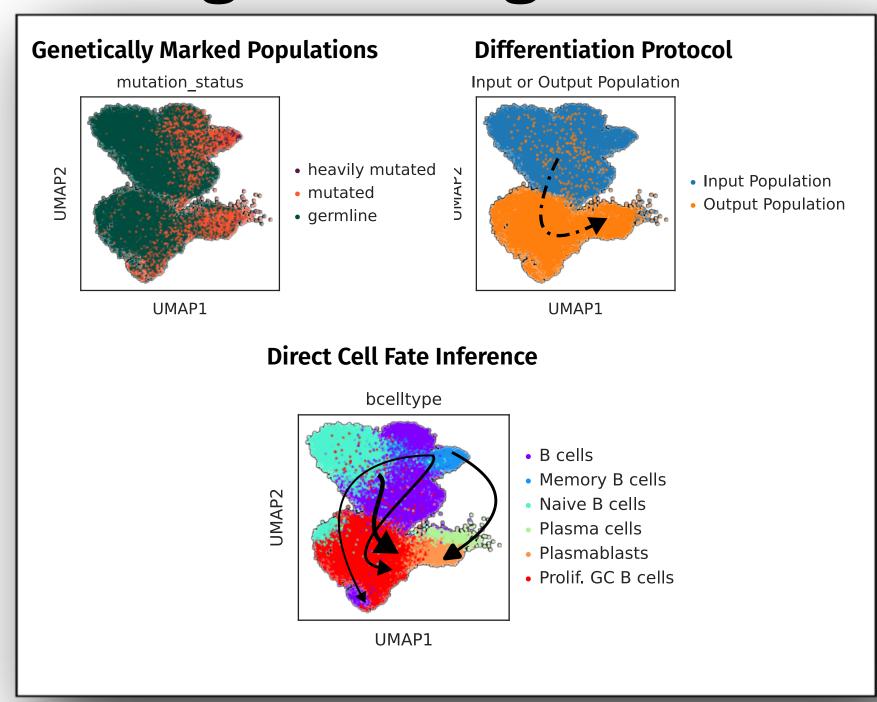
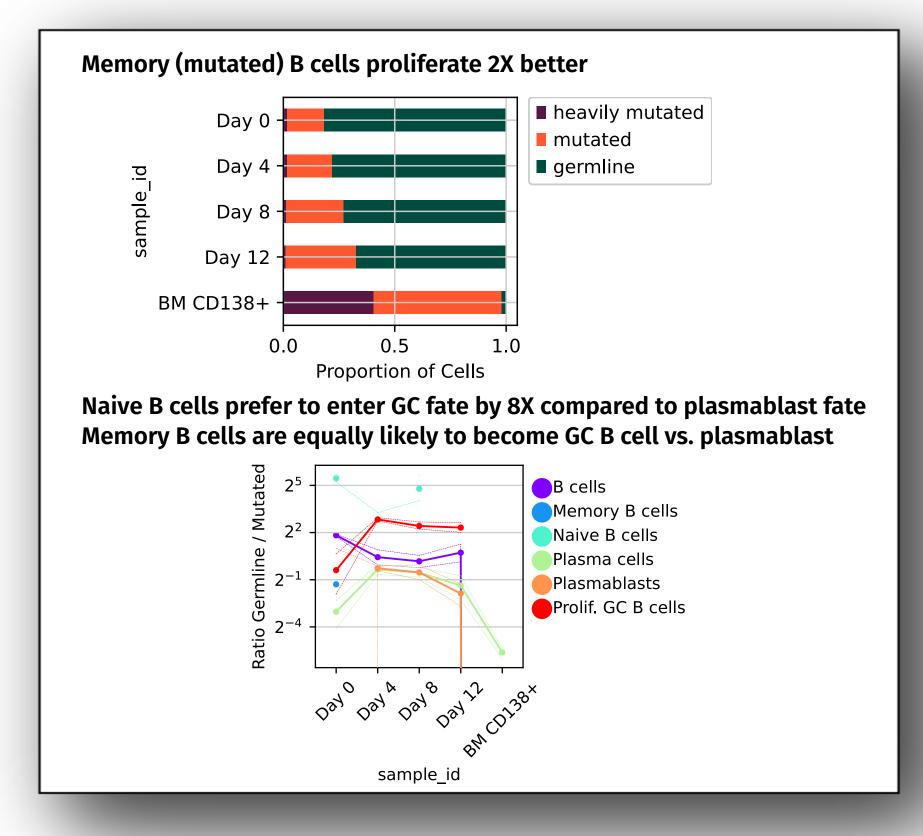
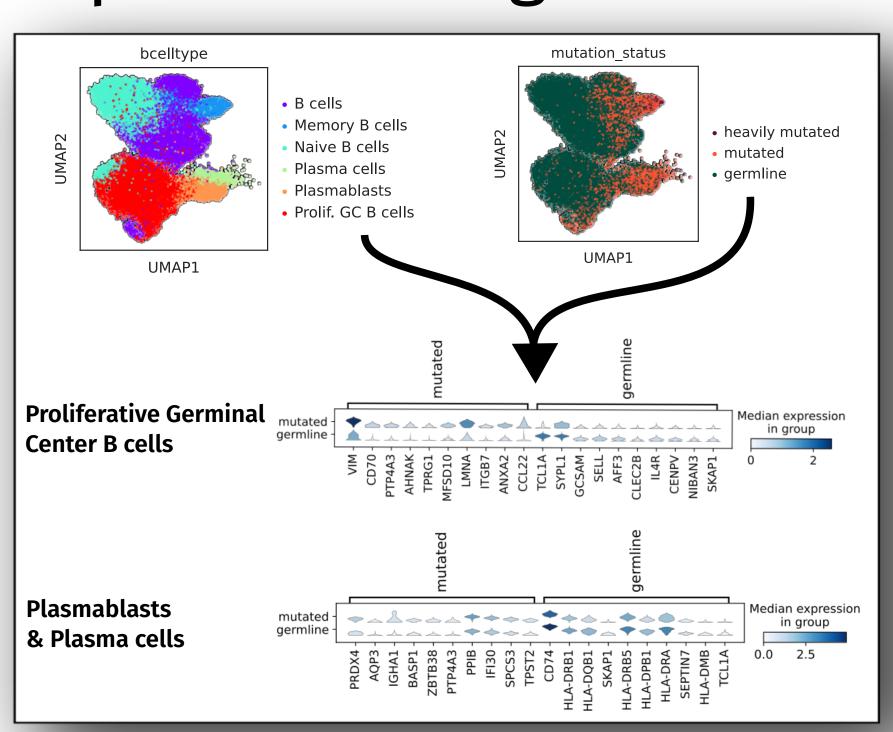
Population Lineage Tracing



