Figure S1. (**A**) Schematic of the main steps of single nuclei isolation protocol E. (**B**) FACS histogram analyses of non-stained and 7-AAD stained samples from ovarian cancer tissue. (**C**) Representative nuclei obtained from the preparation done on ovarian cancer tissue following protocol E. Scale bar represents 50 µm. Protocol E n=1.
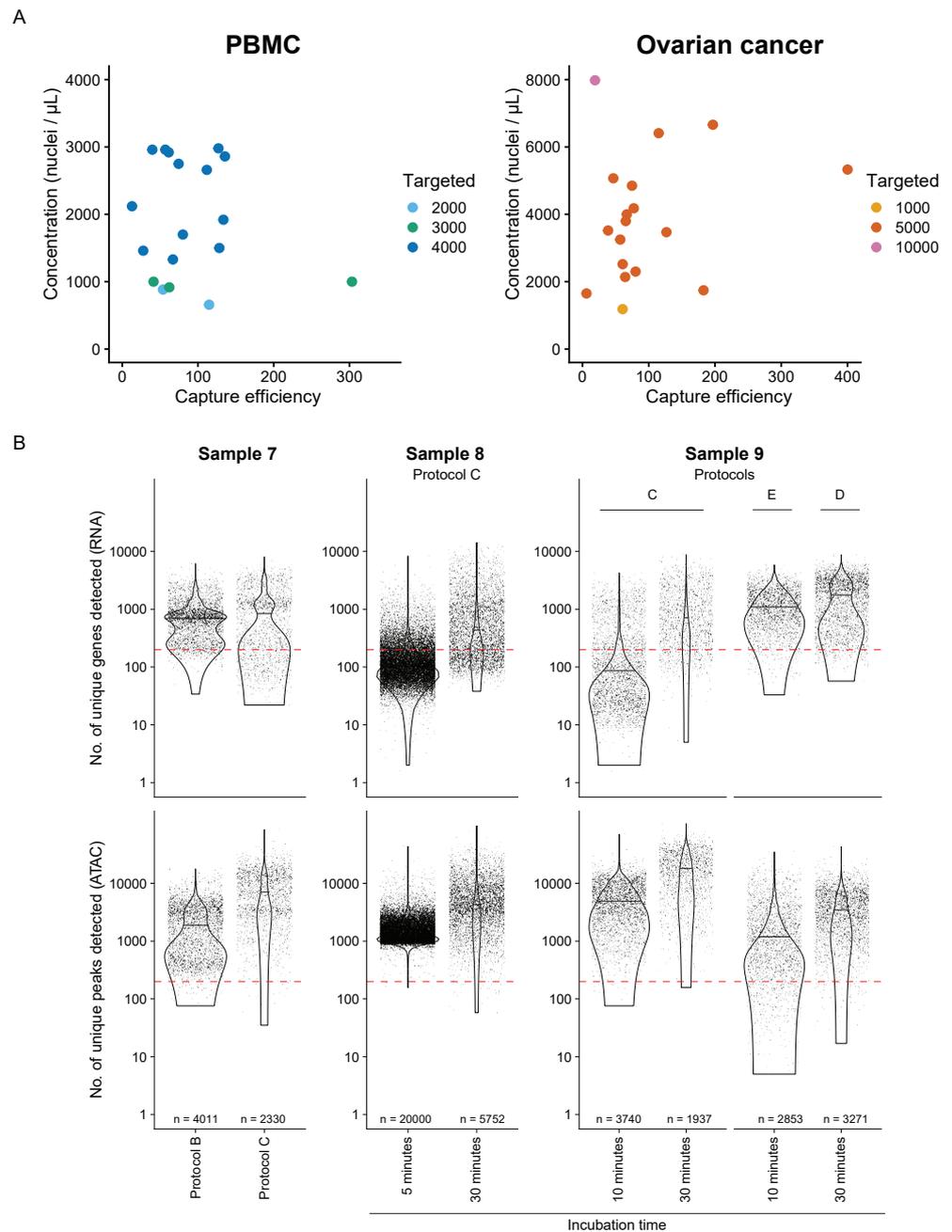
Figure S2. (**A**) Capture efficiency of each sample, defined as the ratio of cells called by Cell Ranger ARC to the targeted number of cells plotted against the nuclei concentration colored by the targeted number of cells. (**B**) Violin plots showing the number of unique genes detected (RNA) and the number of unique peaks detected (ATAC) calculated per cell in Samples 7, 8, and 9 grouped by protocol. The number of cells in each group is listed below the violins plots.
