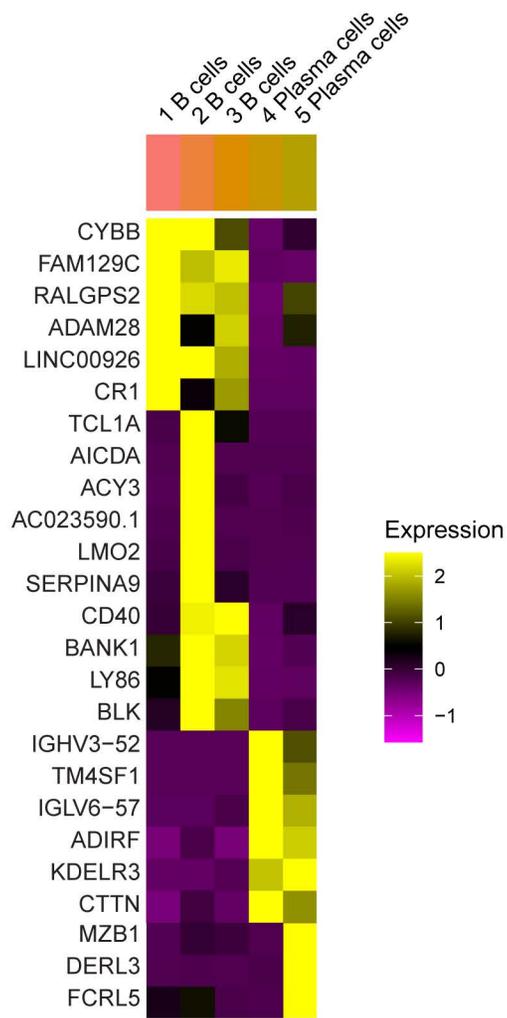
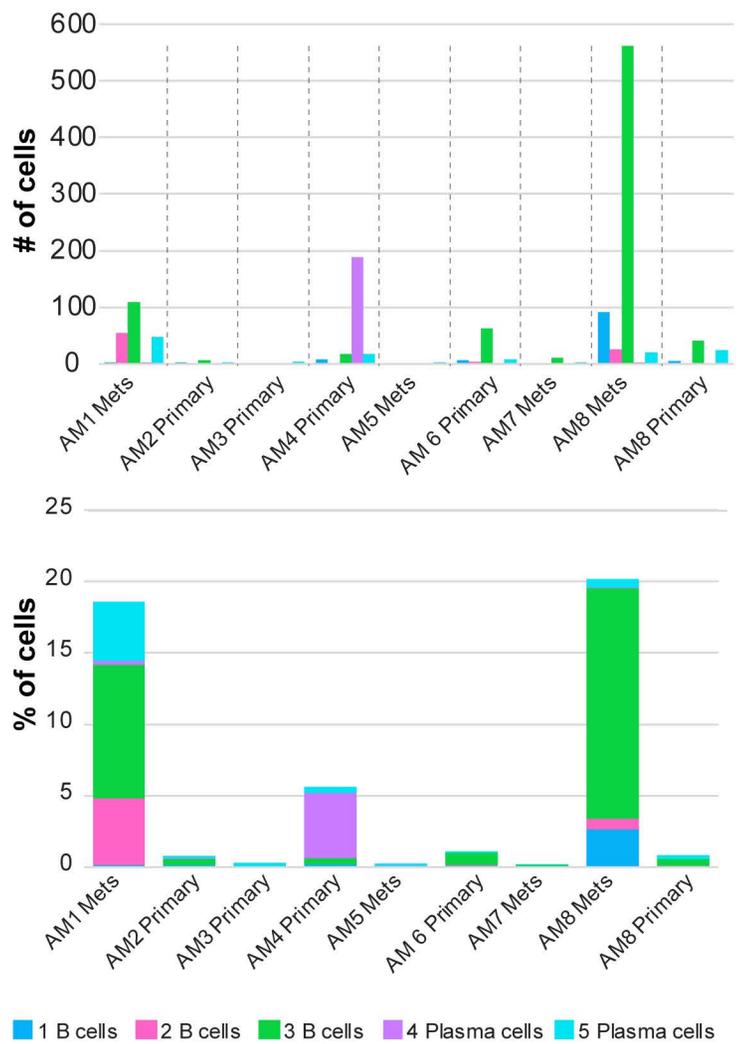


Supplemental Figure 4. Unsupervised clustering identifies 15 subsets of T cells, one cluster of hematopoietic stem cells and 2 sub-clusters of NK cells in acral melanoma samples.



Supplemental Figure 5. Heatmap showing the expression of immune cell lineage markers across the identified immune cell populations (known markers on left Y axis and measured gene expression in our dataset on X axis).

A**B**

Supplemental Figure 6. A. Unsupervised clustering identifies 3 subsets of B cells and 2 clusters of plasma cells. **B.** Bar graphs showing the number (top) and percentage of each B cell and Plasma cell cluster by sample.