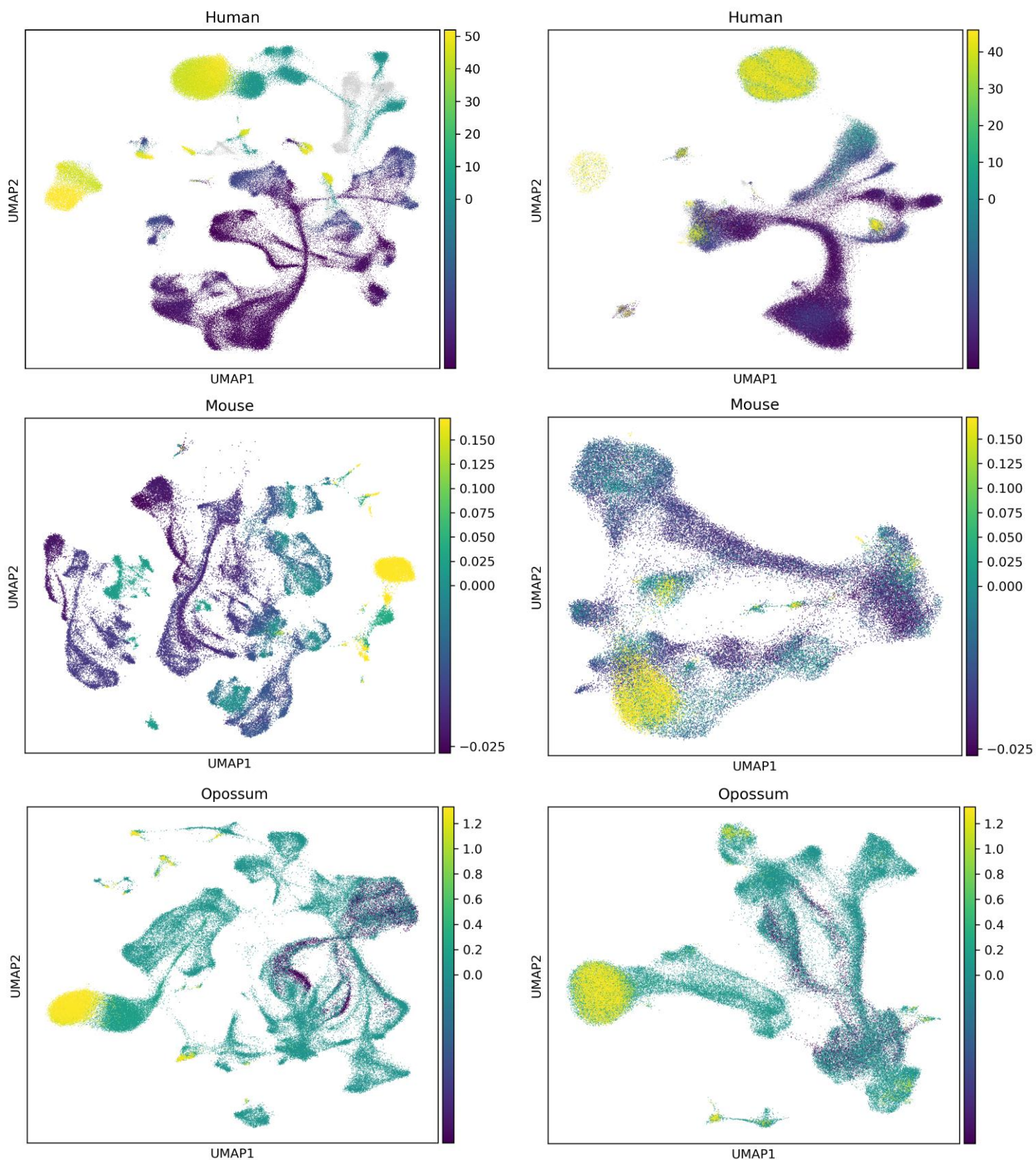
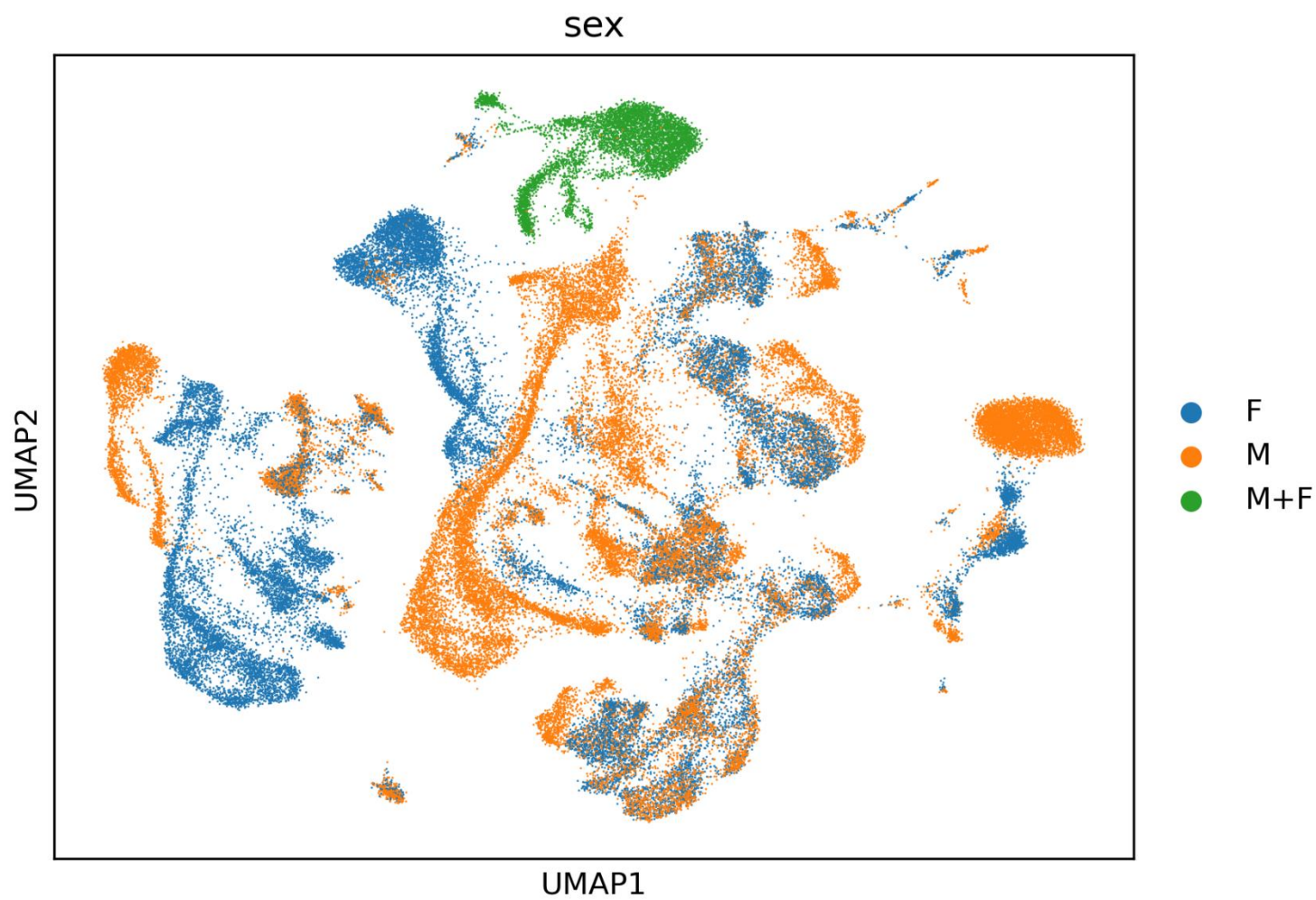


