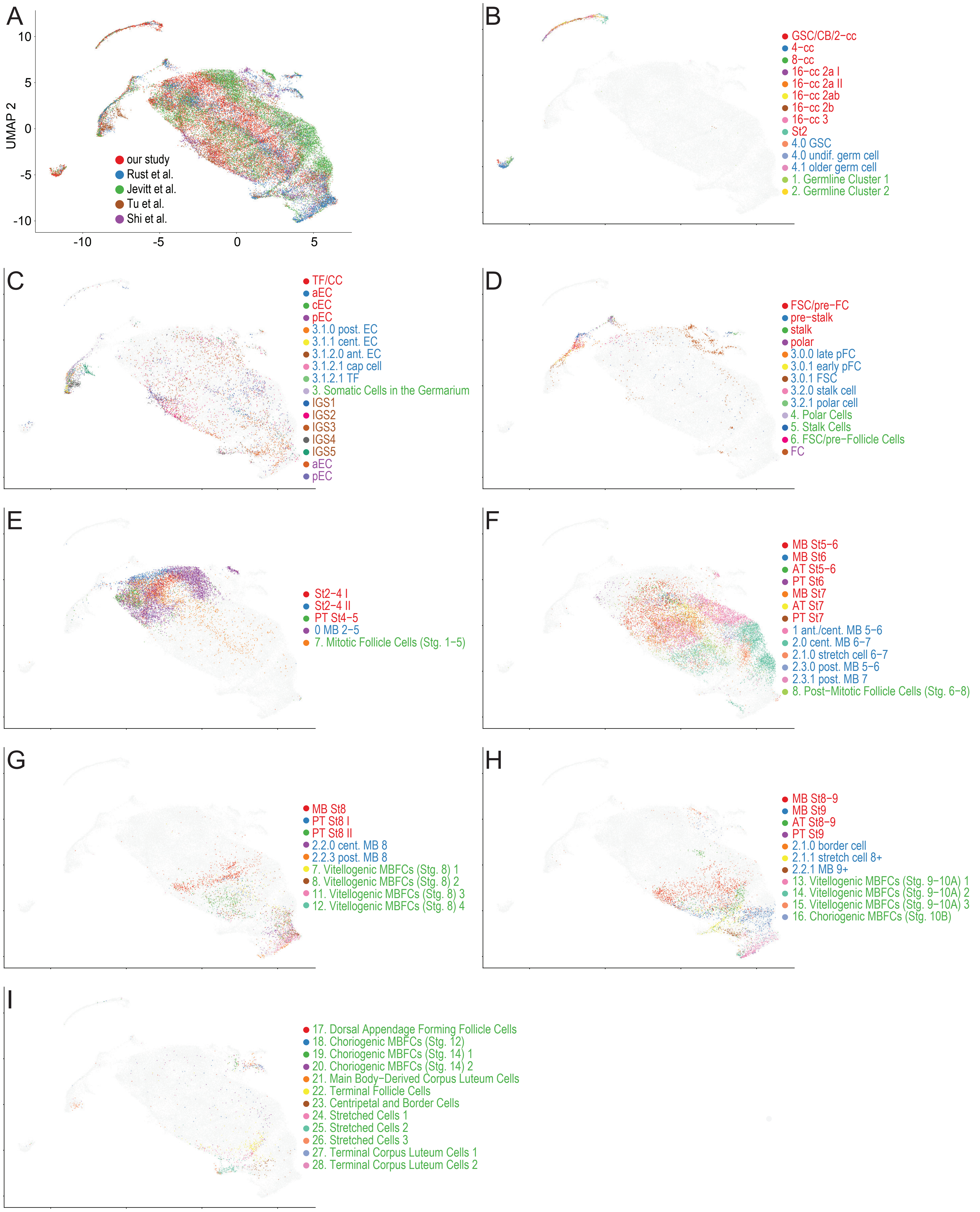

**Supplemental Figure 8.**

A - UMAP plot visualizing the integration of datasets from 5 distinct studies. Each dot represents a transcriptome of a single cell, and is color-coded according to the sample of origin. B - UMAP plot visualizing germ cell clusters. Each dot represents a transcriptome of a single cell, and is color coded according to cluster membership in the legend, while other cells are gray. C - UMAP plot visualizing TF, CC and EC containing clusters. Each dot represents a transcriptome of a single cell, and is color coded according to cluster membership in the legend, while other cells are gray. D - UMAP plot visualizing FSC, pre-FC, stalk and polar cells containing clusters. Each dot represents a transcriptome of a single cell, and is color coded according to cluster membership in the legend, while other cells are gray. E - UMAP plot visualizing clusters containing epithelial FCs from stage 2-4/5 follicles. Each dot represents a transcriptome of a single cell, and is color coded according to cluster membership in the legend, while other cells are gray. F - UMAP plot visualizing clusters containing epithelial FCs from stage 5/6-7 follicles. Each dot represents a transcriptome of a single cell, and is color coded according to cluster membership in the legend, while other cells are gray. G - UMAP plot visualizing clusters containing epithelial FCs from stage 8 follicles. Each dot represents a transcriptome of a single cell, and is color coded according to cluster membership in the legend, while other cells are gray. H - UMAP plot visualizing clusters containing epithelial FCs from stage 8-10 follicles. Each dot represents a transcriptome of a single cell, and is color coded according to cluster membership in the legend, while other cells are gray. I - UMAP plot visualizing clusters containing epithelial FCs from follicles beyond stage 10. Each dot represents a transcriptome of a single cell, and is color coded according to cluster membership in the legend, while other cells are gray.