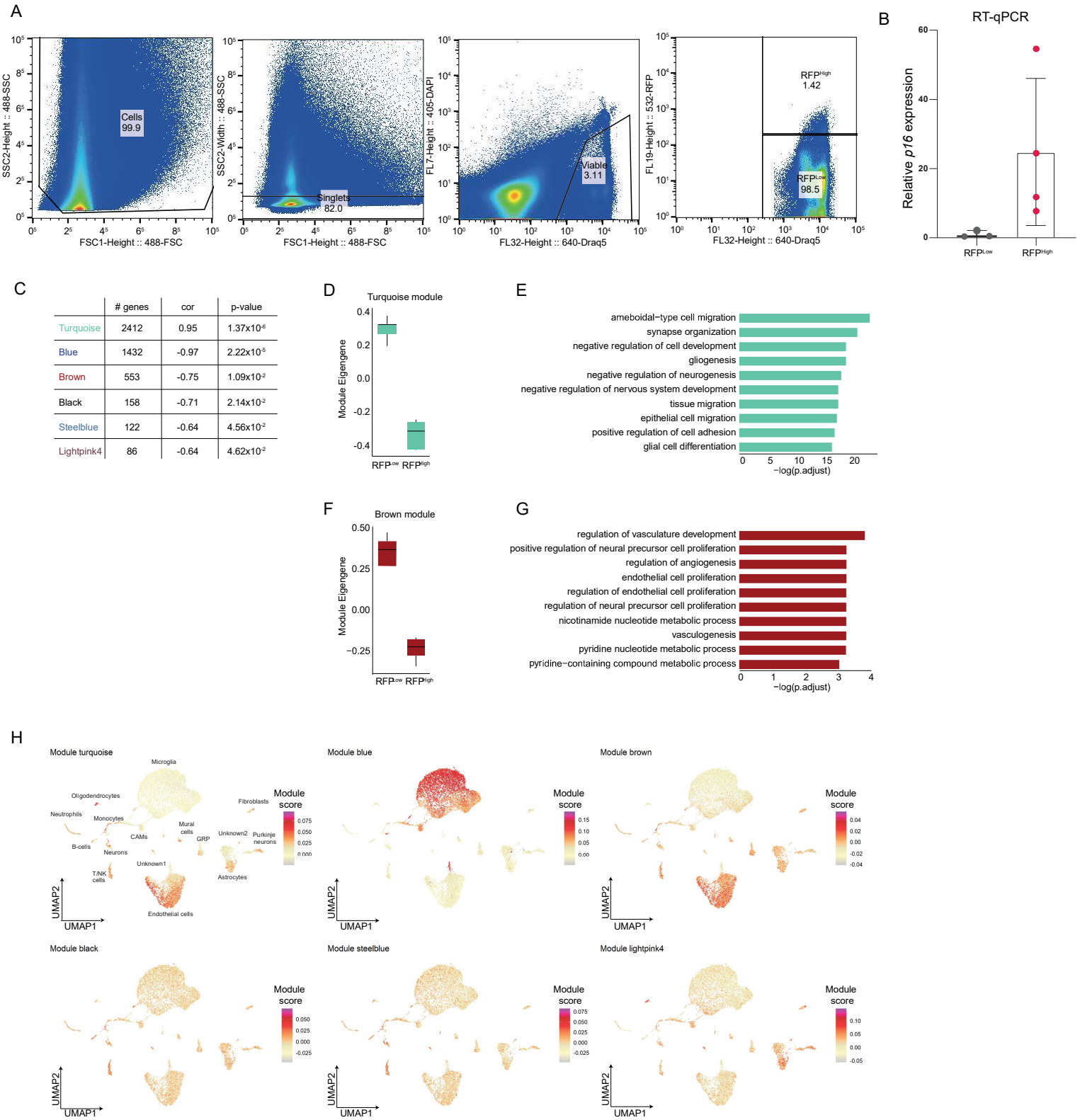

Figure S1: WGCNA module expression between cell types.

A: Gating strategy for sorting RFP^{High}cells by FACS. B: p16 expression measured by qPCR in old mouse brains. C: List of significant weighted gene correlation network analysis (WGCNA) modules between RFP^{Low} and RFP^{High} samples. D-G: ModuleEigengene expression levels and gene ontology analysis of WGCNA modules enriched in RFP^{Low} samples. H: UMAPs depicting the expression of WGCNA modules in all isolated cell types in single cell data set.

