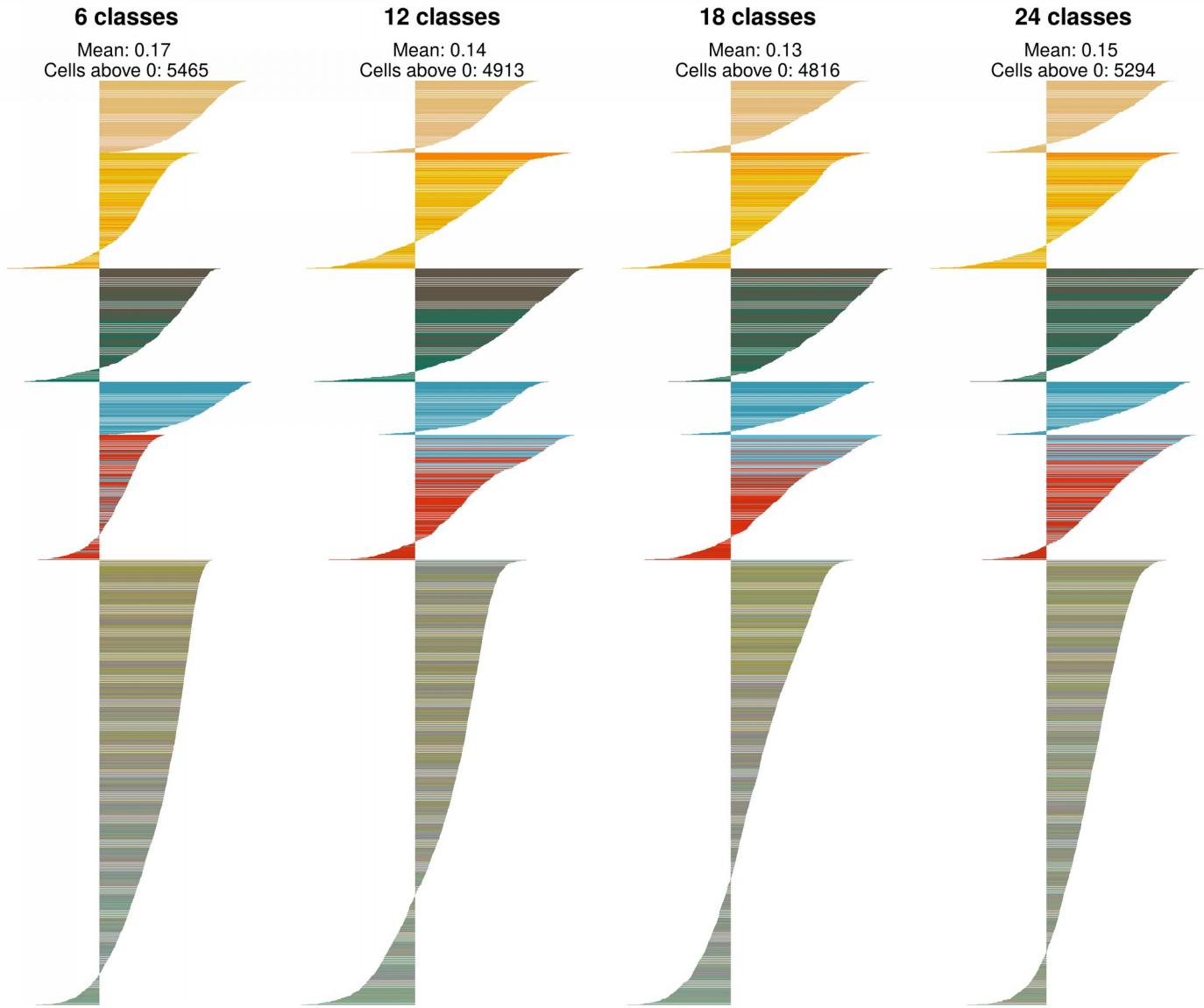
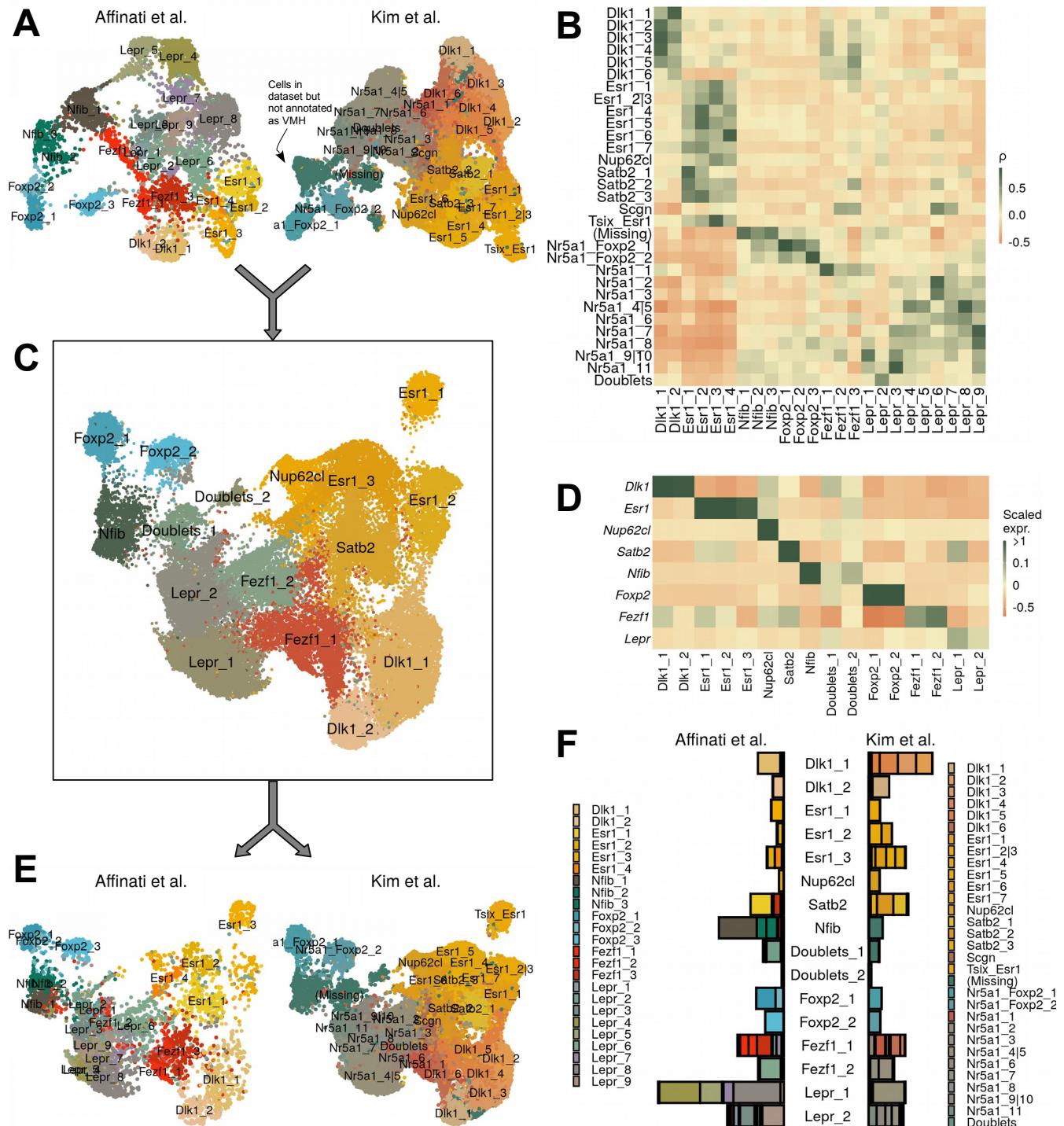


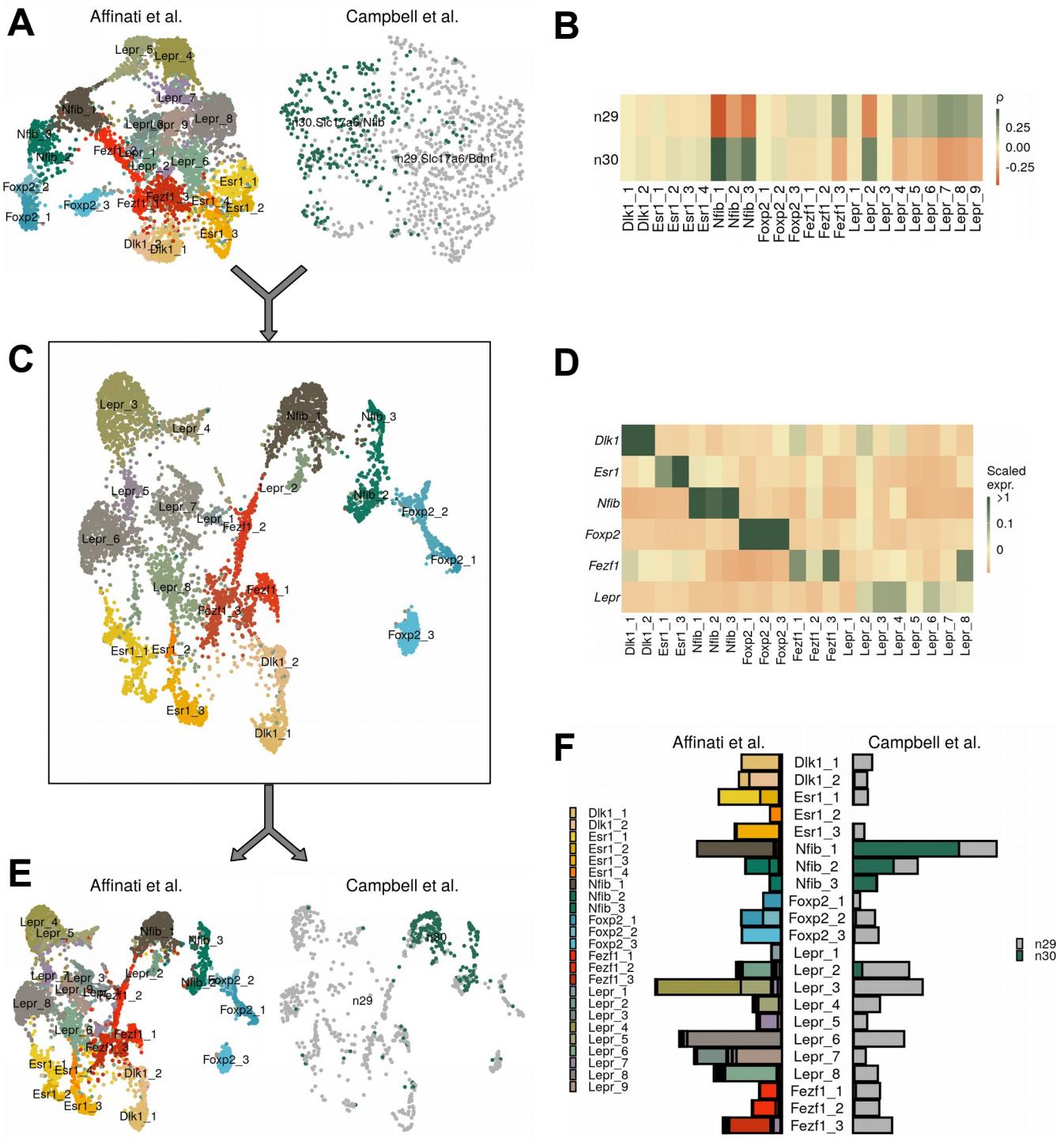
**Figure S1: Mouse snRNA-seq identifies major CNS classes.** (A–C) The number of (A) cells, (B) genes, and (C) UMIs detected per sample used in this study after quality control. (D) UMAP projection of all 42,040 cells, colored by cluster. (E) Average percent of cells in each cluster across all samples. (F) Representative marker genes for each of the major CNS cell types. (G) Expression profile of top enriched genes for each cluster. (H) UMAP representation of cell type classification. (I) Quantification of cell classes per sample.



