

Description of Supplementary Files

Supplementary Data 1 – Bulk ATAC-seq differential analysis on human adult blood for TS cell subsets.

Statistically significant DARs.

Supplementary Data 2 – Bulk H3K4me3 CUT&RUN on human adult blood for T2M^{hi} and T2M^{lo} cells.

Statistically significant differentially enriched regions.

Supplementary Data 3 – Bulk ATAC-seq differential analysis on human cord blood between T2M^{hi} and T2M^{lo} cells.

Statistically significant DARs.

Supplementary Data 4 – RNA assay from CITE-seq dataset.

Statistically significant DEGs for labeled B cell subsets in comparison to other B cells.

Supplementary Data 5 – ATAC assay from Multiome dataset for transitional B cell subset.

Statistically significant DARs for labeled transitional B cells compared to other transitional cells.

Supplementary Data 6 – RNA assay from Multiome dataset for transitional B cell subset.

Statistically significant DEGs for labeled transitional B cells compared to other transitional cells.

Supplementary Data 7 – Gene Ontology analysis for DEGs and DARs in transitional cells.

Supplementary Data 8 – Monocle and scMEGA trajectory analyses.

Statistically significant DEGs and TFs in the trajectory analyses performed with Monocle and scMEGA along identified trajectories.

Supplementary Data 9 – RNA assay from Multiome dataset for all B cells.

Statistically significant DEGs for labeled B cells compared to all other B cells.

Supplementary Data 10 – ATAC assay from Multiome dataset for all B cells.

Statistically significant DARs for labeled B cells compared to all other B cells.

Supplementary Data 11 – Bulk ATAC-seq differential analysis between memory and MZB cells from human adult blood.

Statistically significant DARs.

Supplementary Data 12 – GeneActivity assay from Multiome dataset for all B cells.

Statistically significant differentially accessible genes for labeled B cells compared to all other B cells.

Supplementary Data 13 – ChromVAR assay from Multiome dataset for all B cells.

TFs showing differential activity in labeled B cells compared to all other B cells, along with associated binding motifs.

Supplementary Data 14 – Metadata of Regions of Interest included in IMC study.