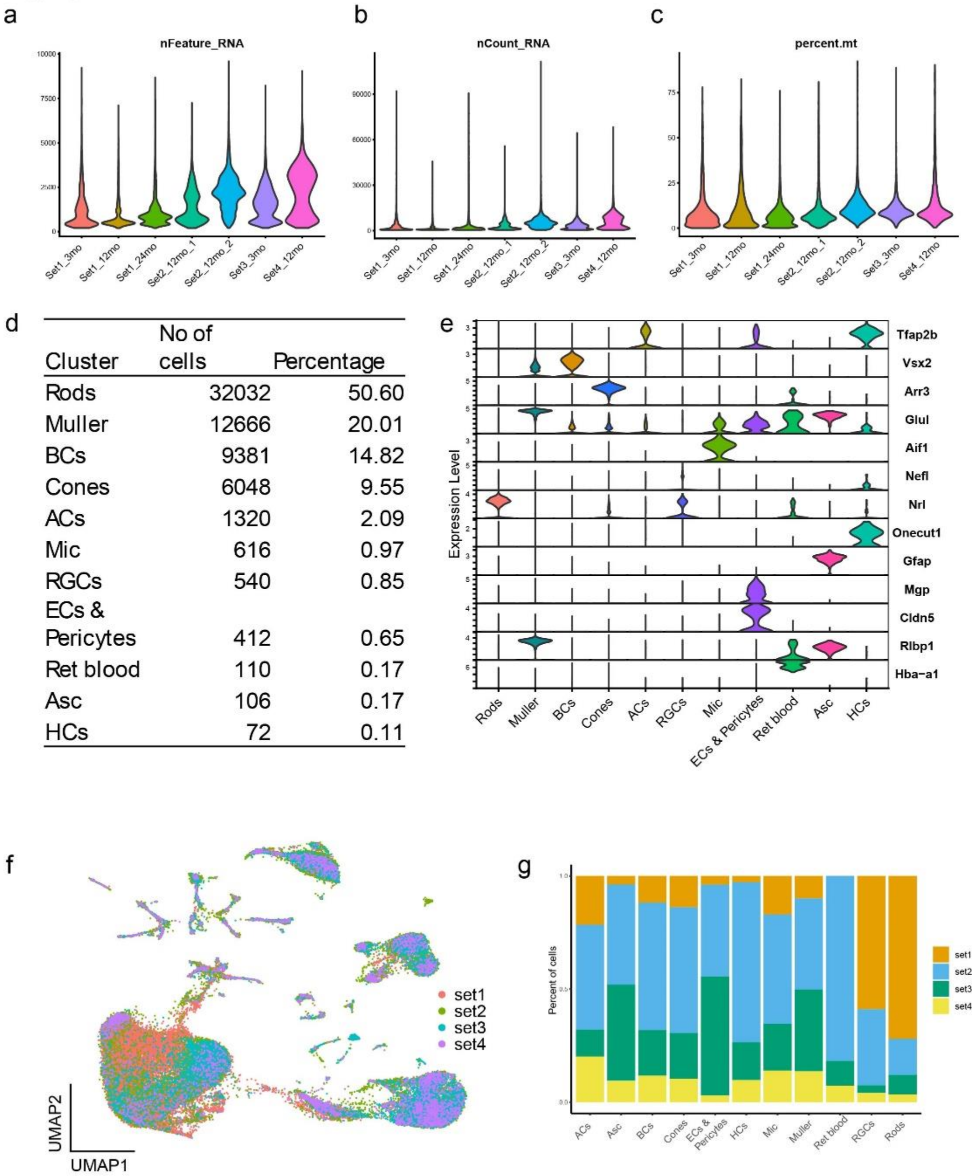
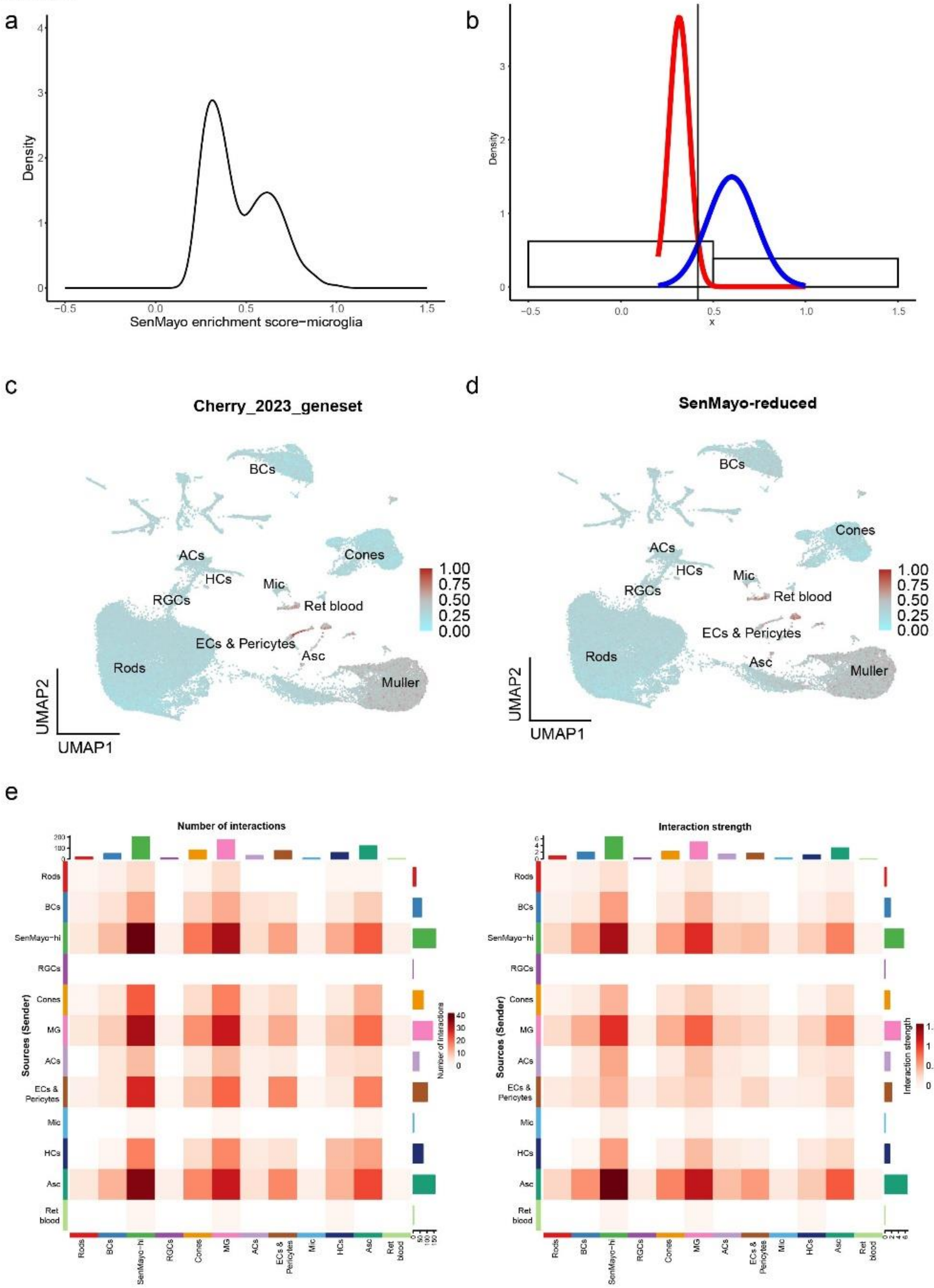
Supp fig 1



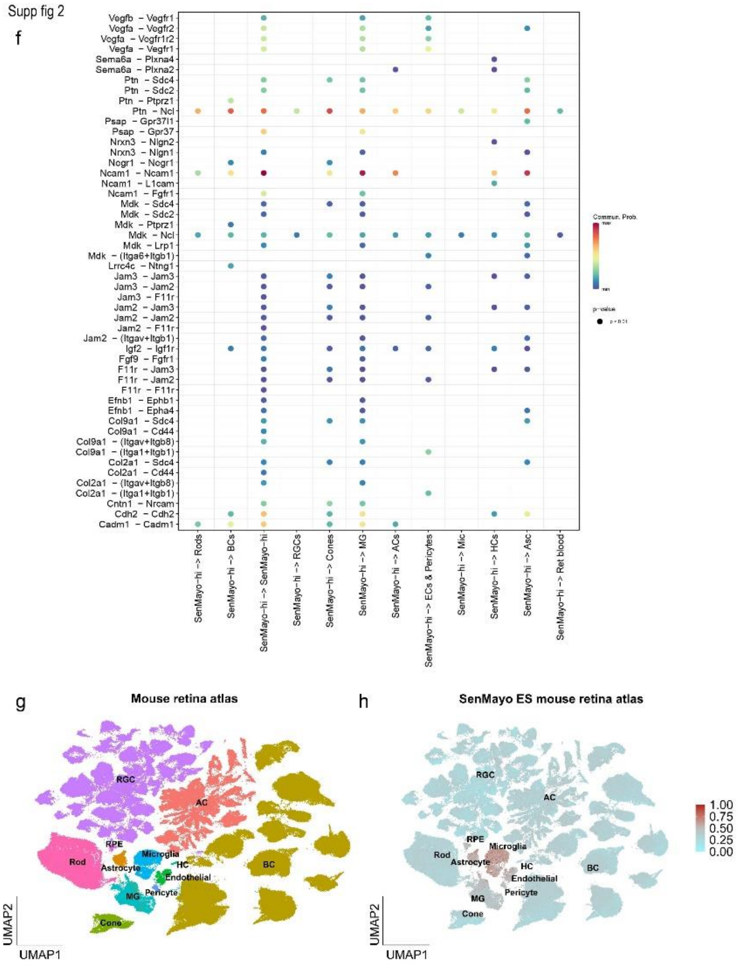
Cluster	No of cells	Percentage
Rods	32032	50.60
Muller	12666	20.01
BCs	9381	14.82
Cones	6048	9.55
ACs	1320	2.09
Mic	616	0.97
RGCs	540	0.85
ECs & Pericytes	412	0.65
Ret blood	110	0.17
Asc	106	0.17
HCs	72	0.11

Supplementary fig 1: **Quality control data for mouse retinal scRNA dataset:** (a-c) Violin plots depicting (a) genes, (b) Unique molecular identifiers (UMIs) and (c) percentage of mitochondrial genes detected per cell per sample in the mouse retinal dataset. (d) Table depicting number of cells detected per cell type. (e) Violin plots depicting marker gene expression of the different cell type detected. As commonly known, Rod gene contamination is often observed in retinal datasets (ref 105). (f) UMAP plot depicting the sample collection set wise distribution of the cells. (g) Proportion plot depicting the contribution of the different sets to various cell types.

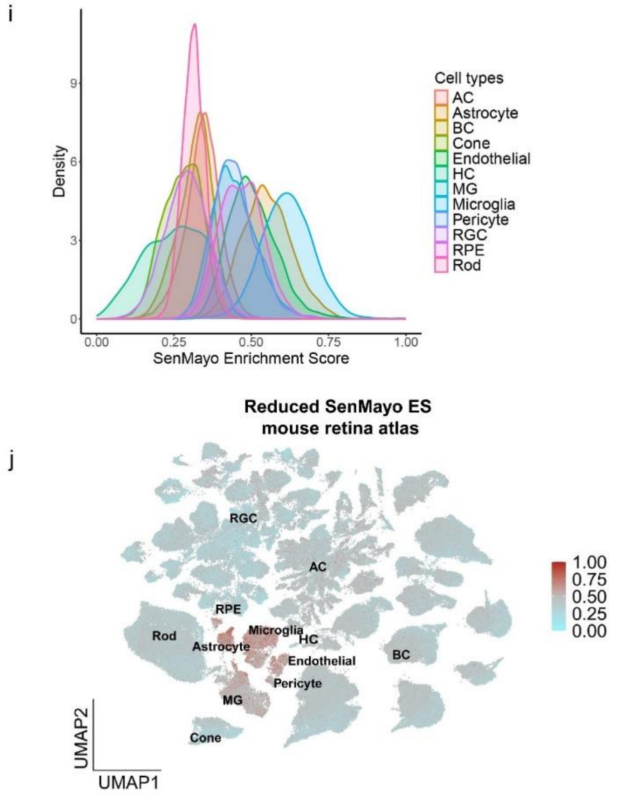
Supp fig 2


a
Density
SenMayo enrichment score−microglia
b
Density
x
c
Cherry_2023_geneset
BCs
ACs
HCs
RGCs
Mic
Cones
Ret blood
ECs & Pericytes
Asc
Rods
Muller
UMAP2
UMAP1
1.00
0.75
0.50
0.25
0.00
d
SenMayo-reduced
BCs
Cones
ACs
HCs
RGCs
Mic
Ret blood
ECs & Pericytes
Asc
Rods
Muller
UMAP2
UMAP1
e
Number of interactions
Interaction strength
Sources (Sender)
Rods
BCs
SenMayo−hi
RGCs
Cones
MG
ACs
ECs & Pericytes
Mic
HCs
Asc
Ret blood
Number of interactions
Interaction strength

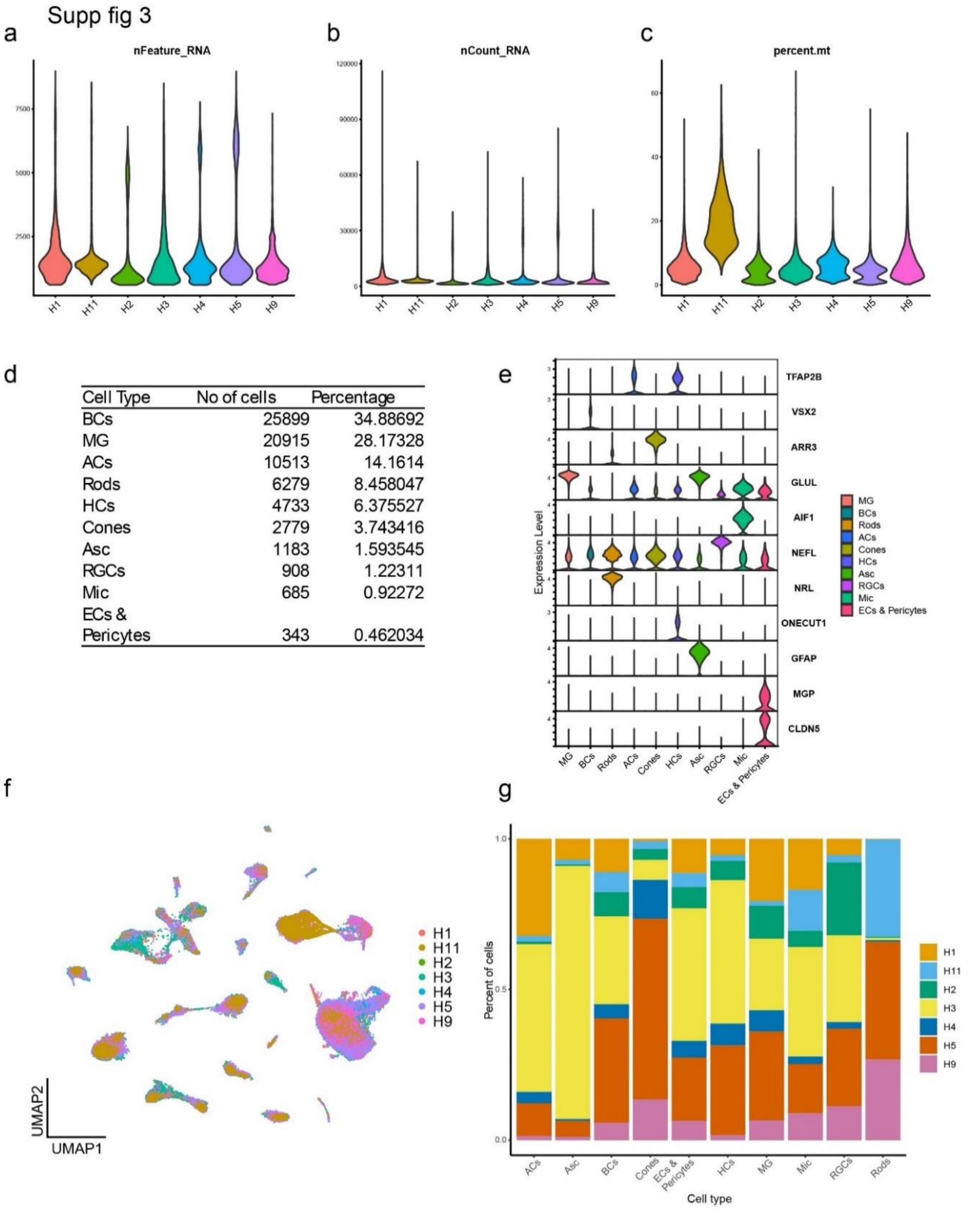
Supp fig 2



Supp fig 2



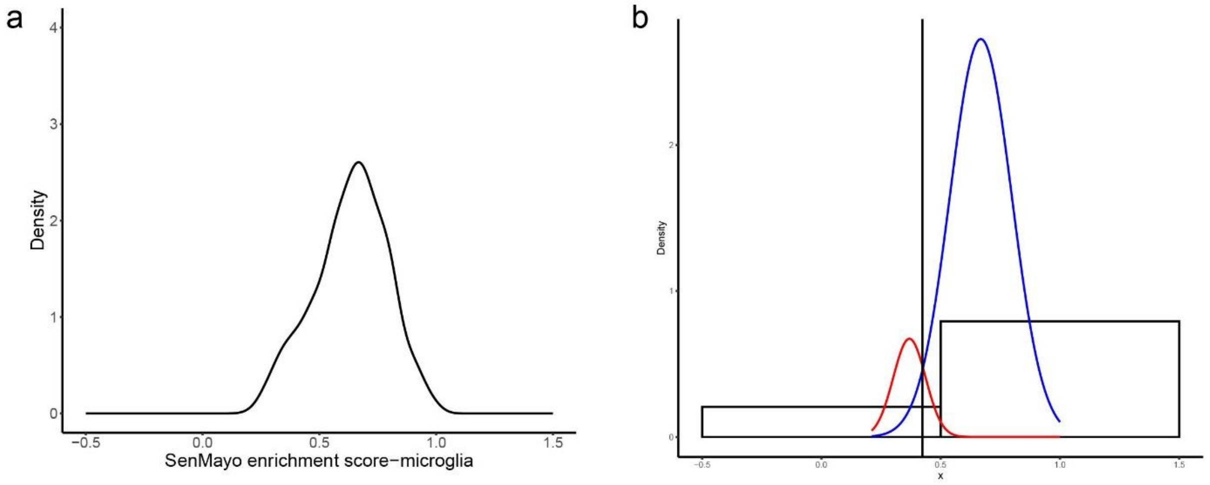
Supplementary fig 2: Method of determining SenMayo-hi cells in the mouse retinal dataset: (a) The microglia (Mic) subcluster which scored highest for SenMayo enrichment was used to set the threshold for SenMayo-hi cells. Distribution of the SenMayo panel enrichment scores were observed to be bimodal. (b) The mixtools package uses a Gaussian mixture model to cluster the data. The intersection point of the two clusters was set as the threshold and cells that scored higher were labelled SenMayo-hi and those that scored lower were labelled SenMayo-low cells. (c)Using another published panel of senescence related genes (Cherry_2023), once again Mic, Asc and MG were the cell types that scored high for this independent panel as observed in the UMAP. (d) To ensure the microglial genes in the SenMayo panel did not skew the analysis, we removed microglial marker genes using the Hu_Fetal_Retinal_Microglia geneset from MSigDB and ran an enrichment analysis using the SenMayo reduced gene panel. Once again Mic, Asc and MG scored high. (e) Heatmaps depicting the number (left) and strength (right) of interactions between SenMayo-hi cells and other cells in the mouse retina. (f) Bubble plot depicting significant pathways of interactions from SenMayo-hi cells to other retinal cells. (g) UMAP depicting the mouse retinal atlas from the Chen lab[117]. (h) UMAP depicting the SenMayo enrichment scores in the mouse retina atlas showed that glial cells scored high in this independent mouse retinal dataset. (i) SenMayo enrichment score (ES) distribution in the mouse retinal atlas by cell type. (j) SenMayo reduced panel enrichment analysis using the mouse retina atlas once again showed that the glial cells were the highest scorers.



Cell Type	No of cells	Percentage
BCs	25899	34.88692
MG	20915	28.17328
ACs	10513	14.1614
Rods	6279	8.458047
HCs	4733	6.375527
Cones	2779	3.743416
Asc	1183	1.593545
RGCs	908	1.22311
Mic	685	0.92272
ECs & Pericytes	343	0.462034

Supplementary fig 3: QC data for human retinal scRNA dataset: (a-c) Violin plots depicting (a) genes, (b) Unique molecular identifiers (UMIs) and (c) percentage of mitochondrial genes detected per cell per sample in the human retinal dataset. (d) Table depicting number of cells detected per cell type. (e) Violin plots depicting marker gene expression of the different cell type detected. (f) UMAP plot depicting the sample wise distribution of the cells detected following Seurat integration. (g) Proportion plot depicting the contribution of the different samples to various cell types. Note that this distribution is not even due to the fact that different samples were taken from different parts of the retina with varying cell type distribution.

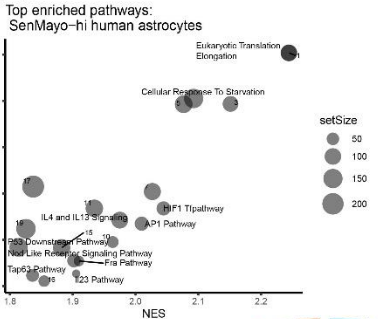
Supp fig 4



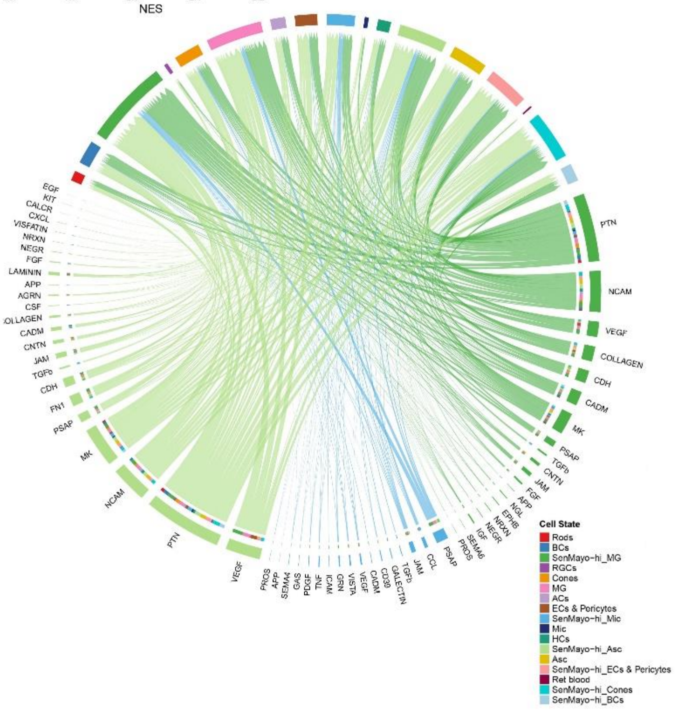
Supplementary fig 4: Method of determining SenMayo-hi cells in the human retinal dataset: (a) Microglia (Mic) subcluster which scored highest for SenMayo enrichment was used to set the threshold for SenMayo-hi cells. (b) The R package mixtools was used to set the threshold and cells that scored higher were labelled SenMayo-hi and those that scored lower were labelled SenMayo-low cells.