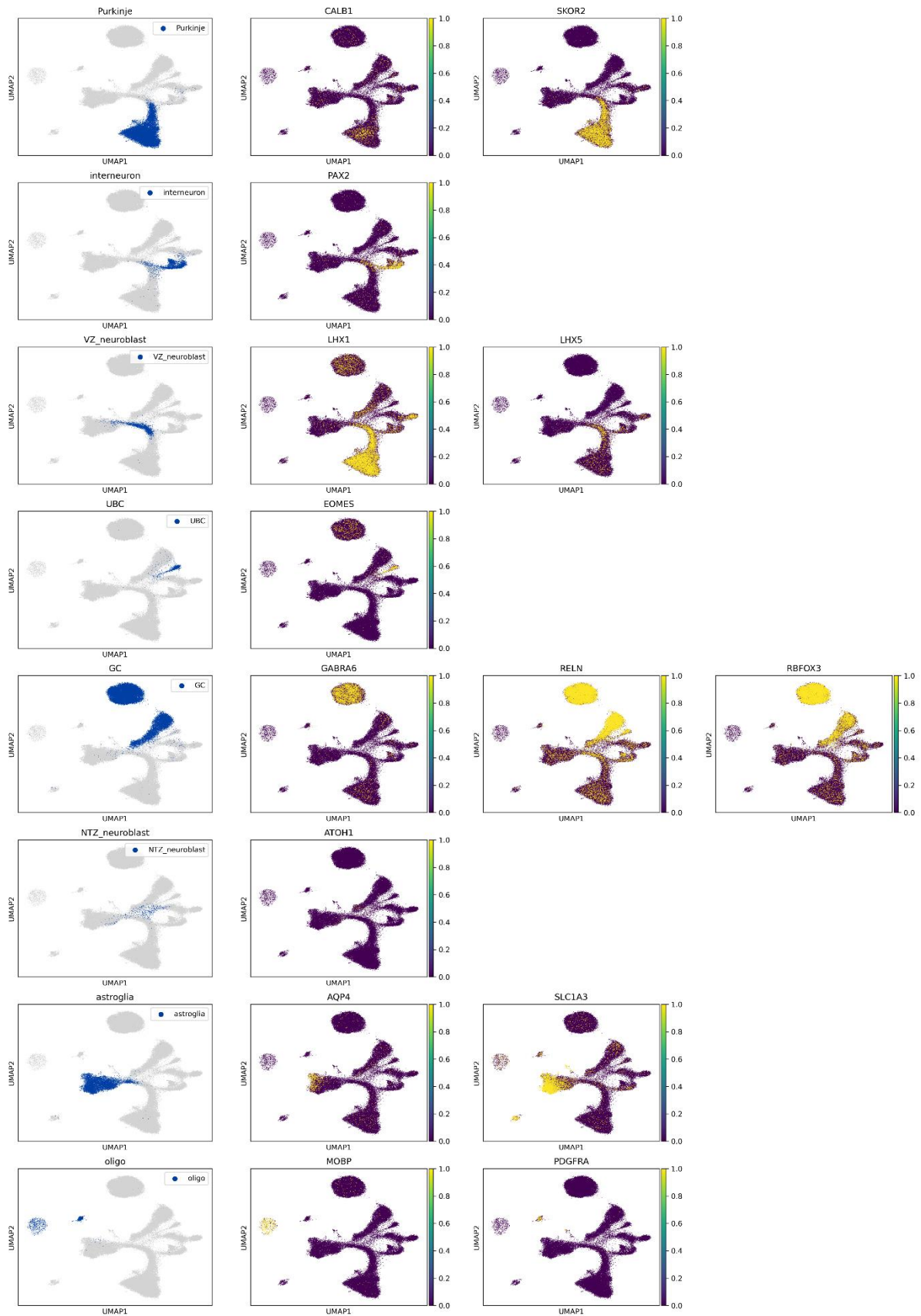
Supplementary Figure 1: Summary of the number of nuclei per dataset which passed quality control, grouped by broad cell type and developmental stage.



