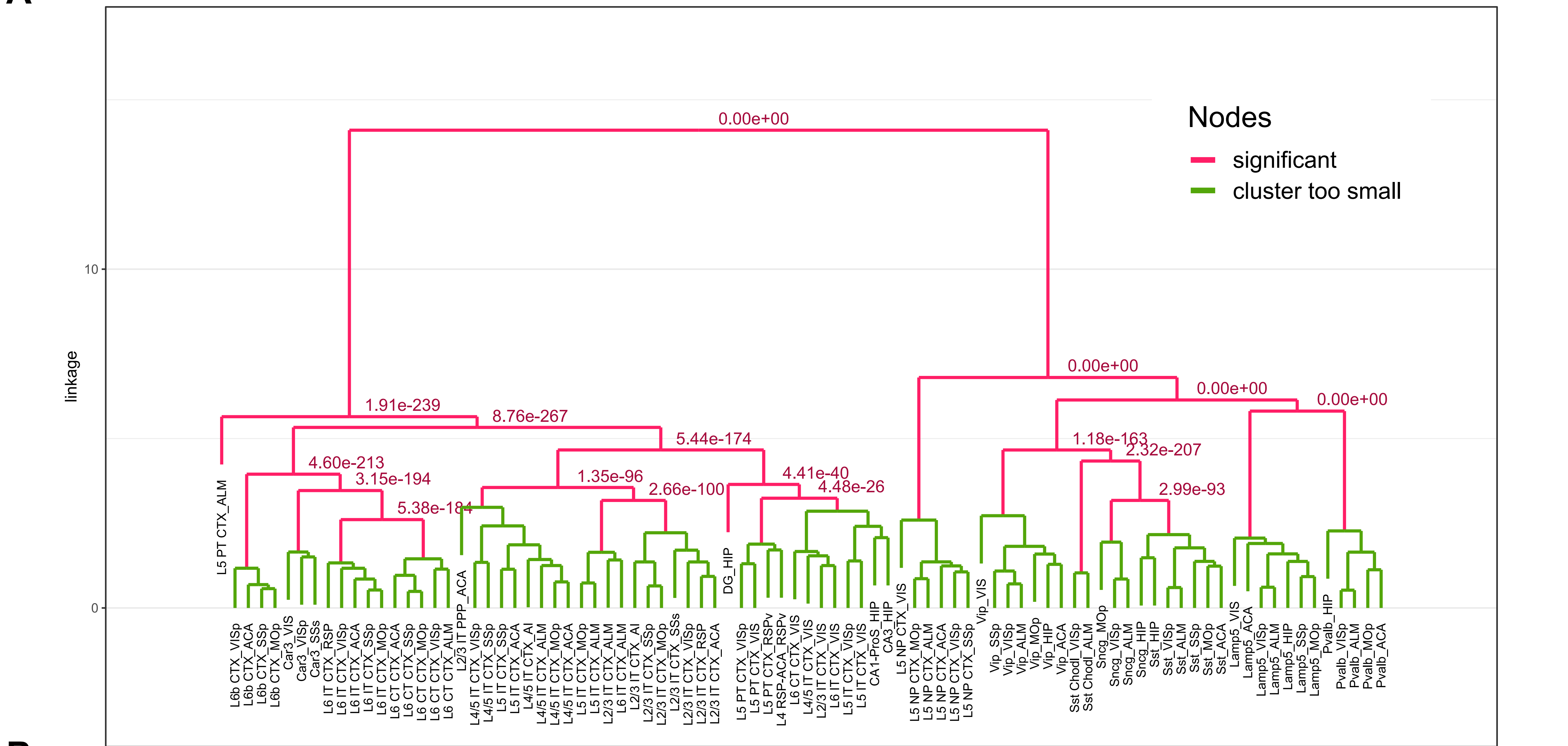


A showing all p-values below 0.05 cutoff (FWER corrected)



