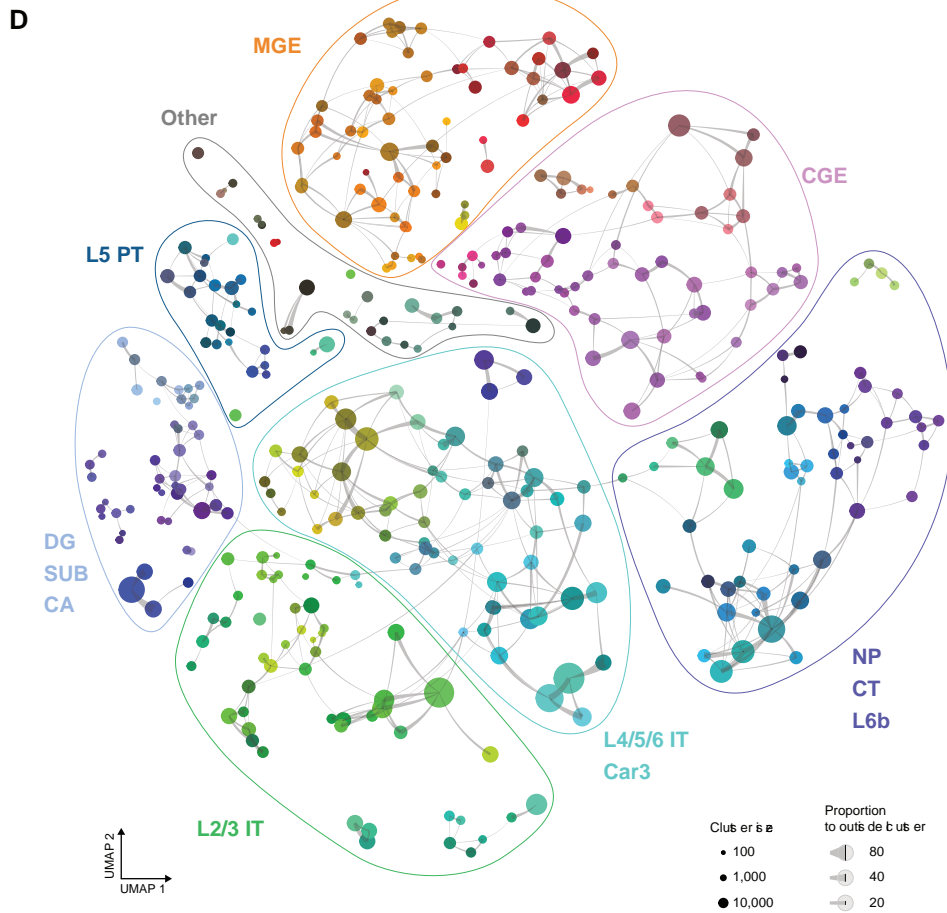
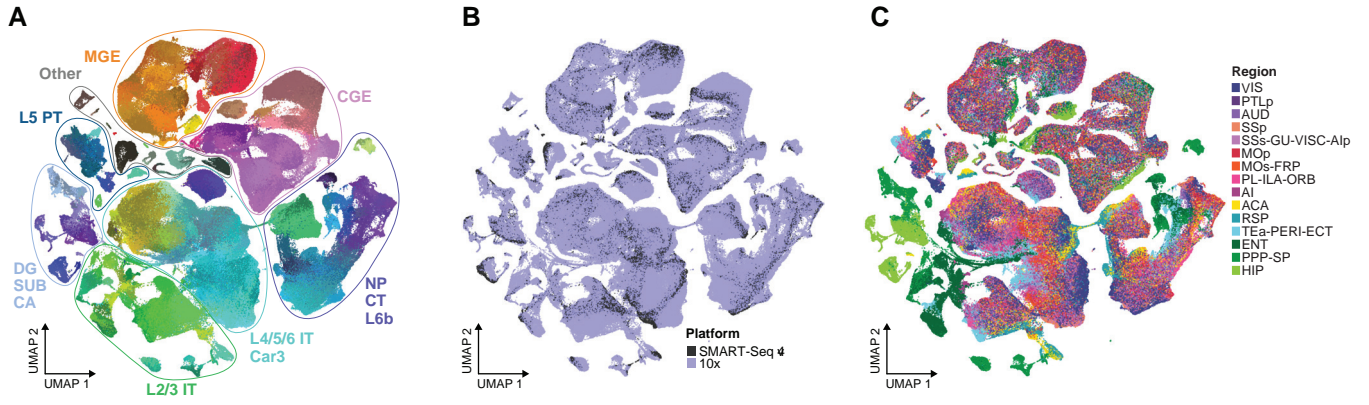


