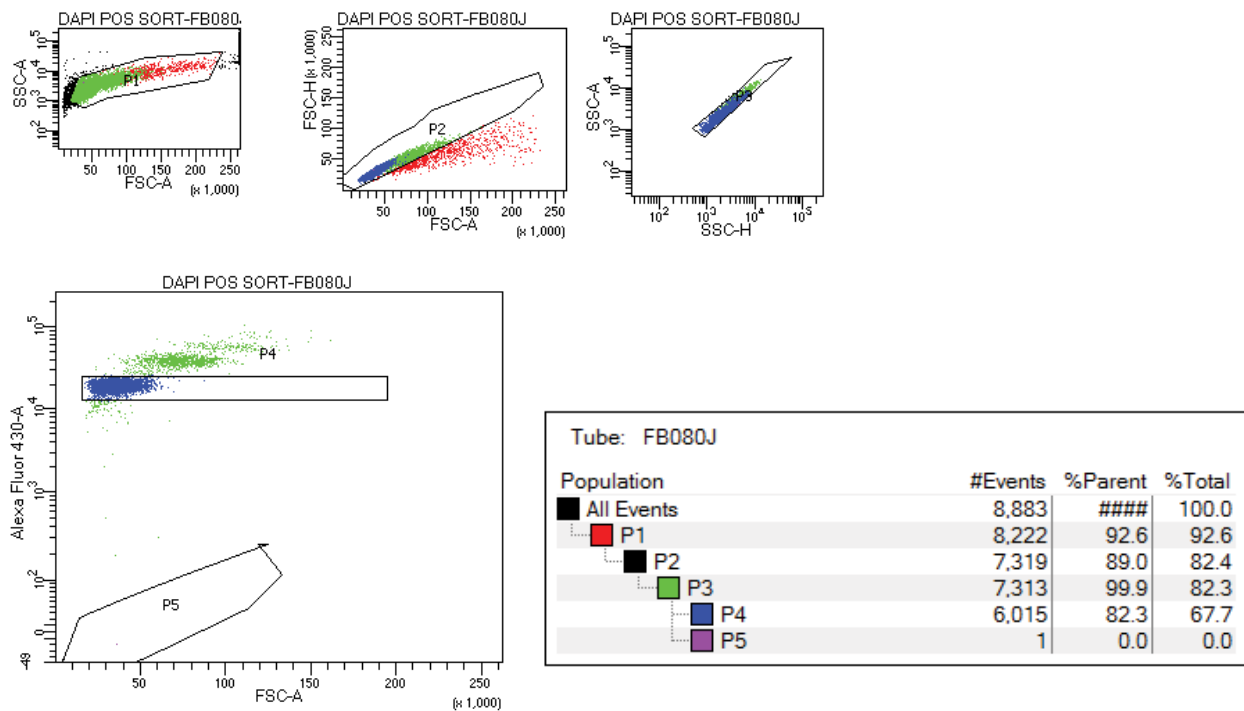

Supplementary information

**Spatial transcriptomics reveals human
cortical layer and area specification**

In the format provided by the
authors and unedited

Supplemental Figure



Supplemental Figure 1. Sorting strategies used for single nucleus used in snRNAseq.

Representative fluorescence-activated nuclear sorting (FANS) using Dapi to label 2N nuclei for separation from debris and multiplet nuclei. Gate P4 shows Dapi-positive 2N nuclei sequenced for this study.

Supplementary Table 1:

Glossary of acronyms.

Supplementary Table 2:

Meta information table for samples used in the study.

Supplementary Table 3:

MERFISH 300 gene panel list with annotation for selection criterion.

Supplementary Table 4:

Merscope encoding probe design for the 300 and 960 gene panels.

Supplementary Table 5:

Cluster annotations for integrated clustering.

Supplementary Table 6:

Differentially expressed genes between anteriorly and posteriorly enriched EN subtypes.

Supplementary Table 7:

Annotation for clustering by individual gestational age.

Supplementary Table 8:

MERFISH 960 gene panel used for additional experiments included in revision.

Supplementary Table 9:

Annotations for additional experiments clustered individually.

Supplementary Table 10:

Differentially expressed genes between V1 and V2 EN subtypes and their overlaps from MERFISH analysis.

Supplementary Table 11:

List of differentially expressed genes between V1 and V2 at different gestational ages.

Supplementary Table 12:

Connection fraction values in constellation plot.

Supplementary Table 13:

Differentially expressed genes between EN-IT-L4-V1 and EN-IT-UL-2 clusters from snRNAseq, used for GO analysis.