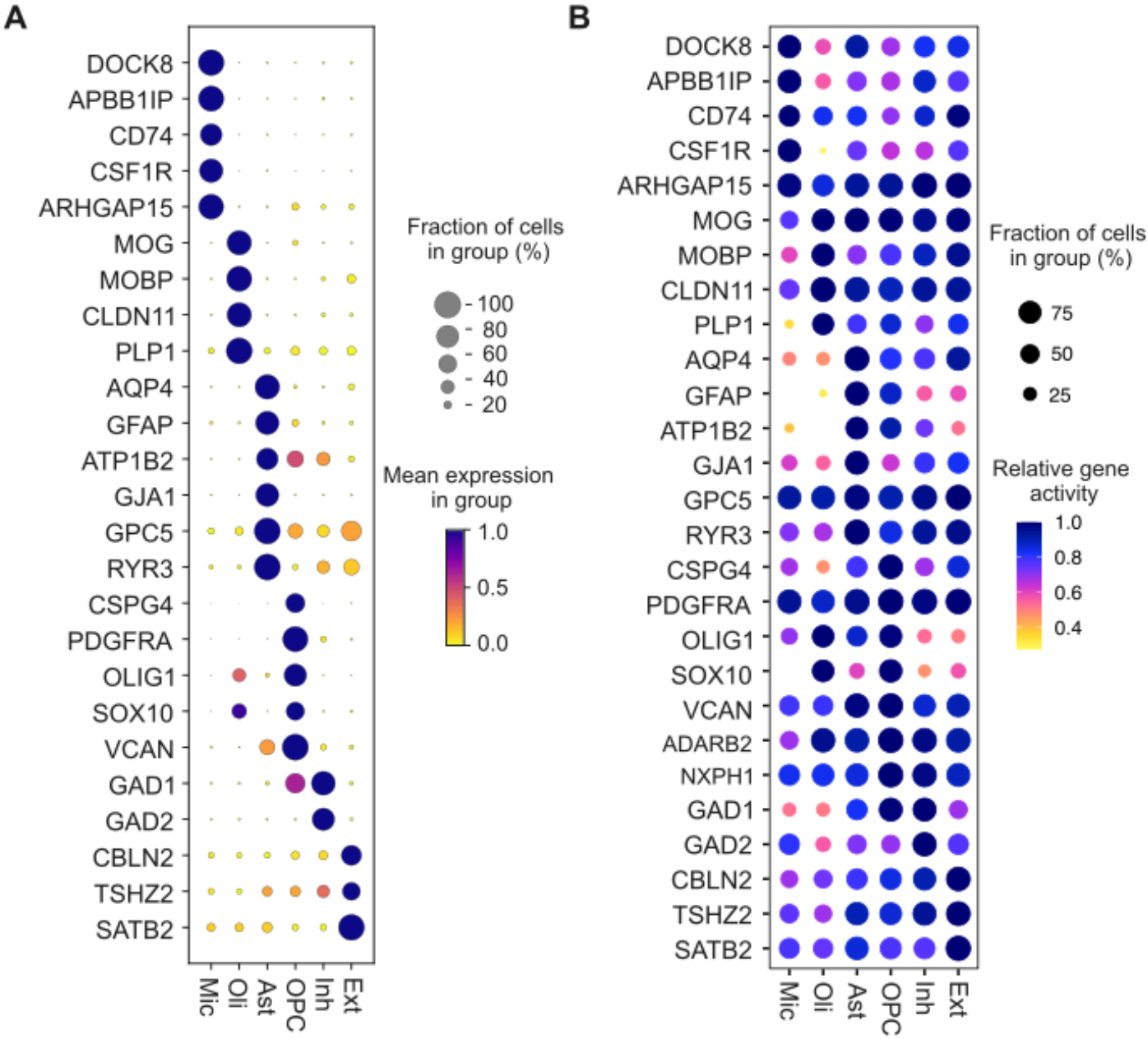

Fig. S1 Marker genes used for cell type annotation. (A) snRNA gene expression for marker genes for each snRNA-seq cluster. (B) snATAC gene activity scores for the gene markers.

