Supplementary Figure 1 |

A Violin plot of total IGHV region mutation frequencies across all isotypes by polyp. **B** Stacked barplots showing CD19 expression by isotype. **C** Barplots showing ASC light chain frequency stratified by CD19 expression. **D-H** Violin plots of IGHV framework regions 1-3 (**D-F**) and complementarity determining regions 1 and 2 (**G, H**) mutation frequencies by isotype. **I** Heatmaps showing IGHV gene frequency with the inclusion (left) and exclusion (right) of gene *IGHV 3-15*.

Statistical significance was determined using Kruskal-Wallis testing with Dunn's multiple comparisons testing between groups. *P ≤ 0.05; **P ≤ 0.01; ***P ≤ 0.001; ****P ≤ 0.0001; ns, not significant.

Supplementary Figure 2 |

A Scatter plot showing the number of unique molecular identifiers (UMIs) per cell against percent of total reads being mitochondrial transcripts. **B** Scatter plot showing the number of unique molecular identifiers (UMIs) per cell against the total number of genes detected per cell. **C** Scatter plot showing the number of unique molecular identifiers (UMIs) per cell against the percent of total reads being immunoglobulin transcripts. **D** Preliminary clustering prior to contaminated cell type detection and removal depicted as a two-dimensional UMAP. **E** Marker genes shown as log normalized counts of ASCs and other cell types shown on a two-dimensional UMAP of preliminary clustering prior to detection and removal to potentially contaminating cell types. Marker genes for ASCs include *JCHAIN*, *PRDM1, IRF4, XBP1*, *SDC1*, *CD19*, and *CD38* while *MS4A1* is used to detect Non-ASC B cells. *IL7R* and *S100A4* are used to identify Memory $CD4^+$ T cells while *CD8A* is used to identify $CD8^+$ T cells. *FCER1A* and *CST3* are used to identify dendritic cells. *FCGR3A* and *MS4A7* are used to identify $FCGR3A^+$ Monocytes, while *CD14* and *LYZ* are used to identify CD14+ Monocytes. *GNLY* and *NKG7* are used to identify natural killer cells. **F** Dot plot showing the same marker genes in **E** as scaled,

log normalized counts for gene markers to identify ASCs and potentially contaminating cells for preliminary clusters in **D**.

Supplementary Figure 3 |

A Dot plot showing the gene expression of heavy chain isotype genes as scaled log normalized counts for each identified isotype determined from either VDJ or gene expression assignment. **B** Violin plots showing the log normalized counts of each heavy chain isotype gene expressed in each identified isotype determined from either VDJ or gene expression assignment sorted from highest to lowest expression (left to right).

Supplementary Figure 4 |

A Gene ontology analysis for genes differentially expressed in each cluster. Blue indicates increased gene ontology enrichment of genes in the associated pathways, while red indicates decreased enrichment.

Supplementary Figure 5 |

Two dimensional UMAP of transcriptomic clustering with colors indicating the location of each isotype in red, with **A** showing the location for IgA1 cells, **B** showing the location for IgA2 cells, **C** showing the location for IgG1 cells, **D** showing the location for IgG2 cells, **E** showing the location for IgG3 cells, **F** showing the location for IgG4 cells, **G** showing the location for IgE cells, and **H** showing the location for IgM cells.

Supplementary Figure 6 |

A Cluster confusion matrix heatmap illustrating the stability of clustering with and without the inclusion of immunoglobulin genes. The working cluster set referenced in the text shows

increased stability of clustering without immunoglobulin genes for clusters 9, 8, 5, 2, 6, 4 and 10, while clusters 3, 7, 0, and 1 are less stable without immunoglobulin genes.