Supplementary Information

Pharmacologically reversible zonation-dependent endothelial cell transcriptomic changes with neurodegenerative disease associations in the aged brain

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Supplementary Fig. 1. Marker gene expression patterns in different cell types and subtypes. a, Violin plots of the expression patterns of marker genes for major cell type clusters identified. Each column corresponds to one primary cell type. Cell type abbreviations: same as **Fig. 1b**. **b,** Heatmap showing the expression patterns of variable genes along the arteriovenous axis employed for classification of EC subtypes (see Methods). Up to 30 genes are shown for each EC subtype. **c,** Relative average expression levels of marker genes of artery/arteriole (*Bmx* and *Vegfc*), capillary (*Tfrc* and *Mfsd2a*), vein (*Slc38a5* and *Nr2f2*), and artery/vein (*Vcam1* and *Vwf*) in the EC subtypes.

Supplementary Fig. 2. Dependence of differential expression analysis on EC subtype classification and cell number. a, Number of significant DEGs plotted against total number of cells sampled (young adult + aged groups) for each EC subtype. **b,** Venn diagram of EC-subtype DEGs and pooled-EC DEGs. The expression changes of a substantial proportion (22.0%, 103 out of 469) of DEGs would not be detected without subtype classification. **c,** *lnFC* in EC subtypes (x-axis) plotted against *lnFC* in all ECs pooled (y-axis) for DEGs significant in both subtype- and pooled EC-based comparisons across age groups. Note that genes with significant differential expression in more than one EC subtype have multiple points. For up- or downregulated DEGs, the majority of points (60.1%, 424 out of 706, $P = 4.5 \times 10^{-8}$ compared to chance level by one-sided, one proportion *z*-test) fall below or above the line with unit slope respectively.

Supplementary Fig. 3. *Vcam1* **expression level in the avEC subtype across age.** Violin plots of *Vcam1* expression levels compared across age for **a,** all avECs (*lnFC* = -0.39; FDR-adjusted *P*-value = 1), or **b,** avECs with non-zero *Vcam1* transcript count $(lnF\overline{C} = -0.19; F\overline{DR}$ -adjusted *P*-value = 1).

Supplementary Fig. 4. RNA fluorescent *in situ* **hybridization (FISH) of selected genes.** RNA FISH of selected genes (one gene per row, from top to down: *Afdn*, *Lef1*, *Ptprb*, *Mfsd2a*, *Smad7*, *Flt1*, *Ifitm3*, *Jund*, *Slc9a3r2*, *Nostrin*) in young adult (left three columns) and aged (right three columns) mouse brain sections, co-stained with lectin and DAPI for visualization of endothelium and cell nuclei (number of staining experiments carried out for each target gene: 2).

Supplementary Fig. 5. Supplementary comparative analysis with the Mayo Clinic AD brain bulk RNA-seq dataset. a, Similar to **Fig. 3b** but with additional genes from comparative analysis using the Mayo Clinic AD brain bulk RNA-seq dataset. Human AD brain differential expressions relative to age-matched control subjects (FDR-adjusted *P*-value < 0.05, y-axis) plotted against expression changes in pooled aged mouse brain ECs (x-axis), showing aged mouse brain EC DEGs whose human orthologs had concordant (first and third quadrants, light green) or discordant (second and fourth quadrants, light red) expression changes in human AD brains. Only DEGs with at least two-fold EC-enrichment (*lnFC* of EC expression relative to other cell types > 0.7) are shown, with color of dots representing the degree of enrichment. **b,** Human brain expression levels of genes with concordant expression changes in human AD and aged mouse brains identified from the Mayo Clinic AD brain bulk RNA-seq dataset (*n* = 78 samples from control brains, 82 samples from AD brains; two-sided unpaired *t*-test with adjustment for multiple comparisons). Black horizontal line: median; upper and lower bounds of box: 75th and 25th percentiles respectively; upper and lower bounds of vertical lines: upper quartile + $1.5 \times$ interquartile range or maximum (whichever is smaller), and lower quartile - $1.5 \times$ interquartile range or minimum (whichever is larger), respectively.