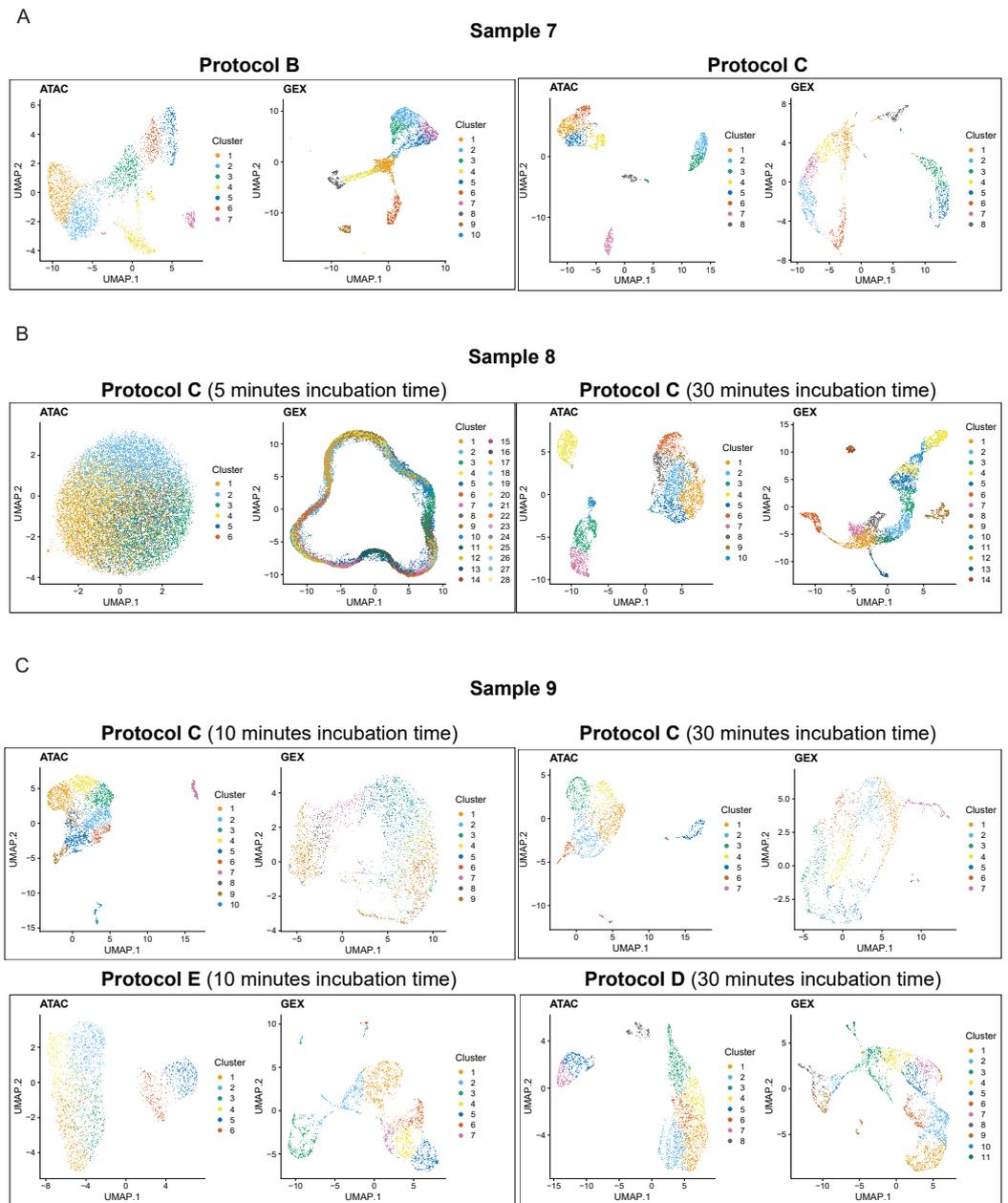
Figure S3. UMAP projection of cells from Samples 7 (**A**), 8 (**B**), and 9 (**C**) processed using different protocols and incubation time points.