Supp fig 5

a

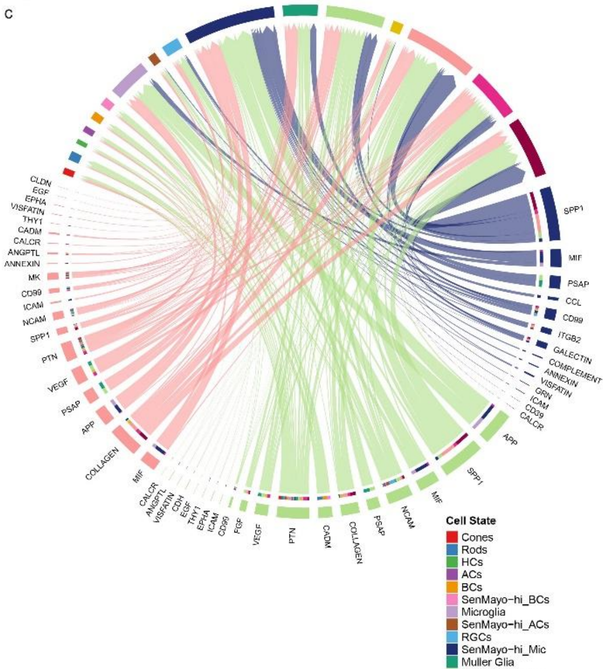


b

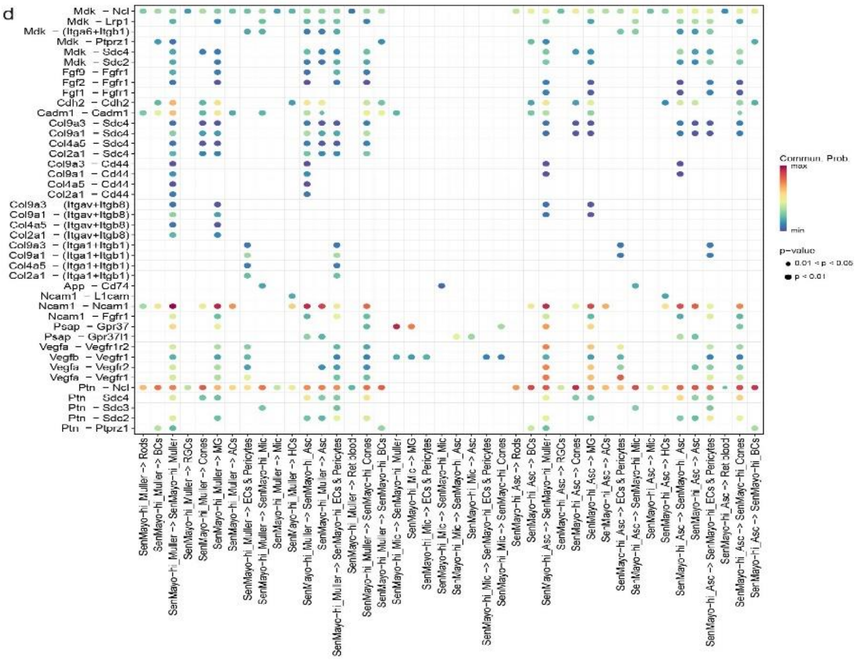


Supp fig 5

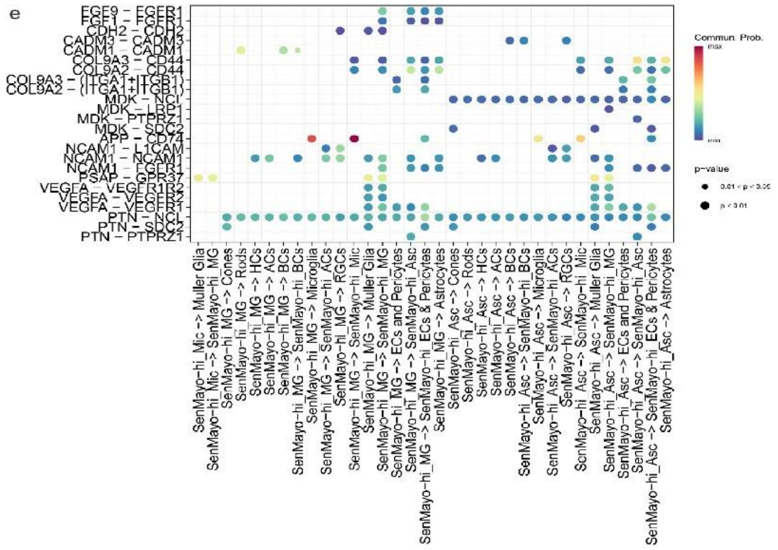
c



Supp fig 5

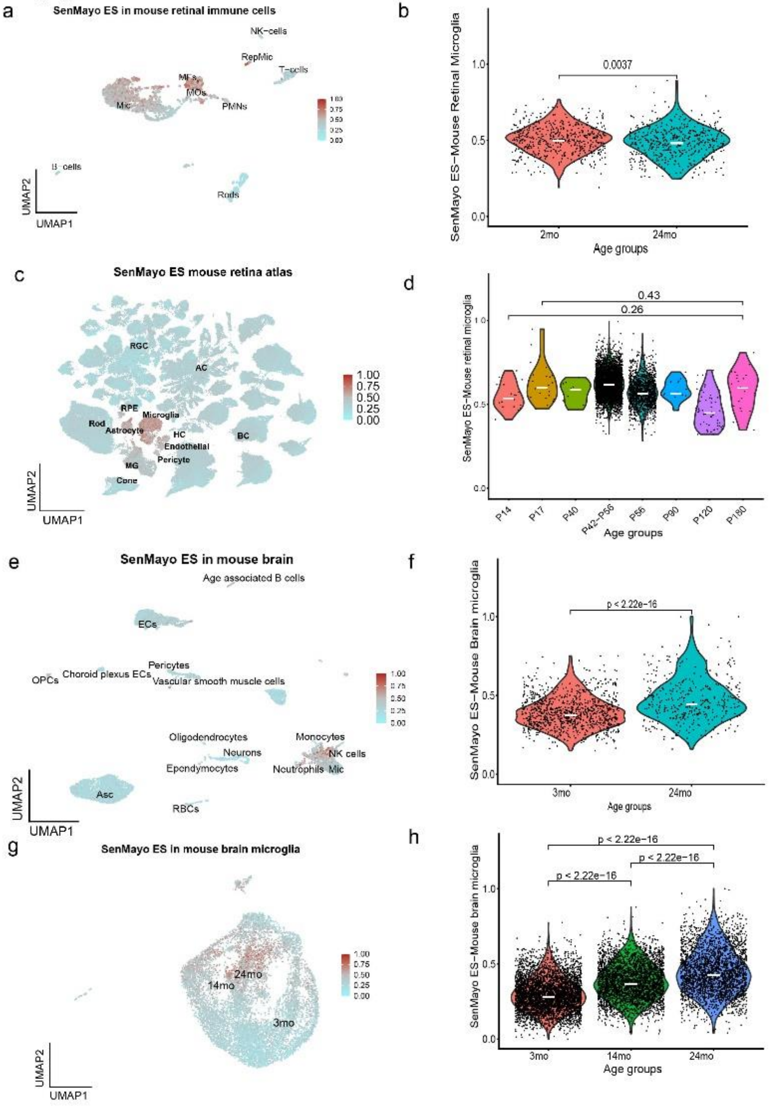


Supp fig 5

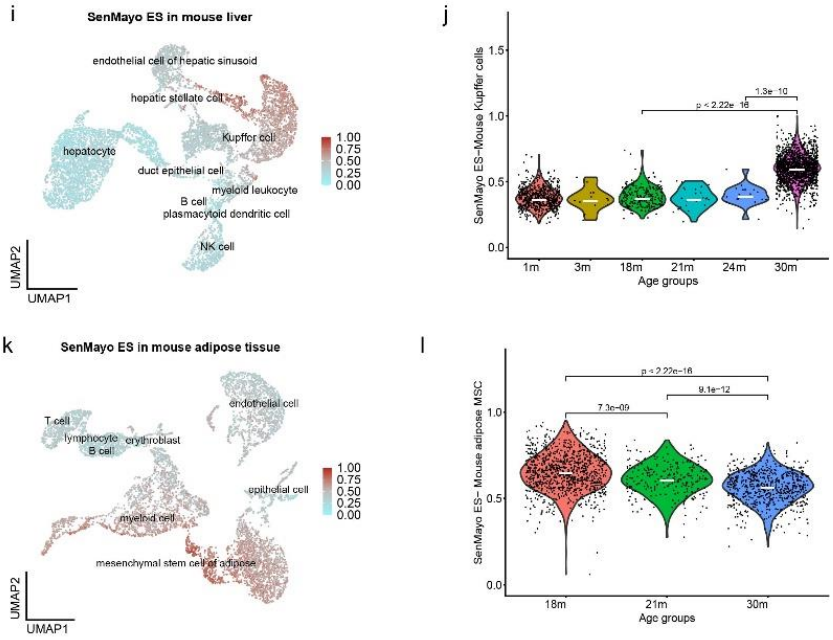


Supplementary fig 5: Comparison of mouse and human SenMayo-hi glial cells: (a) Dotplot of the enriched pathways identified in SenMayo-hi human astrocytes (FDR < 0.01). See Supp table 7c for full list. (b, c) Pathway analysis indicates that PTN, NCAM, VEGF, PSAP, APP, COLLAGEN are among pathways of interaction from SenMayo-hi cells to other retina cells that are conserved in human (c) and mouse (b) retina. (d, e) L-R (Ligand-Receptor) interactions depicting these pathways from SenMayo-hi cells to other retinal cell types in (d) mouse and (e) human datasets.

Supp fig 6



Supp fig 6

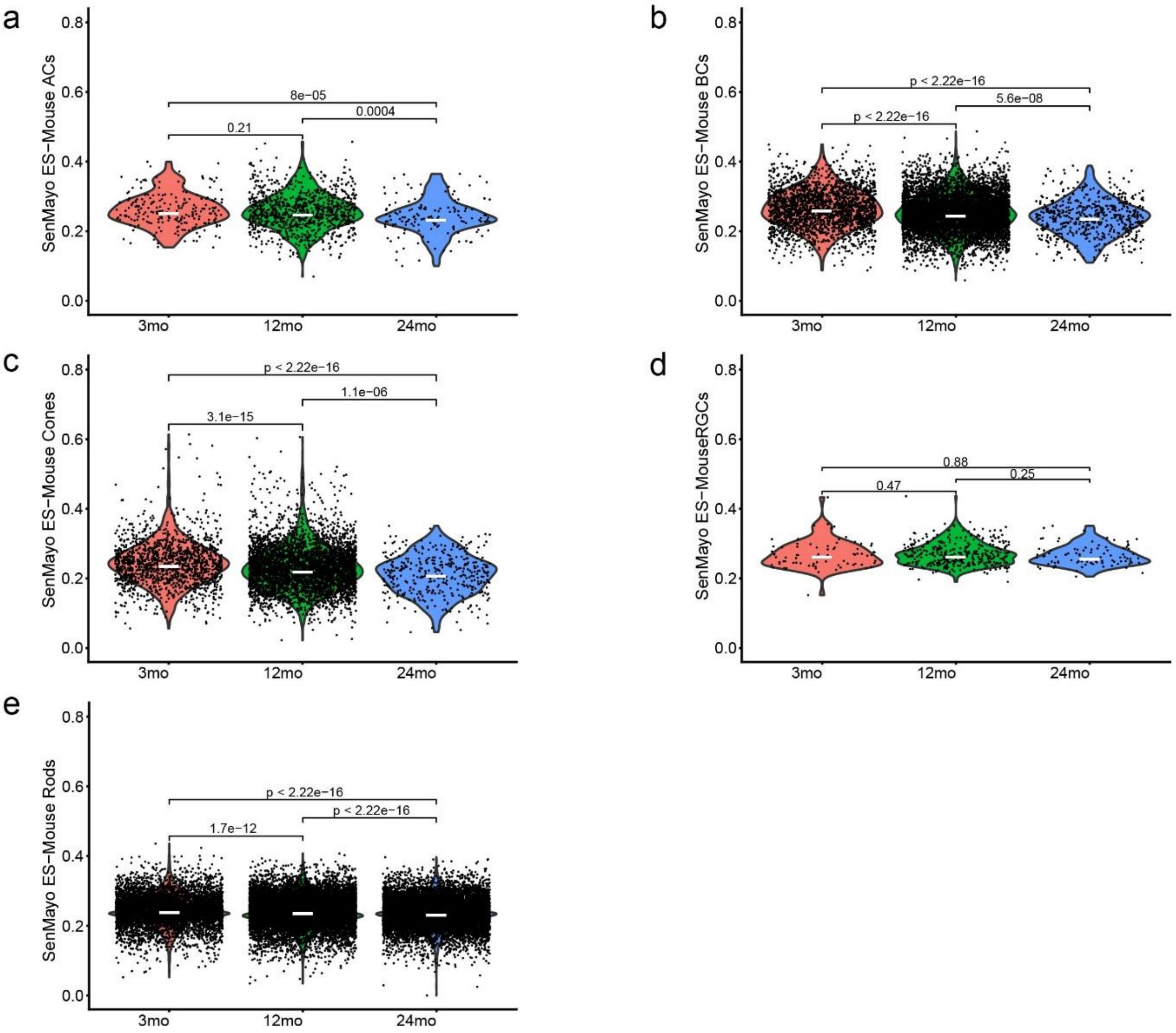


Supplementary fig 6 : SenMayo panel enrichment with age in retinal and non-retinal tissues: (a) UMAP plot of mouse retinal immune cells (GSE: GSE195891) from the Saban lab[116] showing SenMayo enrichment scores and microglia are among the highest scorers. (b) No trend of SenMayo score with age is observed in retinal microglia, as observed in our dataset.

(c) UMAP plot of the mouse retinal atlas from the Chen lab[117] showing SenMayo enrichment scores where glial cells are among the top scorers. (d) Once again, no trend of SenMayo scores with age is observed in mouse retinal microglia. (e) UMAP plot of mouse brain samples (GEO: GSE208292) from the Peng[119] lab, showing SenMayo enrichment scores (ES) and microglia are among the highest scoring cell types. (f)Increased expression of SenMayo score with age in brain microglia (2-mo vs 24-mo) (g) UMAP plot depicting ageing mouse brain microglia samples (GEO:GSE207932) from the Peng[119] lab, showing SenMayo enrichment scores (h) Increased expression of SenMayo scores with age is observed in this independent ageing series (3-, 14-, 24-mo) of mouse brain microglia. (i)UMAP plot of mouse liver[118] showing SenMayo enrichment scores with Kupffer cells scoring highest. (j) Increased SenMayo scores with age in mouse Kupffer cells with age, with the significant increase in scores from 24mo to 30mo.

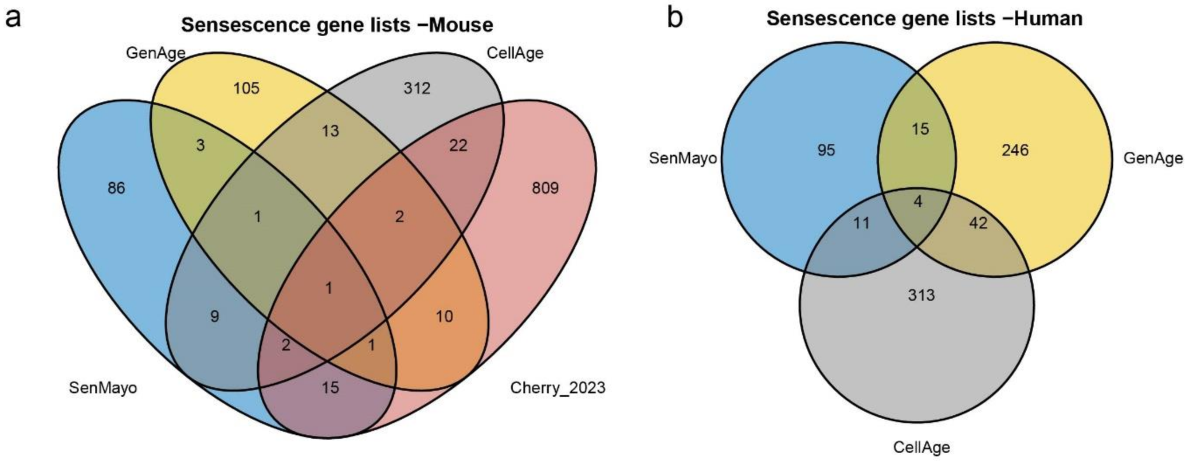
(k) UMAP plot of mouse adipose tissue[118] showing SenMayo enrichment scores with mesenchymal stem cells (MSCs) of adipose scoring the highest. (l)Significant decrease in the SenMayo enrichment scores observed with age in MSCs of adipose.

Supp fig 7



Supplementary fig 7: SenMayo scores in mouse retinal neurons across age: There was no increase in SenMayo score observed with age in mouse retinal neurons that were identified such as (a)Amacrine cells, (b)Bipolar cells, (c) cone photoreceptors, (d) Retinal ganglion cells (RGCs) and (e) rod photoreceptors.

Supp fig 8



Gene list- mouse	No of unique genes	Total no of genes	Percentage of unique genes
SenMayo	86	118	72.9
GenAge	105	136	77.2
CellAge	312	362	86.2
Cherry_2023	809	862	93.9

Gene list- human	No of unique genes	Total no of genes	Percentage of unique genes
SenMayo	95	125	76
GenAge	246	307	80.1
CellAge	313	370	84.6

Supplementary fig 8: Overlap of genes in the various senescence related gene lists used for analysis: (a & b) Venn diagram showing the overlap of genes in the various senescence/ageing gene lists used for the (a) mouse retinal dataset (b) human retinal dataset.

List of supplementary tables

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Supplementary table 4b: Mouse retinal microglia-SenMayo-hi vs SenMayo-low –GSEA pathway enrichment terms – top 50 terms

Supplementary table 5: Top 50 differentially expressed genes- mouse retinal Mueller glia - SenMayo-hi vs SenMayo-low (p-val-adj < 0.01)

Supplementary table 6a: Mouse retinal Mueller glia-SenMayo-hi vs SenMayo-low – GSEA GO: BP – top 50 terms

Supplementary table 6b: Mouse retinal Mueller glia-SenMayo-hi vs SenMayo-low – GSEA pathway enrichment terms – top 50 terms

Supplementary table 7a: Human retinal microglia-SenMayo-hi vs SenMayo-low –GSEA pathway enrichment terms – top 30 terms

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Supplementary table 7c: Human retinal astrocytes-SenMayo-hi vs SenMayo-low –GSEA pathway enrichment terms – top 30 terms

Supplementary table 8a: DEG list for mouse Mueller glia: 12-mo vs 3-mo (p-val-adj < 0.01, | LFC | > 0.25, top 25 up and downregulated)

Supplementary table 8b: DEG list for mouse Mueller glia: 24-mo vs 3-mo (p-val-adj < 0.01, | LFC | > 0.25, top 25 up and downregulated)

Supplementary table 8c: IPA canonical pathway- comparison analysis for mouse Mueller Glia (p-value < 0.05)

Supplementary table 9a: DEG list for mouse Rod photoreceptors: 12-mo vs 3-mo (p-val-adj < 0.01, | LFC | > 0.25, top 25 up and downregulated)

Supplementary table 9b: DEG list for mouse Rod photoreceptors: 24-mo vs 3-mo (p-val-adj < 0.01, | LFC | > 0.25, top 25 up and downregulated)

Supplementary table 9c: IPA canonical pathway- comparison analysis for mouse Rod photoreceptors (p-value < 0.05)

Supplementary table 10a: DEG list for mouse Cone photoreceptors: 12-mo vs 3-mo (p-val-adj < 0.01, | LFC | > 0.25, top 25 up and downregulated)

Supplementary table 10b: DEG list for mouse Cone photoreceptors: 24-mo vs 3-mo (p-val-adj < 0.01, | LFC | > 0.25, top 25 up and downregulated)

Supplementary table 10c: IPA canonical pathway- comparison analysis for mouse Cone photoreceptors (p-value < 0.05)

Supplementary table 11a: DEG list for mouse Bipolar cells: 12-mo vs 3-mo (p-val-adj < 0.01, | LFC | > 0.25, top 25 up and downregulated)

Supplementary table 11b: DEG list for mouse Bipolar cells: 24-mo vs 3-mo (p-val-adj < 0.01, | LFC | > 0.25, top 25 up and downregulated)

Supplementary table 11c: IPA canonical pathway- comparison analysis for mouse Bipolar cells (p-value < 0.05)

Supplementary table 12: Mouse retinal microglia- Saban lab dataset (GSE195891) - SenMayo-hi vs SenMayo-low –GSEA pathway enrichment terms (FDR-q-value < 0.05, NES > 1.5)

Supplementary table 13a: Mouse retinal microglia-SenMayo-hi vs SenMayo-low –Top 50 GSEA pathway enrichment terms obtained after removing the microglial activation genes (Marsh et al, 2022) from the input gene list (FDR-q-value < 0.05, NES > 1.5)

Supplementary table 13b: Human retinal microglia- (GSE148077) -SenMayo-hi vs SenMayo-low –GSEA pathway enrichment terms obtained after removing the microglial activation genes (Marsh et al, 2022) from the input gen e list (FDR-q-value < 0.05, NES > 1.5)

Supplementary table 13c: Mouse retinal microglia- Saban lab dataset (GSE195891) - SenMayo-hi vs SenMayo-low –GSEA pathway enrichment terms obtained after removing the microglial activation genes (Marsh et al, 2022) from the input gene list (FDR-q-value < 0.05, NES > 1.5)

Supplementary table 1: Markers used to annotate retinal cell types (From Peng et al., 2019 and Yan et al., 2020)

Cell type	**Marker genes**
Rods	Rho,Pdc,Nrl,Sag,Gnat1,Gngt1,Nr2e3,Gnb1
Cones	Arr3,Rcvrn,Gnat2,Gngt2,Opn1sw,Opn1mw,Pde6h,Guca1a,Opn1lw
Bipolar cells	Vsx2, Otx2, Grm6, Prkca, Trpm1, Grik1, Vsx1,Cabp5
RGCs	Rbpms, Pou4f1, Pou4f2, Thy1, Slc17a6,Nefl, Nefm, Sncg, Pou4f3
Amacrine cells	Tfap2a, Tfap2b, Tfap2c, Gad1, Gad2, Slc6a9, C1ql1,C1ql2
Horizontal cells	Lhx1,Onecut1,Onecut2,Calb1
Endothelial cells	Cldn5,Igfbp7,Col4a1
Pericytes	Mgp,Kcnj8,Myl9, Col4a1, Rgc5
Microglia	C1qa,C1qb, C1qc, Hexb, Ctss, P2ry12, Tmem119,B2m
Mueller glia	Rlbp1,Glul, Apoe, Crabp1, Clu, Slc1a3,Dkk3, Crym
Astrocytes	Gfap,Sod3,Gypc, Gsn, Hilpda, Cd44, Sparcl1,Mgst1,Emp1, Mt3,Adm,Anxa1

Supplementary table 2: Senescence and ageing gene lists used in the study

SenMayo mouse (Saul et al., 2023)	*Acvr1b, Ang, Angpt1, Angptl4, Areg, Axl, Bex3, Bmp2, Bmp6, C3, Ccl1, Ccl2, Ccl20, Ccl24, Ccl26, Ccl3, Ccl4, Ccl5, Ccl7, Ccl8, Cd55, Cd9, Csf1, Csf2, Csf2rb, Cst10, Ctnnb1, Ctsb, Cxcl1, Cxcl10, Cxcl12, Cxcl16, Cxcl2, Cxcl3, Cxcr2, Dkk1, Edn1, Egf, Egfr, Ereg, Esm1,Ets2, Fas, Fgf1, Fgf2, Fgf7, Gdf15, Gem, Gmfg, Hgf, Hmgb1, Icam1, Icam5, Igf1, Igfbp1,Igfbp2, Igfbp3, Igfbp4, Igfbp5, Igfbp6, Igfbp7, Il10, Il13, Il15, Il18, Il1a, Il1b, Il2, Il6, Il6st, Il7, Inha, Iqgap2, Itga2, Itpka, Jun, Kitl, Lcp1, Mif, Mmp13, Mmp10, Mmp12, Mmp14, Mmp2, Mmp3, Mmp9, Nap1l4, Nrg1, Pappa, Pecam1, Pgf, Pigf, Plat, Plau, Plaur, Ptbp1, Ptger2, Ptges, Rps6ka5, Scamp4, Selplg, Sema3f, Serpinb3a, Serpine1, Serpine2, Spp1, Spx, Timp2, Tnf, Tnfrsf11b, Tnfrsf1a, Tnfrsf1b, Tubgcp2, Vegfa, Vegfc, Vgf, Wnt16, Wnt2*
SenMayo-human (Saul et al., 2023)	ACVR1B, ANG, ANGPT1, ANGPTL4, AREG, AXL, BEX3, BMP2, BMP6, C3, CCL1, CCL13, CCL16, CCL2, CCL20, CCL24, CCL26, CCL3, CCL3L1, CCL4, CCL5, CCL7,CCL8 , CD55, CD9, CSF1, CSF2, CSF2RB, CST4, CTNNB1, CTSB, CXCL1, CXCL10, CXCL12, CXCL16, CXCL2, CXCL3, CXCL8, CXCR2, DKK1, EDN1, EGF, EGFR, EREG, ESM1, ETS2, FAS, FGF1, FGF2, FGF7, GDF15, GEM, GMFG, HGF, HMGB1, ICAM1, ICAM3, IGF1, IGFBP1, IGFBP2, IGFBP3, IGFBP4, IGFBP5, IGFBP6, IGFBP7, IL10, IL13, IL15, IL18, IL1A, IL1B, IL2, IL32, IL6, IL6ST, IL7, INHA, IQGAP2, ITGA2, ITPKA, JUN, KITLG, LCP1, MIF, MMP1, MMP10, MMP12, MMP13, MMP14, MMP2, MMP3, MMP9, NAP1L4, NRG1, PAPPA, PECAM1, PGF, PIGF, PLAT, PLAU, PLAUR, PTBP1, PTGER2, PTGES, RPS6KA5, SCAMP4, SELPLG, SEMA3F, SERPINB4, SERPINE1, SERPINE2, SPP1, SPX, TIMP2, TNF, TNFRSF10C, TNFRSF11B, TNFRSF1A, TNFRSF1B, TUBGCP2, VEGFA, VEGFC, VGF, WNT16, WNT2
GenAge-mouse (de Magalhaes et al., 2009)	*Adcy5, Adra1a, Adra1b, Agtr1a, Akt1, Akt2, Apoe, Arhgap1, Arntl, Atg5, Atm, Atr, Bax, Brca1, Bub1b, Bub3, Casp2, Cat, Cav1, Cdc14b, Cdk7, Cdkn1a, Cebpa, Cebpb, Chek2, Cisd2, Clock, Col1a1, Coq7, Ctf1, Dgat1, Dmd, Eef1e1, Efemp1, Eif5a2, Eps8, Ercc1, Ercc2, Ercc4, Fgf21, Fgf23, Fn1, Foxm1, Fxn, G6PD, Gdf15, Gh, Ghr, Ghrh, Ghrhr, GMFB, Gpx4, Grn, Gsk3a, Gsta4, Hells, Hnrnpd, Htr1b, Htra2, Htt, Igf1, Igf1r, Ikbkb, Insr, Irs1, Irs2, Jund, Kcna3, Kl, Lmna, Mcm2, Mgat5, Mif, Mir17, Mir29a, Msh2, Msra, Mstn, Mt1, Mtbp, Mtor, Myc, Ncor2, Neil1, Nfkb1, Nos3, NUDT1, Pappa, Parp1, Pawr, Pck1, Per2, Plau, Polg, Pou1f1, Pparg, Ppm1d, Prdx1, Prkar2b, Prop1, Pten, Rae1, Rbm38, Rictor, Rps6kb1, Serpine1, Shc1, Siglece, Sirt1, Sirt6, Sirt7, Slc13a1, Slc25a4, Socs2, Sod2, SOD3, Sqstm1, Stub1, Surf1, Terf2, Tert, Top3b, Topors, Tpp2, Trp53, Trp53bp1, Trp63, Trp73, Trpv1, Txn1, Ubd, Ucp2, Xpa, Xrcc5, Xrcc6, Zmpste24*
GenAge-human (de Magalhaes et al., 2009)	GHR, GHRH, SHC1, POU1F1, PROP1, TP53, TERC, TERT, ATM, PLAU, ERCC2, ERCC8, WRN, LMNA, IGF1R, TXN, KL, E2F1, PTPN11, NFKB2, STAT5B, STAT3, STAT5A, NRG1, HDAC3, GH1, IL7R, IGF1, IGF2, INS, NGF, IRS1, PTPN1, IRS2, AKT1, PIK3CB, NGFR, HRAS, MYC, EGFR, ERBB2, INSR, NCOR1, NBN, JUND, IL2, PDGFB, EGF, IL2RG, FOS, PDGFRB, EPOR, SST, PRKCD, PPARA, RET, PLCG2, PEX5, TCF3, PARP1, BRCA1, PIN1, PTEN, CREBBP, HIF1A, UBB, RPA1, BLM, BCL2, S100B, VCP, POLG, IGFBP3, HSP90AA1, NR3C1, EGR1, VEGFA, ABL1, BRCA2, TOP2A, TOP2B, NFKB1, TOP1, RAD51, UBE2I, TNF, PDPK1, CEBPA, CEBPB, MXI1, TGFB1, ERCC6, STK11, EP300, APTX, PML, GSK3B, HTT, PRKCA, SSTR3, HELLS, APOC3, EEF2, ERCC3, TERF1, PRKDC, CAT, ERCC5, AR, GTF2H2, XRCC5, PCNA, FEN1, FAS, TERF2, XRCC6, POLD1, BAX, , RB1, EMD, GRB2, FOXO3, FOXO1, HSF1, XPA, MSRA, RECQL4, SOD2, SOD1, FOXM1, COQ7, CACNA1A, LRP2, AIFM1, UCHL1, APP, APOE, A2M, SNCG, PRDX1, PON1, RELA, IL6, RGN, ATP5O, RAD52, TOP3B, ERCC1, SIRT1, HDAC1, HSPA9, GPX1, GSR, GSS, GSTA4, GSTP1, MT-CO1, HSPD1, HSPA1A, HSPA1B,