Supplementary Fig. 6. Comparative analysis with normal human aging brain data from the Genotype-Tissue Expression (GTEx) project database. a, Aged human brain (≥ 60 years old) differential expressions relative to younger subjects (< 60 years old) (FDR-adjusted *P*-value < 0.05, y-axis) plotted against expression changes in pooled aged mouse brain ECs (x-axis), showing aged mouse brain EC subtype DEGs whose human orthologs had concordant (first and third quadrants, light green) or discordant (second and fourth quadrants, light red) expression changes in aged human brains (GTEx dataset v7). Only DEGs with at least twofold enrichment in EC (i.e. *lnFC* of expression in ECs relative to other cell types > 0.7) were included, with color of dots representing the degree of EC enrichment. **b,** Similar to **a.**, but with y-axis being the slope of regression of expression level with respect to age (GTEx dataset v8). Only genes with significant slope on linear regression (i.e. *P* < 0.05) are included. **c,** Human brain expression levels of selected genes associated with neurovascular regulation (*Iqgap1*, *Ptprb*, *Timp3*, *Flt1*) and AD (P-gp gene, *Adamts1*, *Ahnak*, *Mecom*) with concordant changes in aged human and mouse brains (≥ 60 versus < 60 years old human brains, FDR-adjusted *P*-value < 0.05), or with important functional roles at the BBB and yet discordant changes (≥ 60 versus < 60 years old human brains, *Cldn5*, *Slc2a1* and *Ifitm3*: FDR-adjusted *P*-value < 0.05; *Mfsd2a*: FDR-adjusted *P*-value = 0.0505, *n* = 215 samples from 38 ≥ 60 years old brains, 147 samples from 23 < 60 years old brains, GTEx dataset v7; two-sided unpaired *t*-test with FDR-adjustment for multiple comparisons). Black horizontal line: median; upper and lower bounds of box: 75th and 25th percentiles respectively; upper and lower bounds of vertical lines: upper quartile + 1.5 × interquartile range or maximum (whichever is smaller), and lower quartile - 1.5 × interquartile range or minimum (whichever is larger), respectively. **d,** Human brain expression levels of selected genes plotted against age and the respective linear regression fits (*n* = 388 samples from 61 subjects, GTEx dataset v8, *P*values for linear regression shown are for each gene independently without adjustment for multiple comparisons).

Supplementary Fig. 7. Confirmation of the blood-brain barrier (BBB) rescue effect of exenatide over saline vehicle. a, Threedimensional rendered images (top view) of *in vivo* two-photon imaging of cerebral vasculature and blood-brain barrier (BBB) leakage in the mouse somatosensory cortex by co-injection of 70 kDa FITC-conjugated dextran (FITC-dextran, green) and 40 kDa TRITC-conjugated dextran (TRITC-dextran, red). FITC-dextran remained in the vasculature and allowed reconstruction of vessels, while extravasation of TRITC-dextran served as an indicator of BBB leakage which was quantified for young adult, saline vehicleand exenatide-treated aged mouse groups. **b,** Volumetric quantification of TRITC-dextran extravasation showing BBB breakdown in saline vehicle-treated aged $(18 - 20$ months old) relative to young adult mice $(2 - 3$ months old) (mean fold change (*FC*) in volume of extravasated TRITC-dextran relative to young adult group \pm S.E.M. = 20.5 \pm 2.3; $P = 1.7 \times 10^{4}$ for saline vehicletreated aged vs young adult mouse group, 3 image stacks were acquired to obtain the mean for each animal, *n* = 3 mice for each group, one-way ANOVA with Tukey's post-hoc test), which was significantly reduced by exenatide treatment (5 nmol/kg/day I.P. for $4 - 5$ weeks starting at $17 - 18$ months old, mean fold change relative to young adult group \pm S.E.M. = 10.3 ± 0.9 ; $P = 5.4 \times$ 10-3 for exenatide-treated vs saline vehicle-treated aged mouse group, 3 image stacks were acquired to obtain the mean for each animal, $n = 3$ mice for each group, one-way ANOVA with Tukey's post-hoc test). Source data are provided as a Source Data file.

Supplementary Fig. 8. Reversal of ageing-associated transcriptomic changes by exenatide treatment in the EC subtypes. *P*values of linear regression shown are for each cell subtype independently without adjustment for multiple comparisons.

Supplementary Fig. 9. Attenuation of microglial ageing- and neurodegenerative disease-associated signatures by exenatide treatment. a, IBA1 immunostaining in young adult, aged, and exenatide-treated aged mouse cortex. **b,** IBA1+ cell density across the different groups, revealing a trend of increased IBA1+ microglia density in the aged brain which was reduced by exenatide treatment (mean IBA1+ cell density \pm S.D. = 141 \pm 36 per mm² in young adult group, 171 \pm 34 per mm² in aged group, 154 \pm 28 per mm2 in exenatide-treated aged group brain sections; *n* = 9, 8 and 12 imaged hippocampal and cortical regions of 4, 3 and 3 mice from young adult, aged and exenatide-treated aged groups respectively; $P = 0.17$, one-way ANOVA). Source data are provided as a Source Data file. **c,** t-SNE visualization of the expression of four ageing- and neurodegenerative disease-enriched genes in microglia (*Apoe*, *Ccl6*, *Cd9*, *Timp2*) in the different groups. **d,** Dot plots showing the differential expressions of a panel of microglial ageing-, neurodegenerative disease- and activation-associated genes in the aged mouse brain (relative to young adult group), and the effects of exenatide treatment.