Quantifying Cell Fate Biases

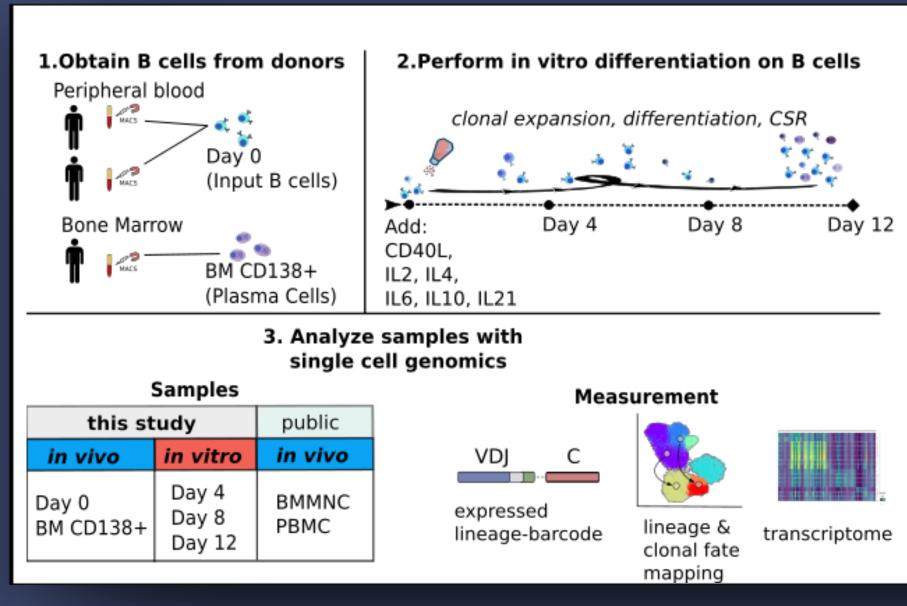


Dissecting cell-intrinsic Expression Programs



Lineage Tracing adds power to single-cell RNA sequencing

We combined lineage tracing with single-cell genomics to understand cell fate decisions



determination. We combined single cell transcriptomics and lineage tracing to better understand fate-choice in human B cells. Using the antibody sequence to trace cell lineage during in vitro differentiation, we parameterized intrinsic proliferative and cell fate biases of B cell subtypes. Clonal analysis revealed a subset of IgM memory B cells which were more proliferative than any other B cell type. We also found clones had restricted cell fates; there were three-times more single-fate clones than would be expected given the diversity of fates in the population. We foundpersistent transcriptional states within clones, with strongest persistence in genes related to cell fate determination. Similar persistent transcriptional programs were observed in human plasma cells from bone marrow, suggesting that these programs maintain long-term cell fate in vivo. These results show how cell-intrinsic fate bias influences human B cell differentiation and reveal molecular programs underpinning cell fate determination in B cells.

We identified and characterized cell fate biases in human B cells. These biases were explanable by intrinsic cell states, which could only be inferred using lineage tracing. Current cell classification schemes do not account for the strong clonal identities characterized here.