	PCMT1, MAPK8, YWHAZ, PTK2B,PTK2, IL7, MAPK14, FGFR1, SP1, FLT1, JUN, MED1, MAPK9, MAPK3, HMGB1, CCNA2, HMGB2, MAP3K5, TAF1, LMNB1, SDHC, FOXO4, HESX1, PIK3R1, BSCL2, AGPAT2, BMI1, EEF1A1, TFAP2A, BDNF, CREB1, ATF2, TBP, APEX1, HBP1, BUB1B, PTGS2, HSPA8, SIN3A, CDK1, TFDP1, DDIT3, POLA1, MAPT, CTGF, HDAC2, MAX, MXD1, MDM2, SUMO1, H2AFX, HOXB7, HOXC4, JAK2, ESR1, LEP, LEPR, NFKBIA, CLU, MTOR, GHRHR, CTNNB1, PSEN1, DLL3, CDKN2A, PPP1CA, DBN1, NOG, ELN, ATR, UCP3, ZMPSTE24, TP63, UCP2, POLB, GCLC, GCLM, SIRT6, BUB3, RAE1, PMCH, MLH1, CSNK1E, STUB1, PPM1D, CHEK2, PCK1, ARHGAP1, CDC42, ARNTL, CLOCK, HIC1, PAPPA, ADCY5, PPARGC1A, GPX4, UCP1, FGF23, EFEMP1, ERCC4, CETP, PPARG, AGTR1, CISD2, EEF1E1, EPS8, KCNA3, SIRT7, SLC13A1, SOCS2, TPP2, TP53BP1, SIRT3, NCOR2, SUN1, BAK1, IGFBP2, PYCR1, TP73, CNR1, NFE2L2, CDKN1A, PDGFRA, PIK3CA, 1QA, CDKN2B, EIF5A2, MIF, DGAT1, MT1E, FGF21, HTRA2, GSK3A, NUDT1, IKBKB, SQSTM1, CDK7, GRN, SERPINE1, SPRTN, RICTOR, CTF1, TRAP1, TRPV1, NFE2L1, IFNB1, GDF11
CellAge **(Avelar et al., 2020)**	AAK1, ABCB1, ABI3, ABI3BP, ACKR1, ADCK5, AGT, AHR, AKT1, ALOX15B, AR, ARF1, ARG2, ARID1A, ARID1B, ARID4B, ARPC1B, ARRB1, ASF1A,ASXL2 , ATF6, ATG10, ATR, ATRAID, ATRX, ATXN10, AXL, BAP1, BCL2, BCL2L2, BCLAF1, BHLHE40, BIN1, BLK, BMP4, BMPR2, BNIP3L, BRAF, BRD7, BTG1, BTG2, CAPNS1, CARF, CASP2, CAV1, CAVIN1, CCL2, CCN2, CCN6, CCND1, CD34, CD82, CDC6, CDK18, CDK5, CDK5R1, CDKN1A, CDKN1B, CDKN1C, CDKN2A, CDKN2AIP, CDKN2B, CEACAM1, CEBPB, CHD5, CHEK1, CHEK2, CHUK, CKB, CLCA2, CPEB1, CREG1, CTNNB1, CXCL1, CXCR2, CYBB, DAO, DDB2, DHCR24, DHRS2, DLC1, DMTF1, DPP4, DUSP1, DYRK1A, E2F1, E2F7, EEF1E1, EGLN1, EGR2, EHF, EID3, EIF2AK2, ENG, ENTPD7, EP300, ERBB2, ERRFI1, ERVW-1, ESRRB, ETS1, ETS2, ETV6, EWSR1, FANCD2, FASN, FASTK, FBXO22, FBXO31, FBXO4, FGFR1, FGFR3, FOXA1, FOXO1, FOXO4, FOXP3, GADD45G, GATA4, GDF15, GEMIN2, GJA1, GKN1, GNG11, GNMT, GRIK2, GRK4, GRK6, HBP1, HDAC1, HEPACAM, HIPK2, HIRA, HK3, HMGA1, HMGA2, HNRNPC, HOPX, HRAS, HSPA9, HTRA1, IFI16, IFNG, IGFBP1, IGFBP3, IGFBP5, IGFBP7, IKBKG, IL1A, IL1R1, IL6, ING1, ING2, ING5 ,IRF1, IRF3, IRF5, IRF7, ITGB3, ITGB4, ITPK1, ITPKB, ITPR1, ITPR2, ITPR3, ITSN2, JAK2, JUNB, KAT5, KCNA1, KDM6B, KEAP1, KLF4, KNDC1, LATS2, LAYN, LIMK1, LPAR1, LY6D, MAD1L1, MAP2K1, MAP2K2, MAP2K6, MAP2K7, MAP3K14, MAP3K5, MAP3K6, MAP3K7, MAPK1, MAPK12, MAPK14, MAPKAPK5, MARCKS, MAST1, MATK, MAVS, MCRS1, MCU, MDP1, MEN1, MEOX1, METTL14, MINK1, MME, MNX1, MOB3A, MORC3, MOS, MST1, MT1G, MVK, MVP, MXD4, NADK, NCAPH2, NDRG1, NDST2, NEK4, NF2, NFKBIA, NINJ1, NLRX1, NOLC1, NOTCH1, NOTCH3, NOX1, NOX4, NQO1, NRAS, NRSN2, NUAK1, OGT, ORAI1, OTX2, PAK2, PAK4, PBRM1, PCGF2, PDCD10, PDGFB, PDIK1L, PDPK1, PDZD2, PEA15, PEBP1, PEX19, PGR, PHB, PI4KB, PIK3R5, PIM1, PIN1, PINX1, PITX1, PLA2G2A, PLA2R1, PML, PMVK, PNPT1, POU3F1, POU5F1, PPARG, PPP2R1A, PPP2R5A, PRKCD, PRKCH, PRKD1, PRODH, PROX1, PTGS2, PTTG1, PURB, RAF1, RAP1GAP, RARB, RASSF1, RASSF5, RB1, RBL1, RBL2, RBM38, RBP1, RBPJ, RELA, RELB,RNASEL , ROMO1, RPL11, RPS14, RPS6KB1, RPTOR, RRP8, RTN4, RUNX1, SALL1, SELENBP1, SERPINB2, SERPINE1, SFN, SFRP1, SIAH1, SIK1, SIN3B, SLC13A3, SLC31A2, SLC5A2, SMAD1, SMAD3, SMAD5, SMARCB1, SMURF2, SOCS1, SOD2, SORBS2, SOX1, SOX2, SOX5, SP1, SPARC, SPI1, SPIN1, SPOP, SREBF1, SRSF1, SSX2, STAG2, STAT1, STAT3, STAT5A, STAT5B, STAT6,STK32C, STK4, STK40, SUMO2, SUMO3, SYK, TAGLN, TBPL1, TGFB1I1, TGFBI, TIGAR, TLR10, TLR2, TLR3, TMEM9B, TNFSF15, TOM1, TOP1, TOP3A, TP53, TP53BP1, TP53BP2, TP53INP1, TP63, TRIM28, TXNIP, TYK2, UBTD1, ULK3, USP28, VCAN, VENTX, WIF1, WNT16, WNT5A, AF1, XPO1, YPEL3, ZCCHC10, ZFP36
Cherry_2023 (Cherry et al., 23)	*Pfkl, Megf6, Tnfrsf10b, Tpm2, Tpm1, Myo1b, Ccdc9b, Myo1e, Snai1, Lrrc32, Rflnb, Glipr1, Pear1, Cyb5r3, Tcim, Cit, Acot7, Fscn1,Impdh1 , Serpina3n, Ccn2, Bgn, Ednra, Spns2, S1pr1, Ptpn14, Emilin1, Vcam1, Cldn1, Sema3f, Myo1d, Lrrfip1,Bcl6b, Dennd4a, Uck2, Ltc4s, Cd82, Slpi, Thbs4, Mmp9, Ulbp1, Itga1, Anxa8, Pld3, Ccnd2, Serpine2, Ank, Trp53inp1,Arhgef5, Notch3, Apold1, Ctsk, Chst11, Zbtb46, Fgd6, Myh9, Ckap4, Rab27a, Cemip2, Plekhg5, Palld, Mmp13, Lbh, Emcn, Mylk, Ddit4l, Col18a1, Plod1, Dusp6, Des, C5ar1, Timp1, Stk17b, Tmc6, Mmp19, Hmcn1, Tmem176a, 11-Sep, Jpt2, Piezo1, Cav1, Cybb, Trp53i11, Sncg, Csf1r, Cd109, Bhlhe41, Scarf2, Rasa3, Nrp2, Col24a1, Ccn3, Rin1, Pdia5, Brinp3, H1f2, Tgfb3, Efnb2, Stab1, Ugcg, Arhgdib, Plk2, Synpo, Serpina3g, Fhl2, Elk3, C77080, Rasd1, Gcnt2, Ugt1a7c, Sipa1l1, Cthrc1, Piezo2, Ica1, Prkacb, Ecscr, Eda2r, Slc20a1, Ltbp2, Cd276, Capn6, Ednrb, Msrb3, S1pr3, Tmem132a, Ggta1, Vstm4, Plpp1, Ptpre, Nkain1, Prag1, Runx1, Grem2, B4galt5, Cdh11, Vegfc, Qsox1, Tgfb1, Cxcl5, Sox18, Ets1, Dio2, Adgrl1, Flt1, Lama5, Inf2, Halr1, Adamts9, Slc40a1, Ppp1r13l, Cacnb3, Plxnd1, Pecam1, Epha2, Tnn, Fam160a1, Susd6, Fli1, Adamts4, Il27ra, Tjp2, Etl4, Cxcl12, Adgrf5, Ppic, Ptp4a3, Col12a1, Tmem98, Kifc3, Pmepa1, Tln2, F11r, Hp, Tubb2a, Cpxm1, Mertk, Ccl9, Kcnj15, Angptl4, C1qtnf3, Fads3, Kctd15, Selp, Acta2, Slc52a3, Igfbp7, Adamts17, Slc39a13, Socs2, Apobec3, Sorcs2, Nlgn2, Kalrn, Colgalt1, Slit2, Pde4d, Parm1, Slc15a3, Igfbp4, Plod3, Pdzrn3, Fzd1, Plec, Mpeg1, Plekhb2, Cdk6, Gsr, Cd80, Nek6, Lgmn, Ppm1j, Mpzl1, Retreg1, Atxn1, Bfar, AU020206, Colec12, Zmat3, Csf2rb2, Cda, Foxs1, Tinagl1, Col15a1, Pdgfrb, Esm1, Adarb1, Psrc1, Slc9a3r1, Notch1, Mcm2, Speg, Tie1, Plvap, Plxdc1, Itgb5, Pdgfrl, Fat1, Map3k11, Mdk, Nectin2, Mafb, Ctsb, 4-Sep, Sh3pxd2a, Hey1, Ezr, Nab1, L3mbtl3, Nr2f2, Extl3, Rcc2, Ajuba, Stmn2, Itga10, Fkbp10, Angpt2, Sfrp2, Rbp1, Cald1, Maged1, Gm42047, Nr5a2,*

	Fuca2, H2bc4, Rrm2, Cyp7b1, Laptm5, Pkig, Col7a1, Crtap, Lman1, Cdh3, Ctsa, Dkk3, Fbln7, Sh3bgrl2, Actr1b, Clec11a, Htr2b, Eno1, Saa3, Olfml3, Il34, Ptprb, Fry, Ctsd, Itgbl1, Pla2g7, Arhgef7, Nupr1, Rnf150, Adam12, Rftn1, Adgre5, Ubash3b, Znrf1, Gmppb, Plscr3, Plpp2, App, Ak1, Ormdl3, Gpr68, C1qb, Chsy1, P3h1, Creld2, Plaat3, Kctd11, Pmaip1, Nrarp, Slc39a1, BC028528, Itpr3, Hif1a, Scap, Rgs16, P3h2, Scube3, Frem1, Phactr1, Nudt4, Lxn, Spon1, Epb41l4a, Cnn2, Nt5dc2, Hdlbp, Mex3a, Rasal2, Kctd10, Cdk1, Aplp1, Prss35, Rarres1,,Fzd2, Parvb, Creb3l1, Tor4a, Bcr, Trim46, Ano1, Pofut2, Rpn1, Adra2a, Plxna4, Flt4, Hc, Nlrc3, Tspan11, Rasgrp4, Tsc22d1, Bok, Man2b1, Ryk, Clca3a1, Foxc2, Stra6, Gm9889, Bpgm, Wls, Tpd52, Foxf1, Gpr107, Avpr1a, C1qa, Myh11, Pdgfa, Chst15, Rasgrf2, Gucy1a1, Rcn1, Acpp, Add2, Zfp608, Tceal9, Cdyl2, Kdelr2, Edil3, Reg3g, Runx2, Serpinb2, Fabp5, Mmp15, Pawr, Gm13889, Traf1, Pltp, Copz2, Sigmar1, Arl1, Clec7a, P4ha1, Lyz2, Chil1, Ptprv, Dnajb11, Pard6g, AI506816, Dio3, Pik3r3, Slc9a3r2, Etv6, Serpinb9, B4galnt1, Fkbp5, Neurl1b, Cmpk1, C1qc, Zswim4, P3h3, Lrrc59, Gng2, Marcksl1, Col6a4, Lclat1, Zfp46, Hs6st1, Atp6v0d2, Top2a, Ssr2, Rnf125, Bak1, Dock5, Phc2, Jph2, Jak3, Serpinh1, Myo1c, Slc35a2, P2rx7, F2rl3, Nr2f6, Chd7, Ass1, Fibin, Unc119, Atp6v0a2, Cgref1, Xpnpep1, Slc38a10, Calr, Praf2, Cpe, Adamts6, Adamts18, Efna1, Ctrl, Ahr, Pf4, Gm48878, B4galt7, Trib2, Aldh1l2, Furin, Cpxm2, Herc3, Traf2, St6galnac4, Pxylp1, Mtss1, Smc4, Gas2, Dcakd, Mpp2, Sfrp1, Dysf, Ift20, Gna12, Cdkn2b, Fam217b, Slc10a7, Nfe2l1, Hdac9, Tspan17, Ncs1, Ccng1, Gcnt4, Prkar2b, Plcg2, Myzap, Clcf1, Pcdhgc5, Fgfr3, cfd2, , A930004D18Rik, Itpripl2, Tmem86a, Cep170b, Abhd2 , Azin2, Rtn4rl2, Lrig3, Pdia4, Hs2st1, Gas6, Tiam2, Ucp2, 2410131K14Rik, Tnfrsf21, Crip1, Cd300a, Nmt1, Ctnnb1, Tmem268, Prickle1, Inhba, Ereg, Sesn2, Btk, Dab2ip, Scn1b, Gdpgp1, Ost4, Slc16a3, Ushbp1, Rgcc, Unc5c, Bace1, Mcam, Pigs, H2aj, Rasgrf1, Gpr176, Cav2, Grsf1, Layn, Chl1, Col1a1, Nfkbid ,Nhsl2, Lrrc15, Specc1, Fcgr1, Amn, Gsto1, Rhod, Vwf, Twf1, Mthfd2, Evl, Rnf152, Mark4, Tmem189, Ighm, Mthfr, 5031439G07Rik, Map4k4, Syngr2, Chpf2, Prdm1, Surf4, Ms4a4a, Mmp8, Ubtd1, Rasgef1b, Arg1, Fnbp1, Hspb6, Ripor3, Eva1b, Cfh, Fjx1, Acvr1, Cryzl2, Prelid1, Tmem44, Dnajc25, Sox4, Fam102a, Cep85, C1qtnf12, Pilra, Fbn2, Gns, Prkcsh, Mdfic, Wdfy4, Kctd5, Slc9a5, 4921524J17Rik, Mlec, Scn4b, Incenp, Hopx, B4galt6, Pgk1, Dram1, Vmp1, Zfp809, Lrfn4, Commd9, Yap1, Cenpb, Olfr810, Lipa, Col11a2, Gapdh, Cdkn1a, Fam110b, Enpp1, Ppp4r1, Mfap4, Chst2, Igsf3, Fnbp1l, Frrs1, Emilin3, Bcl2l11, Gja5, Ccrl2, Yipf5, Mfge8, Cpz, Ptk2b, Tbc1d2, Plod2, BC004004, Cdh5, Col1a2,Kdelr1, Mif, Cttn, Cd79a, Cdh23, Mical3, Ager, Entpd5, Inppl1, Col8a2, Aebp1, Eps8l2,Lzts1, Kctd17, Cldn5, Hexa, Plxnb2, Smox , Ripk3, Exoc3l2, Bicc1, Lhfp, Mboat1, Zbtb34, Col27a1, Tmem176b, Otulinl, Xrcc6, Ncln, Cfi, Aspn, Steap2, Mvp, Robo4, 1700058P15Rik, Arhgef17, Plpp5, Tnni1, Tmtc1, Ptchd1, 9930111J21Rik2, Atf6b, Tmem119, Il10, Washc5, Tedc1, Trim59, Dnm3, Plekhg2, Itprid2, Orai2, Plekha7, Gpr153, Pomgnt1, Cryaa, Sf3b3, Slc39a11, Ndufa4l2, Ghr, Ctbp1, Rrbp1, Plekhg4, Itgav, Syt15, Cd63, Tbx2, Sfxn5, H6pd, Yif1a, Large1, Col5a2, B4galt4, Sgsh, Crlf2, Copb2, Cstb, Tmem214, Nod1, P4ha2, Gnptab, Manba, Dhx34, Actn4, Parp8, Nup93, Ehd3, Pten, Slc16a12, Mogs, Entpd7, Foxp1, Wipi1, Ptpn22 ,Ssr1 H13, Abcc3 ,Castor2 ,Golm1 ,Ttc9, Pdrg1 Doc2b, Arfgap1, Slc31a1 Nrros, Ube2ql1, , Ddb1, Mcrip1, Stum, Amdhd2, Spry1, Serpine1, Npl, Rdh10, Fndc10, Bmi1, Adgra2, Arhgap25, Jag2, Nans, Slc44a2, Myo5a, Shtn1, Prdm11, Ifi30 Itpr1, Slc16a1, Dclk2, Sec22b, Dlg2, Hes1, Tmed9, Mark1, Aim2, Col6a1, Plbd2, Nsd2, Prr7, Ankrd37, Nuak1, Ptafr, Lmtk3, Ppp2r2c, Snx8, Wnt9a, Lyve1, Itga7, Tmed3, Tpi1, Fam214b, Oaz2, Als2cl, Bcar1, Zfp979, Gm42517, Ccdc166, Srprb, Pdia6, Rab3d, Cmtm4, AI427809, Ephb3, 4930555A03Rik, Ccl8, Serpinb8, Gab2, Gm5976, Tmem123, Copg1, Klhl5, Ctif, Cdk17, Sil1, Laptm4b, Hyou1, Gas2l1, Tnfsf8, Ptprk, Itprip, Tm7sf3, Tbcd, Fbxo32, Ptprf, Cnnm2, Sema5b, Gucy1b1, Mtap, Ttc12, Cemip, Mtch1, Tead2, Dnajc1, Sec61a1, Ankrd28, Cd93, Cdca3, Naglu, Ifngr2, Lrp12, P4ha3, Zfp618, Tapbp, Bcat1, Pld4, Gorasp2, Snd1, Akt1s1, Dpp6, Pabpc4l, Krt18, Adamts15, Kif1c, Iqgap3, Col22a1, Tmem104, Dnmt3a, Ly96, Cdh2, Tulp4, Gtse1, Abr, Lmna, Tubb5, Rrm1, Casp8, Plaur, Dusp4, Ada, Epha3, Gm49759, Mras, Nr4a2, AI115009, Mgat3, Zbtb7c, Mib1, Fdxr, Aopep, F730043M19Rik, Mmp11, Col6a3, Shisa5
SenMayo-mouse reduced: SenMayo mouse panel - HU_FETAL_RETINA_MICROGLIA (Hu et al., 2019)	*Acvr1b,Ang,Angpt1,Angptl4,Areg,Axl,Bex3,Bmp2,Bmp6,Ccl1,Ccl2,Ccl20,Ccl24,Ccl26,Ccl5,Ccl7,* *Ccl8,Cd55,Cd9,Csf1,Csf2,Csf2rb,Cst10,Ctnnb1,Cxcl1,Cxcl10,Cxcl12,Cxcl2,Cxcl3,Cxcr2,Dkk1,* *Edn1,Egf,Egfr,Ereg,Esm1,Fas,Fgf1,Fgf2,Fgf7,Gdf15,Gem,Hgf,Hmgb1,Icam1,Icam5,Igf1,Igfbp1,* *Igfbp2,Igfbp3,Igfbp4,Igfbp5,Igfbp6,Igfbp7,Il10,Il13,Il15,Il18,Il1a,Il1b,Il2,Il6,Il7,Inha,Iqgap2, Itga2,Itpka,Jun,Kitl,Mif,Mmp13,Mmp10,Mmp12,Mmp13,Mmp14,Mmp2,Mmp3,Mmp9,Nap1l4, Nrg1,Pappa,Pecam1,Pgf,Pigf,Plat,Plau,Ptbp1,Ptger2,Ptges,Rps6ka5,Scamp4,Sema3f,Serpinb3a,* *Serpine1,Serpine2,Spx,Timp2,Tnf,Tnfrsf11b,Tubgcp2,Vegfa,Vegfc,Vgf,Wnt16,Wnt2*
SenMayo genes also found in HU_FETAL_RETINA_MICROGLIA	*C3,Ccl3,Ccl4,Ctsb,Cxcl16,Ets2,Gmfg,Il6st,Lcp1,Plaur,Selplg,Spp1,Tnfrsf1a,Tnfrsf1b*
Marsh et al., 2022 Microglia/Myeloid activation genes	*Rgs1,Hist2h2aa1,Hist1h4i,Nfkbiz,Klf2,Junb,Dusp1,Ccl3,Hspa1a,Hsp90aa1,Fos,Hspa1b,Jun, Jund,Nfkbid,Gem,Ccl4,Ier5,Txnip,Hist1h2bc,Zfp36,Hist1h1c,Egr1,Atf3,Rhob*
Marsh et al., 2022 All CNS cells activation genes	*Fos,Junb,Zfp36,Jun,Hspa1a,Socs3,Rgs1,Egr1,Btg2,Fosb,Hist1h1d,Ier5,1500015O10Rik, Atf3,Hist1h2ac,Dusp1,Hist1h1e,Folr1,Serpine1*

Supplementary table 3: Top 50 DEGs- mouse retinal microglia - SenMayo-hi vs SenMayo-low (pvaladj < 0.01)