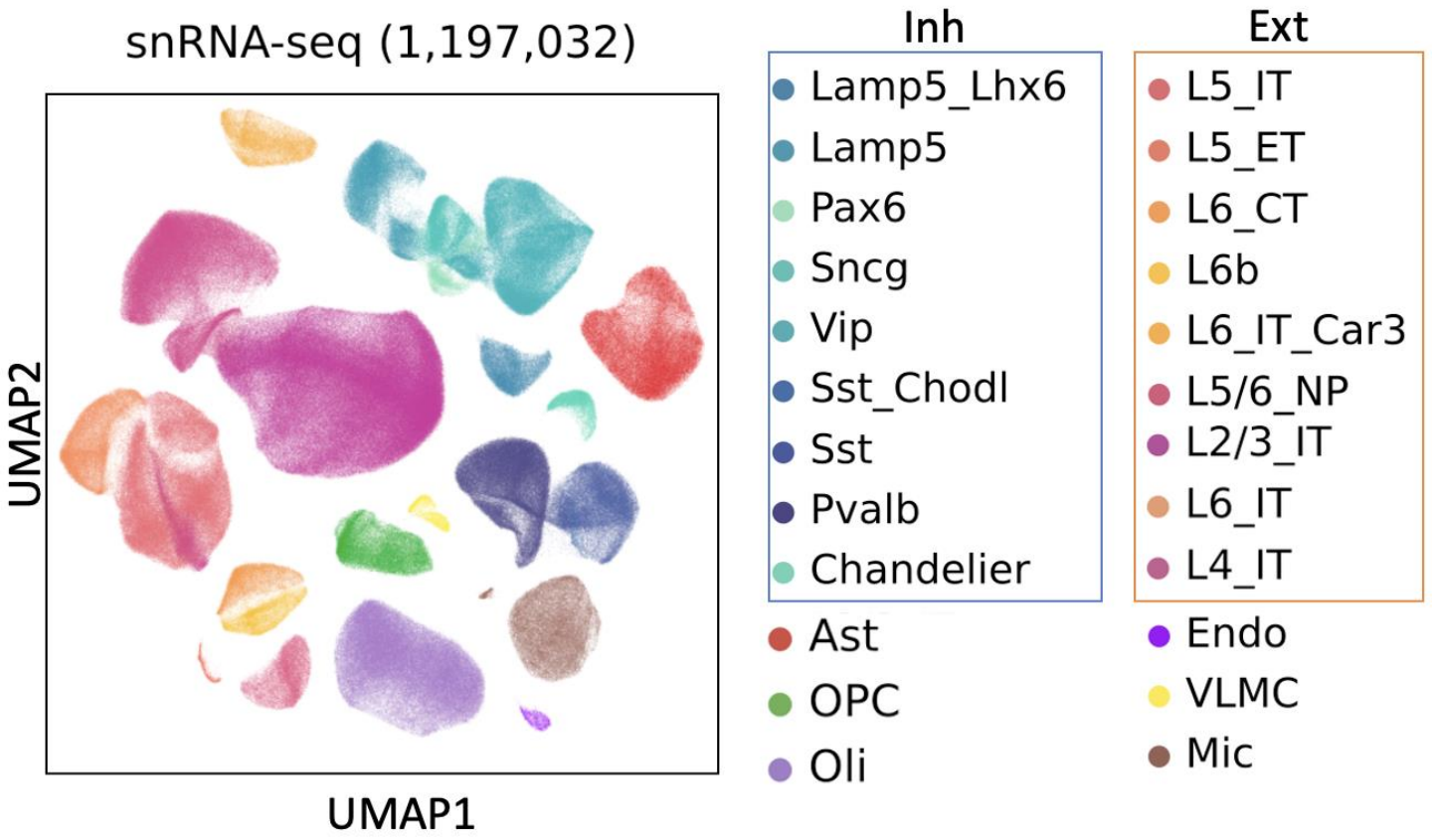

Fig. S2 UMAP representation of snRNA-seq, including sub-class of neuron cell. The blue gradient color represents sub-class of inhibitory neurons, the orange gradient color represents sub-class of excitatory neurons.

