

Description of Additional Supplementary Files

Supplementary Data 1. Markers of CCS components from scRNA-seq data. Statistics were performed using the Wilcoxon rank sum test. Pct.1 refers to the percentage of cells expressing gene in the cluster of interest, and pct.2 refers to the that in the rest of the cells in the dataset.

Supplementary Data 2. Markers of CCS components from GeoMx Digital Profiler spatial transcriptomics data. Absolute fold change values calculated between the CCS component of interest and its non-CCS counterpart, as well as the rest of the CCS regions are shown. A two-tailed unpaired student t-test was performed for statistics.

Supplementary Data 3. Comparison between embryonic (E14.5) and early postnatal CCS profiles. Statistics were performed using the Wilcoxon rank sum test. Pct.1 refers to the percentage of cells expressing gene in the embryonic CCS component indicated in the title of each tab. Pct.2 refers to the postnatal counterpart. P_val_adj refers to the adjusted p-value based on the Bonferroni correction.

Supplementary Data 4. Regulon activity quantification in each CCS component. Averaged area under the curve (AUC) scores of activating regulons in each CCS component calculated by AUCell, performed by 'pySCENIC' (version 0.12.1).

Supplementary Data 5. Sequences of tdTomato and Cre used for alignment of reads in scRNA-seq.

Supplementary Data 6. Sequences of primers used for quantitative PCR in the study.