Genes	pval	avg_log2 FC	pct. 1	pct. 2	p.adj
Ccl4	1.47E-64	3.886951	0.762	0.08	3.05E-60
Ccl3	1.80E-83	3.809437	0.89	0.086	3.75E-79
Atf3	1.95E-81	3.798743	0.834	0.052	4.05E-77
Nfkbia	6.41E-79	3.456228	0.814	0.049	1.33E-74
Jun	1.15E-81	3.437646	0.921	0.181	2.39E-77
Cxcl2	5.02E-13	3.381985	0.166	0.006	1.04E-08
Ccl2	4.74E-56	3.203148	0.7	0.061	9.85E-52
Zfp36	8.28E-83	3.196552	0.893	0.098	1.72E-78
Btg2	1.23E-82	3.17878	0.91	0.12	2.56E-78
Junb	1.27E-83	3.17813	0.941	0.218	2.64E-79
Egr1	7.26E-80	3.162584	0.917	0.19	1.51E-75
Dusp1	1.02E-77	3.146724	0.872	0.11	2.13E-73
Klf2	1.53E-65	3.132573	0.769	0.067	3.17E-61
Fos	3.57E-76	3.071351	0.928	0.291	7.43E-72
Klf6	2.26E-78	2.942725	0.838	0.055	4.71E-74
Klf4	4.13E-62	2.93656	0.697	0.037	8.60E-58
Ccl7	2.43E-13	2.932145	0.169	0.006	5.05E-09
Nfkbiz	3.96E-74	2.906782	0.776	0.034	8.24E-70
Fosb	6.65E-68	2.704742	0.848	0.12	1.38E-63
Ier5	3.61E-82	2.700169	0.903	0.083	7.51E-78
Ier3	1.33E-55	2.659714	0.672	0.049	2.78E-51
Neat1	7.35E-70	2.642397	0.79	0.058	1.53E-65
Jund	2.40E-72	2.60552	0.924	0.224	5.00E-68
Ubc	2.33E-76	2.54719	0.952	0.322	4.85E-72
Rgs1	4.31E-43	2.427852	0.514	0.021	8.96E-39
Rhob	1.84E-64	2.399563	0.824	0.101	3.83E-60
Ier2	1.40E-67	2.357977	0.862	0.126	2.92E-63
Ccl12	1.38E-40	2.319579	0.797	0.227	2.88E-36
Slc15a3	1.36E-66	2.304062	0.728	0.034	2.83E-62
Mafb	8.58E-56	2.231184	0.828	0.153	1.79E-51
Ccnl1	1.03E-71	2.230491	0.838	0.071	2.15E-67
Tnf	6.00E-50	2.159021	0.583	0.021	1.25E-45
Hspa5	4.60E-60	2.140125	0.859	0.15	9.56E-56
Socs3	4.22E-52	2.102302	0.686	0.074	8.78E-48
Cx3cr1	7.74E-63	2.100993	0.931	0.307	1.61E-58
Il1a	7.37E-43	2.086557	0.497	0.012	1.53E-38
Ppp1r15a	1.80E-57	2.070882	0.669	0.037	3.75E-53
Mcl1	5.03E-62	2.065362	0.879	0.147	1.05E-57
Rgs2	7.27E-59	2.049254	0.803	0.104	1.51E-54
Zfp36l1	2.40E-60	2.047064	0.821	0.11	4.98E-56
Marcksl1	1.02E-41	1.872481	0.476	0.009	2.12E-37
Adrb2	3.22E-49	1.864653	0.566	0.018	6.69E-45
Cd14	2.73E-55	1.860593	0.707	0.061	5.68E-51
Il1b	1.55E-15	1.817226	0.179	0	3.22E-11
Btg1	1.07E-55	1.801105	0.838	0.144	2.23E-51
Gm26532	1.08E-45	1.751434	0.521	0.012	2.24E-41
Tmcc3	2.57E-59	1.731883	0.686	0.034	5.34E-55
Kctd12	1.49E-48	1.674408	0.852	0.202	3.10E-44
Srsf5	4.05E-54	1.673511	0.897	0.206	8.41E-50
Cxcl10	4.42E-12	1.665091	0.138	0	9.18E-08

Supplementary table 4a: Mouse retinal microglia-SenMayo-hi vs SenMayo-low –GSEA GO:BP – top 50 terms (FDR-qvalue < 0.05, NES > 1.5). Legend for Fig 2b- refer to top 30 terms.

No	ID	ES	NES	pval	p.adj	qval
1	GOBP_LEUKOCYTE_DIFFERENTIATION	0.735117	2.090111	1.00E-10	8.18E-09	5.71E-09
2	GOBP_LEUKOCYTE_MIGRATION	0.749685	2.083389	1.00E-10	8.18E-09	5.71E-09
3	GOBP_MONONUCLEAR_CELL_MIGRATION	0.788782	2.083272	1.00E-10	8.18E-09	5.71E-09
4	GOBP_RESPONSE_TO_MOLECULE_OF_BACTERIAL_ORIGIN	0.758338	2.081374	1.00E-10	8.18E-09	5.71E-09
5	GOBP_MYELOID_LEUKOCYTE_DIFFERENTIATION	0.776039	2.074237	1.00E-10	8.18E-09	5.71E-09
6	GOBP_RESPONSE_TO_CHEMOKINE	0.863865	2.073511	1.47E-10	1.09E-08	7.61E-09

No	ID	ES	NES	pval	p.adj	qval
7	GOBP_LEUKOCYTE_CELL_CELL_ADHESION	0.743264	2.060158	1.00E-10	8.18E-09	5.71E-09
8	GOBP_MYELOID_LEUKOCYTE_MIGRATION	0.770156	2.058511	1.00E-10	8.18E-09	5.71E-09
9	GOBP_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	0.754222	2.05537	1.00E-10	8.18E-09	5.71E-09
10	GOBP_POSITIVE_REGULATION_OF_LEUKOCYTE_MIGRATION	0.79563	2.046334	1.00E-10	8.18E-09	5.71E-09
11	GOBP_REGULATION_OF_HEMOPOIESIS	0.734157	2.037158	1.00E-10	8.18E-09	5.71E-09
12	GOBP_CELLULAR_RESPONSE_TO_BIOTIC_STIMULUS	0.758294	2.03703	1.00E-10	8.18E-09	5.71E-09
13	GOBP_MONONUCLEAR_CELL_DIFFERENTIATION	0.727668	2.035915	1.00E-10	8.18E-09	5.71E-09
14	GOBP_ERK1_AND_ERK2_CASCADE	0.741288	2.035026	1.00E-10	8.18E-09	5.71E-09
15	GOBP_CELLULAR_RESPONSE_TO_MOLECULE_OF_BACTERIAL_ORIGIN	0.766492	2.033631	1.00E-10	8.18E-09	5.71E-09
16	GOBP_LEUKOCYTE_CHEMOTAXIS	0.757527	2.031122	1.00E-10	8.18E-09	5.71E-09
17	GOBP_REGULATION_OF_LEUKOCYTE_MIGRATION	0.75797	2.029227	1.00E-10	8.18E-09	5.71E-09
18	GOBP_CELL_CHEMOTAXIS	0.744182	2.028887	1.00E-10	8.18E-09	5.71E-09
19	GOBP_GRANULOCYTE_MIGRATION	0.784679	2.018556	1.47E-10	1.09E-08	7.61E-09
20	GOBP_NEUTROPHIL_MIGRATION	0.801044	2.015137	1.52E-09	9.07E-08	6.34E-08
21	GOBP_REGULATION_OF_MONONUCLEAR_CELL_MIGRATION	0.798461	2.013132	1.93E-09	1.11E-07	7.78E-08
22	GOBP_POSITIVE_REGULATION_OF_LEUKOCYTE_CELL_CELL_ADHESION	0.747623	2.008365	1.00E-10	8.18E-09	5.71E-09
23	GOBP_RESPONSE_TO_BACTERIUM	0.707203	2.006723	1.00E-10	8.18E-09	5.71E-09
24	GOBP_T_CELL_ACTIVATION	0.710497	2.003258	1.00E-10	8.18E-09	5.71E-09
25	GOBP_CYTOKINE_MEDIATED_SIGNALING_PATHWAY	0.715037	2.002224	1.00E-10	8.18E-09	5.71E-09
26	GOBP_ADAPTIVE_IMMUNE_RESPONSE	0.717477	1.999956	1.00E-10	8.18E-09	5.71E-09
27	GOBP_LYMPHOCYTE_MIGRATION	0.805585	1.999237	4.17E-09	2.27E-07	1.59E-07
28	GOBP_MYELOID_CELL_DIFFERENTIATION	0.716723	1.997085	1.00E-10	8.18E-09	5.71E-09
29	GOBP_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	0.792459	1.996006	2.99E-09	1.68E-07	1.18E-07
30	GOBP_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	0.784432	1.991436	1.96E-09	1.12E-07	7.81E-08
31	GOBP_INTERLEUKIN_6_PRODUCTION	0.770507	1.987439	2.09E-10	1.48E-08	1.03E-08
32	GOBP_LYMPHOCYTE_CHEMOTAXIS	0.865076	1.986729	4.39E-07	1.41E-05	9.86E-06
33	GOBP_POSITIVE_REGULATION_OF_HEMOPOIESIS	0.763347	1.984638	8.53E-10	5.49E-08	3.84E-08
34	GOBP_GRANULOCYTE_CHEMOTAXIS	0.785294	1.984439	4.65E-09	2.51E-07	1.75E-07
35	GOBP_NEUTROPHIL_CHEMOTAXIS	0.806063	1.983922	1.79E-08	8.68E-07	6.07E-07
36	GOBP_POSITIVE_REGULATION_OF_CELL_ACTIVATION	0.715279	1.98307	1.00E-10	8.18E-09	5.71E-09
37	GOBP_NEGATIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	0.709857	1.980494	1.00E-10	8.18E-09	5.71E-09
38	GOBP_SENSORY_PERCEPTION_OF_PAIN	0.802398	1.975316	3.64E-08	1.70E-06	1.19E-06
39	GOBP_POSITIVE_REGULATION_OF_ERK1_AND_ERK2_CASCADE	0.741534	1.973619	1.00E-10	8.18E-09	5.71E-09
40	GOBP_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	0.746075	1.972986	1.18E-10	9.19E-09	6.42E-09
41	GOBP_MONOCYTE_CHEMOTAXIS	0.858156	1.97262	1.46E-07	5.62E-06	3.93E-06

No	ID	ES	NES	pval	p.adj	qval
42	GOBP_T_CELL_DIFFERENTIATION	0.723067	1.961559	1.00E-10	8.18E-09	5.71E-09
43	GOBP_CELLULAR_EXTRAVASATION	0.819018	1.959999	1.26E-07	4.93E-06	3.44E-06
44	GOBP_POSITIVE_REGULATION_OF_CELL_CELL_ADHESION	0.721889	1.959731	1.00E-10	8.18E-09	5.71E-09
45	GOBP_REGULATION_OF_CHEMOTAXIS	0.730333	1.958208	1.00E-10	8.18E-09	5.71E-09
46	GOBP_REGULATION_OF_LYMPHOCYTE_ACTIVATION	0.695682	1.950923	1.00E-10	8.18E-09	5.71E-09
47	GOBP_B_CELL_DIFFERENTIATION	0.768486	1.95027	4.94E-09	2.64E-07	1.84E-07
48	GOBP_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	0.737033	1.947733	1.45E-09	8.85E-08	6.18E-08
49	GOBP_REGULATION_OF_T_CELL_ACTIVATION	0.707803	1.9431	1.00E-10	8.18E-09	5.71E-09
50	GOBP_POSITIVE_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	0.787993	1.939854	1.62E-07	6.09E-06	4.25E-06

Supplementary table 4b: Mouse retinal microglia-SenMayo-hi vs SenMayo-low –GSEA pathway enrichment terms top 50 terms – (FDR- qvalue < 0.05, NES > 1.5). Legend for Fig 2d- refer to top 30 terms.

No	ID	ES	NES	pval	p.adj	qval
1	REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS	0.862706	2.220181	1.00E-10	6.66E-09	5.10E-09
2	KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	0.813186	2.152557	1.00E-10	6.66E-09	5.10E-09
3	REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	0.931389	2.061244	3.24E-10	2.08E-08	1.60E-08
4	REACTOME_INTERLEUKIN_4_AND_INTERLEUKIN_13_SIGNALING	0.816951	2.049147	1.00E-10	6.66E-09	5.10E-09
5	REACTOME_CLASS_A_1_RHODOPSIN_LIKE_RECEPTORS	0.750866	2.029038	1.00E-10	6.66E-09	5.10E-09
6	KEGG_LEISHMANIA_INFECTION	0.869227	2.022064	1.40E-09	8.12E-08	6.22E-08
7	PID_AP1_PATHWAY	0.85073	2.008975	5.47E-09	2.89E-07	2.21E-07
8	REACTOME_INTERLEUKIN_10_SIGNALING	0.920799	2.002904	1.41E-08	7.03E-07	5.39E-07
9	KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.80706	1.970677	9.09E-09	4.67E-07	3.58E-07
10	KEGG_HEMATOPOIETIC_CELL_LINEAGE	0.818121	1.95968	9.14E-08	4.01E-06	3.07E-06
11	PID_IL6_7_PATHWAY	0.863833	1.952983	4.12E-07	1.54E-05	1.18E-05
12	REACTOME_SIGNALING_BY_INTERLEUKINS	0.689115	1.931653	1.00E-10	6.66E-09	5.10E-09
13	REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPTION_FACTOR_ACTIVATION	0.822975	1.927769	3.85E-07	1.47E-05	1.13E-05
14	PID_NFAT_TFPATHWAY	0.88615	1.927537	9.95E-07	3.44E-05	2.64E-05
15	PID_IL23_PATHWAY	0.911681	1.920539	1.08E-06	3.67E-05	2.81E-05
16	PID_IL12_2PATHWAY	0.823573	1.900182	2.53E-06	7.91E-05	6.06E-05
17	KEGG_JAK_STAT_SIGNALING_PATHWAY	0.7486	1.897009	7.68E-08	3.54E-06	2.71E-06
18	REACTOME_NGF_STIMULATED_TRANSCRIPTION	0.854059	1.890107	6.55E-06	0.000171	0.000131
19	PID_FRA_PATHWAY	0.867331	1.886602	8.41E-06	0.00021	0.000161
20	REACTOME_TOLL_LIKE_RECEPTOR_CASCADES	0.72388	1.882177	8.47E-08	3.80E-06	2.91E-06
21	KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION	0.742878	1.878243	3.31E-07	1.29E-05	9.90E-06
22	KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.810743	1.870581	7.42E-06	0.000188	0.000144
23	PID_SMAD2_3NUCLEAR_PATHWAY	0.778271	1.863265	2.14E-06	7.11E-05	5.45E-05

No	ID	ES	NES	pval	p.adj	qval
24	KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	0.816624	1.86275	6.17E-06	0.000167	0.000128
25	KEGG_LYSOSOME	0.735391	1.862376	6.05E-07	2.17E-05	1.67E-05
26	PID_BCR_5PATHWAY	0.787702	1.854001	6.86E-06	0.000176	0.000135
27	KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	0.810656	1.850407	3.89E-05	0.000848	0.00065
28	KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	0.766359	1.848144	1.02E-05	0.00025	0.000192
29	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	0.824129	1.823869	5.83E-05	0.001191	0.000913
30	REACTOME_INTERFERON_ALPHA_BETA_SIGNALING	0.785989	1.813467	3.92E-05	0.000848	0.00065
31	PID_FCER1_PATHWAY	0.77972	1.812243	3.47E-05	0.000769	0.00059
32	PID_IL4_2PATHWAY	0.787215	1.804182	5.10E-05	0.001068	0.000818
33	BIOCARTA_MAPK_PATHWAY	0.736785	1.78968	6.48E-06	0.000171	0.000131
34	PID_AMB2_NEUTROPHILS_PATHWAY	0.828907	1.786433	0.000101	0.001993	0.001527
35	REACTOME_SIGNALING_BY_NTRKS	0.689883	1.783641	2.39E-06	7.68E-05	5.88E-05
36	REACTOME_INTERFERON_GAMMA_SIGNALING	0.732595	1.783371	3.33E-05	0.000749	0.000574
37	REACTOME_TOLL_LIKE_RECEPTOR_TLR1_TLR2_CASCADE	0.71039	1.778671	4.48E-05	0.000958	0.000734
38	KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	0.707871	1.776125	1.63E-05	0.000381	0.000292
39	BIOCARTA_KERATINOCYTE_PATHWAY	0.785497	1.769928	0.000269	0.00484	0.003709
40	REACTOME_MYD88_INDEPENDENT_TLR4_CASCADE	0.708787	1.767321	5.11E-05	0.001068	0.000818
41	KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	0.800965	1.759921	0.000401	0.00668	0.005118
42	REACTOME_INTERLEUKIN_2_FAMILY_SIGNALING	0.790487	1.756	0.000452	0.007317	0.005606
43	KEGG_MAPK_SIGNALING_PATHWAY	0.644167	1.75411	1.67E-07	6.65E-06	5.10E-06
44	KEGG_GRAFT_VERSUS_HOST_DISEASE	0.858336	1.753878	0.000473	0.007514	0.005757
45	PID_PDGFRB_PATHWAY	0.678673	1.746284	1.59E-05	0.000376	0.000288
46	REACTOME_NEUTROPHIL_DEGRANULATION	0.620758	1.744091	1.78E-09	9.70E-08	7.44E-08
47	BIOCARTA_IL1R_PATHWAY	0.826055	1.74016	0.000718	0.010076	0.00772
48	BIOCARTA_PPARA_PATHWAY	0.761102	1.737295	0.000787	0.010739	0.008228
49	BIOCARTA_NKT_PATHWAY	0.905378	1.737082	0.000137	0.00257	0.001969
50	REACTOME_PERK_REGULATES_GENE_EXPRESSION	0.818218	1.737063	0.000791	0.010739	0.008228

Supplementary table 5: Top 50 DEGs- mouse retinal Mueller glia - SenMayo-hi vs SenMayo-low (pvaladj < 0.01)

Genes	pval	avg_log2 FC	pct. 1	pct. 2	p.adj
Vegfa	1.11E-248	0.563909	0.649	0.305	2.31E-244
Cebpd	1.43E-119	0.543643	0.879	0.652	2.98E-115
Socs3	7.80E-105	0.531604	0.655	0.443	1.62E-100
Jun	9.34E-176	0.508356	0.981	0.765	1.94E-171
Fos	2.65E-163	0.495905	0.968	0.78	5.51E-159
Fosb	7.63E-145	0.492667	0.932	0.674	1.59E-140

Genes	pval	avg_log2 FC	pct. 1	pct. 2	p.adj
Ccn1	6.55E-132	0.481493	0.898	0.644	1.36E-127
Btg2	2.25E-143	0.479724	0.949	0.719	4.68E-139
Zfp36	6.45E-117	0.469961	0.839	0.601	1.34E-112
Timp3	4.77E-147	0.466381	0.964	0.715	9.93E-143
Junb	5.59E-136	0.462877	0.955	0.736	1.16E-131
Adamts1	8.97E-103	0.458981	0.782	0.552	1.86E-98

Genes	pval	avg_log2 FC	pct.1	pct.2	p.adj
Il6st	3.10E-225	0.451357	0.628	0.3	6.45E-221
Egr1	7.31E-135	0.44264	0.955	0.731	1.52E-130
Igfbp4	1.41E-197	0.436479	0.573	0.272	2.94E-193
Dusp1	1.97E-116	0.432177	0.89	0.655	4.10E-112
Gas1	1.88E-86	0.428557	0.816	0.592	3.91E-82
Timp2	6.01E-192	0.428106	0.885	0.566	1.25E-187
Ctsb	1.07E-214	0.427234	0.852	0.504	2.22E-210
Zfp36l1	4.30E-123	0.424775	0.95	0.703	8.95E-119
Ier2	7.97E-116	0.405636	0.945	0.738	1.66E-111
Gadd45g	9.66E-51	0.397938	0.381	0.245	2.01E-46
Mmp14	8.61E-184	0.397103	0.389	0.151	1.79E-179
Nfkbiz	5.23E-98	0.394704	0.591	0.373	1.09E-93
Ier3	8.64E-59	0.393421	0.584	0.415	1.80E-54
Jund	1.54E-116	0.383791	0.98	0.791	3.21E-112
Aqp4	1.13E-118	0.379814	0.984	0.791	2.35E-114
Cebpb	1.90E-66	0.378762	0.477	0.31	3.96E-62
Hes1	7.30E-85	0.367614	0.949	0.742	1.52E-80
Ubc	1.69E-93	0.367603	0.975	0.778	3.52E-89
Bsg	2.77E-98	0.361527	0.998	0.874	5.76E-94
Cxcl16	1.10E-168	0.35663	0.721	0.407	2.29E-164
Trf	6.55E-68	0.355519	0.697	0.509	1.36E-63
Ccn2	6.57E-41	0.354584	0.43	0.302	1.37E-36
Ppp1r15a	9.01E-57	0.35378	0.506	0.344	1.87E-52
Atf3	7.71E-35	0.353285	0.266	0.169	1.60E-30
Cp	2.41E-102	0.350238	0.984	0.783	5.01E-98
Dkk3	2.28E-120	0.346962	0.995	0.846	4.74E-116
Mcl1	1.12E-99	0.346813	0.717	0.481	2.32E-95
Isg15	3.02E-16	0.346525	0.167	0.112	6.29E-12
Sox9	4.18E-96	0.345192	0.94	0.704	8.69E-92
Malat1	1.16E-126	0.343009	1	0.998	2.42E-122
Zfp36l2	1.20E-91	0.341559	0.903	0.664	2.49E-87
Ifit3	5.20E-31	0.339698	0.432	0.309	1.08E-26
Gpr37	1.17E-98	0.335353	0.979	0.748	2.43E-94
Plpp3	3.34E-104	0.333593	0.952	0.691	6.95E-100
Egfr	1.03E-146	0.333264	0.35	0.142	2.13E-142
Slc1a3	1.36E-96	0.332514	0.988	0.775	2.84E-92
Klf6	2.96E-63	0.328786	0.517	0.342	6.16E-59
Irf2bpl	6.25E-91	0.326296	0.746	0.509	1.30E-86

Supplementary table 6a: Mouse retinal Mueller glia-SenMayo-hi vs SenMayo-low –GSEA GO:BP – top 50 terms (FDR-qvalue < 0.05, NES > 1.5). Legend for Fig 3b- refer to top 30 terms.

