

Gliovascular transcriptional perturbations in Alzheimer's disease reveal molecular mechanisms of blood brain barrier dysfunction

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Supplementary Table of Abbreviations

Abbreviations:

A β :	Amyloid β
AD:	Alzheimer's disease
AG:	Angular gyrus
Ast:	Astrocytes
BBB:	Blood-brain barrier
CNS:	Central nervous system
CSF:	Cerebrospinal fluid
DEG:	Differentially expressed genes
DLPFC:	Dorsolateral prefrontal cortex
EC:	Entorhinal cortex
ECM:	Extracellular matrix
FACS:	Fluorescence-activated cell sorting
FANS:	Fluorescence-activated nuclear sorting
ICC:	Immunocytochemistry
IF:	Immunofluorescence
IHC:	Immunohistochemistry
IPSC:	Induced pluripotent stem cells
GO:	Gene ontology
GVU:	Gliovascular unit
HC:	Hippocampus
MTX:	Midtemporal cortex
Per:	Pericytes
PFC:	Prefrontal cortex
QC:	Quality control
RNAseq:	RNA sequencing
scRNAseq:	Single cell RNA sequencing
SFX:	Superior frontal cortex
SMC:	Smooth muscle cells
snRNAseq:	Single nucleus RNA sequencing
TH:	Thalamus
TCX:	Temporal cortex
UMAP:	Uniform Manifold Approximation and Projection
UMI:	Unique molecular identifier

Supplementary Results

Postmortem Results:

Ligand-target interactions between astrocytic and vascular AD-associated genes:

For completeness, expression levels of the six prioritized vascular target genes were also tested for associations with AD-related neuropathologies (**Supplementary Figure 12B**), age, sex and *APOEε4* (**Supplementary Figure 12C**). The results are detailed below. In summary, neuropathology associations are consistent with that expected from AD-related DEG findings, and some associations were also detected with sex and age, but not with *APOEε4*.

We explored the expression profile of the 6 prioritized vascular genes for association with key AD variables including Braak stage, Thal phase, age, sex, and *APOEε4*. We hypothesized that elevated expression of these genes is associated with increased AD pathology. For *ANGPT2*, expression in endothelial cl.26 is used, whereas for other genes expression in pericyte cl.25 is used, per their NicheNet results. As expected, all 6 vascular target genes that are higher in AD brains also have higher expression with increasing Braak stages and Thal phase (**Supplementary Figure 12B**). These associations are statistically significant ($q < 0.05$) except for the Thal phase association with *AHNAK* levels ($q = 0.13$). All genes are also higher in the presence of TDP-43 pathology with *ANGPT2* and *TSC22D3* reaching significance ($q < 0.05$).

There are also significant associations with age and sex, but not *APOEε4*. Brain levels of *ANGPT2*, *ECE1*, *STAT3* and *SMAD3* are reduced with aging (**Supplementary Figure 12C**). These associations are driven by the AD group for *ECE1* and *SMAD3*, which have significant diagnosis by age interaction for expression associations, but not the other genes. Regarding sex differences, *ANGPT2* and *STAT3* expression is significantly lower in males in the combined group, which seems to be driven by controls, especially for the latter. *SMAD3* is lower in AD males. Collectively, these results demonstrate that while

109 all 6 vascular targets are higher in AD temporal cortex and associated with increasing AD-related
110 pathologies, the levels of some of these genes are also influenced by age and sex in a differential manner
111 by diagnosis.