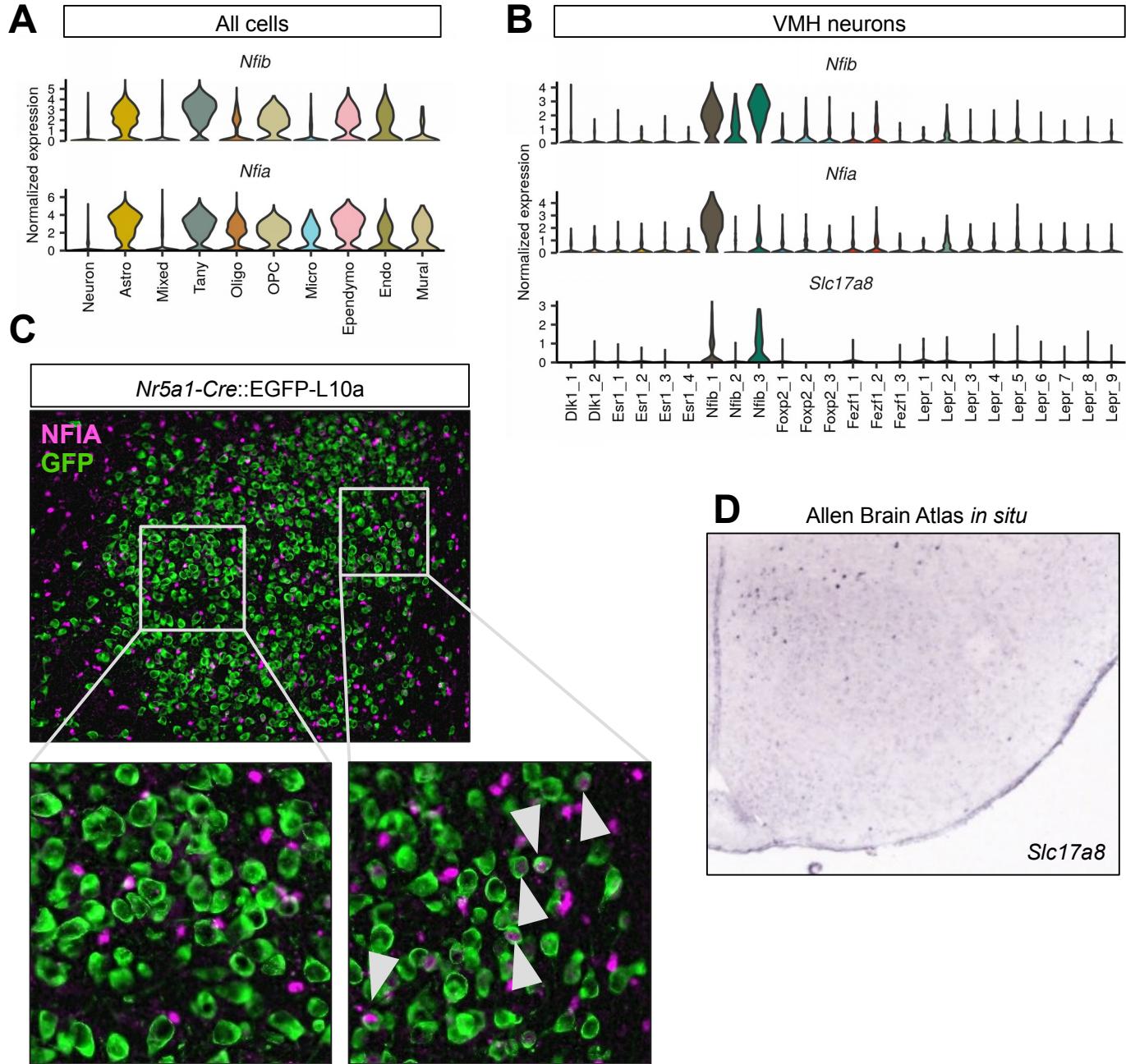
**Figure S2: Identification of VMH neuronal “classes.”** The silhouette width for each cell for each level of VMH neuron classification. The mean silhouette width and the number of cells with a silhouette width greater than 0 are noted above the plot. Cells are colored by their cluster color in Fig. 2A.