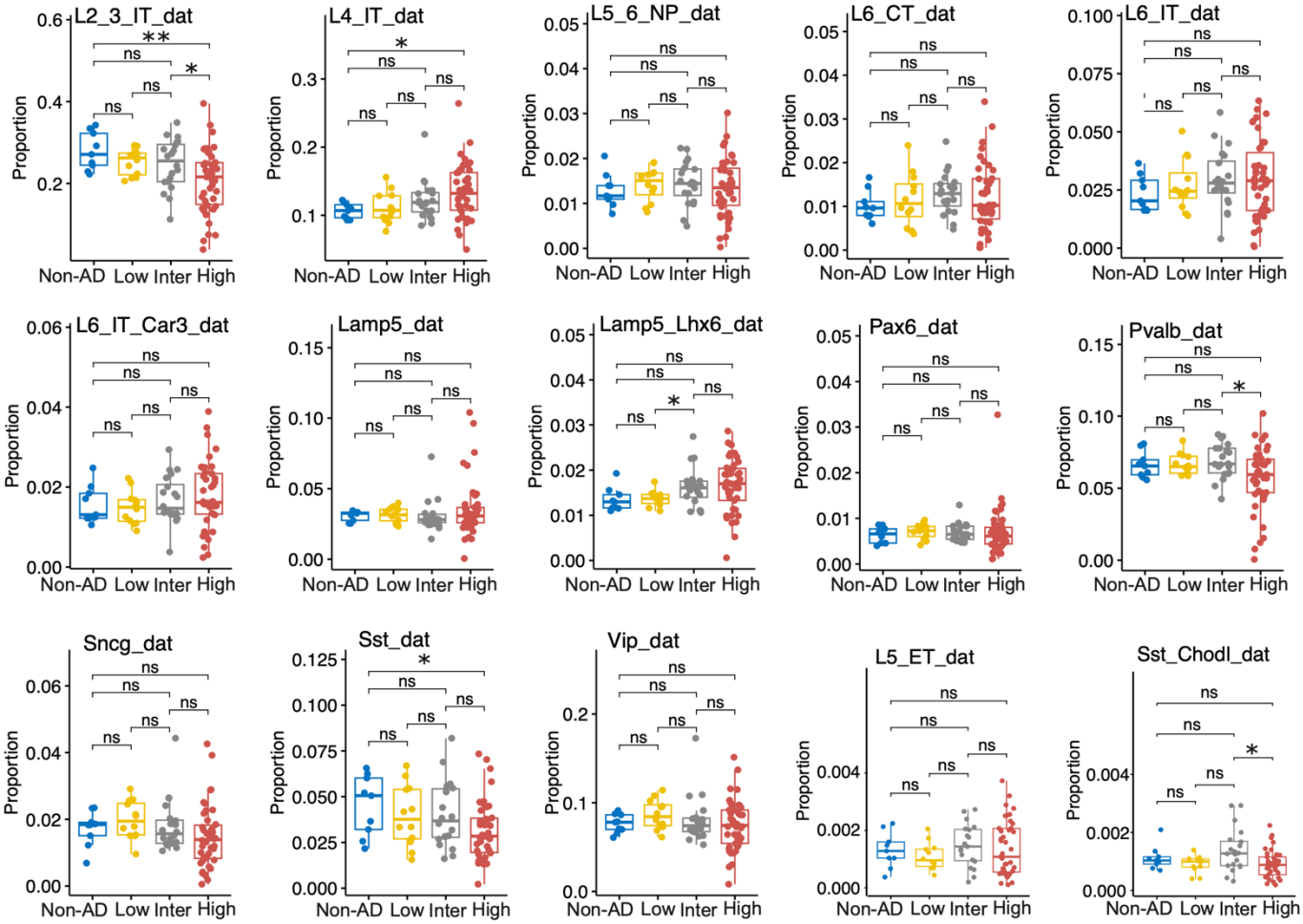

Fig.S3 Proportion of cell numbers for subtypes of neurons across the stages of AD progression. Statistical analysis was conducted using the Kruskal-wallis test. *: p-value < 0.05, **: p-value < 0.01, ns: no significant.