**Data S1. Taxonomy, taxonomy comparison, glutamatergic subclasses, HPF markers, HPF gradients, and IT layer markers. Related to Figures 1, 2, 6, 7, S5 and S6.**

**Taxonomy. Transcriptomic cell type taxonomy of the isocortex (CTX) and hippocampal formation (HPF).**

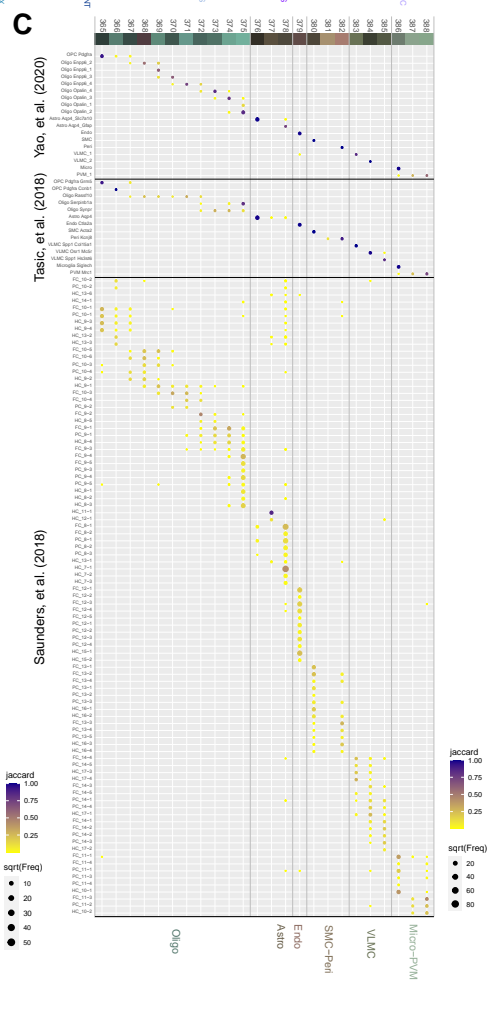
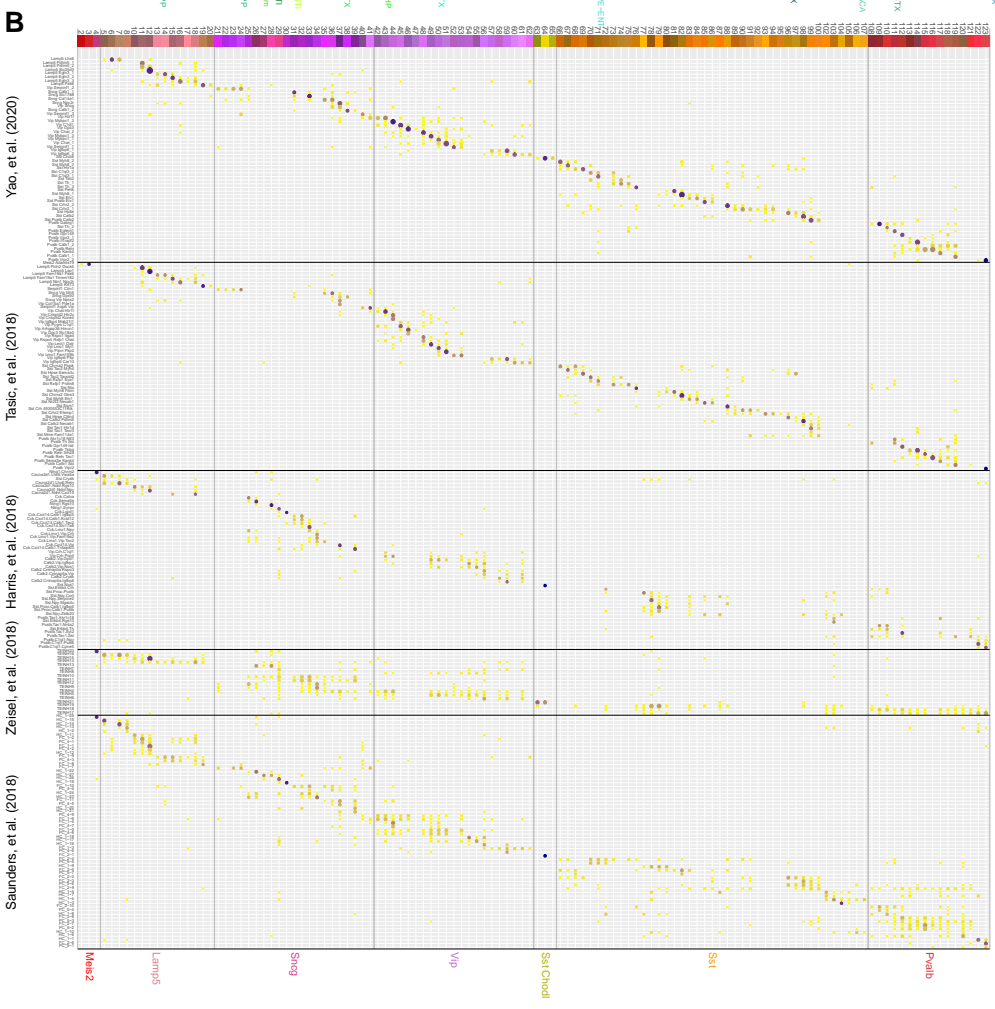
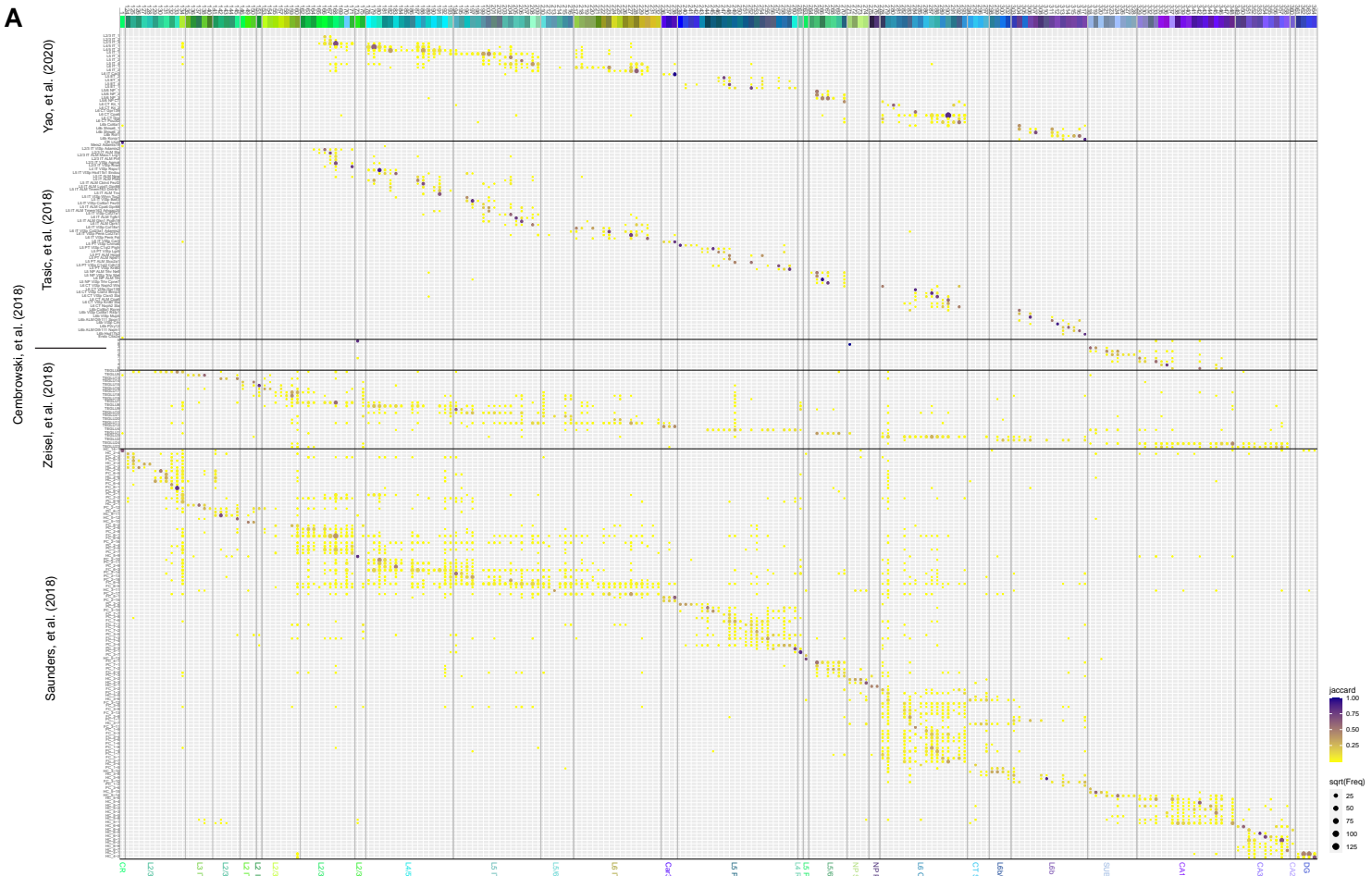
(A-C) UMAP representation of the entire transcriptomic dataset as in **Figure 1B**, colored by cluster (A), platform (B), or region (C).