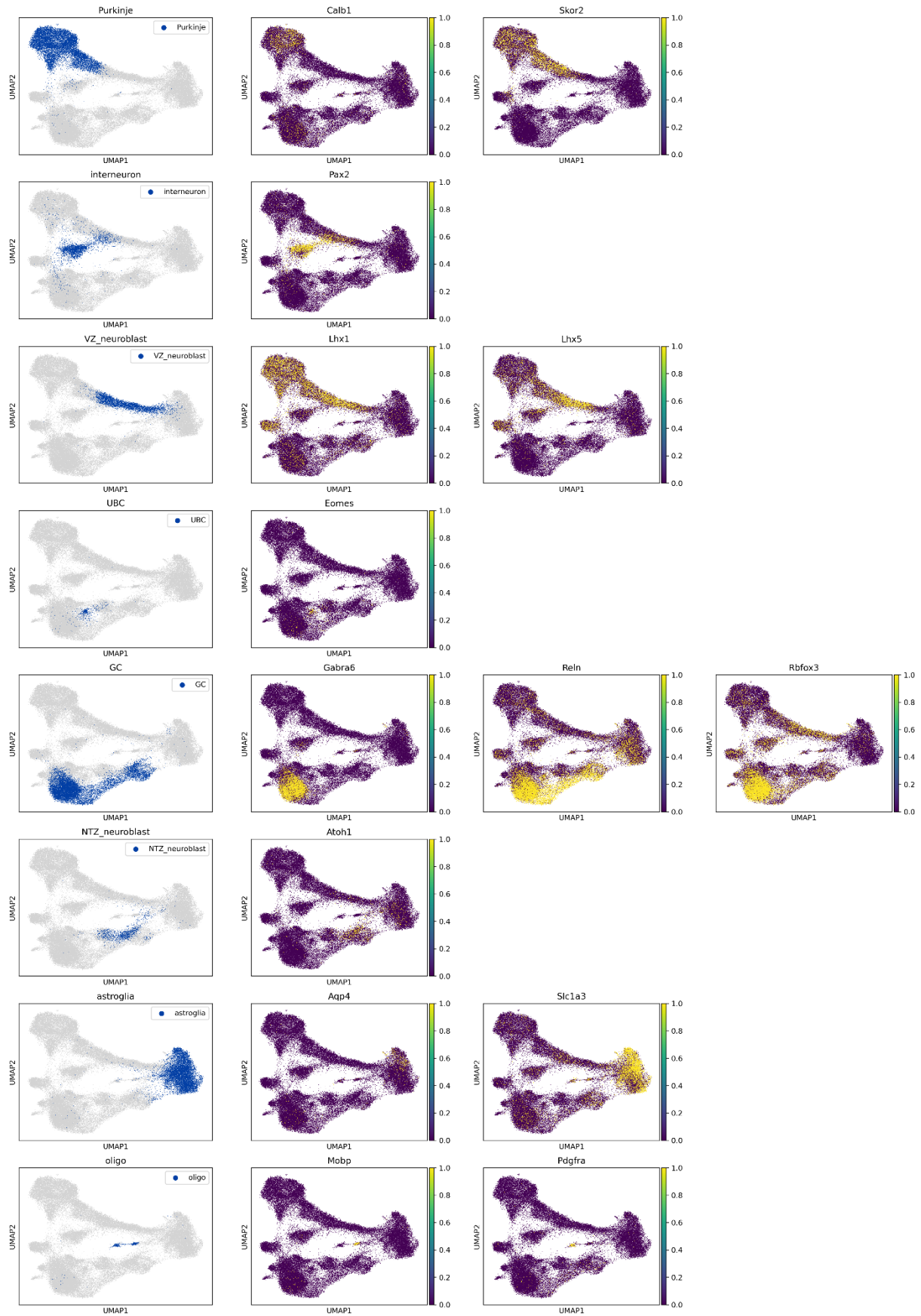
Supplementary Figure 2: UMAP plots visualising nuclei for each dataset before (left) and after (right) integration with Harmony. Colouration shows sample age using a numerical scale in years, where zero is at birth.