B

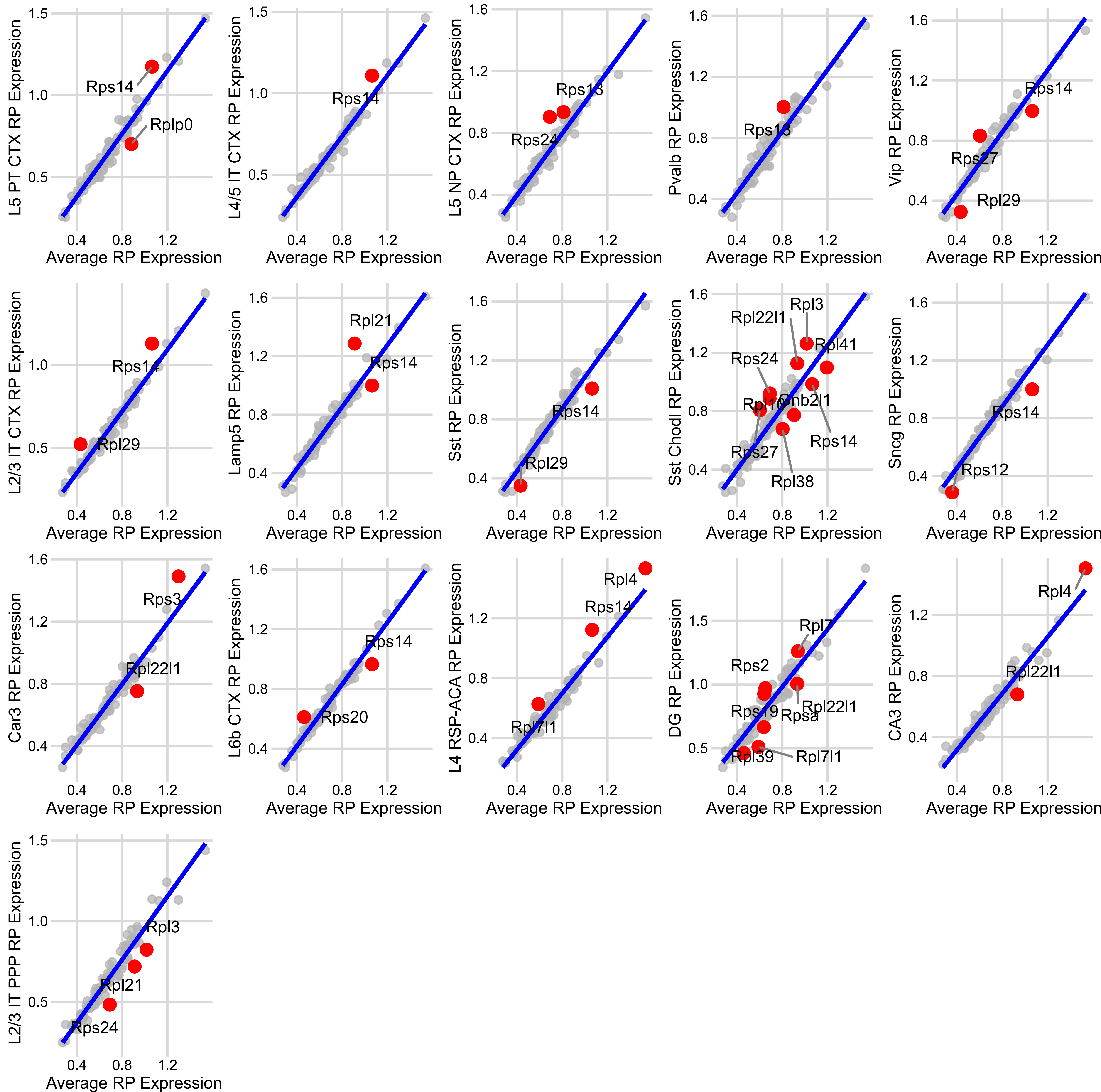


Figure S3. Neuronal subclasses show distinct and specific ribosomal protein (RP) expression profiles. (A) Hierarchical clustering of neuronal subclasses based on their mean RP expression profiles reveals significant subclass groupings. Node significance was calculated using sigclust2. (B) Identification of subclass-specific RP genes. Each scatter plot displays the mean expression of RP genes in a single subclass (y-axis) relative to the overall average expression (x-axis). Genes with subclass-specific expression, identified by a specificity score corresponding to a deviation of more than 2.5 standard deviations from the mean, are highlighted in red.