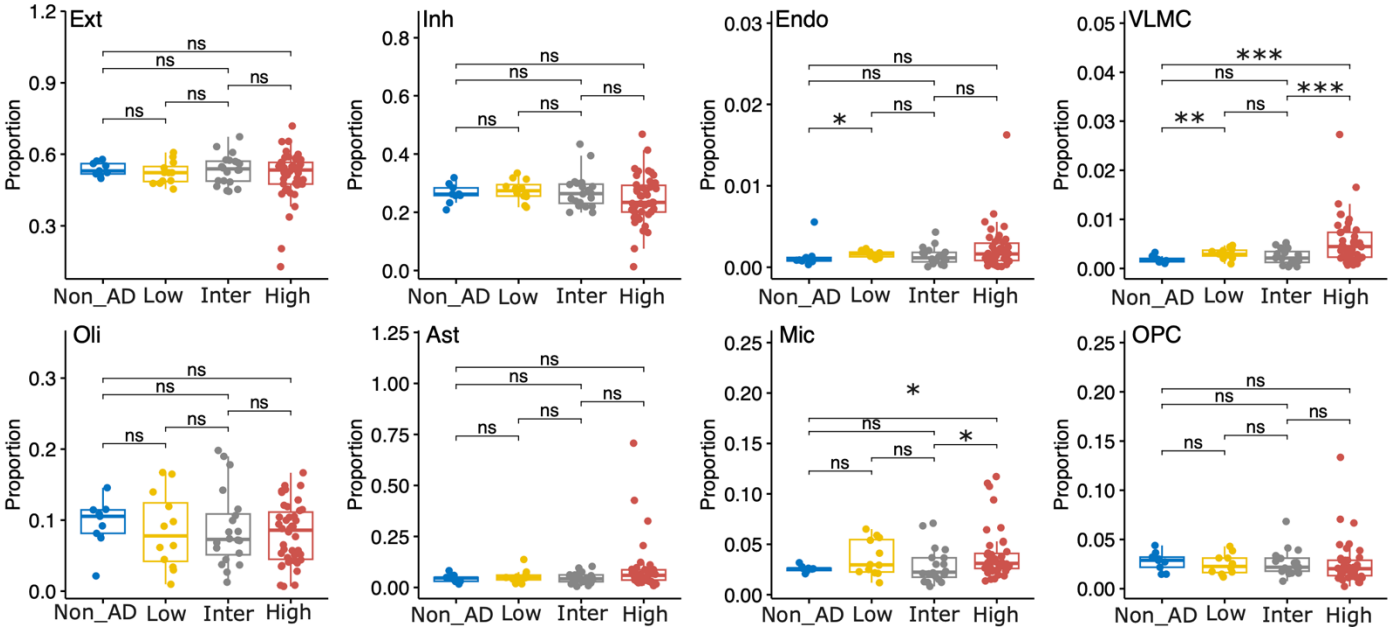

Fig.S4 Proportion of cell numbers for each major cell type across the stages of AD progression. Statistical analysis was conducted using the Kruskal-wallis test. *: p-value < 0.05, **: p-value < 0.01, ns: no significant.