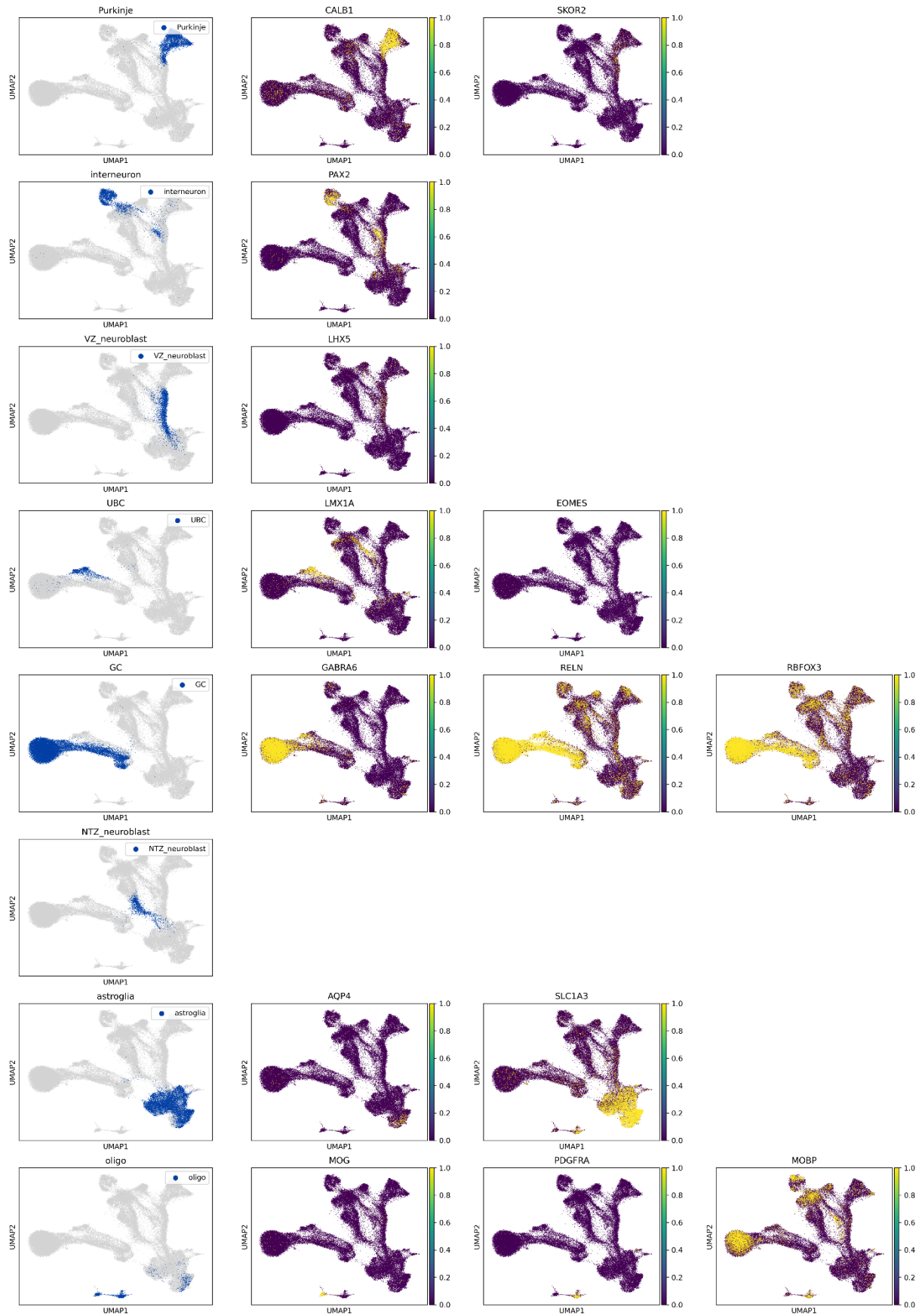
Supplementary Figure 3: UMAP plot for the Sepp mouse dataset with colourations showing sample sex; F = female, M = male, M + F = pooled male and female.



Supplementary Figure 4: Integrated UMAP plots visualising major cerebellar cell types and the primary marker genes used to verify cell identities for the Sepp human dataset.



Supplementary Figure 5: Integrated UMAP plots visualising major cerebellar cell types and the primary marker genes used to verify cell identities for the Sepp mouse dataset.



Supplementary Figure 6: Integrated UMAP plots visualising major cerebellar cell types and the primary marker genes used to verify cell identities for the Sepp opossum dataset.