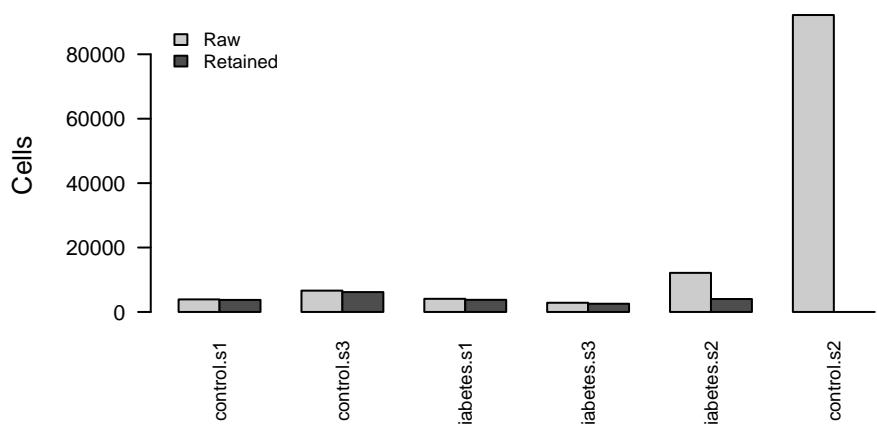
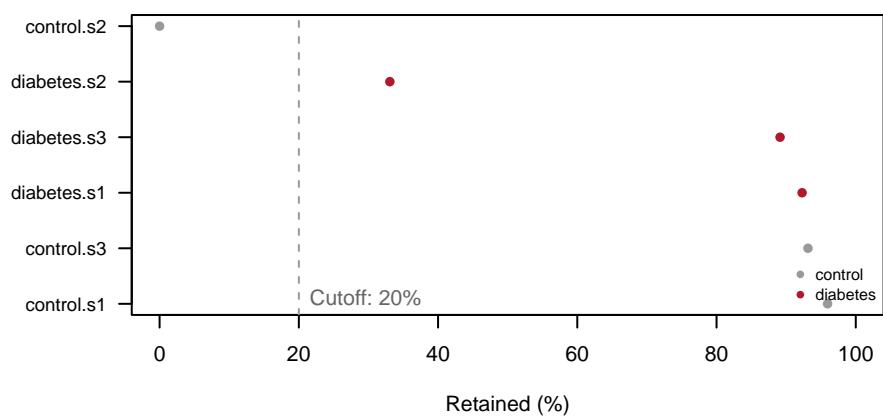
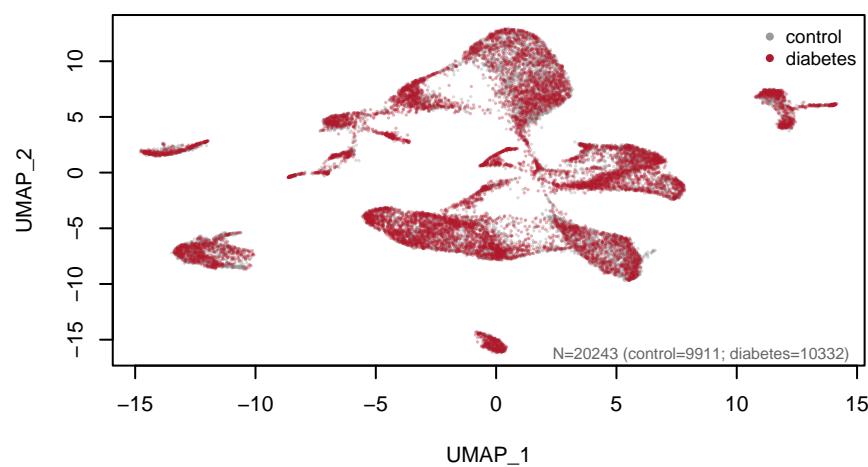
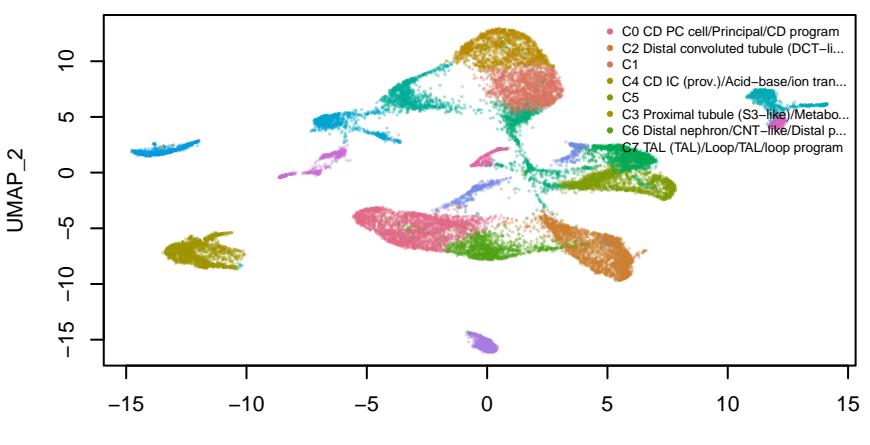
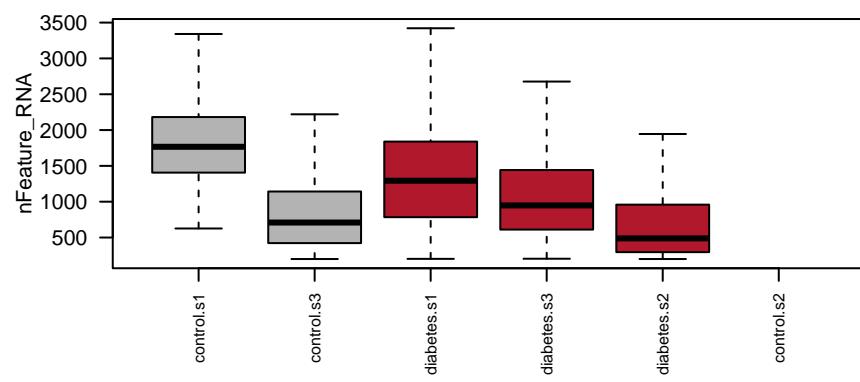
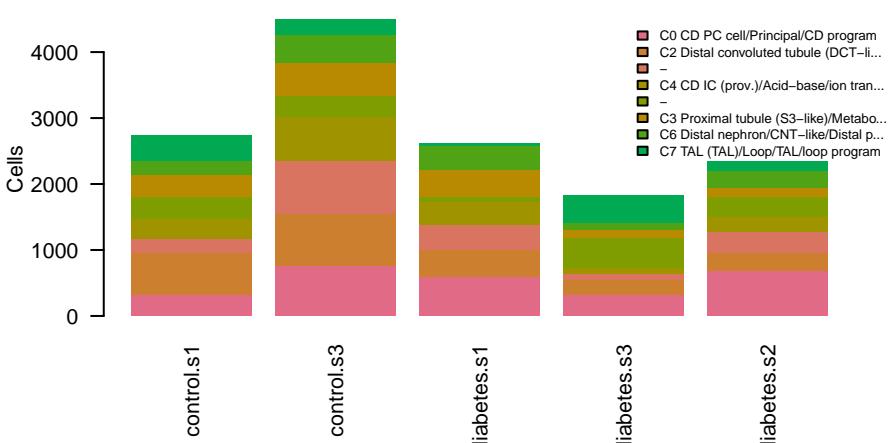
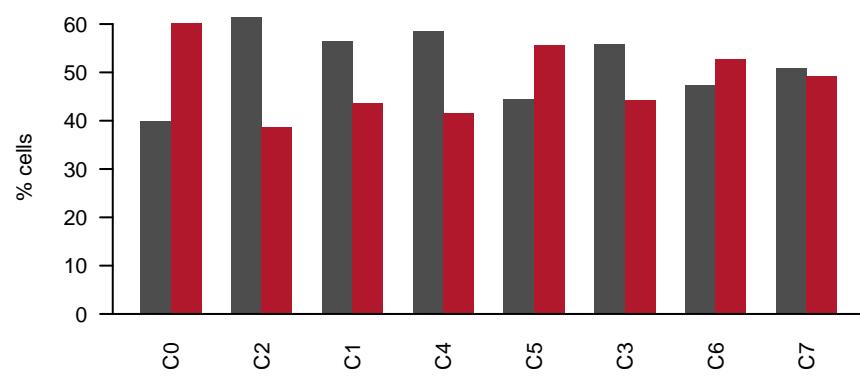


A**Atlas input vs retained cells****B****Retention per sample****C****Atlas UMAP (by group)****D****Atlas UMAP (by cluster)****E****QC: detected genes per cell (nFeature_RNA)****F****Cluster composition per sample (top clusters)****G****Cluster composition by group (%)****H****QC: mitochondrial fraction (percent.mt)**