(D) Constellation plot of the same dataset as in A-C. Each cluster is represented by a dot, positioned at the cluster centroid in UMAP coordinates in A, with dot size proportional to the number of cells in the cluster. Connecting lines represent the proportion of nearest neighbors between pairs of clusters. Clusters are grouped by neighborhood.



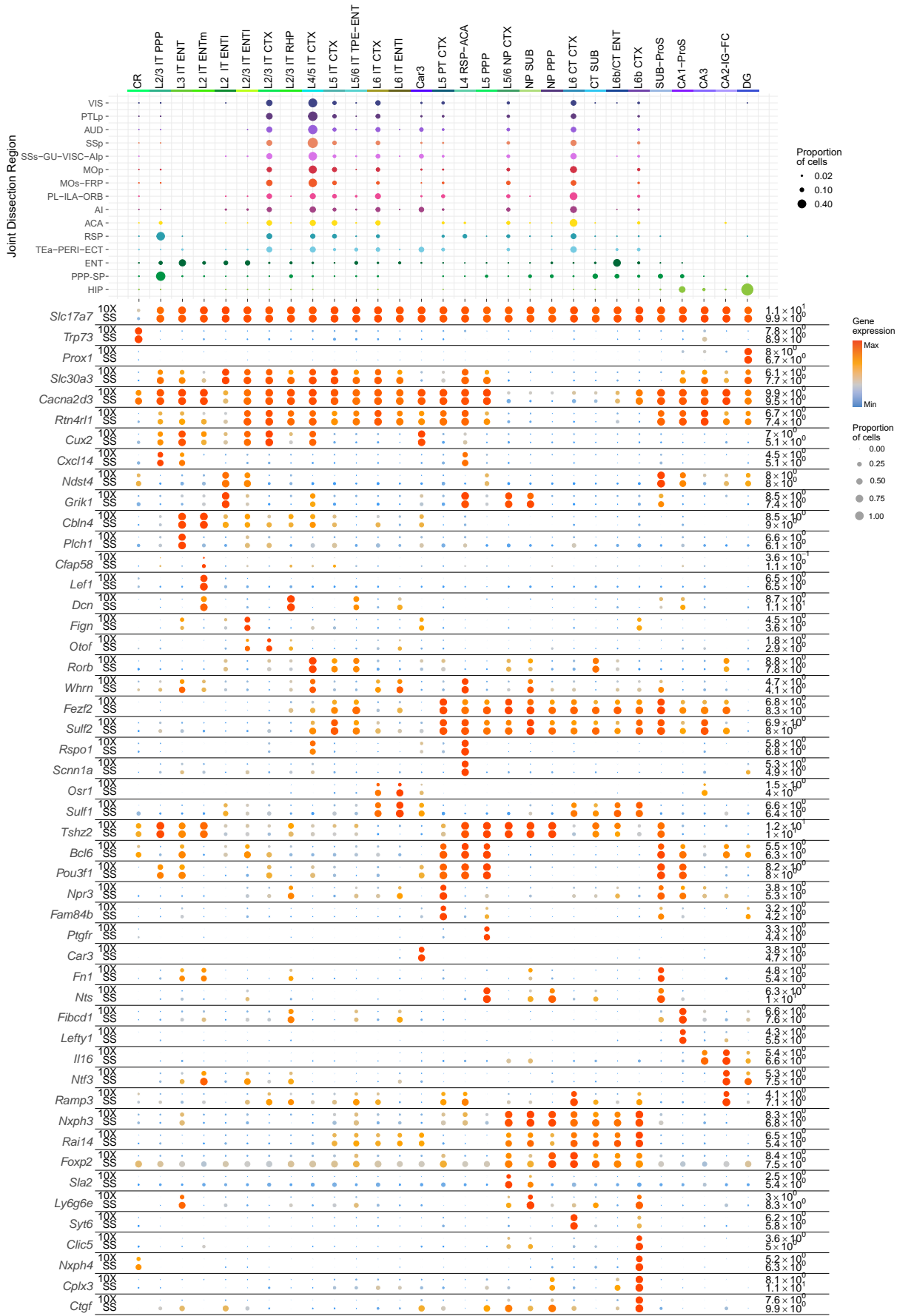
### **Taxonomy comparison. Correspondence between the current transcriptomic taxonomy and previously published ones.**

