

Description of Additional Supplementary Files

Supplementary Data 1: List of differentially-expressed genes between IAMs (cluster 10) and non-IAM microglia clusters. Genes are listed with the mean expression value for each population, the fold change and *P*-value. Statistical analysis was performed using default settings within the DESeq2 pipeline in Partek Flow, which uses the Wald test with FDR multiple correction.

Supplementary Data 2: List of cell-cycle genes present in the sequencing dataset, their classification for cell-cycle stage and whether reads for indicated gene were detected in IAMs population (cluster 10).