The lineage tracing approach we developed helps identify the molecular underpinnings of cell fate determination, and should become routine in developmental biology.

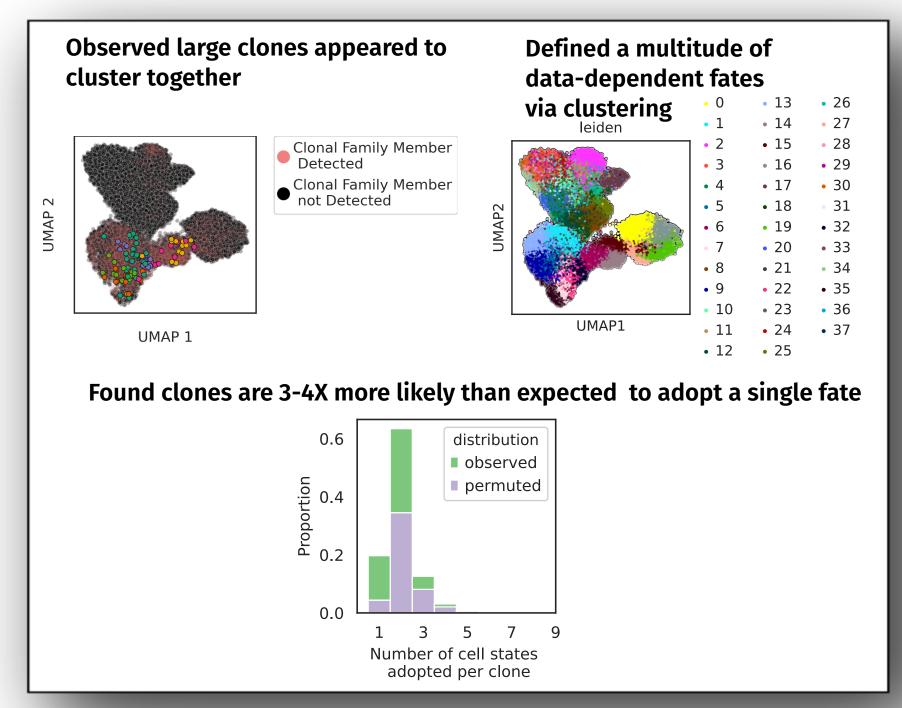
Fate Bias and Transcriptional Memory of human B cells

Michael Swift, Felix Horns, Stephen R. Quake

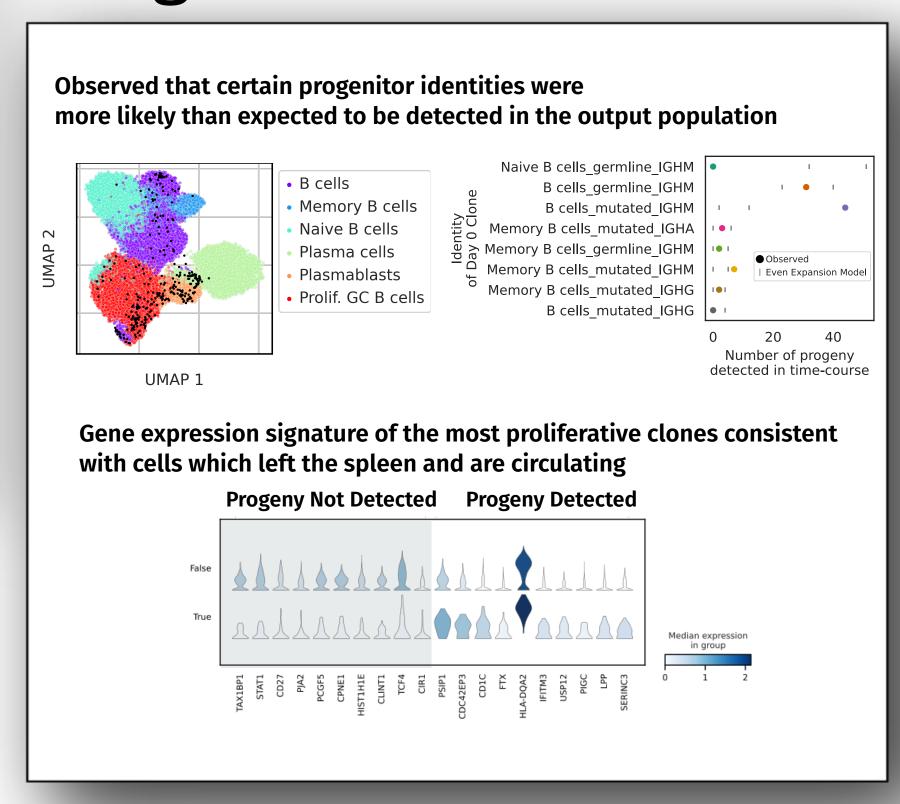
doi: https://doi.org/10.1101/2022.07.14.499766

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Clonal Lineage Tracing



Identifying rare, circulating Marginal Zone B cells



Clones have stable gene expression identities

