Supplemental Figure Legends

Figure S1: Bovine samples were filtered to ensure high-quality scRNA-seq data. *Data was filtered to remove cell barcodes* ***(A & D)*** *with fewer unique molecular identifiers than the majority of cell barcodes from the sample (i.e., below 1,000),* ***(B & E)*** *with a total number of gene counts significantly higher than barcodes within the same sample (i.e., greater than 30,000) and* ***(C & F)*** *with high percentage of mitochondrial gene expression. Red dashed lines indicate filter parameters for each processing stage.*

Figure S2: Sample B8D1 had minimal bias on scRNA-seq analysis. *(A) UMAP of cell populations annotated by sample origin with sample B8D1 removed. (B) Cluster annotation of identified subpopulations. (C) Phylogenetic tree outline population level distance relationships to predict divergence points in global dataset. (D) Heatmap of top DEGs per cluster identified by avg_logFC value. Cell IDs are subsetted for 60 representative cells per cluster. Expression value represents scaled expression of the specified gene on an individual cell barcode ID.*