No	ID	ES	NES	pval	p.adj	qval
1	GOBP_MORPHOGENESIS_OF_A_BRANCHING_STRUCTURE	0.751748	2.059233	1.00E-10	1.91E-08	1.39E-08
2	GOBP_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY	0.698313	2.052856	1.00E-10	1.91E-08	1.39E-08
3	GOBP_BRANCHING_MORPHOGENESIS_OF_AN_EPITHELIAL_TUBE	0.754244	2.012238	1.43E-10	2.62E-08	1.91E-08
4	GOBP_MULTI_MULTICELLULAR_ORGANISM_PROCESS	0.725379	1.989689	1.00E-10	1.91E-08	1.39E-08
5	GOBP_REGULATION_OF_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY	0.698637	1.972143	1.00E-10	1.91E-08	1.39E-08
6	GOBP_REGULATION_OF_EPITHELIAL_CELL_DIFFERENTIATION	0.748315	1.966853	6.70E-09	7.38E-07	5.38E-07
7	GOBP_EPITHELIAL_CELL_PROLIFERATION	0.665288	1.963904	1.00E-10	1.91E-08	1.39E-08
8	GOBP_RESPONSE_TO_BMP	0.728206	1.963363	1.24E-09	1.62E-07	1.18E-07
9	GOBP_REGULATION_OF_MORPHOGENESIS_OF_A_BRANCHING_STRUCTURE	0.855071	1.95202	1.71E-07	1.05E-05	7.62E-06
10	GOBP_RESPIRATORY_SYSTEM_DEVELOPMENT	0.701974	1.944848	5.93E-10	8.90E-08	6.48E-08
11	GOBP_SMAD_PROTEIN_SIGNAL_TRANSDUCTION	0.783834	1.94414	3.62E-07	1.93E-05	1.41E-05
12	GOBP_REGULATION_OF_ANIMAL_ORGAN_MORPHOGENESIS	0.743723	1.940978	1.85E-08	1.73E-06	1.26E-06
13	GOBP_REPRODUCTIVE_SYSTEM_DEVELOPMENT	0.654169	1.929693	1.00E-10	1.91E-08	1.39E-08

No	ID	ES	NES	pval	p.adj	qval
14	GOBP_RESPONSE_TO_FIBROBLAST_GROWTH_FACTOR	0.749465	1.927064	1.11E-07	7.77E-06	5.66E-06
15	GOBP_NEGATIVE_REGULATION_OF_VASCULATURE_DEVELOPMENT	0.752671	1.923341	2.03E-07	1.17E-05	8.53E-06
16	GOBP_REGULATION_OF_LIPID_BIOSYNTHETIC_PROCESS	0.712804	1.921837	1.09E-08	1.12E-06	8.17E-07
17	GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION	0.754805	1.913075	2.64E-07	1.47E-05	1.07E-05
18	GOBP_REGULATION_OF_MORPHOGENESIS_OF_AN_EPITHELIUM	0.807612	1.907477	1.17E-06	5.10E-05	3.72E-05
19	GOBP_NEGATIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_GROWTH_FACTOR_STIMULUS	0.752415	1.907299	2.53E-07	1.43E-05	1.04E-05
20	GOBP_MICROGLIAL_CELL_ACTIVATION	0.852182	1.906746	6.68E-07	3.25E-05	2.37E-05
21	GOBP_LEUKOCYTE_CELL_CELL_ADHESION	0.649517	1.905834	1.00E-10	1.91E-08	1.39E-08
22	GOBP_POSITIVE_REGULATION_OF_MORPHOGENESIS_OF_AN_EPITHELIUM	0.88579	1.905482	7.30E-07	3.44E-05	2.51E-05
23	GOBP_ASTROCYTE_DIFFERENTIATION	0.76774	1.904119	1.58E-06	6.30E-05	4.59E-05
24	GOBP_MATERNAL_PROCESS_INVOLVED_IN_FEMALE_PREGNANCY	0.808299	1.902081	2.32E-06	8.70E-05	6.34E-05
25	GOBP_POSITIVE_REGULATION_OF_LIPID_BIOSYNTHETIC_PROCESS	0.766257	1.898591	8.98E-07	4.05E-05	2.95E-05
26	GOBP_T_CELL_ACTIVATION	0.636442	1.896708	1.00E-10	1.91E-08	1.39E-08
27	GOBP_POSITIVE_REGULATION_OF_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY	0.729016	1.895115	1.32E-07	8.81E-06	6.42E-06
28	GOBP_REGULATION_OF_OSTEOBLAST_DIFFERENTIATION	0.72125	1.892225	1.99E-07	1.16E-05	8.47E-06
29	GOBP_REGULATION_OF_CELL_CELL_ADHESION	0.640464	1.889786	1.00E-10	1.91E-08	1.39E-08
30	GOBP_ERK1_AND_ERK2_CASCADE	0.650064	1.884651	2.07E-10	3.42E-08	2.49E-08
31	GOBP_NEGATIVE_REGULATION_OF_CELL_ADHESION	0.661685	1.883913	6.73E-10	9.53E-08	6.95E-08
32	GOBP_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_DIFFERENTIATION	0.865442	1.883817	2.83E-06	9.96E-05	7.26E-05
33	GOBP_ENDOTHELIUM_DEVELOPMENT	0.714376	1.879957	1.32E-07	8.81E-06	6.42E-06
34	GOBP_KIDNEY_MORPHOGENESIS	0.75128	1.879905	2.66E-06	9.68E-05	7.05E-05
35	GOBP_NEGATIVE_REGULATION_OF_REPRODUCTIVE_PROCESS	0.815163	1.879719	3.39E-06	0.000117	8.50E-05
36	GOBP_MESENCHYMAL_CELL_PROLIFERATION	0.854337	1.878932	1.42E-06	5.80E-05	4.22E-05
37	GOBP_POSITIVE_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING	0.756636	1.878079	2.38E-06	8.80E-05	6.41E-05
38	GOBP_POSITIVE_REGULATION_OF_CELL_CELL_ADHESION	0.663603	1.87434	1.96E-09	2.49E-07	1.81E-07
39	GOBP_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	0.6594	1.873077	2.06E-09	2.56E-07	1.86E-07
40	GOBP_MYELOID_LEUKOCYTE_DIFFERENTIATION	0.675958	1.872769	2.90E-08	2.52E-06	1.84E-06
41	GOBP_REGULATION_OF_MESENCHYMAL_CELL_PROLIFERATION	0.885411	1.870628	6.40E-06	0.000193	0.000141
42	GOBP_REGULATION_OF_CARTILAGE_DEVELOPMENT	0.773961	1.870077	4.50E-06	0.000145	0.000106
43	GOBP_GLAND_MORPHOGENESIS	0.716831	1.868461	8.67E-07	3.94E-05	2.87E-05
44	GOBP_NEGATIVE_REGULATION_OF_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY	0.710588	1.867693	6.18E-07	3.06E-05	2.23E-05
45	GOBP_GLIAL_CELL_DIFFERENTIATION	0.668454	1.866625	3.79E-08	3.13E-06	2.28E-06
46	GOBP_REGULATION_OF_BMP_SIGNALING_PATHWAY	0.732172	1.864162	2.82E-06	9.96E-05	7.26E-05
47	GOBP_REGULATION_OF_STEROID_BIOSYNTHETIC_PROCESS	0.781681	1.861921	4.46E-06	0.000145	0.000105
48	GOBP_FEMALE_SEX_DIFFERENTIATION	0.71315	1.861707	9.61E-07	4.25E-05	3.10E-05

No	ID	ES	NES	pval	p.adj	qval
49	GOBP_REGULATION_OF_T_CELL_ACTIVATION	0.641498	1.859814	9.68E-10	1.30E-07	9.45E-08
50	GOBP_POSITIVE_REGULATION_OF_ANIMAL_ORGAN_MORPHOGENESIS	0.889905	1.859629	5.67E-06	0.000178	0.00013

Supplementary table 6b: Mouse retinal Mueller glia-SenMayo-hi vs SenMayo-low –GSEA pathway enrichment terms – top 50 terms (FDR-qvalue < 0.05, NES > 1.5). Legend for Fig 3d- refer to top 30 terms.

No	ID	ES	NES	pval	p.adj	qval
1	KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	0.738025	2.044729	1.00E-10	7.49E-09	6.02E-09
2	REACTOME_INTERLEUKIN_4_AND_INTERLEUKIN_13_SIGNALING	0.785449	2.014442	1.97E-09	1.22E-07	9.79E-08
3	PID_AP1_PATHWAY	0.8221	1.988276	1.25E-08	7.47E-07	6.00E-07
4	REACTOME_DEGRADATION_OF_THE_EXTRACELLULAR_MATRIX	0.740191	1.946345	2.98E-08	1.73E-06	1.39E-06
5	REACTOME_INTERFERON_ALPHA_BETA_SIGNALING	0.822258	1.934929	2.90E-07	1.35E-05	1.08E-05
6	PID_IL6_7_PATHWAY	0.836911	1.920796	1.04E-06	4.36E-05	3.50E-05
7	REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION	0.670793	1.919089	1.00E-10	7.49E-09	6.02E-09
8	KEGG_JAK_STAT_SIGNALING_PATHWAY	0.724194	1.89763	1.02E-07	5.39E-06	4.33E-06
9	KEGG_CELL_ADHESION_MOLECULES_CAMS	0.729457	1.896061	1.61E-07	8.03E-06	6.46E-06
10	PID_NFAT_TFPATHWAY	0.85207	1.873947	8.24E-07	3.52E-05	2.83E-05
11	REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS	0.697564	1.863704	5.02E-07	2.20E-05	1.77E-05
12	PID_FGF_PATHWAY	0.793514	1.854784	5.28E-06	0.000183	0.000147
13	REACTOME_INTERLEUKIN_10_SIGNALING	0.839139	1.845509	1.94E-06	7.60E-05	6.10E-05
14	REACTOME_O_LINKED_GLYCOSYLATION	0.720441	1.840983	1.72E-06	6.85E-05	5.51E-05
15	REACTOME_COLLAGEN_DEGRADATION	0.782113	1.840461	1.10E-05	0.000358	0.000288
16	REACTOME_COLLAGEN_FORMATION	0.731369	1.834468	3.45E-06	0.000127	0.000102
17	KEGG_LEISHMANIA_INFECTION	0.760308	1.811013	4.88E-05	0.00127	0.001021
18	REACTOME_DISEASES_ASSOCIATED_WITH_O_GLYCOSYLATION_OF_PROTEINS	0.760698	1.80298	1.62E-05	0.000493	0.000396
19	REACTOME_CELL_CELL_COMMUNICATION	0.687115	1.80047	5.30E-06	0.000183	0.000147
20	REACTOME_CELL_SURFACE_INTERACTIONS_AT_THE_VASCULAR_WALL	0.692169	1.79914	5.21E-06	0.000183	0.000147

No	ID	ES	NES	pval	p.adj	qval
21	PID_INTEGRIN2_PATHWAY	0.902309	1.791389	1.77E-05	0.00053	0.000426
22	PID_ATF2_PATHWAY	0.771093	1.785354	3.36E-05	0.00093	0.000747
23	REACTOME_INTERFERON_GAMMA_SIGNALING	0.707895	1.775589	2.22E-05	0.000644	0.000517
24	KEGG_ADHERENS_JUNCTION	0.71332	1.767427	8.64E-05	0.002016	0.00162
25	PID_IL27_PATHWAY	0.877915	1.763778	7.65E-05	0.001833	0.001473
26	REACTOME_COLLAGEN_BIOSYNTHESIS_AND_MODIFYING_ENZYMES	0.727573	1.759659	0.000134	0.00264	0.002122
27	REACTOME_INTEGRIN_CELL_SURFACE_INTERACTIONS	0.702685	1.758157	5.29E-05	0.001338	0.001075
28	PID_INTEGRIN_A9B1_PATHWAY	0.863205	1.754074	0.00012	0.002517	0.002023
29	REACTOME_CELL_JUNCTION_ORGANIZATION	0.700597	1.753351	9.49E-05	0.002159	0.001735
30	REACTOME_DISEASES_OF_GLYCOSYLATION	0.655604	1.751597	2.38E-05	0.000679	0.000545
31	PID_S1P_S1P3_PATHWAY	0.828419	1.750219	0.000193	0.003417	0.002747
32	PID_IL12_2PATHWAY	0.74058	1.742726	0.000194	0.003417	0.002747
33	PID_TCR_CALCIUM_PATHWAY	0.843073	1.740513	0.000328	0.005312	0.004269
34	PID_SHP2_PATHWAY	0.738437	1.735544	0.000134	0.00264	0.002122
35	PID_FRA_PATHWAY	0.78792	1.732862	0.000137	0.00264	0.002122
36	PID_IL12_STAT4_PATHWAY	0.836308	1.726547	0.000491	0.007298	0.005866
37	BIOCARTA_INFLAM_PATHWAY	0.912058	1.724923	5.84E-05	0.001436	0.001154
38	REACTOME_CELL_CELL_JUNCTION_ORGANIZATION	0.732489	1.721567	0.000161	0.002985	0.002399
39	REACTOME_CONSTITUTIVE_SIGNALING_BY_ABERRANT_PI3K_IN_CANCER	0.694098	1.719748	0.000397	0.006098	0.004901
40	REACTOME_PHASE_I_FUNCTIONALIZATION_OF_COMPOUNDS	0.69277	1.719556	0.000289	0.004767	0.003831
41	REACTOME_NGF_STIMULATED_TRANSCRIPTION	0.768356	1.716848	0.00031	0.005072	0.004076
42	REACTOME_O_GLYCOSYLATION_OF_TSR_DOMAIN_CONTAINING_PROTEINS	0.770937	1.716453	0.000341	0.005479	0.004403
43	PID_GLYPICAN_1PATHWAY	0.830838	1.715253	0.000668	0.009227	0.007416
44	REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPHOID_CELL	0.680216	1.711397	0.000239	0.004099	0.003294

45	PID_TCPTP_PATHWAY	0.760724	1.708903	0.000435	0.006626	0.005325
46	REACTOME_UNFOLDED_PROTEIN_RESPONSE_UPR	0.670308	1.70478	0.000108	0.002338	0.001879
47	REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FACTOR_IGF_TRANSPORT_AND_UPTAKE_BY_INSULIN_LIKE_GROWTH_FACTOR_BINDING_PROTEINS_IGFBPS	0.661284	1.702604	0.000109	0.002338	0.001879
48	REACTOME_ASSEMBLY_OF_COLLAGEN_FIBRILS_AND_OTHER_MULTIMERIC_STRUCTURES	0.724354	1.702446	0.000266	0.004419	0.003551
49	REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	0.760643	1.699613	0.000486	0.007282	0.005852
50	REACTOME_ADHERENS_JUNCTIONS_INTERACTIONS	0.795848	1.697511	0.000454	0.006862	0.005515

Supplementary table 7a: Human retinal microglia (GSE148077) -SenMayo-hi vs SenMayo-low –GSEA pathway enrichment terms – top 30 terms (FDR-qvalue < 0.05, NES > 1.5). Legend for Fig 5c- refer to top 20 terms.

No	**ID**	**ES**	**NES**	**pval**	**p.adj**	**qval**
1	REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS	0.81218	2.282878	1.00E-10	1.83E-08	1.54E-08
2	KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	0.781286	2.268892	1.00E-10	1.83E-08	1.54E-08
3	REACTOME_INTERLEUKIN_4_AND_INTERLEUKIN_13_SIGNALING	0.806695	2.191156	1.73E-10	2.88E-08	2.42E-08
4	REACTOME_INTERLEUKIN_10_SIGNALING	0.907875	2.137208	1.12E-07	9.32E-06	7.84E-06
5	REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	0.896509	2.128728	1.74E-08	2.12E-06	1.79E-06
6	KEGG_LEISHMANIA_INFECTION	0.839961	2.111814	2.52E-08	2.87E-06	2.41E-06
7	REACTOME_CLASS_A_1_RHODOPSIN_LIKE_RECEPTORS	0.701693	2.088308	1.00E-10	1.83E-08	1.54E-08
8	KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	0.836646	2.061345	2.77E-07	2.03E-05	1.71E-05
9	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	0.860436	2.025531	1.29E-05	0.000493	0.000414
10	PID_FRA_PATHWAY	0.872392	2.005632	7.42E-06	0.000316	0.000266
11	REACTOME_INTERFERON_GAMMA_SIGNALING	0.743489	1.991636	1.18E-06	7.00E-05	5.89E-05
12	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	0.820198	1.984209	9.85E-06	0.000384	0.000323
13	PID_AP1_PATHWAY	0.792065	1.965024	2.57E-06	0.000135	0.000113
14	KEGG_AUTOIMMUNE_THYROID_DISEASE	0.867722	1.964329	2.54E-05	0.00088	0.00074
15	PID_NFAT_TFPATHWAY	0.839071	1.957601	6.65E-05	0.001748	0.001471
16	KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.735987	1.954415	5.25E-06	0.000253	0.000213
17	KEGG_ALLOGRAFT_REJECTION	0.873335	1.94759	2.62E-05	0.000887	0.000747
18	KEGG_ASTHMA	0.940623	1.946889	7.86E-06	0.000327	0.000275
19	PID_IL23_PATHWAY	0.871152	1.942723	2.81E-05	0.0009	0.000757
20	BIOCARTA_NKT_PATHWAY	0.934767	1.934769	1.34E-05	0.000502	0.000423
21	KEGG_GRAFT_VERSUS_HOST_DISEASE	0.853355	1.901049	6.87E-05	0.001763	0.001483
22	BIOCARTA_INFLAM_PATHWAY	0.924361	1.884004	5.86E-05	0.001602	0.001348
23	KEGG_TYPE_I_DIABETES_MELLITUS	0.800643	1.860757	0.000338	0.006202	0.005218
24	KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	0.739324	1.827281	0.000147	0.003134	0.002636

No	Description	ES	NES	pval	p.adj	qval
25	BIOCARTA_NTHI_PATHWAY	0.880643	1.826771	0.000484	0.008176	0.006879
26	BIOCARTA_TH1TH2_PATHWAY	0.919942	1.826087	0.000116	0.002698	0.00227
27	KEGG_HEMATOPOIETIC_CELL_LINEAGE	0.711289	1.823674	5.36E-05	0.001488	0.001252
28	KEGG_VIRAL_MYOCARDITIS	0.732814	1.818835	0.000196	0.003946	0.00332
29	REACTOME_SCAVENGING_BY_CLASS_A_RECEPTORS	0.897849	1.782232	0.000462	0.007907	0.006652
30	KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.718173	1.769449	0.000322	0.006094	0.005127

Supplementary table 7b: Human retinal Mueller glia (GSE148077) -SenMayo-hi vs SenMayo-low –GSEA pathway enrichment terms – top 30 terms (FDR-qvalue < 0.05, NES > 1.5). Legend for Fig 5d- refer to top 20 terms.

No	Description	ES	NES	pval	p.adj	qval
1	REACTOME_RESPONSE_OF_EIF2AK4_GCN2_TO_AMINO_ACID_DEFICIENCY	0.834127	1.997514	7.02E-09	1.84E-06	1.65E-06
2	REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION	0.843902	1.992297	1.19E-08	2.43E-06	2.18E-06
3	KEGG_RIBOSOME	0.840627	1.968646	6.09E-08	1.02E-05	9.10E-06
4	KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	0.745742	1.942426	1.13E-09	3.46E-07	3.10E-07
5	REACTOME_SELENOAMINO_ACID_METABOLISM	0.797735	1.91338	2.94E-07	4.15E-05	3.72E-05
6	REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	0.905215	1.886394	6.11E-07	7.00E-05	6.27E-05
7	REACTOME_NONSENSE_MEDIATED_DECAY_NMD	0.779545	1.873252	3.88E-07	4.85E-05	4.35E-05
8	REACTOME_INTERLEUKIN_10_SIGNALING	0.89762	1.84359	4.19E-06	0.000334	0.000299
9	PID_NFAT_TFPATHWAY	0.900024	1.840551	2.50E-06	0.000241	0.000216
10	REACTOME_EUKARYOTIC_TRANSLATION_INITIATION	0.759408	1.833904	4.45E-06	0.00034	0.000304
11	REACTOME_INTERLEUKIN_4_AND_INTERLEUKIN_13_SIGNALING	0.75807	1.815378	9.63E-06	0.000608	0.000545
12	PID_P53_DOWNSTREAM_PATHWAY	0.717056	1.76282	9.41E-06	0.000608	0.000545
13	KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.799599	1.757325	0.000134	0.004714	0.004226
14	REACTOME_NGF_STIMULATED_TRANSCRIPTION	0.852726	1.74253	0.000259	0.007914	0.007094
15	REACTOME_RRNA_PROCESSING	0.671617	1.716055	7.04E-06	0.000497	0.000445
16	PID_IL6_7_PATHWAY	0.818869	1.706456	0.000592	0.014091	0.012631
17	REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPTION_FACTOR_ACTIVATION	0.764352	1.701678	0.000546	0.013352	0.011969
18	PID_FRA_PATHWAY	0.834438	1.699974	0.000382	0.010142	0.009091
19	REACTOME_CELLULAR_RESPONSE_TO_STARVATION	0.676243	1.686687	6.92E-05	0.002881	0.002582
20	PID_HIV_NEF_PATHWAY	0.843516	1.677034	0.001381	0.027214	0.024395
21	PID_HIF1_TFPATHWAY	0.741297	1.675015	0.000634	0.01472	0.013196
22	REACTOME_INFLUENZA_INFECTION	0.666711	1.674684	8.77E-05	0.003417	0.003063
23	PID_AP1_PATHWAY	0.739496	1.670945	0.000666	0.015069	0.013508
24	REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS	0.655179	1.652596	9.39E-05	0.003442	0.003085
25	PID_IL12_STAT4_PATHWAY	0.840236	1.642522	0.002685	0.04543	0.040725
26	REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES	0.835741	1.642127	0.001982	0.035617	0.031928

No	ID	ES	NES	pval	p.adj	qval
27	BIOCARTA_HIVNEF_PATHWAY	0.751025	1.63143	0.001433	0.027496	0.024649
28	PID_ATF2_PATHWAY	0.745644	1.624164	0.001766	0.033039	0.029617
29	PID_IL12_2PATHWAY	0.741404	1.619714	0.001455	0.027496	0.024649
30	BIOCARTA_GRANULOCYTES_PATHWAY	0.956674	1.616256	0.000318	0.008893	0.007972

Supplementary table 7c: Human retinal astrocytes (GSE148077) -SenMayo-hi vs SenMayo-low –GSEA pathway enrichment terms – top 30 terms (FDR-qvalue < 0.05, NES > 1.5). Legend for Supp fig 5a- refer to top 20 terms.

No	ID	ES	NES	pval	p.adj	qval
1	REACTOME_RESPONSE_OF_EIF2AK4_GCN2_TO_AMINO_ACID_DEFICIENCY	0.789653	2.244382	1.00E-10	9.17E-08	8.32E-08
2	REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION	0.803945	2.244175	1.00E-10	9.17E-08	8.32E-08
3	KEGG_RIBOSOME	0.778534	2.15139	2.53E-09	1.16E-06	1.05E-06
4	REACTOME_CELLULAR_RESPONSE_TO_STARVATION	0.698754	2.092566	1.45E-09	8.87E-07	8.05E-07
5	REACTOME_EUKARYOTIC_TRANSLATION_INITIATION	0.723646	2.076676	3.21E-09	1.18E-06	1.07E-06
6	PID_HIF1_TFPATHWAY	0.773086	2.044637	1.03E-06	0.00021	0.000191
7	REACTOME_SELENOAMINO_ACID_METABOLISM	0.707968	2.026849	3.47E-07	9.10E-05	8.25E-05
8	PID_AP1_PATHWAY	0.759936	2.00986	2.69E-06	0.000449	0.000407
9	REACTOME_INTERLEUKIN_4_AND_INTERLEUKIN_13_SIGNALING	0.694876	1.975003	2.06E-06	0.000377	0.000342
10	REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	0.801381	1.963701	8.55E-06	0.001119	0.001016
11	REACTOME_NONSENSE_MEDIATED_DECAY_NMD	0.672489	1.93453	9.23E-07	0.00021	0.000191
12	PID_FRA_PATHWAY	0.804846	1.909859	3.15E-05	0.002885	0.002618
13	PID_IL23_PATHWAY	0.820421	1.90554	7.07E-05	0.0054	0.0049
14	KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.729771	1.901911	2.92E-05	0.002821	0.002559
15	REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	0.657123	1.882321	1.30E-05	0.001489	0.001351
16	REACTOME_INTERLEUKIN_10_SIGNALING	0.771088	1.854483	0.000111	0.007839	0.007113
17	KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	0.59504	1.837039	2.32E-07	7.09E-05	6.44E-05
18	PID_TAP63_PATHWAY	0.723098	1.836051	8.02E-05	0.005878	0.005333
19	PID_HIF2PATHWAY	0.788605	1.831642	0.000301	0.016723	0.015173
20	REACTOME_INFLUENZA_INFECTION	0.608098	1.825568	4.11E-06	0.000579	0.000525
21	PID_P53_DOWNSTREAM_PATHWAY	0.619174	1.813956	1.19E-05	0.001456	0.001321
22	BIOCARTA_LAIR_PATHWAY	0.912272	1.811718	6.20E-05	0.004942	0.004484
23	PID_DELTA_NP63_PATHWAY	0.74048	1.797287	0.000444	0.023243	0.021089
24	PID_ATF2_PATHWAY	0.684028	1.761698	0.001193	0.046515	0.042205
25	REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_CAP_BINDING_COMPLEX_AND_EIFS_AND_SUBSEQUENT_BINDING_TO_43S	0.675497	1.759778	0.000706	0.030268	0.027463
26	BIOCARTA_GRANULOCYTES_PATHWAY	0.89729	1.733212	0.000704	0.030268	0.027463
27	BIOCARTA_GHRELIN_PATHWAY	0.945468	1.707186	0.000292	0.016723	0.015173
28	PID_CMYB_PATHWAY	0.620718	1.698656	0.001363	0.049048	0.044504

No	ID	ES	NES	pval	p.adj	qval
29	REACTOME_RRNA_PROCESSING	0.543455	1.658366	5.45E-05	0.004755	0.004315
30	REACTOME_CELL_SURFACE_INTERACTIONS_AT_THE_VASCULAR_WALL	0.544773	1.595989	0.000716	0.030268	0.027463

Supplementary table 8a: DEG list for mouse Mueller glia: 12-mo vs 3-mo (pvaladj < 0.01,| LFC | > 0.25, top 25 up and downregulated)

Genes	pval	avg_log2FC	pct.1	pct.2	p.adj
Prss56	6.21E-152	1.478028	0.313	0.113	1.29E-147
Xist	5.95E-144	1.326191	0.2	0.037	1.24E-139
Nupr1	0	1.19632	0.67	0.323	0
Ifit1	4.31E-149	1.19426	0.21	0.042	8.96E-145
Ifit3	1.33E-43	1.064545	0.397	0.27	2.77E-39
Isg15	5.87E-83	1.018049	0.173	0.055	1.22E-78
Ifi27	1.44E-269	1.015639	0.519	0.203	3.00E-265
Rho	0	1.001992	0.908	0.607	0
Gnat1	1.06E-268	0.911875	0.703	0.347	2.21E-264
Rsad2	7.10E-97	0.822608	0.138	0.025	1.48E-92
Mt3	2.86E-180	0.797387	0.684	0.439	5.95E-176
Opn1sw	6.69E-85	0.772684	0.277	0.121	1.39E-80
Rom1	1.91E-147	0.742135	0.625	0.35	3.96E-143
Pde6h	4.02E-76	0.734459	0.295	0.141	8.36E-72
Rcvrn	7.03E-113	0.725375	0.403	0.192	1.46E-108
Necab2	4.11E-166	0.700342	0.428	0.182	8.54E-162
Prph2	1.45E-116	0.677221	0.47	0.241	3.02E-112
Guca1a	1.94E-93	0.675987	0.417	0.222	4.04E-89
Pdc	3.23E-117	0.668942	0.574	0.329	6.72E-113
Rpl38	3.81E-270	0.64499	0.929	0.933	7.92E-266
Rp1	3.71E-106	0.630189	0.36	0.164	7.71E-102
Rbp3	5.17E-86	0.624273	0.353	0.176	1.08E-81
Gnb1	1.18E-117	0.610353	0.784	0.571	2.45E-113
Rpl35	4.28E-133	0.608803	0.792	0.682	8.91E-129
Pde6g	2.16E-105	0.595803	0.533	0.303	4.49E-101