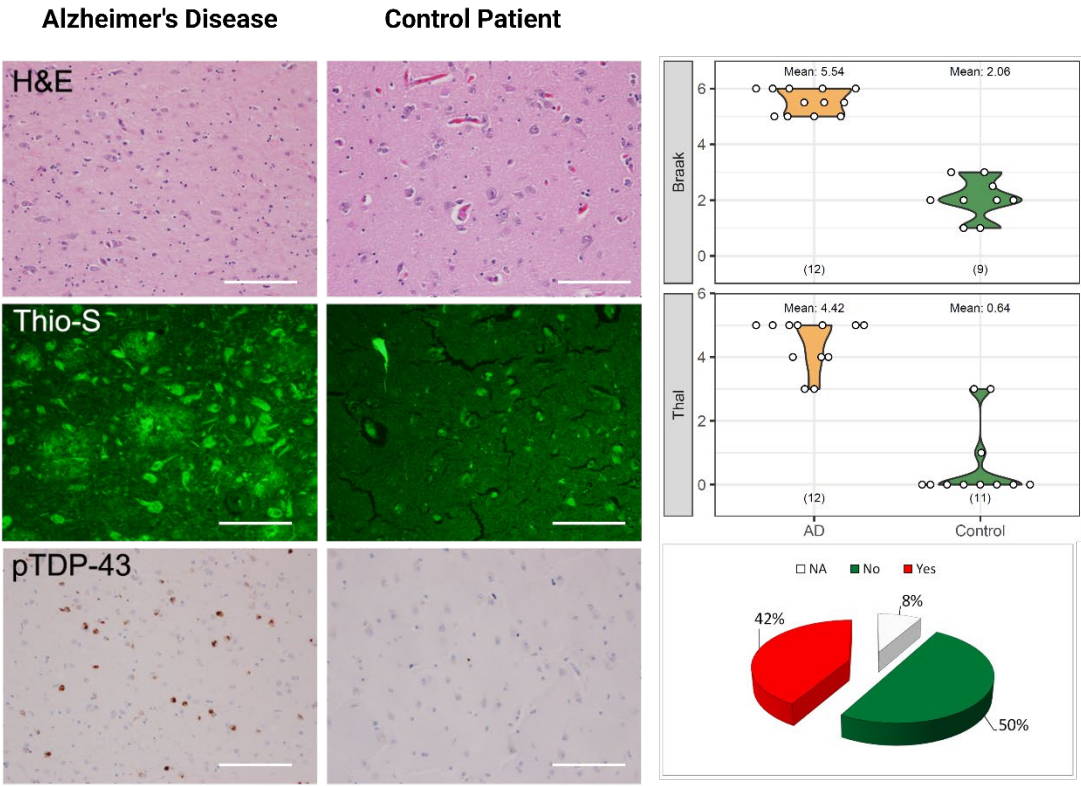
112 **Association of blood *SMAD3* gene expression levels with infarcts, A β deposition and cortical**
113 **atrophy:**

114 Since *APOE* or sex can influence brain vascular burden^{1,2}, we also performed secondary analyses
115 of *SMAD3* locus variants with infarcts and blood *SMAD3* levels, in *APOE*- ϵ 4 or sex-stratified cohorts. The
116 direction of effect remained the same in all strata, though as expected significance was lower given
117 smaller sample sizes (**Supplementary Data 35**). Effect sizes for both infarct and *SMAD3* blood expression
118 associations were similar between *APOE*- ϵ 4 carriers and non-carriers but greater for males compared to
119 females. These findings suggest that higher blood *SMAD3* levels may have a protective effect against
120 infarcts in a non-*APOE* dependent manner, though this effect may be stronger for males.