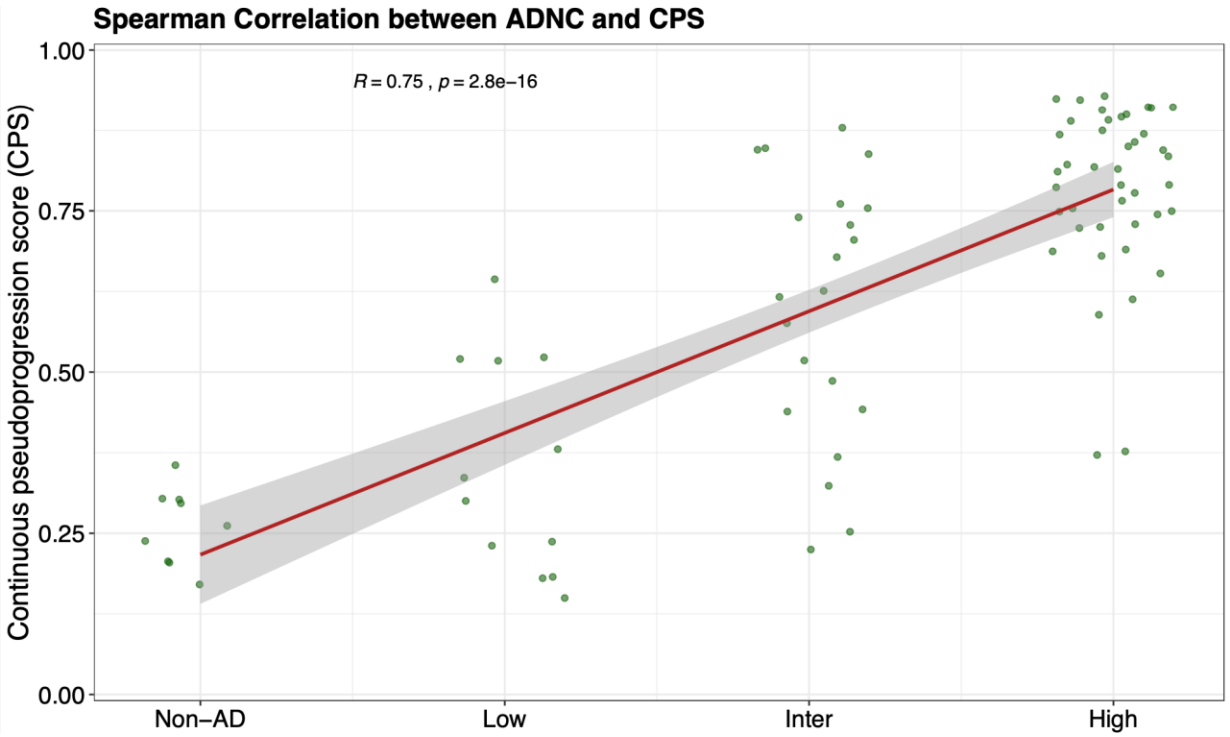

Fig.S5 Association between ADNC stage and continuous pseudoprogression score (CPS). Each point is a sample; the red line is the fitted trend with a 95% CI (shaded). ADNC stage shows a strong relationship with CPS (Spearman ρ = 0.75, p = 2.8×10^{-16}).

Fig.S6 GO function enrichment analysis of each cell for upregulated DEGs during Non-AD to Low ADNC stage.

