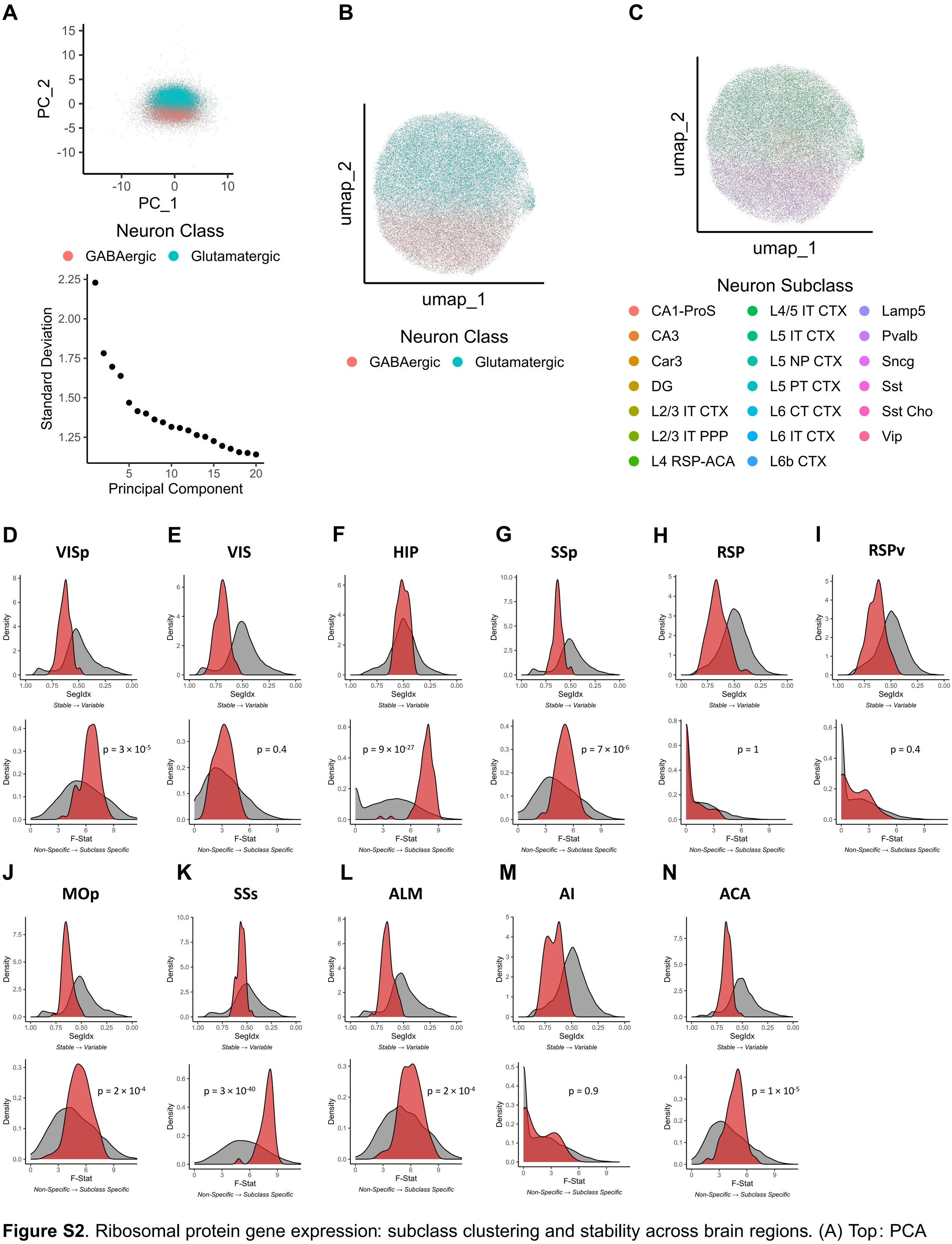

Figure S2. Ribosomal protein gene expression: subclass clustering and stability across brain regions. (A) Top: PCA performed based only on RP gene expression, coloring cells by cell class. Bottom: Elbow plot used to select the 8 most significant principal components from a PCA based on RP gene expression. (B, C) UMAP projection showing that clustering cells based only on RP genes can effectively separate them by neuronal class (B), but is insufficient to resolve finer neuronal subclasses (C). (D-N) Characterization of RP gene stability within individual brain regions. The two-plot layout is consistent for each region: the top row analyzes the expression stability index (SegIdx), showing its distribution; the bottom row analyzes the F-statistic, a measure of subclass-specific expression, showing its distribution along with the p-value from a Wilcoxon test assessing whether RP genes show significantly higher F-statistics than the global gene distribution. In all density plots, RP genes (red) are compared against the background of all detected genes (grey).