Supplementary Figures

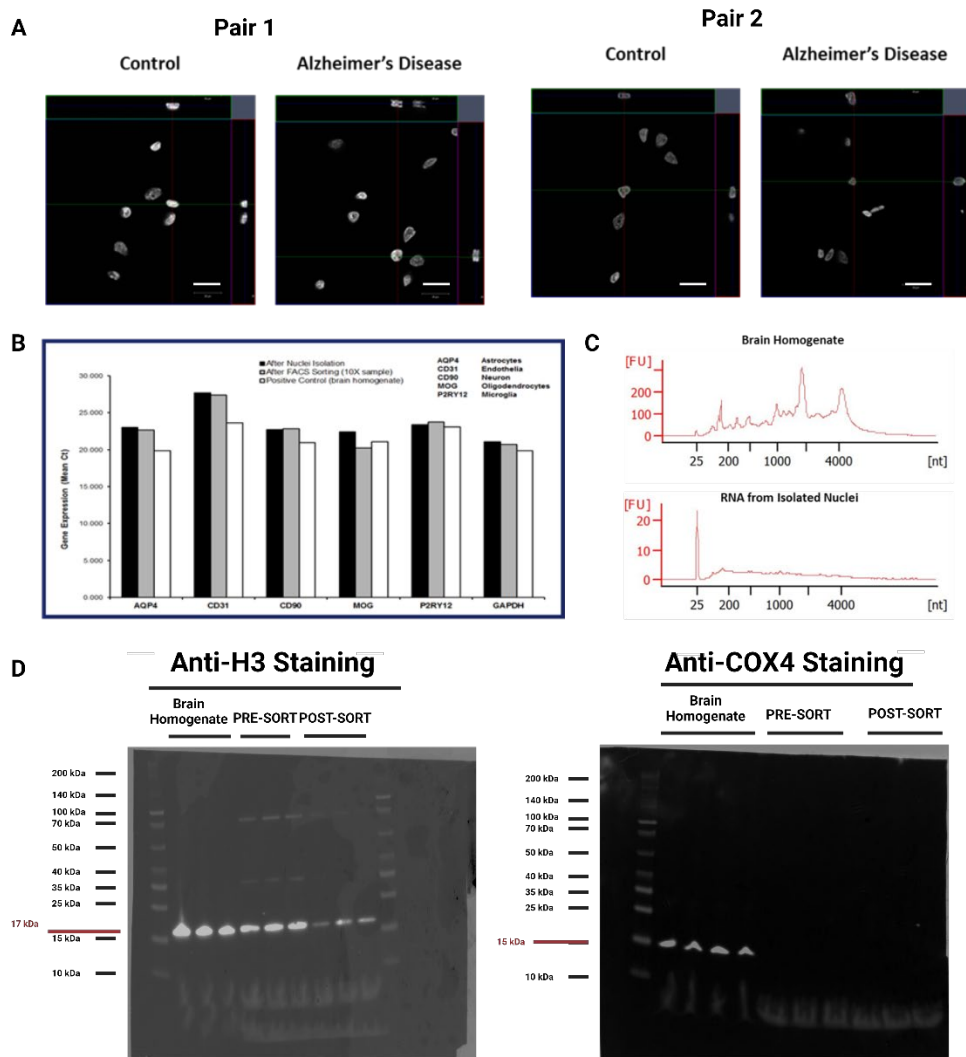
- Supplementary Figure 1** Neuropathological measures in AD and control samples
- Supplementary Figure 2** Purity and quality of isolated and purified nuclei
- Supplementary Figure 3** Effect of fluorescence-activated nuclei sorting (FANS) to cell type distribution
- Supplementary Figure 4** Parametric results of snRNAseq data after quality control and filtration steps
- Supplementary Figure 5** snRNAseq nuclei clusters on UMAP by features
- Supplementary Figure 6** snRNAseq cluster nuclei proportion distributions
- Supplementary Figure 7** Selected signature genes in brain vascular nuclei clusters
- Supplementary Figure 8** Comparison of our study with previous study
- Supplementary Figure 9** Heatmap of 40 astrocyte ligand genes identified in NicheNet analysis
- Supplementary Figure 10** Astrocyte ligands and vascular targets
- Supplementary Figure 11** Heatmap of 26 vascular target genes identified in NicheNet analysis
- Supplementary Figure 12** Validation of six vascular prioritized genes
- Supplementary Figure 13** *SMAD3* is a predicted target for multiple astrocytic ligands in AD
- Supplementary Figure 14** High expression of *VEGFA* is detected in astrocytes
- Supplementary Figure 15** Marker gene expression profile of pericytes in integrated datasets
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- Supplementary Figure 17** Correlation amongst *SMAD3* probes
- Supplementary Figure 18** QC of utilized iPSCs
- Supplementary Figure 19** Validation of *SMAD3* gene expression through RNAscope
- Supplementary Figure 20** Experimental design for the treatment of iPSC derived pericytes
- Supplementary Figure 21** Diagnosis stratified response of iPSC derived pericytes
- Supplementary Figure 22** Pericyte *SMAD3* levels at different VEGF treatment concentration
- Supplementary Figure 23** Validation of human snRNAseq results on transgenic zebrafish
- Supplementary Figure 24** FACS Gating strategy of zebrafish brain cells
- Supplementary Figure 25** QC Results of A β and PBS treated transgenic zebrafish results
- Supplementary Figure 26** Structural comparison of VEGFR2 in human and zebrafish
- Supplementary Figure 27** Zebrafish Immunostaining quantification strategies
- Supplementary Figure 28** FANS Gating strategy of intact nuclei from frozen human brain
- Supplementary Figure 29** Fold change in gene expression profile of iPSC-derived pericytes
- Supplementary Figure 30** Graphical abstract

Supplementary Figure 1:



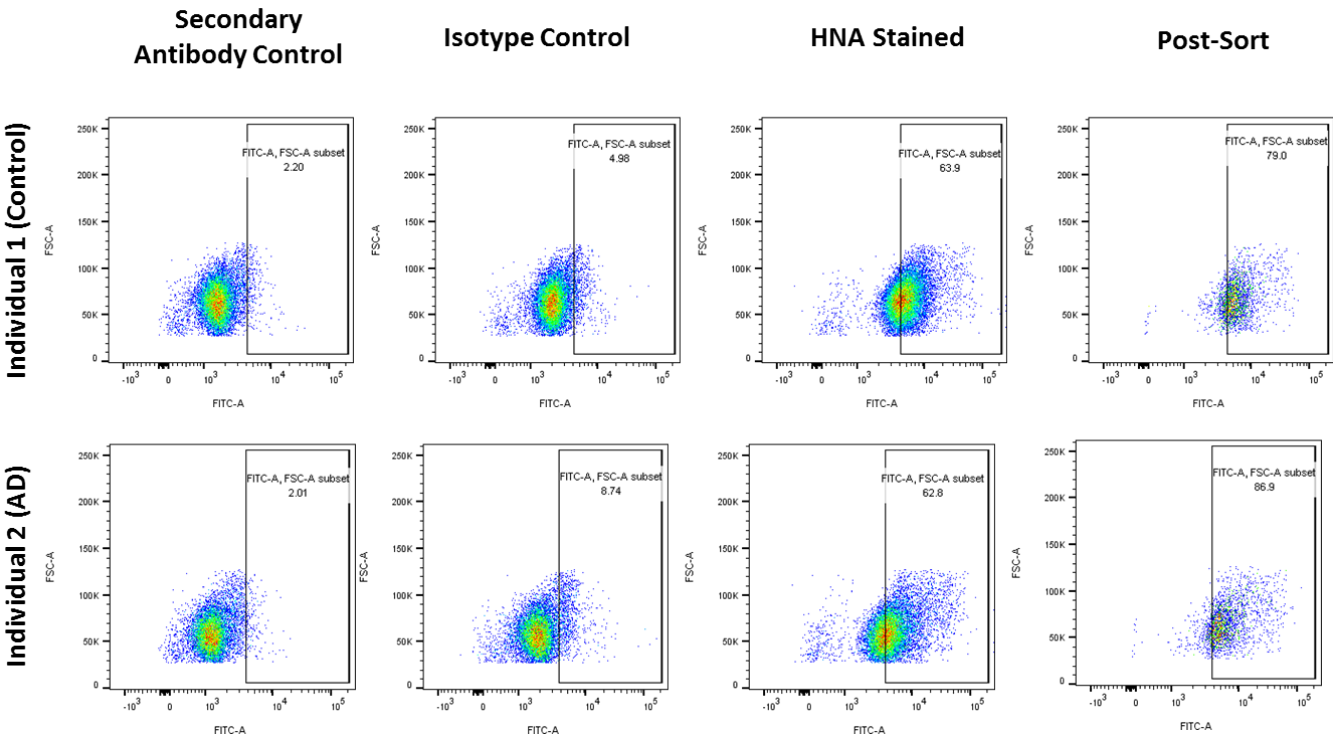
Supplementary Figure 1: Neuropathological measures in AD and control samples. Left panels depict representative immunohistochemistry pictures from an Alzheimer's patient and control brain amygdala tissue slides for H&E, thioflavin-S and TDP-43 staining. The white scale bar in each panel equals 200 µm. Right sided panels from top to bottom show distribution of Thal phase, Braak stage and presence or absence of TDP-43 in the cohort of 12 AD and 12 control brains. Source data are provided as a Source Data file.

Supplementary Figure 2:



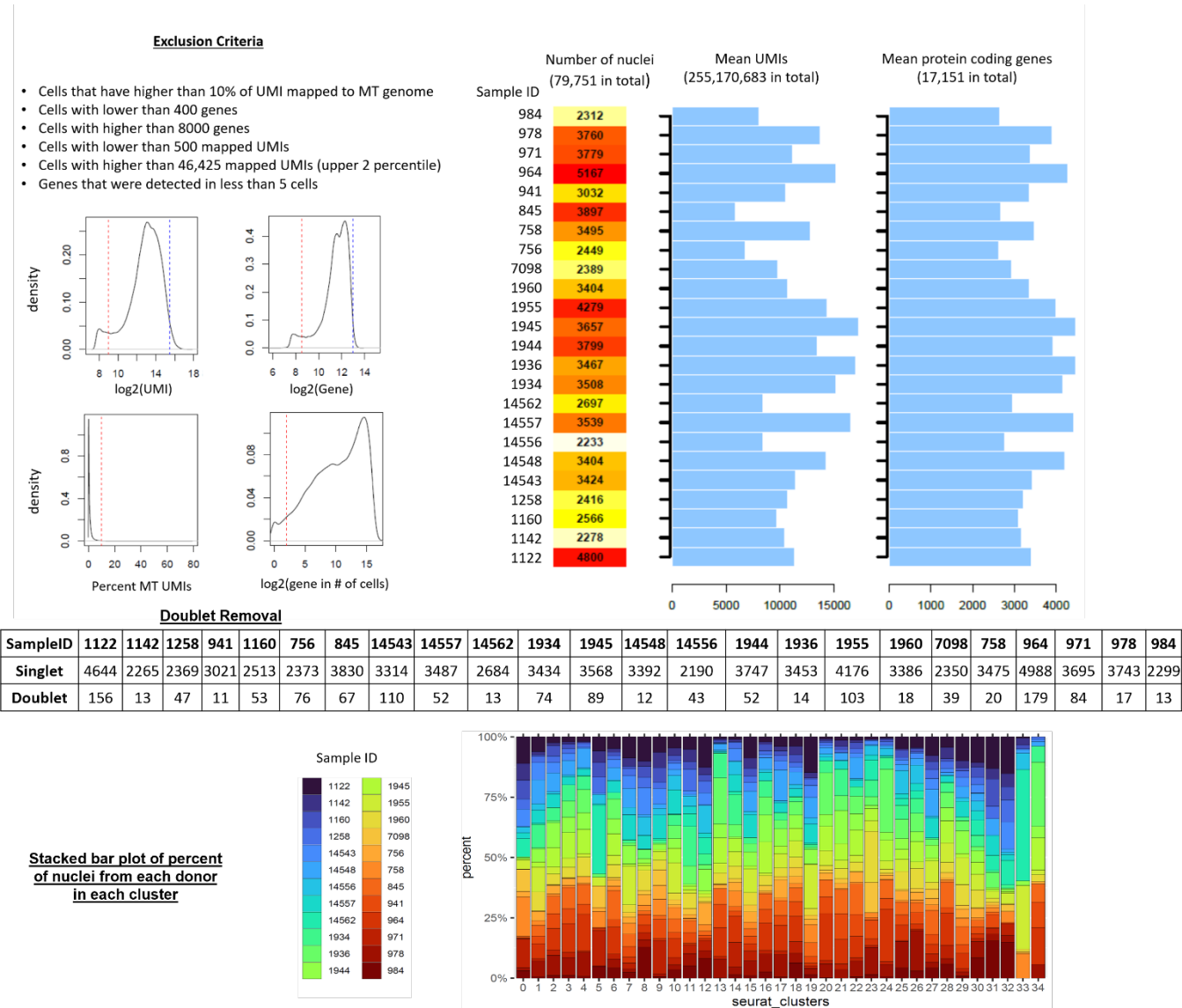
Supplementary Figure 2: Purity and quality of isolated and purified nuclei. (A): Intact nuclei were observed under confocal microscope. The scale bar equals 20 μ m. (B) qPCR was performed with cell type specific TaqMan probes from isolated nuclear RNA demonstrate lack of bias in detecting various cell types. (C) Disappearance of 18S and 28S peaks in Bioanalyzer histogram demonstrates the disappearance of cytoplasmic RNA from the nuclear fraction. (D): Effect of FACS to purity of isolated nuclei was measured using Nuclear (Anti-H3) and mitochondrial (Anti-COX4) antibodies. This experiment was completed once prior to snRNAseq data generation.

