Supplemental Information

Table S1. Differential gene expression analysis comparing each of the 15 clusters to all other 14 clusters, Related to Figure 1.

Table S2. Differentially gene expression analysis comparing P60 IEG+ microglia to P60 homeostatic microglia, Related to Figure 3.

Table S3. Differentially gene expression analysis for bulk RNA-seq and scRNA-seq comparing microglia from each brain region to microglia from all other regions, Related to Figure 3.

Table S4. Cell cycle phase-specific genes identified by pseudotime analysis of dividing microglia, Related to Figure 4.

Table S5. Differentially gene expression analysis comparing P7 microglia clusters, Related to Figure 5 and Figure 6.

Table S6. Gene ontology analysis for enriched biological process and cellular component terms in early postnatal PAM relative to P7-C0 immature microglia, Related to Figure 8.

Table S7. Manually curated genes that were enriched in early postnatal PAM and involved in energy metabolism, lysosomal functions and lipid metabolism/transport, Related to Figure 8.

Movie S1. 63X confocal stack showing CLEC7a$^+$(red) CX3CR1-GFP$^+$ microglia in the P7 cerebellum engulfing other nuclei (see also Figure 8A for a presentative single plane, and Figure 8B for 3D reconstruction of a typical microglia phagocytosing a pyknotic nucleus), Related to Figure 8.

Movie S2. 3D reconstruction of early postnatal PAM (CX3CR1-GFP$^+$) engulfing cCASP3$^+$MBP$^+$ oligodendrocytes in the P7 white matter, Related to Figure 8.