



Figure S1. Individual cell populations identified through scRNA-seq, related to **Figure 1**. **(A)** tSNE representation of scRNA-seq data, with labeling of each cell populations. **(B)** Heatmap of cell lineage and functional markers provides phenotypic information for individual cell populations. Expression values are scaled between minimum and maximum expression for each gene across all clusters. **(C)** Representation of each sample within each cell cluster, colored by tissue of origin.