Genes	pval	avg_log2FC	pct.1	pct.2	p.adj
Slc1a3	1.58E-249	-0.54414	0.798	0.925	3.29E-245
Kdr	1.37E-166	-0.54908	0.757	0.874	2.85E-162
mt-Nd2	0	-0.54964	0.991	0.997	0
Hist1h1b	8.46E-34	-0.55177	0.121	0.192	1.76E-29
Chst2	5.70E-131	-0.56556	0.507	0.623	1.18E-126
Col9a1	5.42E-121	-0.56756	0.618	0.722	1.13E-116
Plk2	3.34E-52	-0.57112	0.236	0.333	6.94E-48
Mt1	4.36E-202	-0.57879	0.856	0.942	9.07E-198
Etnppl	5.29E-64	-0.58212	0.391	0.485	1.10E-59
Abca8a	6.69E-282	-0.61959	0.809	0.919	1.39E-277
Itgb8	5.31E-138	-0.63436	0.347	0.5	1.10E-133
Dkk3	0	-0.64048	0.86	0.949	0
Utp14b	1.04E-144	-0.66757	0.617	0.722	2.17E-140
Hist1h1e	3.91E-240	-0.69669	0.518	0.746	8.13E-236
Spc25	9.64E-308	-0.7042	0.796	0.945	2.00E-303
Galnt13	2.62E-214	-0.70676	0.15	0.37	5.45E-210
Dio2	7.79E-135	-0.73206	0.225	0.386	1.62E-130
Eno1b	1.68E-214	-0.73679	0.476	0.648	3.49E-210
Ccn2	2.14E-39	-0.73743	0.315	0.394	4.45E-35
Slmap	1.15E-304	-0.75615	0.761	0.875	2.39E-300
Fosb	3.59E-183	-0.79954	0.718	0.838	7.47E-179
Dbp	0	-0.90966	0.636	0.838	0
mt-Atp8	0	-0.99264	0.668	0.896	0
Ciart	2.37E-283	-1.00428	0.15	0.411	4.92E-279
Car14	0	-1.07032	0.765	0.912	0

Supplementary table 8b: DEG list for mouse Mueller glia: 24-mo vs 3-mo (pvaladj < 0.01,| LFC | > 0.25, top 25 up and downregulated)

Genes	pval	avg_log2FC	pct.1	pct.2	p.adj
Bc1	2.19E-115	2.16122	0.741	0.371	4.56E-111
Rp1	1.05E-237	2.074836	0.73	0.164	2.19E-233
Rho	4.06E-206	1.925375	0.989	0.607	8.44E-202
Rpgrip1	5.41E-137	1.837112	0.606	0.182	1.13E-132
Pdc	5.81E-168	1.805171	0.843	0.329	1.21E-163
Pde6b	9.54E-160	1.765033	0.562	0.131	1.98E-155
Gnat1	6.13E-159	1.733958	0.841	0.347	1.27E-154
Pde6a	1.10E-148	1.667705	0.492	0.107	2.29E-144
Pde6g	1.37E-110	1.5974	0.727	0.303	2.84E-106
Rcvrn	1.73E-107	1.581029	0.573	0.192	3.59E-103
Rom1	2.82E-114	1.570666	0.773	0.35	5.87E-110
Kcnb1	2.67E-107	1.549813	0.552	0.182	5.56E-103
Mir124a-1hg	1.04E-131	1.532951	0.43	0.09	2.15E-127
Tulp1	3.38E-99	1.526832	0.584	0.208	7.02E-95
Mir124-2hg	6.19E-94	1.479731	0.546	0.193	1.29E-89
Nr2e3	7.20E-142	1.470954	0.414	0.076	1.50E-137
Gm42418	1.91E-218	1.456251	1	1	3.97E-214
Hk2	1.45E-72	1.453487	0.417	0.141	3.01E-68
Guca1a	8.57E-101	1.436068	0.606	0.222	1.78E-96
Sag	4.76E-108	1.428923	0.784	0.382	9.89E-104
Slc24a1	6.83E-72	1.419624	0.465	0.17	1.42E-67
Prph2	4.65E-112	1.418754	0.662	0.241	9.66E-108
Gnb1	8.19E-85	1.365061	0.843	0.571	1.70E-80
Gngt1	5.59E-120	1.358523	0.895	0.478	1.16E-115
Neurod1	7.74E-72	1.358507	0.389	0.121	1.61E-67

Genes	pval	avg_log2FC	pct.1	pct.2	p.adj
Car14	1.43E-93	-1.0435	0.632	0.912	2.97E-89
Gm26532	3.85E-36	-1.05593	0.143	0.378	8.01E-32
Hes5	7.06E-28	-1.05992	0.41	0.604	1.47E-23
Timp3	1.72E-80	-1.07038	0.548	0.868	3.57E-76
Gas1	1.27E-40	-1.08163	0.454	0.698	2.64E-36
Klf4	2.87E-35	-1.09635	0.097	0.335	5.97E-31
Ccn2	4.51E-25	-1.10342	0.203	0.394	9.38E-21
Col9a1	1.18E-73	-1.11167	0.408	0.722	2.46E-69
Zfp36l1	7.33E-78	-1.11336	0.517	0.851	1.52E-73
Klf6	1.35E-44	-1.15286	0.168	0.437	2.80E-40
Ciart	6.36E-66	-1.21701	0.065	0.411	1.32E-61
Mt1	2.48E-129	-1.2243	0.694	0.942	5.15E-125
Nfkbiz	4.74E-66	-1.26943	0.178	0.506	9.86E-62
Socs3	4.82E-45	-1.27393	0.251	0.515	1.00E-40
Jun	1.02E-116	-1.30709	0.567	0.897	2.12E-112
Dbp	1.71E-133	-1.3505	0.433	0.838	3.55E-129
Btg2	3.42E-119	-1.5354	0.54	0.858	7.12E-115
Junb	1.86E-129	-1.54349	0.498	0.881	3.86E-125
Egr1	6.42E-140	-1.55746	0.563	0.87	1.33E-135
Fos	7.54E-147	-1.56699	0.573	0.897	1.57E-142
Ier2	1.04E-147	-1.70768	0.502	0.869	2.17E-143
Zfp36	5.68E-113	-1.74021	0.338	0.75	1.18E-108
Fosb	1.17E-130	-1.83813	0.452	0.838	2.43E-126
Ccn1	2.68E-132	-1.894	0.378	0.799	5.57E-128
Dusp1	3.33E-146	-2.01071	0.373	0.806	6.92E-142

Supplementary table 8c: IPA canonical pathway- comparison analysis for mouse Mueller Glia (pval < 0.05, top 50 based on z-score)

Canonical Pathways	12mo vs 3mo	24mo vs 3mo
Visual phototransduction	4.243	4.264
Nonsense-Mediated Decay (NMD)	4.796	2.828
Eukaryotic Translation Elongation	4.796	2.828
Eukaryotic Translation Termination	4.796	2.828
Eukaryotic Translation Initiation	4.796	2.333
Selenoamino acid metabolism	4.796	2.333
SRP-dependent cotranslational protein targeting to membrane	4.6	2.333

Canonical Pathways	12mo vs 3mo	24mo vs 3mo
Role of Tissue Factor in Cancer	-3	-3.873
Major pathway of rRNA processing in the nucleolus and cytosol	4.491	2.333
Pulmonary Fibrosis Idiopathic Signaling Pathway	-2.84	-3.545
Response of EIF2AK4 (GCN2) to amino acid deficiency	4.796	1.508
Coronavirus Pathogenesis Pathway	-2.714	-3
NGF-stimulated transcription	-2.449	-2.887
Cell junction organization	-2.236	-3

Canonical Pathways	12mo vs 3mo	24mo vs 3mo
EIF2 Signaling	4.123	1
Protein Kinase A Signaling	3.13	1.8
O-linked glycosylation	-2	-2.828
NCAM signaling for neurite out-growth	-2	-2.714
Wound Healing Signaling Pathway	-1.633	-3.051
Signaling by TGF-beta Receptor Complex	-1.342	-3.162
Neutrophil degranulation	2.53	-1.964
Role of Hypercytokinemia/hyperchemokinemia in the Pathogenesis of Influenza	2.236	2.236
Extracellular matrix organization	-1.89	-2.496
Nuclear Cytoskeleton Signaling Pathway	-2.236	-2.111
Molecular Mechanisms of Cancer	0.2	-4.11
RHO GTPase cycle	-1.265	-2.982
Oxidative Phosphorylation	4.243	N/A
TP53 Regulates Metabolic Genes	2.236	-2
Amyloid fiber formation	2.236	-2
G-Protein Coupled Receptor Signaling	2.858	-1.372
Integrin cell surface interactions	-1.414	-2.714
STAT3 Pathway	-2.236	-1.89
SNARE Signaling Pathway	2.646	1.414
Sertoli Cell-Sertoli Cell Junction Signaling	-1.89	-2.138
Pathogen Induced Cytokine Storm Signaling Pathway	-1	-3
Interferon alpha/beta signaling	2.714	1.265
CREB Signaling in Neurons	-1.069	-2.887
Neutrophil Extracellular Trap Signaling Pathway	3	0.905
Signaling by VEGF	-1.342	-2.53
IL-15 Production	-1.342	-2.53
RAF/MAP kinase cascade	-0.707	-3.153
Interferon Signaling	2.449	1.342
Electron transport, ATP synthesis, and heat production by uncoupling proteins	3.771	N/A
D-myo-inositol (3,4,5,6)-tetrakisphosphate Biosynthesis	-1.342	-2.333
D-myo-inositol-5-phosphate Metabolism	-1.342	-2.333
3-phosphoinositide Degradation	-1.342	-2.333
3-phosphoinositide Biosynthesis	-1.342	-2.333
D-myo-inositol (1,4,5,6)-Tetrakisphosphate Biosynthesis	-1.342	-2.333
Superpathway of Inositol Phosphate Compounds	-1.342	-2.333

Supplementary table 9a: DEG list for mouse Rod photoreceptors: 12-mo vs 3-mo (pvaladj < 0.01,| LFC | > 0.25, top 25 up and downregulated)

Genes	pval	avg_log2 FC	pct. 1	pct. 2	p.adj
Hist3h2ba	7.23E-228	1.008311	0.305	0.096	1.50E-223
AY036118	0	0.98591	0.772	0.574	0
Rnpc3	6.62E-149	0.95084	0.31	0.141	1.38E-144
Peg3	4.24E-143	0.93747	0.328	0.16	8.82E-139
Hist3h2a	1.79E-227	0.918432	0.388	0.159	3.71E-223
Eif2s3y	5.55E-116	0.82353	0.123	0.023	1.15E-111
Gria2	6.53E-73	0.778543	0.161	0.069	1.36E-68
Pcp4l1	2.83E-127	0.731408	0.239	0.097	5.88E-123
Ptprn	1.26E-78	0.710402	0.119	0.038	2.62E-74
Gm16982	2.51E-50	0.677225	0.116	0.05	5.23E-46
Glb1l3	5.17E-137	0.633093	0.163	0.038	1.08E-132
Pitpnm3	5.71E-66	0.624353	0.314	0.204	1.19E-61
Gm42418	6.53E-203	0.609506	1	1	1.36E-198
Dnah7b	1.27E-63	0.597683	0.141	0.06	2.63E-59
Frmpd2	7.14E-52	0.593189	0.189	0.106	1.49E-47
Smug1	9.08E-60	0.591271	0.197	0.107	1.89E-55
Ahi1	3.01E-95	0.577239	0.485	0.336	6.26E-91
Adgrv1	1.01E-49	0.561756	0.256	0.166	2.11E-45
Meis2	1.35E-64	0.541322	0.327	0.214	2.82E-60
Pfkp	3.09E-61	0.535691	0.355	0.243	6.42E-57
Rpgrip1	1.27E-121	0.533983	0.779	0.628	2.64E-117
Bcl2	2.94E-50	0.526728	0.11	0.046	6.11E-46
Hdc	2.69E-56	0.522765	0.1	0.036	5.59E-52
Gm11961	6.04E-59	0.52269	0.157	0.075	1.26E-54
Mycbp2	3.31E-49	0.51727	0.298	0.203	6.88E-45
Ubb	4.04E-96	-0.36599	0.789	0.849	8.41E-92
Lrrc2	6.60E-21	-0.3664	0.08	0.12	1.37E-16
Ip6k2	3.38E-21	-0.37947	0.141	0.189	7.03E-17
Tuba1b	1.76E-27	-0.38288	0.372	0.429	3.66E-23
Jun	5.37E-10	-0.38879	0.125	0.152	1.12E-05
Ptms	2.22E-20	-0.3968	0.213	0.263	4.62E-16
Vtn	4.23E-53	-0.40737	0.601	0.65	8.79E-49

Genes	pval	avg_log2FC	pct.1	pct.2	p.adj
Gngt1	1.43E-142	-0.4111	0.976	0.979	2.97E-138
Ndufs2	2.02E-33	-0.42018	0.438	0.489	4.20E-29
Ssu72	2.14E-44	-0.43343	0.436	0.505	4.44E-40
Sncb	9.01E-32	-0.4414	0.24	0.306	1.87E-27
Phpt1	1.01E-42	-0.45513	0.097	0.161	2.09E-38
Glul	1.38E-20	-0.47893	0.165	0.211	2.87E-16
Bloc1s1	2.36E-47	-0.48436	0.079	0.143	4.92E-43
Gm11808	2.55E-36	-0.49419	0.132	0.195	5.30E-32
Ndufaf5	3.50E-57	-0.50692	0.077	0.147	7.27E-53

Genes	pval	avg_log2FC	pct.1	pct.2	p.adj
Rs1	2.87E-74	-0.50962	0.659	0.701	5.96E-70
Apoe	9.09E-13	-0.52977	0.202	0.232	1.89E-08
Rbm3	8.51E-52	-0.56719	0.13	0.208	1.77E-47
Gnb3	1.19E-29	-0.56899	0.14	0.196	2.48E-25
Sag	0	-0.60358	0.981	0.992	0
Eno1b	4.27E-108	-0.69842	0.105	0.216	8.88E-104
Uba52	2.07E-114	-0.82195	0.304	0.422	4.30E-110
Tsix	0	-2.18841	0.024	0.245	0
Xist	0	-2.90352	0.054	0.44	0

Supplementary table 9b: DEG list for mouse Rod photoreceptors: 24-mo vs 3-mo (pvaladj < 0.01,| LFC | > 0.25, top 25 up and downregulated)

Genes	pval	avg_log2FC	pct.1	pct.2	p.adj
Gm42418	0	1.231456	1	1	0
Eif2s3y	7.50E-214	1.052482	0.187	0.023	1.56E-209
Bc1	4.01E-238	1.047307	0.559	0.299	8.33E-234
Hist3h2a	0	1.033233	0.448	0.159	0
Hist3h2ba	6.49E-255	0.985234	0.328	0.096	1.35E-250
Csrp3	7.68E-171	0.899695	0.135	0.011	1.60E-166
Gm11961	1.21E-168	0.897565	0.239	0.075	2.52E-164
Pcp4l1	2.07E-173	0.887248	0.271	0.097	4.31E-169
Glb1l3	1.15E-192	0.806981	0.2	0.038	2.39E-188
Rnpc3	8.24E-151	0.806868	0.32	0.141	1.71E-146
Hk2	0	0.773066	0.869	0.608	0
Peg3	4.84E-133	0.740391	0.33	0.16	1.01E-128
Ptprn	2.94E-113	0.727725	0.145	0.038	6.11E-109
Negr1	5.22E-136	0.667225	0.386	0.204	1.09E-131
Col4a3	1.10E-99	0.649641	0.146	0.043	2.29E-95
Meis2	1.67E-108	0.616657	0.371	0.214	3.48E-104
3222401L13Rik	5.75E-94	0.609178	0.288	0.153	1.20E-89
Mrpl9	7.05E-61	0.603247	0.253	0.147	1.47E-56
Ddx3y	3.03E-98	0.599452	0.105	0.019	6.31E-94
Mef2c	1.29E-182	0.592919	0.722	0.507	2.68E-178
Vax2os	2.54E-171	0.576385	0.719	0.489	5.28E-167
Malat1	1.99E-244	0.574224	1	0.995	4.15E-240
Osbpl1a	1.39E-93	0.567056	0.182	0.07	2.88E-89

Genes	pval	avg_log2FC	pct.1	pct.2	p.adj
Nr2e3	1.47E-226	0.564402	0.85	0.649	3.05E-222
Gria2	7.10E-58	0.560644	0.151	0.069	1.48E-53
Clstn1	7.29E-35	-0.51991	0.393	0.439	1.52E-30
Arl3	1.82E-46	-0.52037	0.502	0.544	3.79E-42
mt-Nd2	4.06E-113	-0.52173	0.852	0.873	8.45E-109
Rps7	2.33E-71	-0.52794	0.585	0.64	4.85E-67
Rps24	1.13E-86	-0.52843	0.648	0.709	2.35E-82
Ndufaf5	1.98E-62	-0.53451	0.071	0.147	4.12E-58
Clu	1.35E-36	-0.53478	0.053	0.102	2.80E-32
Sag	0	-0.54681	0.987	0.992	0
Rpl13	7.43E-77	-0.55498	0.613	0.669	1.55E-72
mt-Cytb	8.16E-157	-0.55889	0.896	0.933	1.70E-152
Rps10	2.64E-61	-0.56203	0.518	0.572	5.50E-57
Cox6c	1.24E-81	-0.56849	0.577	0.637	2.59E-77
Unc119	5.14E-274	-0.60111	0.858	0.886	1.07E-269
Ubb	2.39E-228	-0.62961	0.788	0.849	4.97E-224
Gngt1	3.41E-269	-0.6339	0.975	0.979	7.10E-265
Gnb3	7.10E-36	-0.64766	0.132	0.196	1.48E-31
Gm47283	5.92E-39	-0.64819	0.18	0.255	1.23E-34
Selenow	3.50E-59	-0.69884	0.301	0.386	7.27E-55
Rbm3	1.80E-100	-0.75551	0.097	0.208	3.74E-96
Dbi	1.88E-68	-0.77058	0.095	0.182	3.92E-64
Gnas	8.03E-133	-0.81939	0.093	0.222	1.67E-128

Genes	pval	avg_log2FC	pct.1	pct.2	p.adj
Glul	8.52E-96	-0.90569	0.104	0.211	1.77E-91
Apoe	2.00E-85	-1.00786	0.129	0.232	4.16E-81

Genes	pval	avg_log2FC	pct.1	pct.2	p.adj
Tsix	0	-2.54824	0	0.245	0
Xist	0	-4.14564	0	0.44	0

Supplementary table 9c: IPA canonical pathway- comparison analysis for mouse Rod photoreceptors (pval < 0.05, top 50 based on z-score)

Canonical Pathways	12mo vs 3mo	24mo vs 3mo
Eukaryotic Translation Elongation	-4.583	-7.874
Eukaryotic Translation Initiation	-4.583	-7.746
SRP-dependent cotranslational protein targeting to membrane	-4.583	-7.746
Response of EIF2AK4 (GCN2) to amino acid deficiency	-4.583	-7.681
Selenoamino acid metabolism	-4.583	-7.681
Eukaryotic Translation Termination	-4.583	-7.681
Nonsense-Mediated Decay (NMD)	-4.583	-7.488
Major pathway of rRNA processing in the nucleolus and cytosol	-3.962	-7.298
EIF2 Signaling	-2.714	-5.333
Coronavirus Pathogenesis Pathway	2.673	4.747
Parkinson's Signaling Pathway	2.828	3.441
Processing of Capped Intron-Containing Pre-mRNA	2	2.496
RUNX1 regulates megakaryocyte differentiation and platelet function	2	2.236
RHO GTPase cycle	1.897	2.111
Neutrophil degranulation	1	-2.982
MicroRNA Biogenesis Signaling Pathway	2	1.89
Synaptic Long Term Depression	1.89	1.89
Oxytocin in Brain Signaling Pathway	1.89	1.633
Electron transport, ATP synthesis, and heat production by uncoupling proteins	N/A	-3.464
Oxidative Phosphorylation	N/A	-3.464
Beta-catenin independent WNT signaling	-1.633	-1.667
Ion channel transport	2.236	-0.816
MAPK6/MAPK4 signaling	-1	-2
Endocannabinoid Neuronal Synapse Pathway	1.633	1.134

Canonical Pathways	12mo vs 3mo	24mo vs 3mo
Cellular Effects of Sildenafil (Viagra)	-1.155	-1.5
TP53 Regulates Metabolic Genes	N/A	-2.646
Mitochondrial Dysfunction	-0.447	2.065
Protein folding	-1.342	-1
Vasopressin regulates renal water homeostasis via Aquaporins	-1	-1.342
GPER1 signaling	-1	-1.342
G alpha (z) signalling events	-1	-1.342
Phototransduction Pathway	-1.134	-1.134
Dopamine-DARPP32 Feedback in cAMP Signaling	N/A	-2.236
Amyloid fiber formation	N/A	-2.236
Orexin Signaling Pathway	0.816	-1.414
Gap Junction Signaling	-1.414	-0.816
Visual phototransduction	-1.414	-0.707
Granzyme A Signaling	N/A	2.121
ERK5 Signaling	N/A	2
Transport of inorganic cations/anions and amino acids/oligopeptides	2	N/A
NR1H2 and NR1H3-mediated signaling	N/A	-2
Formation of WDR5-containing histone-modifying complexes	N/A	2
Platelet homeostasis	-1	-1
Class B/2 (Secretin family receptors)	-1	-1
Mitophagy	N/A	-2
L1CAM interactions	0	2
Extra-nuclear estrogen signaling	0.816	1.134
Clathrin-mediated endocytosis	1.134	0.816
Hematoma Resolution Signaling Pathway	N/A	-1.941

Supplementary table 10a: DEG list for mouse Cone photoreceptors: 12-mo vs 3-mo (pvaladj < 0.01,| LFC | > 0.25, top 25 up and downregulated)

Genes	pval	avg_log2FC	pct.1	pct.2	p.adj
Hbb-bs	1.36E-10	1.58721	0.134	0.07	2.82E-06
Pcp4l1	3.55E-178	1.292649	0.545	0.104	7.39E-174
Pcp2	4.93E-30	0.906482	0.249	0.102	1.03E-25
Drd4	1.29E-111	0.86543	0.635	0.283	2.67E-107
Gng13	3.42E-43	0.743891	0.387	0.176	7.10E-39
Fabp7	5.02E-72	0.645879	0.451	0.165	1.04E-67
Ttyh1	1.18E-63	0.609185	0.739	0.482	2.46E-59

Genes	pval	avg_log2FC	pct.1	pct.2	p.adj
Car2	6.10E-65	0.58998	0.83	0.633	1.27E-60
mt-Co1	1.94E-115	0.567281	0.998	0.996	4.04E-111
Mef2c	2.50E-51	0.564951	0.509	0.268	5.19E-47
Plekhb1	3.92E-76	0.546717	0.879	0.801	8.16E-72
Trnp1	6.20E-23	0.488225	0.156	0.054	1.29E-18
Gnat1	1.66E-75	0.477889	0.702	0.363	3.45E-71
Atp2b1	1.17E-48	0.467507	0.87	0.753	2.44E-44

Genes	pval	avg_log2 FC	pct. 1	pct. 2	p.adj
Ptprn	7.26E-33	0.449647	0.477	0.277	1.51E-28
mt-Nd3	4.63E-50	0.449178	0.985	0.976	9.62E-46
Pcp4	3.28E-17	0.446877	0.167	0.075	6.83E-13
Mogat1	5.81E-42	0.432616	0.357	0.157	1.21E-37
Nr2e3	8.82E-18	0.412557	0.227	0.119	1.83E-13
Rnpc3	7.55E-18	0.386607	0.644	0.475	1.57E-13
Rpl35	9.17E-33	0.385839	0.635	0.417	1.91E-28
Rcvrn	2.90E-55	0.378124	0.922	0.929	6.02E-51
Gnb1	9.82E-43	0.376432	0.619	0.366	2.04E-38
Rpl38	1.38E-37	0.372838	0.861	0.731	2.87E-33
Actg1	1.68E-31	0.365001	0.801	0.622	3.48E-27
Jchain	5.24E-15	-0.42046	0.3	0.371	1.09E-10
Rbp3	1.56E-63	-0.4268	0.932	0.945	3.24E-59
Grk1	6.98E-28	-0.43958	0.654	0.685	1.45E-23
Usp2	1.40E-17	-0.44713	0.417	0.48	2.90E-13
Galnt13	1.47E-11	-0.44995	0.364	0.408	3.05E-07
Slc24a2	5.81E-30	-0.47476	0.571	0.629	1.21E-25
Bc1	2.47E-21	-0.48014	0.205	0.313	5.14E-17

Genes	pval	avg_log2 FC	pct. 1	pct. 2	p.adj
Kcne2	9.86E-32	-0.48988	0.669	0.742	2.05E-27
Thrb	1.21E-18	-0.49016	0.628	0.649	2.51E-14
Eno1b	1.01E-27	-0.51691	0.173	0.286	2.10E-23
Rtbdn	1.80E-84	-0.54809	0.895	0.93	3.74E-80
Pdc	2.58E-100	-0.55283	0.942	0.949	5.36E-96
Rbm3	1.72E-29	-0.56913	0.458	0.546	3.58E-25
Olfm1	2.04E-55	-0.57163	0.729	0.807	4.24E-51
Uba52	2.51E-27	-0.57627	0.414	0.491	5.22E-23
Sag	1.40E-155	-0.57824	0.977	0.969	2.91E-151
Ip6k2	1.07E-31	-0.59683	0.41	0.507	2.23E-27
Stxbp1	1.23E-78	-0.63591	0.815	0.848	2.56E-74
Pcdh15	9.26E-73	-0.6602	0.83	0.852	1.93E-68
Adcy1	8.74E-61	-0.67589	0.152	0.331	1.82E-56
Dbp	4.01E-42	-0.7144	0.305	0.453	8.33E-38
mt-Atp8	2.54E-94	-0.76141	0.71	0.843	5.28E-90
Hopx	2.04E-53	-0.78315	0.46	0.581	4.23E-49
Arr3	2.05E-158	-0.78752	0.954	0.962	4.27E-154
Rs1	1.05E-156	-1.02809	0.741	0.851	2.19E-152