EC subtype	Marker genes (source: Nature. 2018 Feb 22;554(7693):475-480 ¹ .)
aEC1	Sncaip/Alpl/Alox12/B4galnt1/Glul/Syt15/Tpgs2/Fam198b/Antxr1/Eml1/Gm609/Rnf144a/Stom/Prdx4/Aig1/Arhgef25/Stc1/Plat/Peak1/Tec/Efnb2/Fbxo7/Unc5b/Tpst1/Hey1/
	Cpm/Hrct1/Unc119b/Hbegf/Tbxa2r/Spry4/Scube2/Plcb1/Hlx/Arl15/Tsc22d1/Filip1/A430090L17Rik/Plk2/Slc36a1/Sez6/Rad54b/Gcnt2/Clec1a/Tgfb2/Slc12a5
aEC2	Egr1/Mgst1/St8sia2/Entpd1/Zbp1/Cables2/Cthrc1/Msx1/St8sia6/Cbr3/Irf6/Lcat/Olfml2a/Slc27a3/Col18a1/Fchsd2/Prkcd/Ifitm3/Mmrn2/Gata2/Fos/Marcks/Edn1/Kdm6b/E
	ps8l2/P2ry2/Pfkfb3/Snx10/Ssfa2/Crispld1/Prr13/Atl2/Galk1/Kazald1/Dsp/Sncg/Rasd1/Nebl/Gadd45b/Lama3/Bmx/Gkn3/Tmem100/Ssbp2/Hmgn3/Slc26a10/Pradc1
capEC	Dll4/Rasgrp3/Akr1c14/Slc25a33/Smarca2/Ets2/Rcan2/Sema6d/Gja1/Enpp2/Angpt2/Col4a3/Prdm1/Cdc42ep3/Hdac9/Pde4b/Arhgap18/Bcl2/Htra3/Gpr85/Cyp2d22/Itga4/T
	rak2/Nrp1/Camk2n1/Nid2/Lrrn3/Plekhh2/Rgcc/Stra6/Rgl1/Pcx/Slc1a1/Osgin1/Klhl6/Cxcl12/Spry1
vcapEC	Nrp2/Frmd5/Tmem98/Pnkd/Atp8a1/Tmem37/Stx3/Pak1/Pitpnm2/Car14/Jak3/Tspan17/Serpinb9/Unc13c/Fcgrt/Pglyrp1/Kcp/Slc40a1/Slc38a3/Ctla2b/Tmtc2/Irf5/Nos2/Rell
	1/Hcn2/Coro2b/Baiap2/Rab4a/Pfkl/Trib2/Prr5l/Tmsb10/Ndnf/Car4/Slc38a5/Fmo2/Cebpd/St6gal1/AU021092/Pcdh19/Igsf5/Odc1/Fam13a/Tbx4/Ankrd37/Pmaip1/Grb7/Iv
	ns1abp/Cdkn2b
vEC	Dixdc1/Nr2f2/Lbp/Adk/Ltc4s/Tspan9/Tcea3/Ndufa8/Lrrc8b/Chn2/Prcp/Icam1/Il1r1/Tbc1d2b/Nckap5/Gm7694/Bst1/Sdk1/Lcn2/Fmo1/Ctsc/Gpr182/Gm5127/Cysltr1/Hspb8
	/Prpf40b/Rp1/Mxra8/Prdm5/Itga3/Hs3st1/Anxa2/Golm1/Homer3/Atp1b1/Nampt/Prrt4/Sytl2/Gjc1/Actn1/Klk8/Ddah1/Smagp/Ramp3
avEC	Tmem176b/Tgtp1/Id2/Ptn/Gngt2/Tpd52l1/Frem2/Hyal2/Ifi27l2a/Tln2/Slc6a6/Car7/Vcam1/Klf4/Rfk/P2ry1/S100a10/Ehd1/Plec/S100a11/Pla2g4a/Cd9/Pdgfa/Ntn1/Thbd/C5
	30008M17Rik/Aldh1a3/Kcnb1/Tnfrsf11a/Klf10/Carhsp1/Aldh1a1/Wnt5a/Icosl/Cfb/Myof/Adh1/Epha4/Tgm2/Slfn2/Vwf/Adcy4/Tmem252/Tbx1

Supplementary Table 1. Arteriovenous zonation marker genes used for EC subtype classification.