Correspondence was determined by mapping cells from previously published datasets to the current taxonomy as described in **Methods** and **Methods S1**. Panels show mapping of glutamatergic types (**A**), GABAergic types (**B**), and non-neuronal types (**C**). In nearly all cases we found gaps in previous datasets suggesting our current taxonomy is the most complete for isocortex and HPF. One exception to this is that Saunders et al. (2018) profiled many more non-neuronal cells and had more types in this class. The two previous whole mouse brain single-cell transcriptomic datasets (Saunders et al., 2018; Zeisel et al., 2018) map poorly with our taxonomy in both glutamatergic and GABAergic classes, exhibiting high degrees of confusion among clusters. Our own previous studies on VISp-ALM (Tasic et al., 2018) and MOp (Yao et al., 2020) as well as the Cembrowski et al. (2018) data on glutamatergic neurons in subiculum and the Harris et al. (2018) data on GABAergic interneurons in CA1 all map well with our current taxonomy.



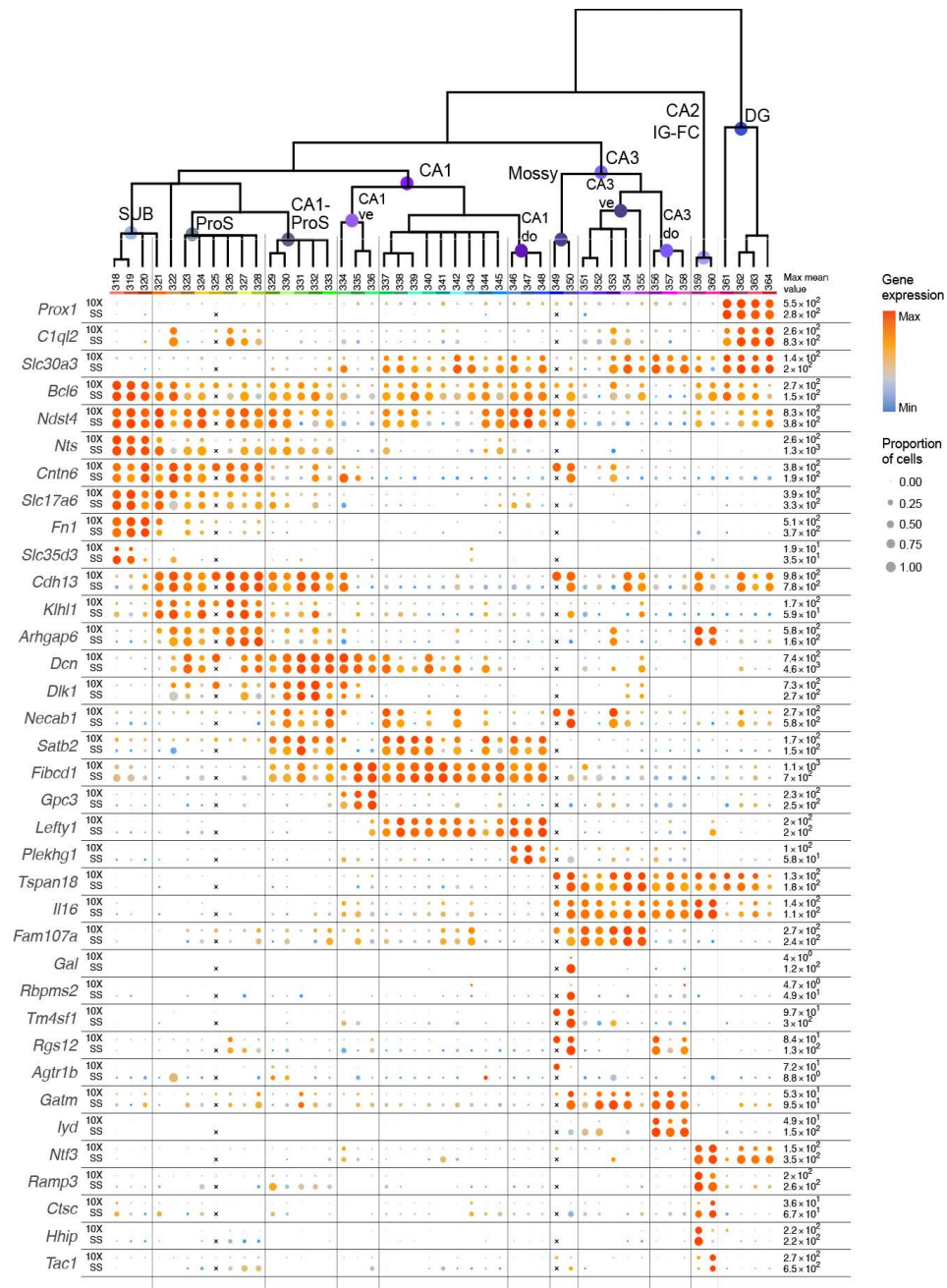
**Glutamatergic subclasses. Regional distribution and marker gene expression for glutamatergic subclasses.