Supplementary table 10b: DEG list for mouse Cone photoreceptors: 24-mo vs 3-mo (pvaladj < 0.01,| LFC | > 0.25, top 25 up and downregulated)

Genes	pval	avg_log2 FC	pct. 1	pct. 2	p.adj
Gnat1	1.95E-73	1.559029	0.862	0.363	4.05E-69
Gnb1	3.52E-64	1.53724	0.82	0.366	7.32E-60
Pcp4l1	1.15E-100	1.530277	0.587	0.104	2.39E-96
Rho	2.39E-87	1.473289	0.995	0.631	4.97E-83
Pde6b	1.92E-76	1.422331	0.677	0.195	3.99E-72
Nr2e3	1.22E-55	1.415527	0.466	0.119	2.53E-51
Bc1	2.50E-25	1.340245	0.598	0.313	5.20E-21
Cngb1	8.90E-48	1.338385	0.497	0.155	1.85E-43
Vax2os	4.38E-49	1.315846	0.458	0.131	9.12E-45
Pde6a	1.51E-45	1.299579	0.63	0.27	3.13E-41
Drd4	5.42E-69	1.285285	0.712	0.283	1.13E-64
Cnga1	3.88E-41	1.198752	0.526	0.188	8.07E-37
Slc24a1	7.73E-41	1.198642	0.566	0.222	1.61E-36
Nrl	4.35E-39	1.13597	0.495	0.174	9.04E-35

Genes	pval	avg_log2 FC	pct. 1	pct. 2	p.adj
Mef2c	2.76E-42	1.007437	0.614	0.268	5.74E-38
Gm42418	3.15E-99	0.936013	1	1	6.55E-95
Samd11	1.57E-32	0.905792	0.426	0.148	3.26E-28
Rp1	6.77E-38	0.79224	0.931	0.805	1.41E-33
AC149090.1	5.63E-21	0.783164	0.548	0.282	1.17E-16
Reep6	1.40E-23	0.763121	0.471	0.213	2.92E-19
mt-Nd3	3.52E-25	0.757601	0.987	0.976	7.32E-21
Rom1	6.14E-39	0.756774	0.963	0.89	1.28E-34
Agpat3	3.00E-27	0.727832	0.817	0.622	6.24E-23
Ybx3	1.55E-18	0.684229	0.651	0.406	3.23E-14
Lynx1	2.72E-07	-0.62214	0.272	0.367	0.005653
Jchain	3.59E-12	-0.62467	0.209	0.371	7.46E-08
Adcy1	1.96E-12	-0.62865	0.167	0.331	4.08E-08
Rs1	1.22E-20	-0.63563	0.786	0.851	2.53E-16

Genes	pval	avg_log2FC	pct.1	pct.2	p.adj
Olfm1	2.17E-20	-0.64291	0.701	0.807	4.52E-16
Dusp1	1.87E-08	-0.68157	0.032	0.13	0.000389
Ppia	4.52E-21	-0.70301	0.701	0.819	9.40E-17
Casp7	3.50E-13	-0.70849	0.288	0.447	7.28E-09
AY036118	1.55E-13	-0.71415	0.783	0.845	3.22E-09
Sag	8.74E-63	-0.72595	0.976	0.969	1.82E-58
Fos	9.31E-12	-0.74543	0.571	0.679	1.94E-07
Hopx	8.58E-15	-0.75953	0.444	0.581	1.78E-10
Rlbp1	1.72E-07	-0.85857	0.061	0.162	0.003576
Stxbp1	1.66E-37	-0.86015	0.754	0.848	3.46E-33
Rbm3	2.59E-23	-0.88878	0.323	0.546	5.39E-19
Pcdh15	2.15E-39	-0.91856	0.743	0.852	4.46E-35
Jun	2.58E-11	-0.97686	0.257	0.401	5.37E-07
Glul	7.38E-16	-0.99077	0.198	0.401	1.53E-11
Fosb	5.22E-13	-0.99684	0.156	0.323	1.08E-08
Dbp	3.24E-23	-1.01068	0.206	0.453	6.74E-19
Dkk3	1.06E-09	-1.03417	0.016	0.121	2.19E-05
Arr3	1.78E-97	-1.41083	0.884	0.962	3.69E-93
Mt1	4.57E-09	-1.60866	0.063	0.18	9.50E-05
Xist	3.21E-14	-1.98391	0	0.137	6.67E-10
Apoe	1.24E-30	-2.55098	0.225	0.518	2.58E-26

Supplementary table 10c: IPA canonical pathway- comparison analysis for mouse Cone photoreceptors (pval < 0.05, top 50 based on z-score)

Canonical Pathways	12mo vs 3mo	24mo vs 3mo
G Beta Gamma Signaling	2.236	1
Phototransduction Pathway	2.673	0.471
Nonsense-Mediated Decay (NMD)	1	2
SNARE Signaling Pathway	-1.633	-1.134
Gap Junction Signaling	-1.89	-0.816
Cilium Assembly	N/A	2.646
Platelet homeostasis	1.342	1
Coronavirus Pathogenesis Pathway	N/A	-2.236
Protein Kinase A Signaling	0.333	1.807
Beta-catenin independent WNT signaling	1	1.134
Oxytocin in Brain Signaling Pathway	2	N/A
Role of PKR in Interferon Induction and Antiviral Response	N/A	-2
Chemokine Signaling	N/A	-2
G-Protein Coupled Receptor Signaling	1.155	-0.816
Visual phototransduction	-0.832	1
Endothelin-1 Signaling	0.816	-1
Estrogen Receptor Signaling	1	-0.816
Molecular Mechanisms of Cancer	1.265	-0.535
GNRH Signaling	0	-1.633
Acetylcholine Receptor Signaling Pathway	-0.447	-1
Eukaryotic Translation Initiation	0.447	1
Synaptogenesis Signaling Pathway	-1.134	-0.302
tRNA Splicing	N/A	1.414
BBSome Signaling Pathway	N/A	1.414
CLEAR Signaling Pathway	1.342	N/A
Insulin Secretion Signaling Pathway	-1.342	N/A
S100 Family Signaling Pathway	0.707	-0.632
Docosahexaenoic Acid (DHA) Signaling	0.816	0.447
G alpha (s) signalling events	0.447	0.816
Opioid Signaling Pathway	1.134	0
Eicosanoid Signaling	1	N/A
Opioid Signalling	0	-1
Colorectal Cancer Metastasis Signaling	N/A	-1
IL-8 Signaling	N/A	-1
Cardiac β-adrenergic Signaling	N/A	1
EIF2 Signaling	1	N/A
Gαi Signaling	N/A	1
cAMP-mediated signaling	-0.447	0.535
Role of NFAT in Cardiac Hypertrophy	0.447	0.447
Ion channel transport	0.447	0.447
Cachexia Signaling Pathway	-0.378	-0.447
Oxytocin Signaling Pathway	0.378	0.447
PPARα/RXRα Activation	N/A	0.816
Cellular Effects of Sildenafil (Viagra)	0	-0.728
G alpha (i) signalling events	0.632	0
RAR Activation	-0.333	-0.218
Cardiac Hypertrophy Signaling (Enhanced)	0	0.535
ESR-mediated signaling	N/A	-0.447

Supplementary table 11a: DEG list for mouse Bipolar cells: 12-mo vs 3-mo (pvaladj < 0.01,| LFC | > 0.25, top 25 up and downregulated)

Genes	pval	avg_log2FC	pct.1	pct.2	p.adj
Meis2	6.61E-33	0.733195	0.182	0.075	1.37E-28
Aldoc	3.62E-56	0.586585	0.429	0.235	7.53E-52
Gnat1	7.43E-109	0.56547	0.663	0.351	1.54E-104
Gsg1	3.80E-15	0.557783	0.228	0.15	7.91E-11
Eno1	3.63E-67	0.538835	0.701	0.507	7.55E-63
Rpl35	6.63E-68	0.501545	0.615	0.393	1.38E-63
Rbp3	2.45E-55	0.494466	0.451	0.242	5.10E-51
Rpl6	5.41E-72	0.491389	0.8	0.726	1.12E-67
Rcvrn	4.07E-38	0.487394	0.372	0.21	8.45E-34
AC149090.1	4.70E-72	0.486066	0.85	0.675	9.77E-68
Rho	8.41E-166	0.477082	0.89	0.615	1.75E-161
Ptprz1	6.11E-32	0.473951	0.42	0.273	1.27E-27
Cplx4	8.90E-27	0.469283	0.317	0.197	1.85E-22
Gm30382	8.86E-37	0.462643	0.405	0.249	1.84E-32
Rpl38	1.57E-63	0.456661	0.795	0.69	3.26E-59
Rps29	3.34E-67	0.453315	0.858	0.822	6.95E-63
3222401L13Rik	3.48E-49	0.447053	0.364	0.184	7.23E-45
Cntn5	2.29E-21	0.44211	0.111	0.043	4.77E-17
Gnb1	2.03E-65	0.418367	0.576	0.335	4.22E-61
Nfia	2.72E-13	0.410982	0.139	0.079	5.67E-09
Rpl37	6.84E-53	0.400063	0.81	0.728	1.42E-48
Rpl10	1.84E-42	0.398636	0.591	0.409	3.83E-38
Hk2	1.31E-30	0.397267	0.195	0.088	2.72E-26
Nr2e3	1.65E-30	0.393723	0.183	0.078	3.42E-26
mt-Nd5	4.86E-77	-0.36036	0.966	0.972	1.01E-72

Genes	pval	avg_log2FC	pct.1	pct.2	p.adj
Zfp365	1.58E-16	-0.36096	0.503	0.541	3.29E-12
Adrb1	1.05E-14	-0.36155	0.39	0.444	2.18E-10
Arglu1	1.09E-40	-0.36322	0.776	0.813	2.26E-36
Gprasp1	2.18E-16	-0.36503	0.46	0.505	4.54E-12
Ndnf	8.05E-21	-0.36517	0.646	0.678	1.67E-16
Lrtm1	3.80E-42	-0.37059	0.835	0.859	7.90E-38
Dnaja1	2.13E-25	-0.3739	0.709	0.748	4.44E-21
Ppm1e	5.22E-23	-0.38179	0.396	0.465	1.08E-18
Slc24a4	3.90E-18	-0.39235	0.322	0.387	8.10E-14
Spc25	9.88E-15	-0.39925	0.065	0.113	2.05E-10
Prdm8	5.72E-19	-0.42474	0.386	0.446	1.19E-14
Gnao1	3.12E-46	-0.43325	0.791	0.815	6.48E-42
Glul	6.17E-13	-0.45021	0.406	0.446	1.28E-08
Uba52	1.04E-20	-0.45932	0.418	0.466	2.16E-16
Mt1	4.84E-32	-0.47961	0.539	0.62	1.01E-27
Vstm2b	1.82E-31	-0.48371	0.464	0.557	3.78E-27
Map4	7.24E-87	-0.51938	0.838	0.881	1.51E-82
Strip2	6.12E-36	-0.54877	0.425	0.521	1.27E-31
Car8	5.39E-35	-0.55108	0.485	0.572	1.12E-30
Gm42418	6.20E-79	-0.58823	1	1	1.29E-74
Adcy1	1.64E-144	-0.70287	0.056	0.243	3.41E-140
Prkca	3.56E-69	-0.80975	0.503	0.602	7.40E-65
Bc1	1.40E-83	-0.9728	0.404	0.581	2.91E-79
mt-Atp8	4.51E-272	-1.20737	0.583	0.838	9.38E-268

Supplementary table 11b: DEG list for mouse Bipolar cells: 24-mo vs 3-mo (pvaladj < 0.01,| LFC | > 0.25, top 25 up and downregulated)

Genes	pval	avg_log2FC	pct.1	pct.2	p.adj
Rp1	1.09E-136	1.769517	0.7	0.183	2.27E-132
Pdc	1.15E-93	1.559296	0.806	0.352	2.40E-89
Rho	9.57E-141	1.529795	0.986	0.615	1.99E-136
Gnb1	9.06E-88	1.486724	0.783	0.335	1.88E-83
Bc1	1.54E-41	1.46184	0.804	0.581	3.21E-37
Gnat1	2.32E-101	1.444294	0.836	0.351	4.82E-97

Genes	pval	avg_log2FC	pct.1	pct.2	p.adj
Rcvrn	2.70E-79	1.412348	0.621	0.21	5.61E-75
Pde6a	1.73E-86	1.392042	0.529	0.146	3.60E-82
Nr2e3	1.58E-99	1.380485	0.434	0.078	3.29E-95
Pde6b	2.73E-103	1.345706	0.58	0.144	5.67E-99
Cnga1	1.11E-75	1.303512	0.492	0.137	2.30E-71
Pde6g	6.06E-87	1.302449	0.781	0.317	1.26E-82

Genes	pval	avg_log2FC	pct.1	pct.2	p.adj
Hk2	3.97E-86	1.297743	0.423	0.088	8.25E-82
Slc24a1	9.74E-69	1.201609	0.547	0.18	2.02E-64
Cplx4	2.31E-44	1.041561	0.476	0.197	4.80E-40
Samd11	1.17E-69	1.040138	0.312	0.056	2.42E-65
Rpgrip1	1.72E-65	1.017759	0.653	0.264	3.58E-61
Guca1a	5.39E-76	1.004415	0.656	0.234	1.12E-71
Grk1	4.39E-75	1.003693	0.363	0.07	9.13E-71
Prph2	1.67E-42	0.995483	0.808	0.517	3.47E-38
Sag	3.81E-59	0.994643	0.799	0.446	7.92E-55
Gngt1	4.57E-55	0.973749	0.884	0.544	9.50E-51
Tulp1	3.22E-48	0.950809	0.605	0.27	6.69E-44
AC149090.1	4.86E-61	0.904003	0.898	0.675	1.01E-56
Rom1	2.61E-39	0.890159	0.871	0.649	5.42E-35
Mt2	6.92E-08	-0.55561	0.21	0.296	0.00144
Rgs7	1.70E-09	-0.5562	0.332	0.416	3.54E-05
Adrb1	8.40E-10	-0.56469	0.344	0.444	1.75E-05
Rgs16	1.04E-08	-0.58117	0.351	0.416	0.000216
Spc25	7.58E-11	-0.58432	0.025	0.113	1.58E-06
Ppm1e	2.00E-13	-0.59105	0.356	0.465	4.15E-09
Junb	5.56E-10	-0.60546	0.192	0.307	1.16E-05
Itm2c	3.72E-17	-0.6251	0.489	0.605	7.74E-13
Rbm3	4.90E-13	-0.62798	0.245	0.368	1.02E-08
Strip2	2.48E-13	-0.68211	0.42	0.521	5.16E-09
Prkca	5.43E-16	-0.68363	0.481	0.602	1.13E-11
Dusp1	1.47E-14	-0.68566	0.06	0.186	3.06E-10
Tsix	2.40E-15	-0.77307	0.004	0.108	4.99E-11
Jun	2.23E-11	-0.80163	0.189	0.304	4.63E-07
Vstm2b	1.02E-19	-0.81024	0.427	0.557	2.11E-15
Cacna2d3	8.74E-23	-0.84248	0.54	0.66	1.82E-18
Glul	3.18E-22	-0.88246	0.261	0.446	6.62E-18
Car8	1.20E-23	-0.95344	0.43	0.572	2.50E-19
Mt1	1.21E-29	-1.04766	0.444	0.62	2.51E-25
Arr3	1.52E-19	-1.10711	0.041	0.195	3.15E-15
Fosb	3.78E-18	-1.17015	0.09	0.253	7.87E-14
AY036118	9.95E-38	-1.21705	0.721	0.833	2.07E-33
Fos	8.35E-39	-1.23563	0.252	0.529	1.74E-34
Apoe	2.92E-45	-1.37216	0.136	0.443	6.08E-41
Xist	7.16E-21	-2.89061	0.002	0.142	1.49E-16

Supplementary table 11c: IPA canonical pathway- comparison analysis for mouse Bipolar cells (pval < 0.05, top 50 based on z-score)

Canonical Pathways	12mo vs 3mo	24mo vs 3mo
Visual phototransduction	2.53	4.379
Nonsense-Mediated Decay (NMD)	3.742	3
Major pathway of rRNA processing in the nucleolus and cytosol	3.742	2.828
Selenoamino acid metabolism	3.742	2.828
Eukaryotic Translation Elongation	3.742	2.828
Eukaryotic Translation Initiation	3.742	2.828
SRP-dependent cotranslational protein targeting to membrane	3.742	2.828
Eukaryotic Translation Termination	3.742	2.828
Response of EIF2AK4 (GCN2) to amino acid deficiency	3.742	2.828
EIF2 Signaling	2.646	2.449
Glutaminergic Receptor Signaling Pathway (Enhanced)	-2.333	-2.673
Coronavirus Pathogenesis Pathway	-2.121	-2.449
Adrenergic Receptor Signaling Pathway (Enhanced)	-1.633	-2.449
Dopamine-DARPP32 Feedback in cAMP Signaling	-2	-2
Pancreatic Secretion Signaling Pathway	-2	-1.89
Synaptic Long Term Potentiation	-2	-1.633
RAR Activation	1.897	1.414
Androgen Signaling	-1	-2.236
Netrin Signaling	-0.816	-2.236
Glycolysis I	3	N/A
Gαi Signaling	1.342	1.414
Cilium Assembly	N/A	2.646
Glucose metabolism	2.646	N/A
Acetylcholine Receptor Signaling Pathway	-0.816	-1.633
GPCR-Mediated Nutrient Sensing in Enteroendocrine Cells	-1.342	-1
SNARE Signaling Pathway	-1	-1.342
Gap Junction Signaling	-1.633	-0.707
Cardiac Hypertrophy Signaling	-1.633	-0.632
Serotonin Receptor Signaling	-1.414	-0.832
Gluconeogenesis I	2.236	N/A
Oxytocin Signaling Pathway	-1.633	-0.577
Phototransduction Pathway	1.897	-0.229
Role of NFAT in Cardiac Hypertrophy	-1.414	-0.632
Signaling by NTRK1 (TRKA)	N/A	2

Canonical Pathways	12mo vs 3mo	24mo vs 3mo
Neurovascular Coupling Signaling Pathway	N/A	1.89
G alpha (q) signalling events	1	0.816
P2Y Purinergic Receptor Signaling Pathway	-1	-0.707
Hepatic Cholestasis	N/A	-1.633
Mitotic Prometaphase	N/A	1.633
Potassium Channels	N/A	1.633
Orexin Signaling Pathway	-0.447	-1.134
Insulin Secretion Signaling Pathway	-0.816	-0.707

Canonical Pathways	12mo vs 3mo	24mo vs 3mo
Corticotropin Releasing Hormone Signaling	-0.816	-0.707
Synaptic Long Term Depression	-1.134	0.333
Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis	N/A	-1.414
CXCR4 Signaling	1	0.378
RANK Signaling in Osteoclasts	N/A	-1.342
Chemokine Signaling	N/A	-1.342
Activation of kainate receptors upon glutamate binding	N/A	1.342

Supplementary table 12: Mouse retinal microglia- Saban lab dataset (GSE195891) -SenMayo-hi vs SenMayo-low –GSEA pathway enrichment terms (FDR-qvalue < 0.05, NES > 1.5)

No	ID	ES	NES	pval	p.adj	qval
1	REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS	0.876355	2.626864	1.00E-10	2.47E-08	2.25E-08
2	REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	0.906001	2.393184	1.00E-10	2.47E-08	2.25E-08
3	REACTOME_CLASS_A_1_RHODOPSIN_LIKE_RECEPTORS	0.739214	2.365217	1.00E-10	2.47E-08	2.25E-08
4	REACTOME_INTERLEUKIN_10_SIGNALING	0.889059	2.346482	1.00E-10	2.47E-08	2.25E-08
5	REACTOME_GPCR_LIGAND_BINDING	0.68151	2.271781	1.00E-10	2.47E-08	2.25E-08
6	KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	0.68867	2.232509	1.00E-10	2.47E-08	2.25E-08
7	KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.774696	2.157461	4.77E-07	5.90E-05	5.37E-05
8	KEGG_TYPE_I_DIABETES_MELLITUS	0.819524	2.109862	5.23E-07	6.03E-05	5.49E-05
9	PID_IL23_PATHWAY	0.822201	2.097101	3.33E-06	0.000281	0.000256
10	REACTOME_INTERFERON_ALPHA_BETA_SIGNALING	0.740183	2.048235	8.18E-06	0.000643	0.000586
11	KEGG_GRAFT_VERSUS_HOST_DISEASE	0.820657	2.011734	4.42E-05	0.002836	0.002582
12	REACTOME_RESOLUTION_OF_SISTER_CHROMATID_COHESION	0.649906	1.993698	7.99E-07	8.20E-05	7.47E-05
13	PID_PLK1_PATHWAY	0.737198	1.981554	3.86E-05	0.002568	0.002337
14	KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	0.747356	1.97319	5.24E-05	0.00324	0.00295
15	REACTOME_MITOTIC_METAPHASE_AND_ANAPHASE	0.587118	1.955958	1.19E-08	2.07E-06	1.88E-06
16	REACTOME_INTERFERON_SIGNALING	0.610779	1.954981	1.67E-07	2.41E-05	2.19E-05
17	REACTOME_KINESINS	0.7046	1.919339	9.24E-05	0.004845	0.00441
18	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	0.727418	1.901845	0.000317	0.011689	0.010641
19	REACTOME_CELL_CYCLE_MITOTIC	0.530441	1.891979	1.00E-10	2.47E-08	2.25E-08
20	REACTOME_INTERLEUKIN_4_AND_INTERLEUKIN_13_SIGNALING	0.630398	1.88817	2.45E-05	0.001766	0.001608
21	KEGG_LEISHMANIA_INFECTION	0.671491	1.881004	0.000154	0.006655	0.006058
22	REACTOME_CONDENSATION_OF_PROPHASE_CHROMOSOMES	0.888407	1.879623	7.74E-05	0.004324	0.003936
23	KEGG_CHEMOKINE_SIGNALING_PATHWAY	0.587547	1.879506	3.41E-06	0.000281	0.000256
24	REACTOME_M_PHASE	0.541266	1.876974	1.78E-09	3.85E-07	3.51E-07
25	REACTOME_GAP_JUNCTION_ASSEMBLY	0.859146	1.865015	0.000227	0.008946	0.008144

No	ID	ES	NES	pval	p.adj	qval
26	PID_IL12_2PATHWAY	0.665663	1.86468	0.00019	0.007818	0.007117
27	PID_IL27_PATHWAY	0.780196	1.864442	0.000473	0.016364	0.014897
28	PID_AURORA_B_PATHWAY	0.718624	1.862496	0.000563	0.019019	0.017314
29	REACTOME_SEPARATION_OF_SISTER_CHROMATIDS	0.573726	1.860034	1.47E-06	0.000134	0.000122
30	KEGG_ALLOGRAFT_REJECTION	0.756658	1.854848	0.000933	0.029378	0.026744
31	REACTOME_MITOTIC_PROMETAPHASE	0.567487	1.849475	8.05E-07	8.20E-05	7.47E-05
32	KEGG_HEMATOPOIETIC_CELL_LINEAGE	0.642669	1.84666	0.000133	0.006155	0.005603
33	BIOCARTA_INFLAM_PATHWAY	0.842159	1.846534	0.000289	0.010865	0.009891
34	REACTOME_NUCLEAR_ENVELOPE_NE_REASSEMBLY	0.642209	1.845338	0.000135	0.006155	0.005603
35	PID_AURORA_A_PATHWAY	0.736508	1.841258	0.000915	0.029333	0.026702
36	REACTOME_SIGNALING_BY_INTERLEUKINS	0.519302	1.830954	3.46E-09	6.66E-07	6.06E-07
37	KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.61722	1.827994	0.000107	0.005124	0.004665
38	REACTOME_TRANSPORT_OF_CONNEXONS_TO_THE_PLASMA_MEMBRANE	0.878586	1.823217	0.000571	0.019019	0.017314
39	REACTOME_SCAVENGING_BY_CLASS_A_RECEPTORS	0.880174	1.818905	0.000378	0.013362	0.012164
40	REACTOME_MITOTIC_SPINDLE_CHECKPOINT	0.593913	1.806775	0.00014	0.006229	0.005671
41	PID_SYNDECAN_1_PATHWAY	0.715949	1.801267	0.001343	0.03749	0.034128
42	REACTOME_CELL_CYCLE_CHECKPOINTS	0.527778	1.786884	9.75E-07	9.37E-05	8.53E-05
43	REACTOME_MHC_CLASS_II_ANTIGEN_PRESENTATION	0.587596	1.77686	9.60E-05	0.004872	0.004435
44	BIOCARTA_ERYTH_PATHWAY	0.885989	1.761975	0.000991	0.030629	0.027883
45	KEGG_CELL_CYCLE	0.570281	1.759545	0.000175	0.007393	0.00673
46	REACTOME_THE_ROLE_OF_GTSE1_IN_G2_M_PROGRESSION_AFTER_G2_CHECKPOINT	0.604767	1.754593	0.000894	0.029192	0.026574
47	KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.639047	1.75415	0.001869	0.046011	0.041885
48	REACTOME_RHO_GTPASES_ACTIVATE_FORMINS	0.563009	1.750539	7.35E-05	0.004243	0.003862
49	REACTOME_CONDENSATION_OF_PROMETAPHASE_CHROMOSOMES	0.879954	1.749975	0.001158	0.034287	0.031213
50	REACTOME_INTRAFLAGELLAR_TRANSPORT	0.642062	1.743791	0.001382	0.037872	0.034476
51	BIOCARTA_CELLCYCLE_PATHWAY	0.754271	1.73722	0.001254	0.036186	0.032942
52	PID_ANTHRAX_PATHWAY	0.804881	1.731182	0.001697	0.043855	0.039923
53	REACTOME_INTERFERON_GAMMA_SIGNALING	0.592633	1.725158	0.001169	0.034287	0.031213
54	REACTOME_APC_C_MEDIATED_DEGRADATION_OF_CELL_CYCLE_PROTEINS	0.580645	1.711123	0.001501	0.039965	0.036382
55	PID_INTEGRIN1_PATHWAY	0.621646	1.706548	0.001941	0.046017	0.041891
56	REACTOME_MITOTIC_PROPHASE	0.576148	1.692777	0.002101	0.049153	0.044746
57	REACTOME_G_ALPHA_I_SIGNALLING_EVENTS	0.514848	1.690573	8.84E-05	0.00478	0.004351
58	REACTOME_SIGNALING_BY_GPCR	0.477054	1.689409	1.32E-07	2.08E-05	1.89E-05
59	PID_AP1_PATHWAY	0.59076	1.675155	0.001879	0.046011	0.041885
60	REACTOME_MITOTIC_G2_G2_M_PHASES	0.51142	1.656646	9.85E-05	0.004872	0.004435