Supplementary Table 3. Disease associations of the human orthologs of aged mouse brain EC DEGs.

Supplementary Table 4. Evidence of human brain endothelial expression of the orthologs of a subset of aged mouse brain EC DEGs.

Abbreviations and annotations: A: arteriole, AD: Alzheimer's disease; C: capillary, DEG: differentially expressed genes, IF: immunofluorescence; IHC: immunohistochemistry, RT-PCR: reverse transcription-polymerase chain reaction, scRNA-Seq: single cell RNA sequencing; snRNA-seq: single nucleus RNA sequencing; V: venule; genes in bold font: have evidence of human brain endothelial expression.

Footnotes

i Gene names were chosen in accordance with Human Protein Atlas. Bold: confirmed expression in endothelium. Italic: unable to find evidence for endothelial expression.

ii Annotated by inspecting available human brain images from Human Protein Atlas and literature, may not be accurate due to sampling error.

iii Annotated by inspecting available human brain images from Human Protein Atlas and literature, cross-compared with Lee et al., 2017^{34} , may not be accurate due to sampling error.

iv Retrieved fro[m https://www.proteinatlas.org/humanproteome/tissue/brain](https://www.proteinatlas.org/humanproteome/tissue/brain) on 10/8/2019.

v Retrieved from<https://celltypes.brain-map.org/rnaseq/human> on 10/8/2019, data was based on snRNA-seq of cells from the middle temporal gyrus.

vi Lee et al 2017³⁴ annotated it as specific for endothelium, we however noted neuropil staining in all samples in Human Protein Atlas.

vii Not commented by Lee et al 2017³⁴ to be specific for endothelium.

viii Difficult to determine due to weak nuclear staining, not present in all samples.

ix Lee et al 2017³⁴ annotated it as specific for endothelium, we however noted that neuronal cell bodies were clearly stained in one sample in Human Protein Atlas and which appeared unlikely due to lipofuscin staining.

x Difficult to determine due to intense neuropil staining.

xi Lee et al 2017³⁴ annotated it as specific for endothelium by IHC, however a transmission electron microscopy study by Cornford et al 2005³² noted potential glial expression. xii Only in some segments of vessels.

Supplementary Table 5. Primer list.

Supplementary Table 6. RNA FISH probe list.

Supplementary References

1. Vanlandewijck, M. *et al.* A molecular atlas of cell types and zonation in the brain vasculature. *Nature* **554**, 475 (2018).

2. Buniello, A. *et al.* The NHGRI-EBI GWAS Catalog of published genome-wide association studies, targeted arrays and summary statistics 2019. *Nucleic Acids Res* **47**, D1005–D1012 (2018).

3. Verhaaren, B. *et al.* Multiethnic Genome-Wide Association Study of Cerebral White Matter Hyperintensities on MRI. *Circulation: Cardiovascular Genetics* **8**, 398–409 (2015).

4. Consortium, N. of the for and in, (SiGN), S. & (ISGC), I. Identification of additional risk loci for stroke and small vessel disease: a meta-analysis of genome-wide association studies. *The Lancet Neurology* **15**, 695–707 (2016).

5. Chang, D. *et al.* A meta-analysis of genome-wide association studies identifies 17 new Parkinson's disease risk loci. *Nat Genet* **49**, 1511–1516 (2017).

6. Kouri, N. *et al.* Genome-wide association study of corticobasal degeneration identifies risk variants shared with progressive supranuclear palsy. *Nat Commun* **6**, 7247 (2015).

7. Höglinger, G. U. *et al.* Identification of common variants influencing risk of the tauopathy progressive supranuclear palsy. *Nat Genet* **43**, 699 (2011).

8. Sailer, A. *et al.* A genome-wide association study in multiple system atrophy. *Neurology* **87**, 1591–1598 (2016).

9. Ferrari, R. *et al.* Frontotemporal dementia and its subtypes: a genome-wide association study. *The Lancet. Neurology* **13**, 686–99 (2014).

10. Rheenen, W. van *et al.* Genome-wide association analyses identify new risk variants and the genetic architecture of amyotrophic lateral sclerosis. *Nature Genetics* **48**, 1043 (2016).

11. Nicolas, A. *et al.* Genome-wide Analyses Identify KIF5A as a Novel ALS Gene. *Neuron* **97**, 1268-1283.e6 (2018).

12. Moss, D. J. *et al.* Identification of genetic variants associated with Huntington's disease progression: a genome-wide association study. *Lancet Neurology* **16**, 701–711 (2017).