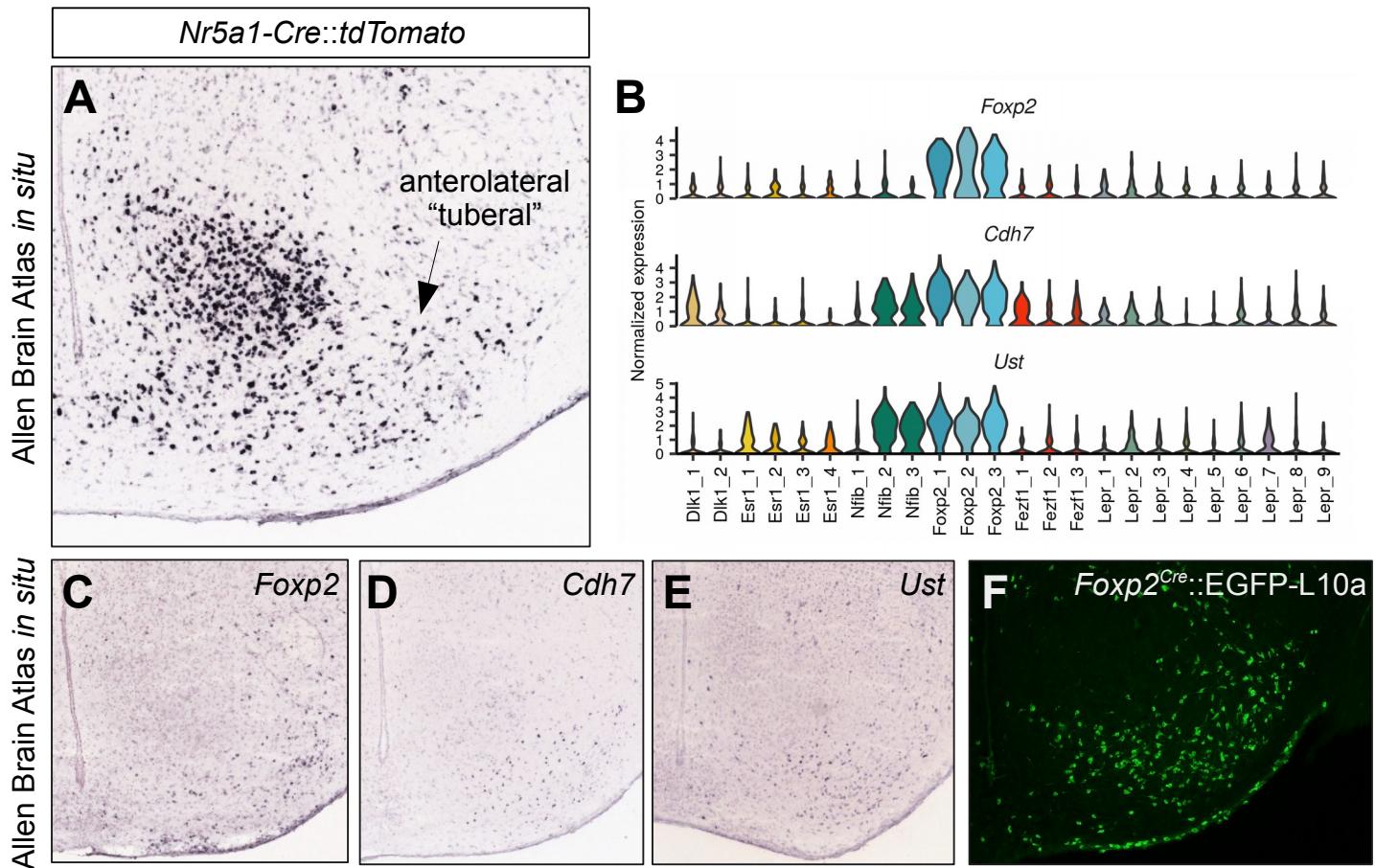
**Figure S3: Comparison with VMH data from Kim et al.** **(a)** UMAP projection of each dataset separately. **(b)** Pair-wise expression correlation of variable genes for each cluster in each dataset. **(c)** UMAP projection of CCA-integrated data, colored by cluster. **(d)** Mean scaled expression of marker genes for each cluster. **(e)** UMAP projection of integrated data, by dataset of origin. **(f)** Breakdown of cluster designation from original dataset and integrated dataset.



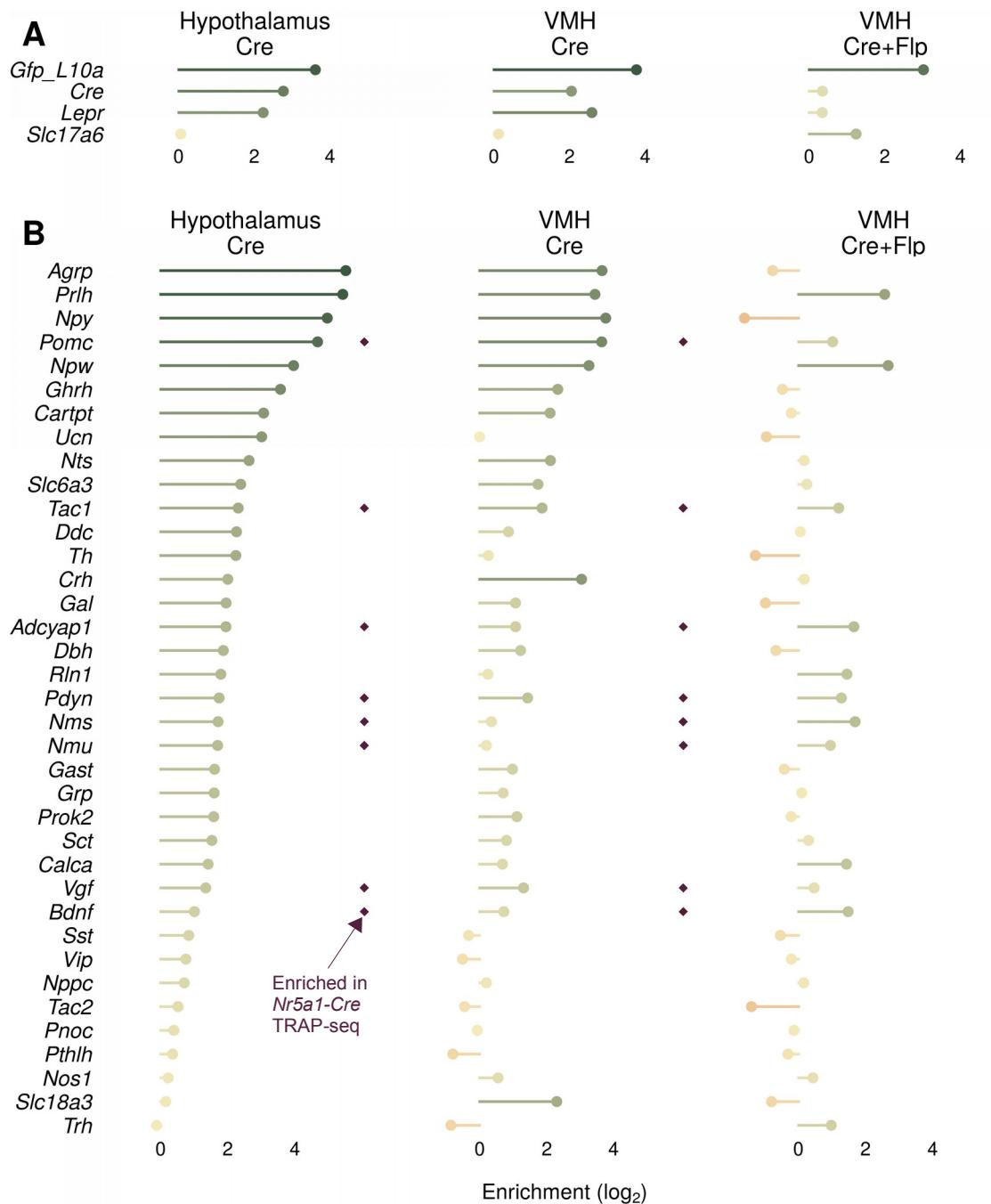
**Figure S4: Comparison of data with VMH data from Campbell et al.** (a) UMAP projection of each dataset separately. (b) Pair-wise expression correlation of variable genes for each cluster in each dataset. (c) UMAP projection of CCA-integrated data, colored by cluster. (d) Mean scaled expression of marker genes for each cluster. (e) UMAP projection of integrated data, by dataset of origin. (f) Breakdown of cluster designation from original dataset and integrated dataset.