No	ID	ES	NES	pval	p.adj	qval
61	REACTOME_CHROMOSOME_MAINTENANCE	0.554509	1.645951	0.001897	0.046011	0.041885
62	REACTOME_RHO_GTPASE_EFFECTORS	0.485009	1.639706	6.54E-05	0.003902	0.003552
63	REACTOME_FACTORS_INVOLVED_IN_MEGAKARYOCYTE_DEVELOPMENT_AND_PLATELET_PRODUCTION	0.520056	1.609959	0.001598	0.041907	0.03815
64	REACTOME_MITOTIC_G1_PHASE_AND_G1_S_TRANSITION	0.505535	1.59791	0.001331	0.03749	0.034128
65	REACTOME_S_PHASE	0.488714	1.56219	0.001766	0.044949	0.040918
66	REACTOME_NEUTROPHIL_DEGRANULATION	0.439447	1.545494	3.73E-05	0.002568	0.002337

Supplementary table 13a: Mouse retinal microglia-SenMayo-hi vs SenMayo-low –Top 50 GSEA pathway enrichment terms obtained after removing the microglial activation genes (Marsh et al, 2022) from the input gene list (FDR-qvalue < 0.05, NES > 1.5)

No	ID	ES	NES	pval	p.adj	qval
1	REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS	0.838671	2.185224	1.00E-10	6.64E-09	5.24E-09
2	KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	0.797586	2.166048	1.00E-10	6.64E-09	5.24E-09
3	REACTOME_INTERLEUKIN_4_AND_INTERLEUKIN_13_SIGNALING	0.809714	2.02672	3.11E-10	1.93E-08	1.52E-08
4	REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	0.916964	1.985409	2.44E-09	1.37E-07	1.08E-07
5	KEGG_LEISHMANIA_INFECTION	0.854765	1.98203	7.73E-09	4.18E-07	3.29E-07
6	REACTOME_CLASS_A_1_RHODOPSIN_LIKE_RECEPTORS	0.717343	1.979697	1.00E-10	6.64E-09	5.24E-09
7	REACTOME_INTERLEUKIN_10_SIGNALING	0.913832	1.9676	7.92E-09	4.18E-07	3.29E-07
8	KEGG_HEMATOPOIETIC_CELL_LINEAGE	0.818981	1.955032	1.59E-08	8.14E-07	6.41E-07
9	KEGG_JAK_STAT_SIGNALING_PATHWAY	0.749343	1.927157	2.12E-08	1.06E-06	8.32E-07
10	PID_IL23_PATHWAY	0.912551	1.912026	4.94E-07	1.97E-05	1.55E-05
11	KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.826364	1.900973	4.33E-07	1.77E-05	1.39E-05
12	REACTOME_SIGNALING_BY_INTERLEUKINS	0.661141	1.896429	1.00E-10	6.64E-09	5.24E-09
13	KEGG_LYSOSOME	0.736151	1.895773	5.46E-08	2.58E-06	2.03E-06
14	KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION	0.74368	1.894009	1.70E-07	7.26E-06	5.72E-06
15	KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	0.836895	1.877501	8.86E-07	3.31E-05	2.61E-05
16	KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.766546	1.872556	1.02E-06	3.65E-05	2.88E-05
17	KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	0.81148	1.846512	5.74E-06	0.000166	0.000131
18	REACTOME_TOLL_LIKE_RECEPTOR_CASCADES	0.701274	1.842943	1.01E-07	4.52E-06	3.56E-06
19	PID_IL6_7_PATHWAY	0.82857	1.835883	4.55E-06	0.000138	0.000109
20	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	0.824997	1.808292	5.43E-05	0.001282	0.00101
21	PID_IL4_2PATHWAY	0.788058	1.805987	1.14E-05	0.000314	0.000248
22	REACTOME_INTERFERON_GAMMA_SIGNALING	0.733366	1.805323	5.23E-06	0.000157	0.000123
23	REACTOME_NEUTROPHIL_DEGRANULATION	0.622667	1.794443	1.00E-10	6.64E-09	5.24E-09
24	PID_AMB2_NEUTROPHILS_PATHWAY	0.829771	1.783259	4.04E-05	0.001006	0.000792
25	REACTOME_FCGAMMA_RECEPTOR_FCGR_DEPENDENT_PHAGOCYTOSIS	0.72119	1.777193	2.52E-05	0.000655	0.000516
26	REACTOME_INTERFERON_ALPHA_BETA_SIGNALING	0.771639	1.775082	3.98E-05	0.001005	0.000792

No	ID	ES	NES	pval	p.adj	qval
27	REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPTION_FACTOR_ACTIVATION	0.763886	1.771298	3.65E-05	0.000935	0.000737
28	PID_FRA_PATHWAY	0.822469	1.769158	5.33E-05	0.001275	0.001005
29	REACTOME_RAC1_GTPASE_CYCLE	0.653693	1.768187	1.29E-06	4.46E-05	3.52E-05
30	PID_IL12_2PATHWAY	0.769386	1.763198	4.68E-05	0.001151	0.000907
31	PID_BCR_5PATHWAY	0.751609	1.757064	9.12E-05	0.00207	0.001632
32	PID_AP1_PATHWAY	0.757288	1.755999	5.59E-05	0.001303	0.001027
33	REACTOME_INTERLEUKIN_2_FAMILY_SIGNALING	0.791227	1.747083	0.000178	0.003705	0.002919
34	KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	0.72678	1.742876	7.63E-05	0.001755	0.001383
35	PID_NFAT_TFPATHWAY	0.813756	1.738059	0.000138	0.002992	0.002358
36	REACTOME_INTERFERON_SIGNALING	0.645094	1.733712	3.46E-06	0.000107	8.42E-05
37	KEGG_GRAFT_VERSUS_HOST_DISEASE	0.859182	1.730761	0.000291	0.005229	0.004121
38	PID_INTEGRIN2_PATHWAY	0.871603	1.728056	0.000371	0.005992	0.004721
39	REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPHOID_CELL	0.701147	1.723974	0.00011	0.002399	0.001891
40	KEGG_APOPTOSIS	0.695713	1.704206	0.000313	0.005278	0.004159
41	BIOCARTA_MAPK_PATHWAY	0.697146	1.701833	0.000193	0.003928	0.003096
42	PID_INTEGRIN_A4B1_PATHWAY	0.796945	1.70022	0.000524	0.007808	0.006153
43	KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	0.7824	1.694051	0.000611	0.008839	0.006965
44	BIOCARTA_NTHI_PATHWAY	0.853308	1.691783	0.000802	0.011066	0.00872
45	REACTOME_TRANSCRIPTIONAL_REGULATION_OF_GRANULOPOIESIS	0.800481	1.691762	0.000752	0.010456	0.008239
46	REACTOME_TOLL_LIKE_RECEPTOR_TLR1_TLR2_CASCADE	0.675175	1.689968	0.000308	0.005278	0.004159
47	BIOCARTA_TID_PATHWAY	0.895241	1.686669	0.000325	0.005399	0.004254
48	REACTOME_PARASITE_INFECTION	0.722122	1.683235	0.000395	0.006185	0.004873
49	REACTOME_MYD88_INDEPENDENT_TLR4_CASCADE	0.672462	1.68169	0.000233	0.004545	0.003581
50	PID_SMAD2_3NUCLEAR_PATHWAY	0.706608	1.68122	0.000287	0.005209	0.004105

Supplementary table 13b: Human retinal microglia- (GSE148077) -SenMayo-hi vs SenMayo-low –GSEA pathway enrichment terms obtained after removing the microglial activation genes (Marsh et al, 2022) from the input gen e list (FDR-qvalue < 0.05, NES > 1.5)

No	ID	ES	NES	pval	p.adj	qval
1	KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	0.760764	2.298222	1.00E-10	1.83E-08	1.53E-08
2	REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS	0.77614	2.234277	1.00E-10	1.83E-08	1.53E-08
3	REACTOME_INTERLEUKIN_4_AND_INTERLEUKIN_13_SIGNALING	0.804936	2.212566	2.72E-10	4.52E-08	3.79E-08
4	KEGG_LEISHMANIA_INFECTION	0.833275	2.172264	7.89E-08	7.60E-06	6.38E-06
5	REACTOME_INTERLEUKIN_10_SIGNALING	0.893446	2.157931	5.15E-08	5.55E-06	4.65E-06
6	KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	0.83738	2.147225	1.72E-07	1.43E-05	1.20E-05
7	REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	0.86892	2.136787	3.94E-07	2.88E-05	2.42E-05
8	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	0.86115	2.107499	2.95E-06	0.000145	0.000122

No	**ID**	**ES**	**NES**	**pval**	**p.adj**	**qval**
9	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	0.82092	2.061664	2.89E-06	0.000145	0.000122
10	REACTOME_CLASS_A_1_RHODOPSIN_LIKE_RECEPTORS	0.658352	2.028361	1.00E-10	1.83E-08	1.53E-08
11	REACTOME_INTERFERON_GAMMA_SIGNALING	0.744229	2.028336	2.71E-06	0.000141	0.000119
12	KEGG_AUTOIMMUNE_THYROID_DISEASE	0.868452	2.007663	1.13E-05	0.000449	0.000377
13	KEGG_ASTHMA	0.941346	1.97359	3.01E-06	0.000145	0.000122
14	KEGG_ALLOGRAFT_REJECTION	0.874064	1.964118	3.97E-06	0.000186	0.000156
15	PID_IL23_PATHWAY	0.87187	1.959187	4.71E-06	0.000215	0.000181
16	PID_FRA_PATHWAY	0.853596	1.951511	2.58E-05	0.000857	0.000719
17	BIOCARTA_INFLAM_PATHWAY	0.925082	1.927423	2.26E-05	0.00078	0.000655
18	KEGG_TYPE_I_DIABETES_MELLITUS	0.801367	1.904909	0.000129	0.002921	0.002451
19	KEGG_GRAFT_VERSUS_HOST_DISEASE	0.854078	1.904133	0.000106	0.002578	0.002163
20	PID_AP1_PATHWAY	0.743816	1.899573	9.06E-05	0.002367	0.001986
21	PID_NFAT_TFPATHWAY	0.808982	1.894631	0.00047	0.007961	0.00668
22	KEGG_VIRAL_MYOCARDITIS	0.733545	1.890969	2.63E-05	0.000858	0.00072
23	KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	0.735187	1.877536	0.000141	0.003078	0.002582
24	BIOCARTA_TH1TH2_PATHWAY	0.920632	1.873445	9.89E-05	0.002477	0.002078
25	KEGG_HEMATOPOIETIC_CELL_LINEAGE	0.712006	1.864989	9.68E-05	0.002458	0.002063
26	KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.724252	1.849609	0.000236	0.004587	0.003849
27	BIOCARTA_NTHI_PATHWAY	0.878883	1.842633	0.000242	0.004639	0.003893
28	BIOCARTA_NKT_PATHWAY	0.892869	1.841207	0.00019	0.00394	0.003306
29	REACTOME_SCAVENGING_BY_CLASS_A_RECEPTORS	0.898429	1.828264	0.000399	0.006891	0.005782
30	KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.674104	1.813033	5.93E-05	0.001778	0.001492
31	REACTOME_BINDING_AND_UPTAKE_OF_LIGANDS_BY_SCAVENGER_RECEPTORS	0.735874	1.804783	0.001638	0.020801	0.017455
32	BIOCARTA_IL1R_PATHWAY	0.825872	1.800705	0.001098	0.015586	0.013078
33	REACTOME_TRANSCRIPTIONAL_REGULATION_OF_GRANULOPOIESIS	0.806898	1.779876	0.001366	0.018111	0.015197
34	BIOCARTA_LAIR_PATHWAY	0.901248	1.778521	0.001287	0.017308	0.014523
35	KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	0.735233	1.765613	0.001259	0.017189	0.014424
36	REACTOME_COLLAGEN_DEGRADATION	0.684533	1.764525	0.000828	0.012515	0.010501
37	PID_UPA_UPAR_PATHWAY	0.741288	1.74425	0.001099	0.015586	0.013078
38	BIOCARTA_GRANULOCYTES_PATHWAY	0.901398	1.729581	0.002945	0.032385	0.027174
39	PID_IL6_7_PATHWAY	0.705083	1.725553	0.003213	0.034365	0.028836
40	REACTOME_COMPLEMENT_CASCADE	0.685009	1.720336	0.002755	0.030723	0.02578
41	PID_INTEGRIN2_PATHWAY	0.79397	1.716426	0.005072	0.047973	0.040255
42	BIOCARTA_TID_PATHWAY	0.850167	1.713383	0.002435	0.028022	0.023513
43	REACTOME_P75NTR_SIGNALS_VIA_NF_KB	0.867667	1.712252	0.003679	0.037794	0.031714

No	ID	ES	NES	pval	p.adj	qval
44	BIOCARTA_TNFR2_PATHWAY	0.883281	1.710175	0.004652	0.045255	0.037974
45	BIOCARTA_COMP_PATHWAY	0.860508	1.707588	0.001287	0.017308	0.014523
46	REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPHOID_CELL	0.602707	1.705392	0.000246	0.004639	0.003893
47	BIOCARTA_NFKB_PATHWAY	0.813101	1.694108	0.004771	0.045929	0.03854
48	KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.667839	1.682842	0.001859	0.022719	0.019064
49	BIOCARTA_CYTOKINE_PATHWAY	0.919763	1.681622	0.002779	0.0308	0.025845
50	REACTOME_DIGESTION_AND_ABSORPTION	0.833434	1.67966	0.004895	0.046626	0.039124
51	PID_INTEGRIN1_PATHWAY	0.651339	1.679055	0.001147	0.01614	0.013543
52	PID_NFKAPPAB_CANONICAL_PATHWAY	0.799077	1.675314	0.004489	0.044137	0.037036
53	BIOCARTA_BLYMPHOCYTE_PATHWAY	0.914668	1.672307	0.00343	0.03585	0.030083
54	REACTOME_ORGANIC_CATION_ANION_ZWITTERION_TRANSPORT	0.890213	1.667234	0.003528	0.036662	0.030764
55	REACTOME_GPCR_LIGAND_BINDING	0.524647	1.656051	7.02E-08	7.13E-06	5.98E-06
56	PID_HIF1_TFPATHWAY	0.639583	1.646441	0.001614	0.020637	0.017317
57	KEGG_CHEMOKINE_SIGNALING_PATHWAY	0.561144	1.634943	0.00016	0.003393	0.002847
58	REACTOME_RIP_MEDIATED_NFKB_ACTIVATION_VIA_ZBP1	0.814396	1.616084	0.005136	0.048171	0.040421
59	REACTOME_UNFOLDED_PROTEIN_RESPONSE_UPR	0.586732	1.613998	0.00404	0.039938	0.033513
60	REACTOME_INTERFERON_SIGNALING	0.534736	1.595681	0.000156	0.003365	0.002823
61	KEGG_LYSOSOME	0.554646	1.567054	0.002075	0.024966	0.02095
62	REACTOME_SIGNALING_BY_INTERLEUKINS	0.497081	1.565471	4.65E-07	3.15E-05	2.64E-05
63	KEGG_CELL_ADHESION_MOLECULES_CAMS	0.548692	1.562432	0.00249	0.028282	0.023732
64	REACTOME_NEUTROPHIL_DEGRANULATION	0.482267	1.544442	1.11E-06	6.55E-05	5.49E-05

Supplementary table 13c: Mouse retinal microglia- Saban lab dataset (GSE195891) -SenMayo-hi vs SenMayo-low –GSEA pathway enrichment terms obtained after removing the microglial activation genes (Marsh et al, 2022) from the input gene list (FDR-qvalue < 0.05, NES > 1.5)

No	ID	ES	NES	pval	p.adj	qval
1	REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS	0.868202	2.599074	1.00E-10	2.88E-08	2.61E-08
2	REACTOME_CLASS_A_1_RHODOPSIN_LIKE_RECEPTORS	0.724838	2.342855	1.00E-10	2.88E-08	2.61E-08
3	REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	0.898987	2.341286	1.00E-10	2.88E-08	2.61E-08
4	REACTOME_INTERLEUKIN_10_SIGNALING	0.882518	2.318811	4.51E-10	1.11E-07	1.01E-07
5	REACTOME_GPCR_LIGAND_BINDING	0.665224	2.22653	1.00E-10	2.88E-08	2.61E-08
6	KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	0.677387	2.219196	1.00E-10	2.88E-08	2.61E-08
7	KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.786376	2.175202	3.48E-08	5.46E-06	4.95E-06
8	KEGG_TYPE_I_DIABETES_MELLITUS	0.819732	2.093872	7.04E-07	8.11E-05	7.35E-05
9	PID_IL23_PATHWAY	0.822359	2.076116	9.92E-06	0.000745	0.000675
10	REACTOME_INTERFERON_ALPHA_BETA_SIGNALING	0.74533	2.058265	3.51E-05	0.002333	0.002112

No	**ID**	**ES**	**NES**	**pval**	**p.adj**	**qval**
11	KEGG_GRAFT_VERSUS_HOST_DISEASE	0.820865	2.019833	7.41E-05	0.004135	0.003743
12	REACTOME_RESOLUTION_OF_SISTER_CHROMATID_COHESION	0.650186	1.993464	1.19E-06	0.000114	0.000103
13	KEGG_LEISHMANIA_INFECTION	0.713397	1.985981	2.22E-05	0.001597	0.001445
14	REACTOME_INTERFERON_SIGNALING	0.613149	1.980785	1.02E-07	1.46E-05	1.32E-05
15	PID_PLK1_PATHWAY	0.737481	1.974634	0.000195	0.008532	0.007724
16	REACTOME_INTERLEUKIN_4_AND_INTERLEUKIN_13_SIGNALING	0.658039	1.969926	4.09E-06	0.000353	0.00032
17	REACTOME_MITOTIC_METAPHASE_AND_ANAPHASE	0.587401	1.967939	1.21E-08	2.09E-06	1.89E-06
18	REACTOME_CELL_CYCLE_MITOTIC	0.533489	1.913379	1.00E-10	2.88E-08	2.61E-08
19	REACTOME_KINESINS	0.704865	1.908376	0.00025	0.01029	0.009316
20	REACTOME_CONDENSATION_OF_PROPHASE_CHROMOSOMES	0.888714	1.906015	0.000115	0.006022	0.005451
21	REACTOME_GAP_JUNCTION_ASSEMBLY	0.859351	1.902891	0.000652	0.020885	0.018908
22	REACTOME_M_PHASE	0.545214	1.900131	1.72E-09	3.30E-07	2.99E-07
23	KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	0.729509	1.899904	0.00016	0.007487	0.006778
24	REACTOME_MITOTIC_PROMETAPHASE	0.57398	1.895452	3.77E-07	4.66E-05	4.22E-05
25	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	0.72772	1.895244	0.000176	0.007993	0.007236
26	PID_IL27_PATHWAY	0.780518	1.885642	0.000572	0.019034	0.017231
27	REACTOME_SEPARATION_OF_SISTER_CHROMATIDS	0.574007	1.884745	1.13E-06	0.000114	0.000103
28	BIOCARTA_INFLAM_PATHWAY	0.84242	1.876147	0.000235	0.009918	0.008978
29	KEGG_ALLOGRAFT_REJECTION	0.756866	1.862355	0.001137	0.031705	0.028703
30	REACTOME_TRANSPORT_OF_CONNEXONS_TO_THE_PLASMA_MEMBRANE	0.87879	1.854178	0.000281	0.011317	0.010245
31	PID_AP1_PATHWAY	0.670179	1.853789	0.000197	0.008532	0.007724
32	PID_AURORA_B_PATHWAY	0.718901	1.850012	0.000398	0.014958	0.013542
33	KEGG_PRION_DISEASES	0.768646	1.847144	0.000624	0.020359	0.018431
34	KEGG_CHEMOKINE_SIGNALING_PATHWAY	0.571605	1.839994	9.54E-06	0.000745	0.000675
35	REACTOME_SIGNALING_BY_INTERLEUKINS	0.521273	1.839799	8.59E-10	1.86E-07	1.68E-07
36	REACTOME_SCAVENGING_BY_CLASS_A_RECEPTORS	0.880385	1.83269	0.000501	0.017689	0.016014
37	REACTOME_SENESCENCE_ASSOCIATED_SECRETORY_PHENOTYPE_SASP	0.667608	1.820676	0.001376	0.037176	0.033655
38	PID_AURORA_A_PATHWAY	0.736803	1.818328	0.000847	0.026614	0.024094
39	KEGG_HEMATOPOIETIC_CELL_LINEAGE	0.64298	1.817806	0.000453	0.016649	0.015072
40	REACTOME_NUCLEAR_ENVELOPE_NE_REASSEMBLY	0.642476	1.816383	0.00047	0.016947	0.015343
41	KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.62148	1.814126	0.000149	0.007147	0.006471
42	REACTOME_MITOTIC_SPINDLE_CHECKPOINT	0.594192	1.809471	4.05E-05	0.002508	0.00227
43	REACTOME_PURINERGIC_SIGNALING_IN_LEISHMANIASIS_INFECTION	0.761406	1.804875	0.000977	0.029127	0.026369
44	PID_FOXM1_PATHWAY	0.70098	1.803895	0.000891	0.027518	0.024912
45	REACTOME_MHC_CLASS_II_ANTIGEN_PRESENTATION	0.587892	1.794695	9.59E-05	0.005179	0.004689

No	**ID**	**ES**	**NES**	**pval**	**p.adj**	**qval**
46	REACTOME_CELL_CYCLE_CHECKPOINTS	0.528005	1.78789	1.93E-06	0.000175	0.000159
47	PID_SYNDECAN_1_PATHWAY	0.716164	1.782575	0.001923	0.047309	0.042829
48	REACTOME_RHO_GTPASES_ACTIVATE_FORMINS	0.570355	1.778378	6.89E-05	0.00411	0.003721
49	PID_IL12_2PATHWAY	0.638302	1.776944	0.001549	0.04057	0.036728
50	REACTOME_THE_ROLE_OF_GTSE1_IN_G2_M_PROGRESSION_AFTER_G2_CHECKPOINT	0.620259	1.763817	0.000526	0.0182	0.016477
51	REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_CYCLIN_B	0.744053	1.76374	0.001927	0.047309	0.042829
52	KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFECTION	0.627923	1.762639	0.000929	0.028186	0.025517
53	KEGG_CELL_CYCLE	0.570528	1.753306	0.000131	0.006683	0.00605
54	REACTOME_INTERFERON_GAMMA_SIGNALING	0.592932	1.712698	0.001016	0.02927	0.026498
55	BIOCARTA_ERYTH_PATHWAY	0.875079	1.708475	0.001943	0.047309	0.042829
56	REACTOME_APC_C_MEDIATED_DEGRADATION_OF_CELL_CYCLE_PROTEINS	0.580922	1.706321	0.001843	0.047309	0.042829
57	REACTOME_MITOTIC_G2_G2_M_PHASES	0.518613	1.703768	4.06E-05	0.002508	0.00227
58	REACTOME_MITOTIC_PROPHASE	0.576415	1.680535	0.002092	0.049557	0.044864
59	REACTOME_G_ALPHA_I_SIGNALLING_EVENTS	0.504593	1.67357	7.41E-05	0.004135	0.003743
60	REACTOME_SIGNALING_BY_GPCR	0.465674	1.659974	1.09E-06	0.000114	0.000103
61	REACTOME_RHO_GTPASE_EFFECTORS	0.488944	1.65324	3.33E-05	0.002301	0.002084
62	REACTOME_MITOTIC_G1_PHASE_AND_G1_S_TRANSITION	0.50578	1.609145	0.001203	0.033024	0.029897
63	REACTOME_NEUTROPHIL_DEGRANULATION	0.452268	1.605896	6.06E-06	0.000499	0.000451
64	REACTOME_FACTORS_INVOLVED_IN_MEGAKARYOCYTE_DEVELOPMENT_AND_PLATELET_PRODUCTION	0.520324	1.604225	0.002011	0.048295	0.043721
65	REACTOME_CELLULAR_SENESCENCE	0.515424	1.598848	0.001061	0.030077	0.027228
66	REACTOME_S_PHASE	0.488933	1.573504	0.001403	0.037331	0.033796