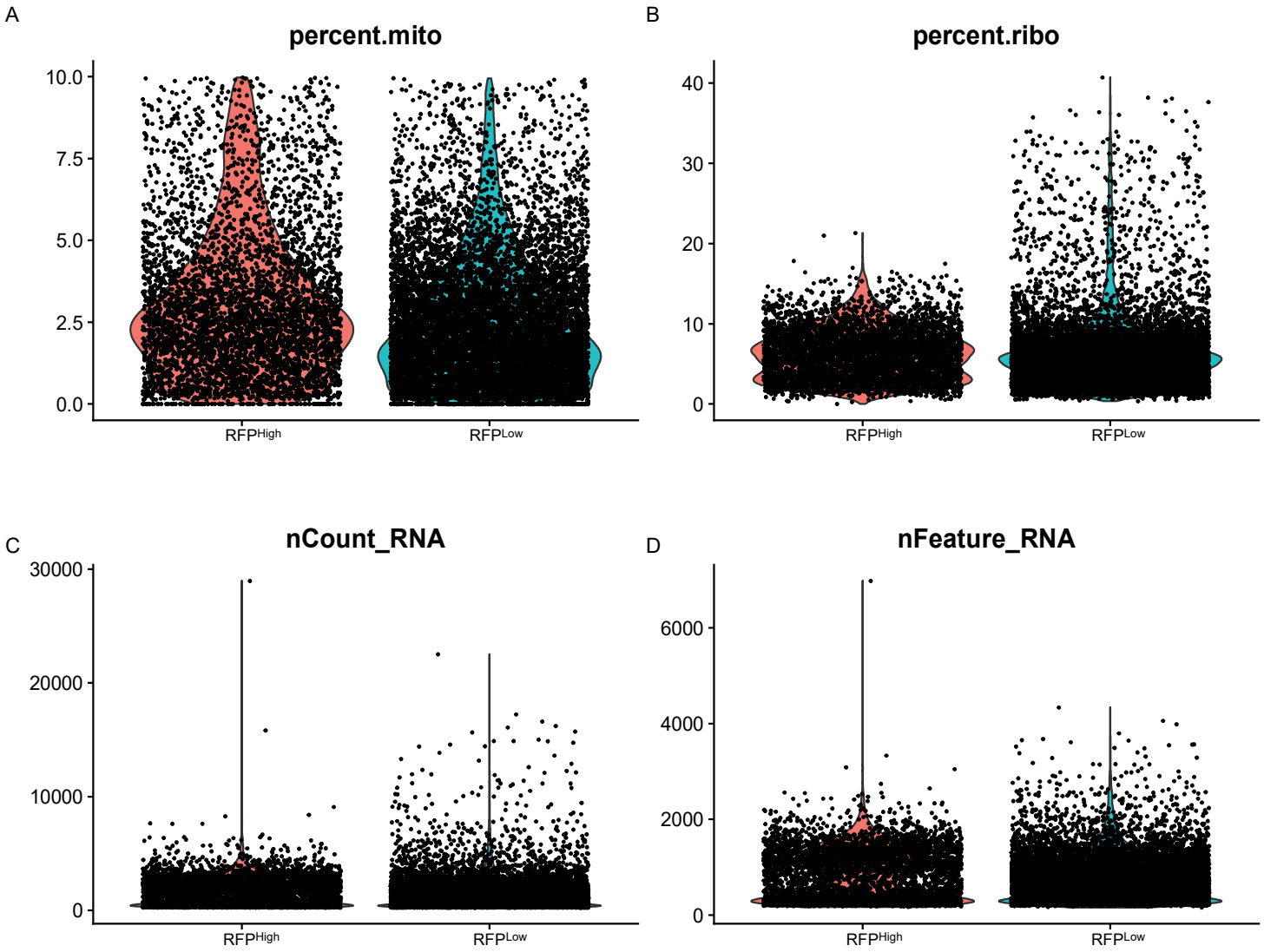

Figure S2: Quality control of scRNAseq

A: Percentage mitochondrial RNA, B: percentage ribosomal RNA, C: read counts and D: number of unique genes detected in RFP^{Low} and RFP^{High}samples.

