**Supplemental tables**

**Table S1 |** Subpopulation gene markers adult brain (GSE60361) dataset (Zeisel et al. 2015).

**Table S2 |** Gene marker list of subpopulations in the 1.3 million brain cells from E18 Mice (10x Genomics dataset).

**Table S3** | Overlaps between the cell type markers of the developmental pallium (10x Genomics) and the markers of the cell types of developmental midbrain. The ventral midbrain scRNA-seq dataset is similar in terms of development (pallium is E18, midbrain is from E12 to E18) and species (both are mouse) to the developmental pallium of the 10x Genomics. Still, the region is largely different as the pallium belongs to the forebrain, the rostral-most portion of the brain, whereas the midbrain belongs to the brainstem, the portion which connects the cerebrum with the spinal cord. Standard hypergeometric test with Bonferroni correction was used to detect significant overlaps, after determining a common background of 16,647 genes. Significant overlaps were found for the non-neuronal population, namely endothelial cells, microglia and pericytes, indicating highly conserved phenotypes for these cells types across brain regions. Significant overlaps were also found between forebrain and midbrain subtypes of radial glia. Further, the neuronal populations showed significant enrichments with some midbrain counterparts, namely gabaergic neurons or neuroblasts. However, the latter comparison is very approximate for two reasons i) the neuronal cells types can be very different in the two brain regions. For instance, Cajal-Retzius neurons (C14) do not exist in the midbrain. ii) Comparing general neuronal signature is not possible because the *BackSPIN* algorithm used for the midbrain analysis does not efficiently captures higher order signatures.

**Table S4** | The cell type markers of the mouse developmental pallium (10x Genomics) showed co-expression in the Allen Brain Atlas: Human Brain spatial transcriptomic dataset. An anatomically comprehensive atlas of the adult human brain transcriptome based on microarray profiling is available in (Hawrylycz et al. 2012). To detect genes specific to sub-areas of each brain region (myelencephalon (MY), mesencephalon (MES), pons, hippocampal formation (Hif), etc.) two alternative analysis were performed by Hawrylycz and coworkers: i) a differential expression ii) a 2D clustering (bi-clustering). We tested for significant overlaps between these Allen Brain Atlas gene sets and our gene sets of the developmental pallium (cell type markers) by standard hypergeometric test with Bonferroni correction. Species conversion for the genes was performed with NCBI’s homologene tool (https://www.ncbi.nlm.nih.gov/homologene) resulting in a common background of 13,648 genes. The upper (lower) part of the table reports the significant overlaps found using the first (second) analysis of Hawrylycz and coworkers. The majority of our genes sets shows significant overlaps with one or more Allen Brain Atlas spatial gene sets, which is a remarkable result considering we are comparing two different species (human, mouse) in two entirely different developmental stages (embryonic, adult). The presence of overlaps indicates that core networks of co-expressed genes remain highly conserved throughout development and specie. For instance, the strongest overlap (p<5.4-34) was found between the Radial Glia 3 markers (C11) and the Allen Brain Atlas gene set Myelencephalon 7 (MY\_7). The overlap consists of a conserved module of 104 genes which is functionally related to cilia morphogenesis (GO p<2.4-5). Interestingly, cilia are thought to play a guiding role in the establishment of apical-basal polarity of the radial glial scaffold.

**Table S5 |** Markers list of the Cajal-Retzius subpopulations.