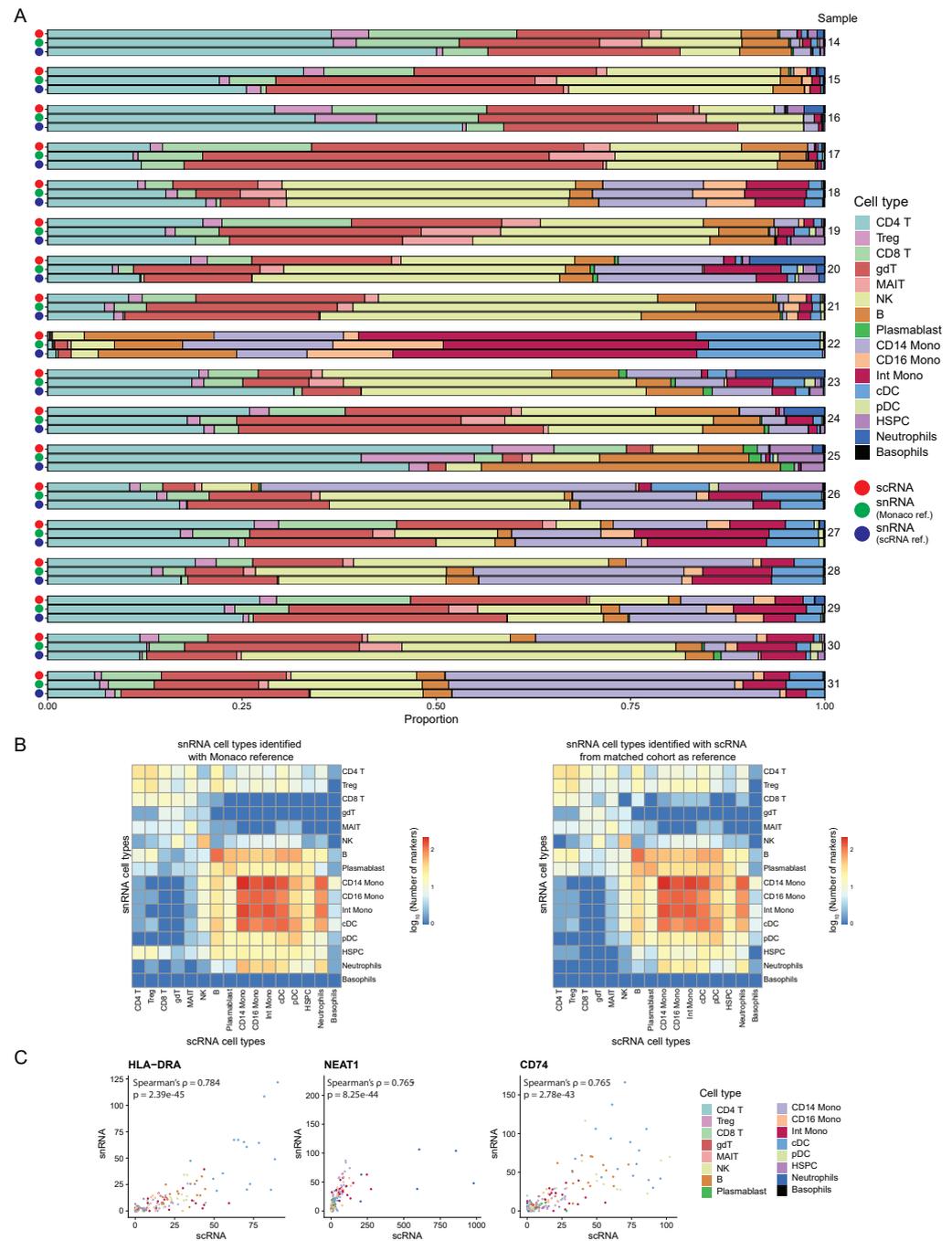
Figure S4. (**A**) Barplots showing the proportion of cells in each cell type in scRNA and snRNA samples with cell type identification in snRNA performed using Monaco reference or using scRNA from the matched cohort as reference. (**B**) Heatmaps showing the log (base 10) of the number of marker genes that overlap between the cell types identified by scRNA and those identified by snRNA with snRNA cell types identified using Monaco reference (left) or using scRNA from the matched cohort as reference (right). (**C**) Scatter plots showing the gene expression averaged over both sample and cell type of the three most significantly correlated genes between scRNA and snRNA measurements.