



Supplementary Figure 8. Details of single-cell transcriptomics.

(a) A heatmap of normalized expression for genes used to assign identities to cell types for a combined analysis of CS-shFoxP2 datasets (corresponding to Figure 4a). Expression was normalized globally across all genes, but a difference for each gene based on the highest normalized value. For marker gene expression, the size of the dot indicates the percent expressed within a cluster expressing a given gene, and the color of the dot indicates the average normalized expression level. (b) A UMAP projection of nuclei from Area X of an independent analysis of CS-shScr+ birds (not merged, corresponding to Figure 4b). Clusters are numbered in ascending order by decreasing size (1-largest; 23-smallest). (c) For CS-shScr+, density plot of the number of UMIs per cell (left) and the percentage of mitochondrial genes in each cell (right). The analysis only included cells with UMI < 10,000 and < 5% mitochondrial genes (indicated by the red dashed lines). (d) For CS-shScr+, a scatterplot of the number of UMIs per nucleus and the number of genes (left) or percentage of mitochondrial genes (right). Each dot is a cell. The cells within the red dashed box, corresponding to the filters in (c), were the cells used for the analysis.