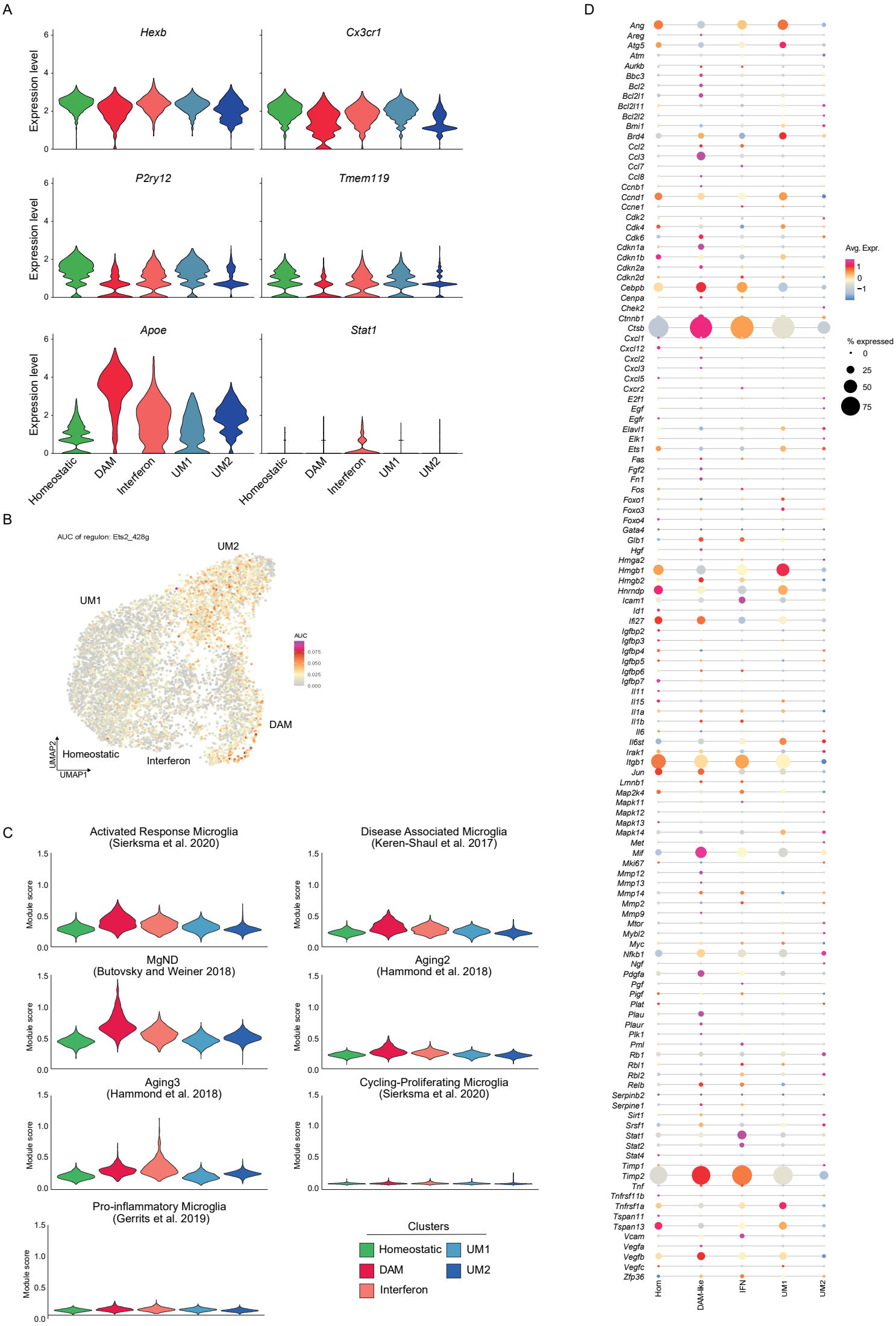
A
Hexb
Cx3cr1
P2ry12
Tmem119
Apoe
Stat1
Expression level
Homeostatic
DAM
Interferon
UM1
UM2
B
AUC of regulon: Ets2_428g
AUC
UMAP1
UMAP2
C
Activated Response Microglia (Sierksma et al. 2020)
Disease Associated Microglia (Keren-Shaul et al. 2017)
MgND (Butovsky and Weiner 2018)
Aging2 (Hammond et al. 2018)
Aging3 (Hammond et al. 2018)
Cycling-Proliferating Microglia (Sierksma et al. 2020)
Pro-inflammatory Microglia (Gerrits et al. 2019)
Module score
Clusters
D
Avg. Expr.
% expressed
Hom
DAM-like
IFN
UM1
UM2

Figure S3: Microglia clusters in literatue do not resemble p16^{pos} microglia.

A: Violin plot depicting the expression of Hexb, Cxcr1, P2ry12,Tmem119, Apoe and Stat1 respectively in each cell of the microglia cluster. B: UMAP depicting Ets2 regulon expression in all microglia. C: Violin plots showing the expression of subtype signatures from the literature in each cluster. D:Dot plot showing expression of senescence genes in microglia clusters.