**

Dot plot illustrating the proportion of cells (dot size) within each glutamatergic subclass derived from each region where the values in each region (row) add up to 100%. Below the regional dot plot, the gene expression dot plot illustrates marker gene expression in glutamatergic excitatory subclasses from the SSv4 (bottom) and 10xv2 (top) datasets. Dot size and color indicate proportion of expressing cells and average expression level in each cluster, respectively.



## HPF markers. Marker gene expression in hippocampal and subicular glutamatergic cell types.

Dendrogram of clusters in the DG/SUB/CA neighborhood followed by dot plot showing marker gene expression in clusters from SSv4 (bottom) and 10xv2 (top) datasets. Dot size and color indicate proportion of expressing cells and average expression level in each cluster, respectively. The small x's under clusters #325 and 349 mean there are no SSv4 cells in them.



**HPF gradients. Multidimensional gradient distribution of hippocampal and subicular glutamatergic cell types.**

(A) Average expression of select marker genes in clusters along the Pr-Di axis in SUB/ProS/CA1 as shown in **Figure S5A**. Gene expression is normalized by dividing the maximal value per gene in range [0,1].

(B) RNA ISH images for select markers showing the Pr-Di transition.

(C) Average expression of select marker genes in clusters along the Do-Ve axis within each subclass (separated by dashed lines) as shown in **Figure S5C**, normalized as in A.

(D) RNA ISH images for select markers showing the Do-Ve transition.

