1		An Atlas of Cortical Arealization Identifies Dynamic Molecular Signatures
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Supplementary Table 2. Cluster markers for the final iteration of whole brain combined clustering analysis. Markers were calculated using the one-sided Wilcoxon rank sum test. Table shows gene name, p-value, average log2 fold change, the percentage of cells within the cluster expressing the gene (pct.1), the percentage of cells outside the cluster expressing the gene (pct.2), and adjusted p-value. Positive log-fold change values indicate that the feature is more highly expressed in the cluster of interest.

Supplementary Table 3. Region specific marker genes, including those at the cell type specific level. Markers were calculated using the one-sided Wilcoxon rank sum test. Table shows gene name, p-value, average log₂ fold change, the percentage of cells within the cluster expressing the gene (pct.1), the percentage of cells outside the cluster expressing the gene (pct.2), and adjusted p-value. Positive log-fold change values indicate that the feature is more highly expressed in the cluster of interest.

- **Supplementary Table 4.** Cell type specific differential expression across the neocortex, allocortex (hippocampus), and proneocortex (cingulate). Markers were calculated using the one-sided Wilcoxon rank sum test. Table shows gene name, p-value, average log₂ fold change, the percentage of cells within the cluster expressing the gene (pct.1), the percentage of cells outside the cluster expressing the gene (pct.2), and adjusted p-value. Positive log-fold change values indicate that the feature is more highly expressed in the cluster of interest.
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