13. Jansen, I. E. *et al.* Genome-wide meta-analysis identifies new loci and functional pathways influencing Alzheimer's disease risk. *Nature Genetics* **51**, 404–413 (2019). 14. Bendayan, R., Ronaldson, P. T., Gingras, D. & Bendayan, M. In Situ Localization of P-glycoprotein (ABCB1) in Human and Rat Brain. *J Histochem Cytochem* **54**, 1159– 1167 (2006).

15. Martino-Echarri, E. *et al.* Relevance of IGFBP2 proteolysis in glioma and contribution of the extracellular protease ADAMTS1. *Oncotarget* **5**, 4295–4304 (2014).

16. Medoro, A. *et al.* Proteases Upregulation in Sporadic Alzheimer's Disease Brain. *J Alzheimer's Dis* **68**, 931–938 (2019).

17. Davies, K. M. *et al.* Localization of copper and copper transporters in the human brain. *Metallomics* **5**, 43–51 (2013).

18. Naeve, G. S. *et al.* Expression profile of the copper homeostasis gene, rAtox1, in the rat brain. *Neuroscience* **93**, 1179–1187 (1999).

19. Sabbagh, M. F. *et al.* Transcriptional and epigenomic landscapes of CNS and non-CNS vascular endothelial cells. *Elife* **7**, e36187 (2018).

20. Du, Y. *et al.* Increased cerebral expressions of MMPs, CLDN5, OCLN, ZO1 and AQPs are associated with brain edema following fatal heat stroke. *Sci Rep-uk* **7**, 1691 (2017).

21. Krumbholz, M. *et al.* Chemokines in multiple sclerosis: CXCL12 and CXCL13 up-regulation is differentially linked to CNS immune cell recruitment. *Brain* **129**, 200–211 (2005).

22. Grubman, A. *et al.* A single-cell atlas of entorhinal cortex from individuals with Alzheimer's disease reveals cell-type-specific gene expression regulation. *Nat Neurosci* **22**, 2087–2097 (2019).

23. Wosik, K., Biernacki, K., Khouzam, M.-P. & Prat, A. Death receptor expression and function at the human blood brain barrier. *J Neurol Sci* **259**, 53–60 (2007).

24. Uranishi, R., Baev, N. I., Ng, P.-Y., Kim, J. H. & Awad, I. A. Expression of Endothelial Cell Angiogenesis Receptors in Human Cerebrovascular Malformations. *Neurosurgery* **48**, 359–368 (2001).

25. Wallgard, E. *et al.* Identification of a Core Set of 58 Gene Transcripts With Broad and Specific Expression in the Microvasculature. *Arteriosclerosis Thrombosis Vasc Biology* **28**, 1469–1476 (2008).

26. Ehrlich, A. T. *et al.* Expression map of 78 brain-expressed mouse orphan GPCRs provides a translational resource for neuropsychiatric research. *Commun Biology* **1**, 102 (2018).

27. Murphy, P. A., Lu, G., Shiah, S., Bollen, A. W. & Wang, R. A. Endothelial Notch signaling is upregulated in human brain arteriovenous malformations and a mouse model of the disease. *Laboratory Investigation J Technical Methods Pathology* **89**, 971–82 (2009).

28. Iqbal, U. *et al.* Molecular imaging of glioblastoma multiforme using anti-insulin-like growth factor-binding protein-7 single-domain antibodies. *Brit J Cancer* **103**, 1606– 16 (2010).

29. Gratzinger, D. *et al.* The transcription factor LMO2 is a robust marker of vascular endothelium and vascular neoplasms and selected other entities. *Am J Clin Pathol* **131**, 264–78 (2009).

30. Hou, A. *et al.* Expression of MECOM is associated with unfavorable prognosis in glioblastoma multiforme. *Oncotargets Ther* **9**, 315–20 (2016).

31. Vuletic, S. *et al.* Widespread distribution of PLTP in human CNS: evidence for PLTP synthesis by glia and neurons, and increased levels in Alzheimer's disease. *J Lipid Res* **44**, 1113–1123 (2003).

32. Cornford, E. M. & Hyman, S. Localization of brain endothelial luminal and abluminal transporters with immunogold electron microscopy. *Neurorx* **2**, 27–43 (2005).

33. Macdonald, J. A., Murugesan, N. & Pachter, J. S. Endothelial cell heterogeneity of blood-brain barrier gene expression along the cerebral microvasculature. *J Neurosci Res* **88**, NA-NA (2009).

34. Lee, S. J. *et al.* Large-scale identification of human cerebrovascular proteins: Inter-tissue and intracerebral vascular protein diversity. *Plos One* **12**, e0188540 (2017).