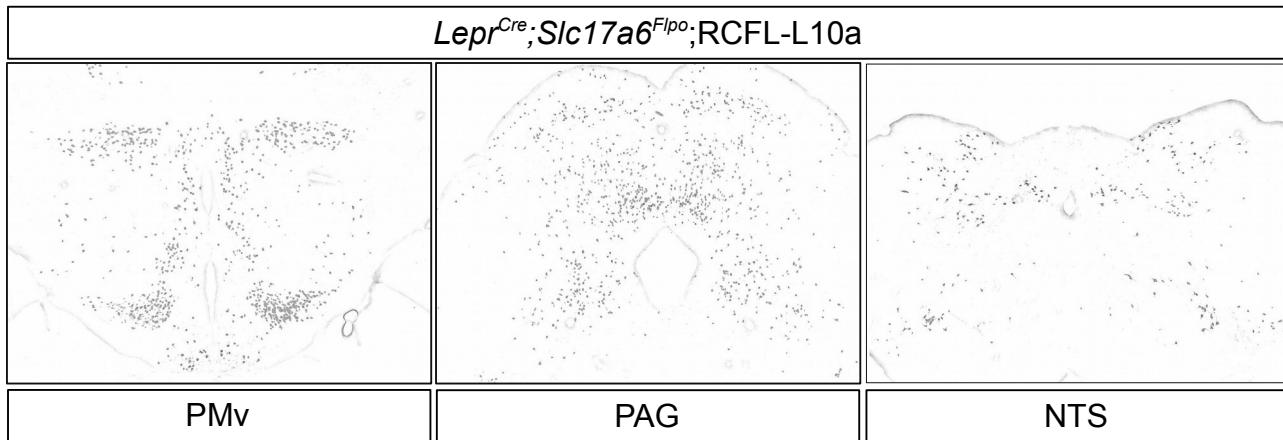
**Figure S5:** VMH *Nfib* population localizes to dorsomedial compartment. **(A–B)** *Nfia* marks **(B)** a subset of VMH<sup>*Nfib*</sup> neurons but is also widely expressed in **(A)** non-neuronal populations in the VMH. **(C)** Immunofluorescence staining for NFIA in *Nr5a1-Cre::EGFP-L10a* mice shows colocalization of GFP (green) and NFIA (magenta) in the most dorsomedial aspect of the VMH. **(B)** *Slc17a8* is a marker for VMH<sup>*Nfib*</sup> cells and **(D)** is expressed in the most dorosmedial VMH according to the Allen Brain Atlas *in situ* database.



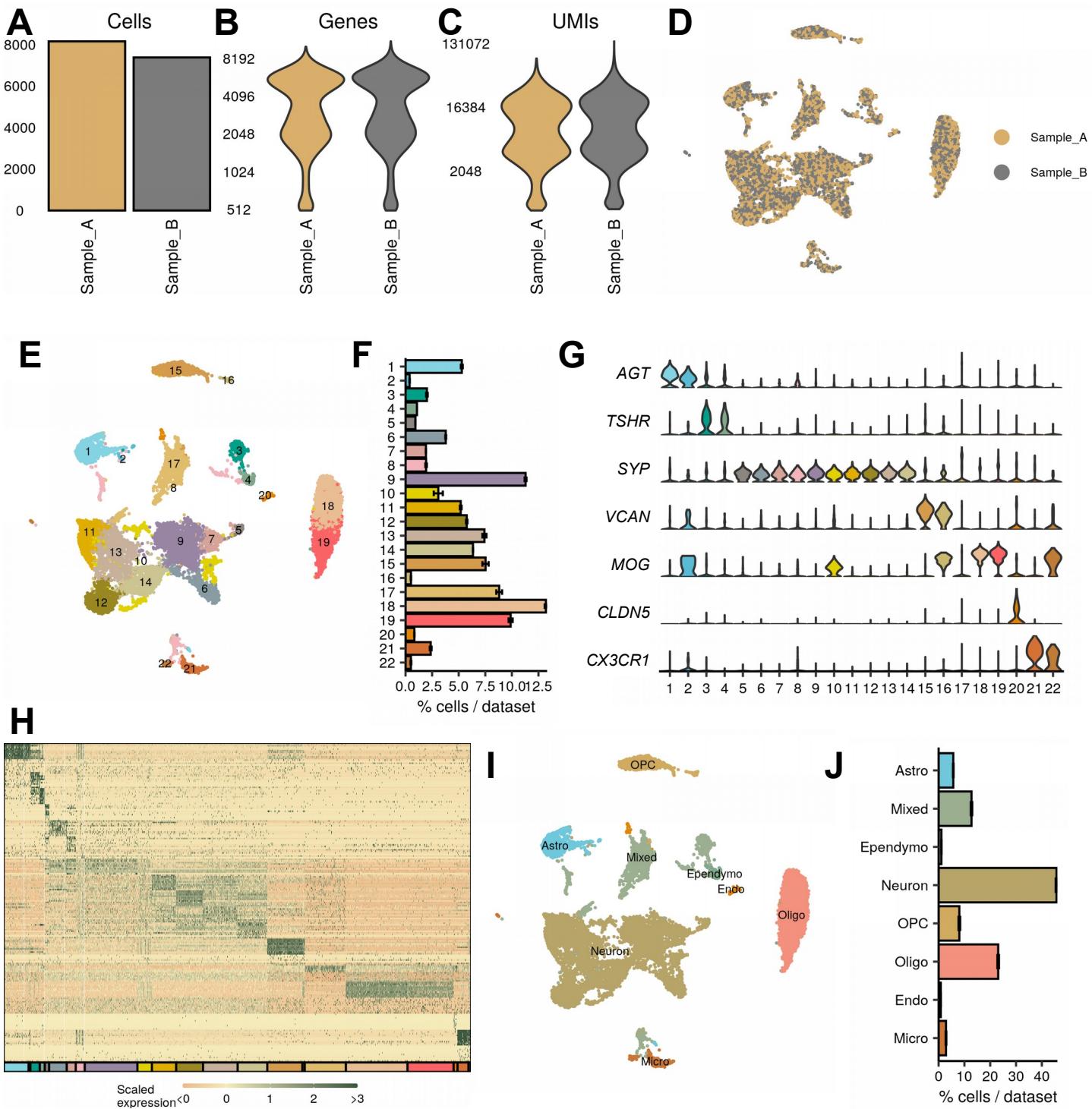
**Figure S6:** *Foxp2* population localizes to anterolateral (“tuberal”) compartment. **(A)** Allen Brain Atlas *in situ* for *tdTomato* in *Nr5a1-Cre::tdTomato* mice shows widespread expression outside of the core VMH in an area referred to as the tuberal nucleus. **(B)** The VMH<sup>*Foxp2*</sup> population is also marked by *Cdh7* and *Ust* expression. **(C–E)** Allen Brain Atlas *in situ* images for **(C)** *Foxp2*, **(D)** *Cdh7*, and **(E)** *Ust* show expression in the tuberal VMH. **(F)** Immunofluorescence for GFP in *Foxp2<sup>Cre</sup>::EGFP-L10a* mice demonstrates expression in the tuberal VMH.



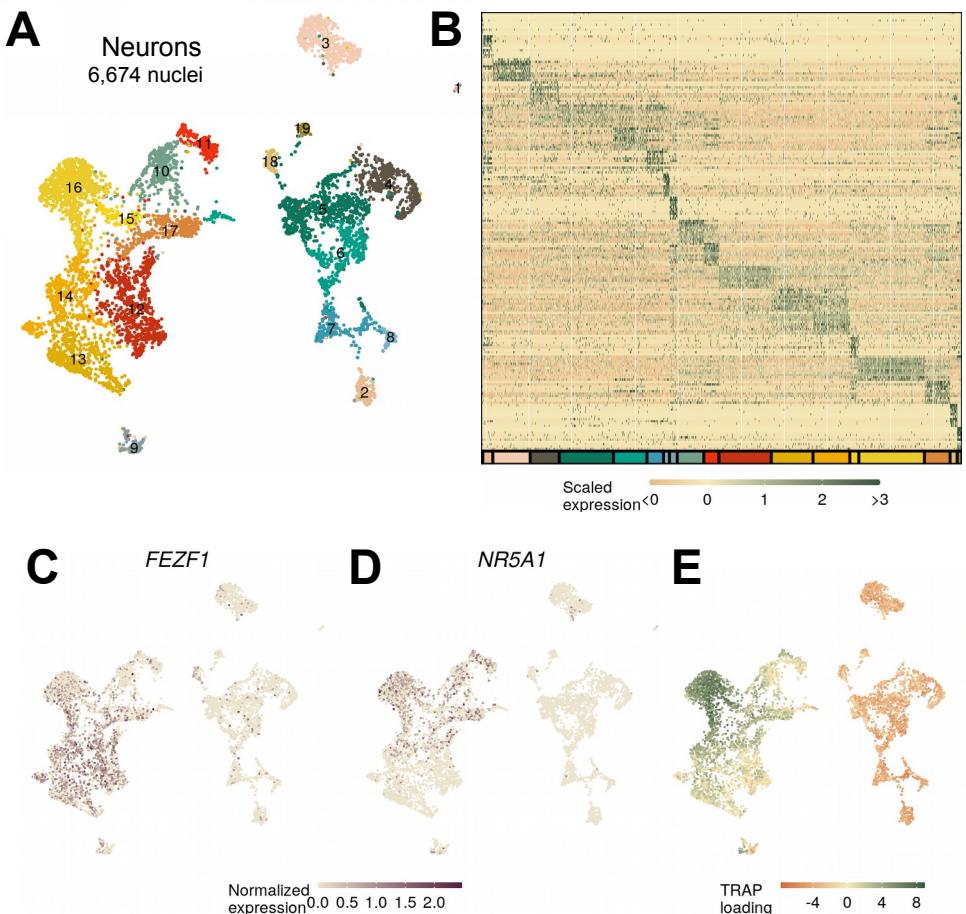
**Figure S7: Comparison of different TRAP-seq approaches for identifying genes enriched in *Lepr* VMH cells.** **(A, B)** Comparison of *Lepr<sup>Cre</sup>::EGFP-L10a* of the whole hypothalamus (Hypothalamus Cre), *Lepr<sup>Cre</sup>::EGFP-L10a* with targeted dissection of the VMH (VMH Cre), and using the dual Flp- and Cre-dependent RCFL-L10a with *Lepr<sup>Cre</sup>;Slc17a6<sup>Flopo</sup>* mice (VMH Cre+Flp). **(A)** Enrichment of control genes in each dataset. **(B)** Enrichment of genes conferring neurochemical identity that are significantly enriched in any of the 3 datasets. Dark red diamonds signify genes that are significantly enriched in the *Nr5a1-Cre::EGFP-L10a* TRAP-seq (presumptive VMH).