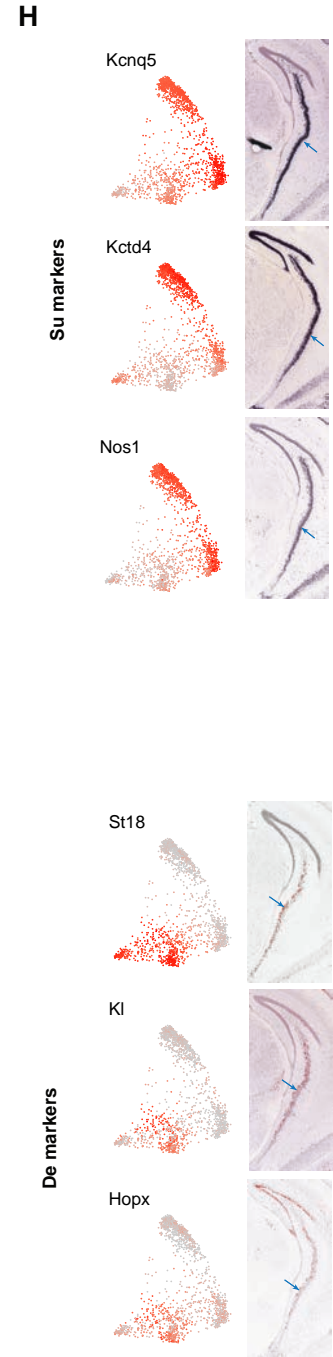
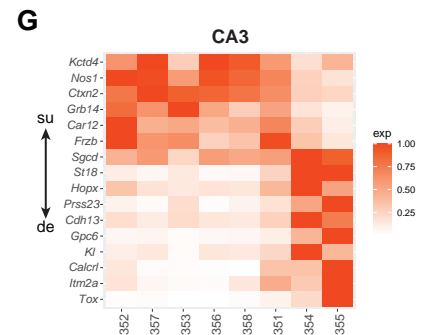
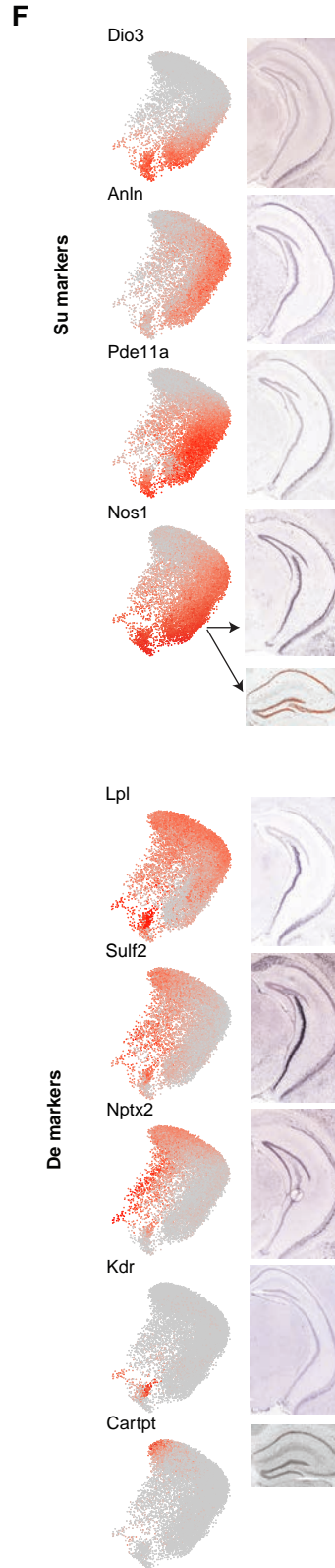
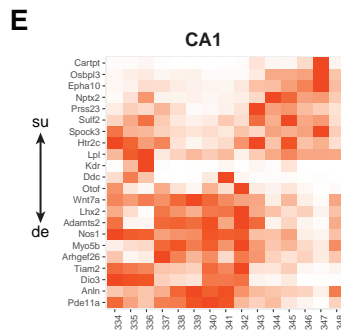
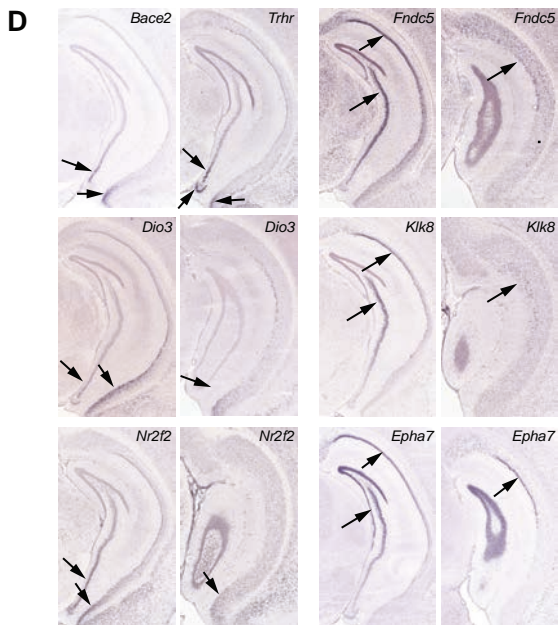
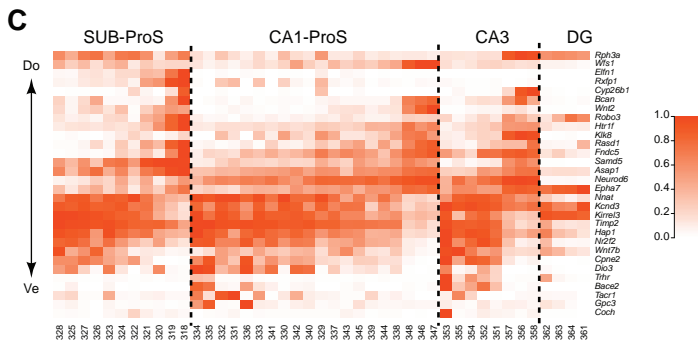
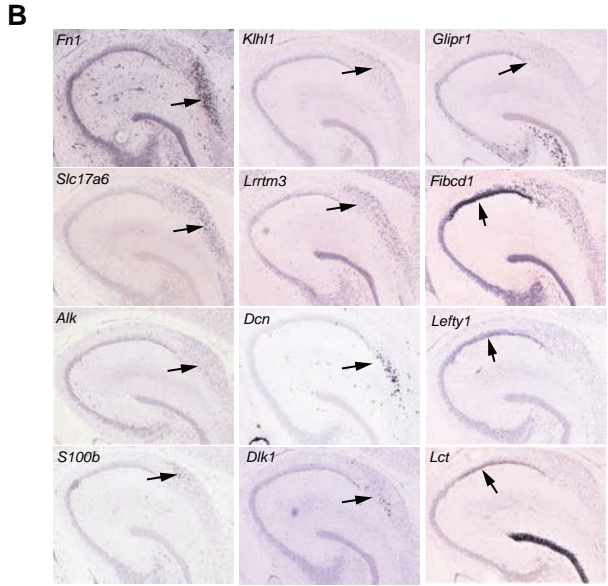
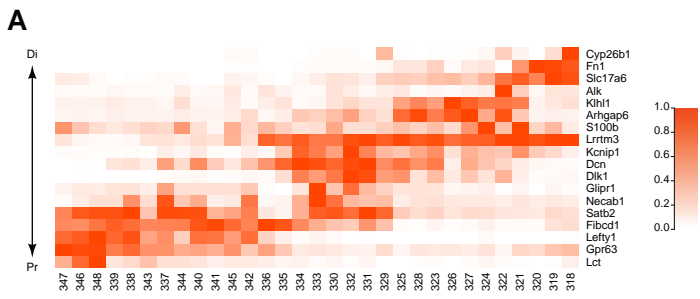
(E) Average expression of selected layer markers in CA1 clusters along the CA1 Su-De axis as shown in **Figure S5G**.

(F) Left: imputed expression of selected layer markers in CA1 2D PC plot. Maximal expression in red, no expression in gray. Right: RNA ISH images of corresponding markers.

(G) Average expression of selected layer markers in CA3 clusters along the CA3 Su-De axis as shown in **Figure S5I**.

(H) Left: imputed expression of selected layer markers in CA3 2D PC plot. Maximal expression in red, no expression in gray. Right: RNA ISH images of these makers.





**IT layer markers. Expression heatmap of IT layer specific markers.**

Heatmap showing the expression of differentially expressed genes between IT subclasses that correspond to different layers. L4/5 IT subclass is further divided into two groups: L4 IT (more superficial, *Rspo1*<sup>+</sup> and *Fezf2*<sup>-</sup>) and L4/5 IT (deeper, *Etv1*<sup>+</sup>, *Fezf2*<sup>+</sup>). L5 IT subclass is further divided into two groups: L5 IT (more superficial, *Foxo1*<sup>+</sup>) and L5/6 IT (deeper, *Cdh9*<sup>+</sup>, *Rxfp1*<sup>+</sup>). For each group, 1,000 cells are randomly sampled, and groups are separated by vertical lines.