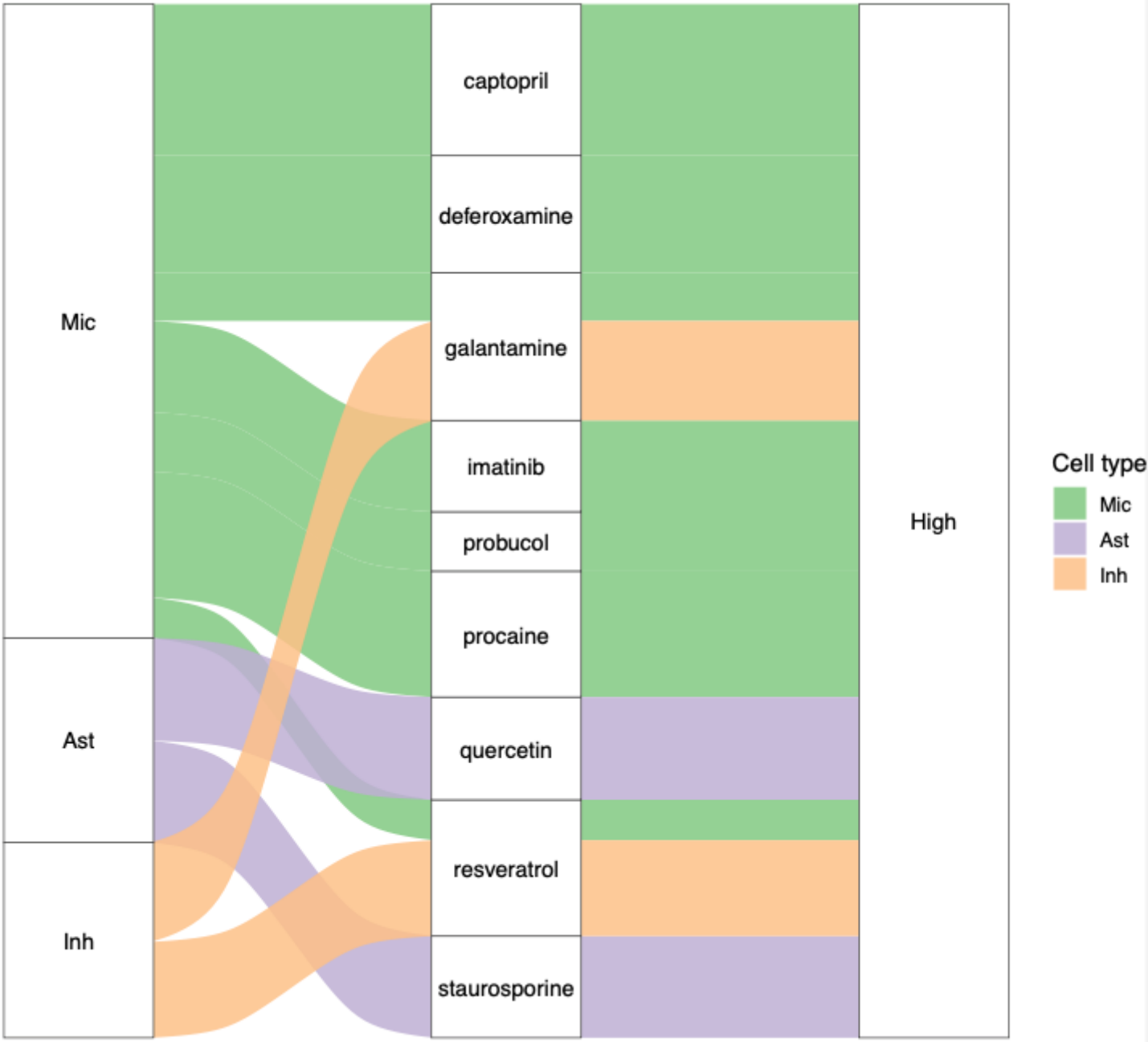

Fig.S7 Stage-specific mapping of candidate drugs across major brain cell types. Alluvial diagram showing the relationships between cell types (left), candidate drugs (middle), and disease stage (right).