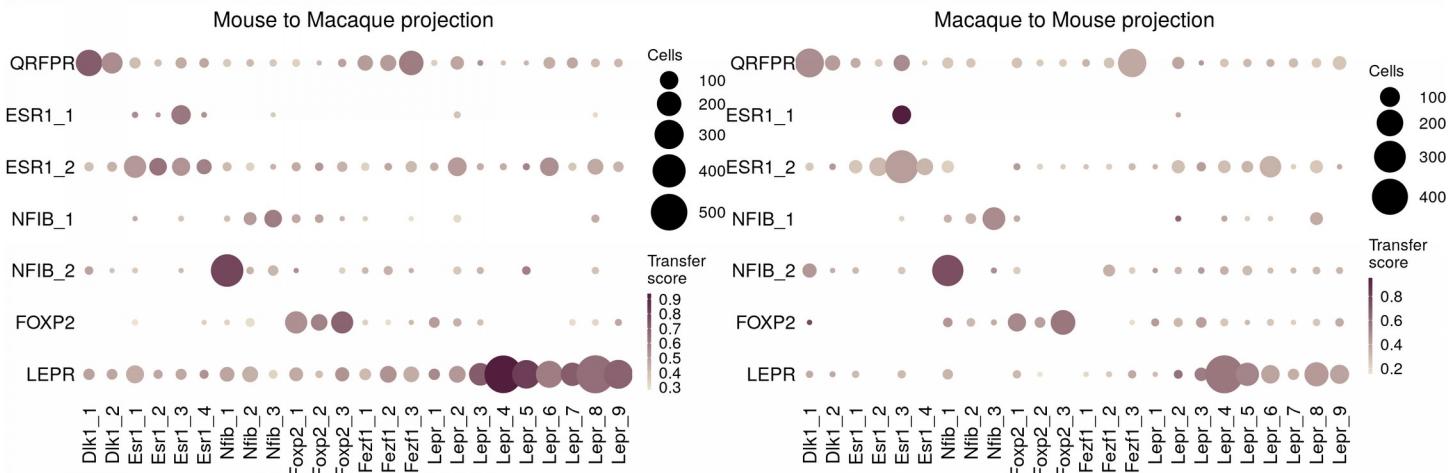
**Figure S8: Expression of *Lep<sup>r</sup><sup>Cre</sup>;Slc17a6<sup>Flopo</sup>;RCFL-L10a* outside of the VMH.** EGFP expression was detected in the ventral premamillary nucleus (PMv), periaqueductal gray (PAG), and nucleus of the solitary tract (NTS).



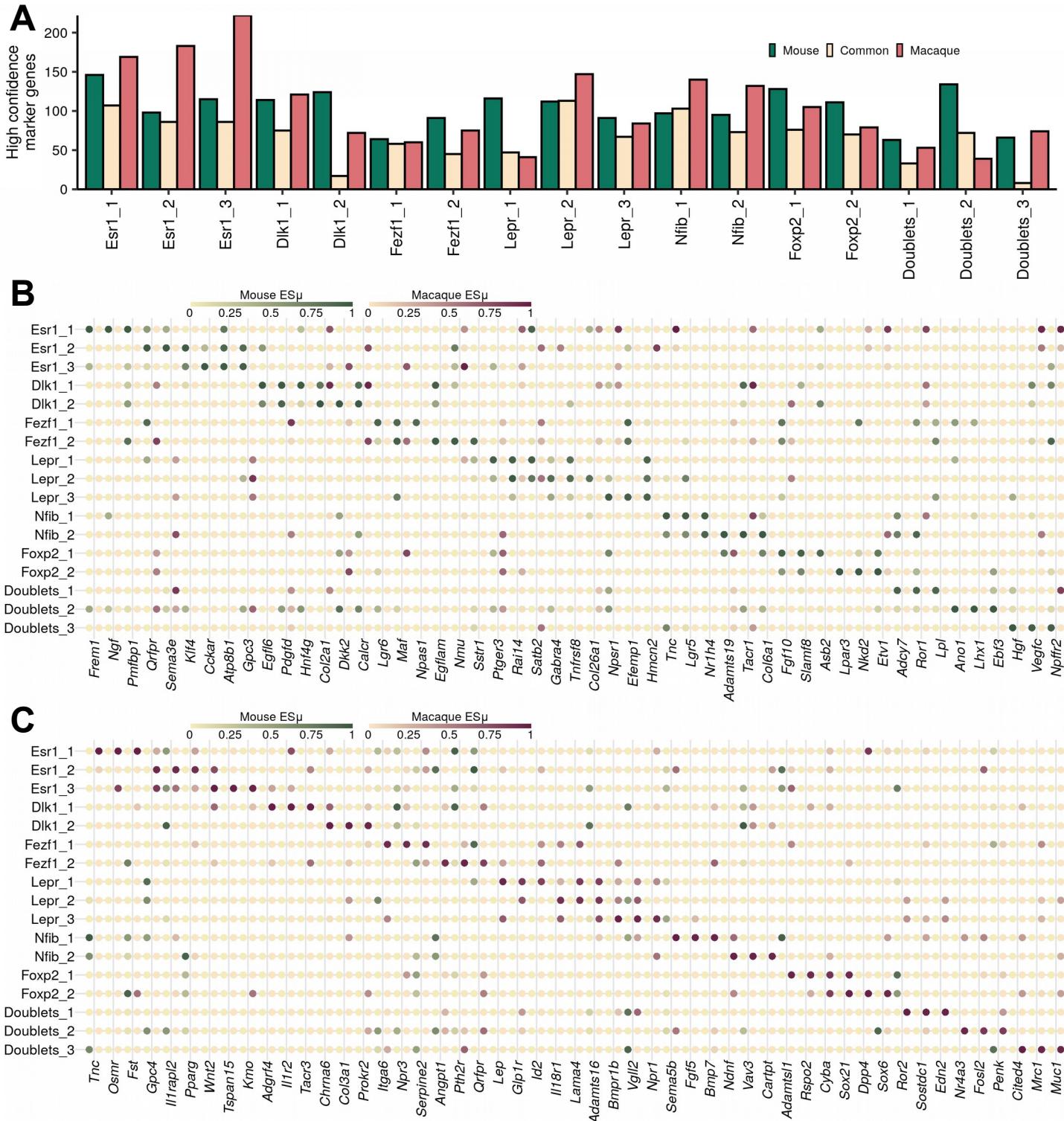
**Figure S9: Macaque snRNA-seq identifies major CNS classes.** (A–C) The number of (A) cells, (B) genes, and (C) UMIs detected per sample used in this study after quality control. (D–E) UMAP projection of all cells, colored by (D) sample and (E) cluster. (F) Average percent of cells in each cluster across all samples. (G) Representative marker genes for each of the major CNS cell types. (H) Expression profile of top 10 enriched genes for each cluster. (I) UMAP representation of cell type classification. (J) Quantification of cell classes per sample.