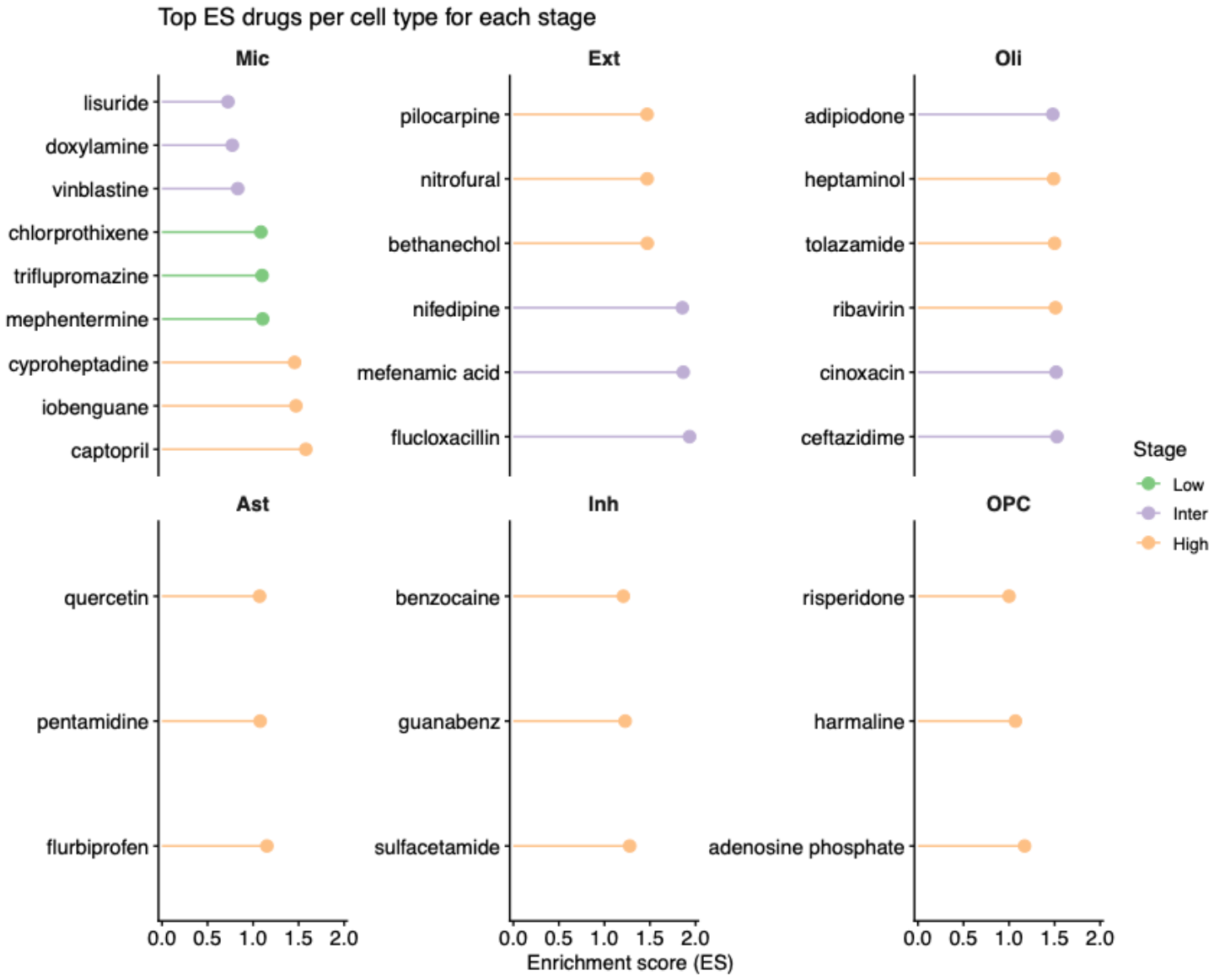

Fig.S8 Top enriched drug candidates across cell types and ADNC stages. Dot plots showing the top drug candidates ranked by enrichment score (ES) for each major brain cell type across ADNC stages