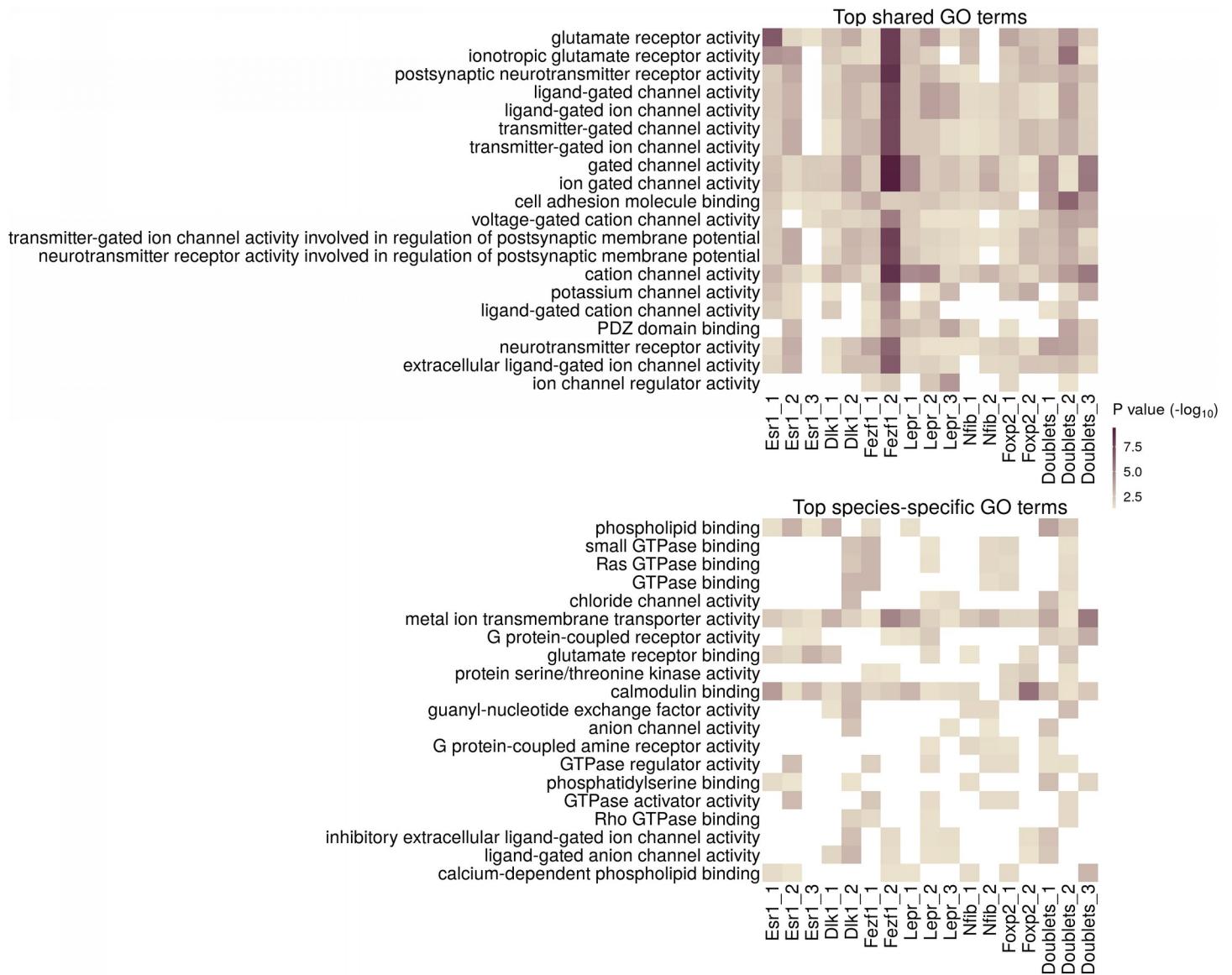
**Figure S10: Identifying VMH neurons in macaque.** (A) UMAP projection and labeling by cluster and (B) expression of top 10 genes for each macaque neuron cluster. (C) *FEZF1* and (D) *NR5A1* expression across the macaque neurons. (E) Loading on the top enriched mouse *Nr5a1-Cre* TRAP-seq genes.



**Figure S11: Transferability of cluster designation between species.** Transferred cluster designations from mouse to macaque (and vice versa) using the Seurat CCA projection, colored by transfer score with dot size corresponding to the number of cells from a given cluster transferred to each cluster.



**Figure S12: Species-specific marker genes for each conserved cluster.** **(A)** The number of high confidence marker genes (CELLEX ES $\mu$  > 0.5) for each cluster and species. **(B-C)** The most highly species-specific marker genes determined by CELLEX score for each cluster for **(B)** mouse and **(C)** macaque.



**Figure S13: GO analysis of genes shared between both species and species-specific genes.** The top GO terms associated with genes common between the species (“Top shared GO terms”) and the top GO terms associated with species-specific genes (“Top species-specific GO terms”).