Supplementary Figure 3:



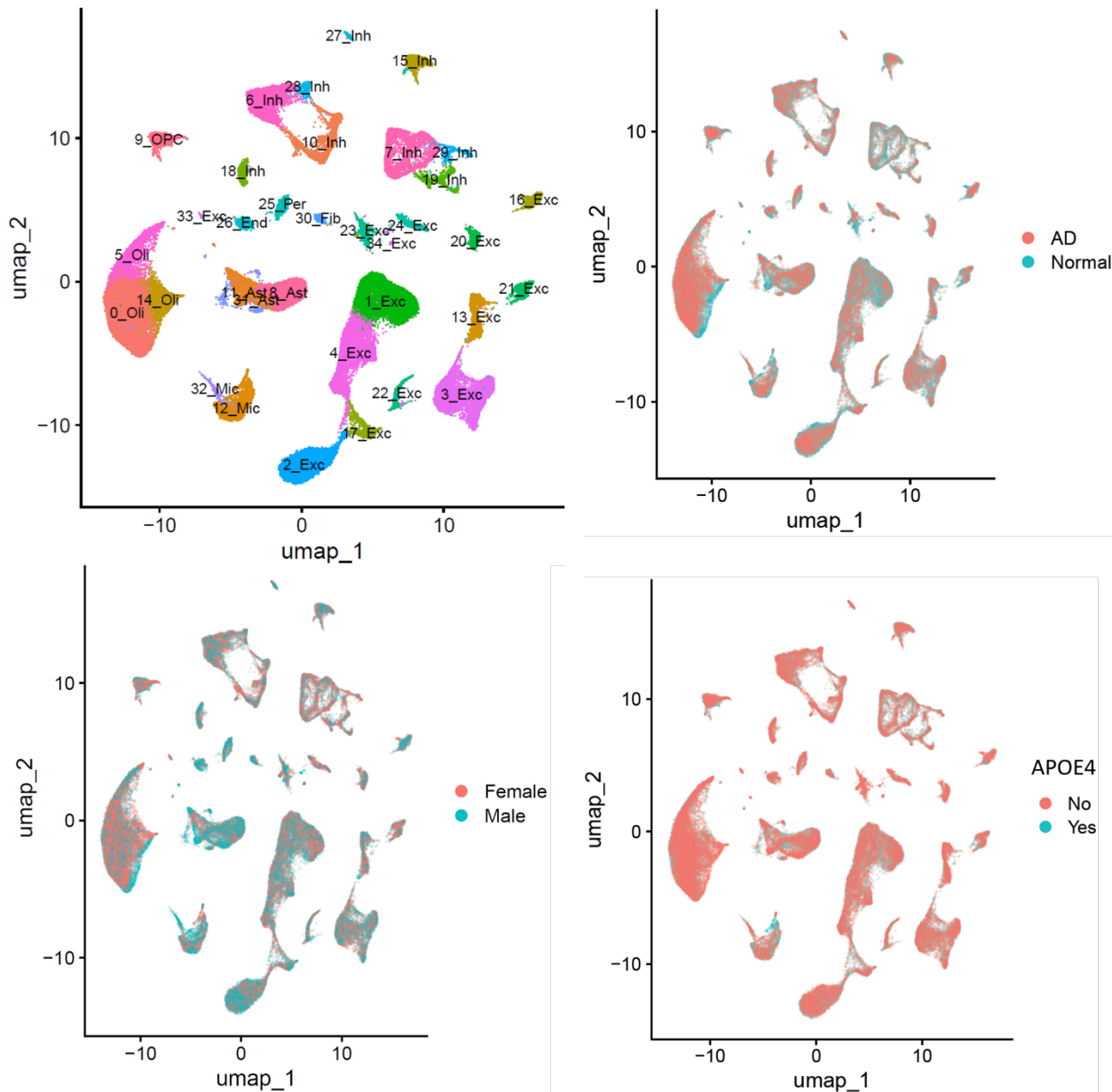
Supplementary Figure 3: Effect of fluorescence-activated nuclei sorting (FANS) to cell type distribution. Upper: FANS profile of the sorted nuclei. Lower: effect of FANS sorting to the distribution of cell types.

Supplementary Figure 4:



Supplementary Figure 4: Parametric results of snRNAseq data after quality control and filtration steps. Top left: Exclusion criteria for nuclei and genes. Bottom left: Density plots: UMI=unique molecular identifier. Top right: Post-QC number of nuclei, mean UMI and number of protein coding genes per each sample. Table: the number of doublets and singlets detected by Scrublet. These doublets were removed from downstream analysis. Lower: To test if there are over-representations of nuclei from donor(s) in each cluster, we followed the approach of Wang et al.³ to perform one-sided Fisher's Exact Test (FET).

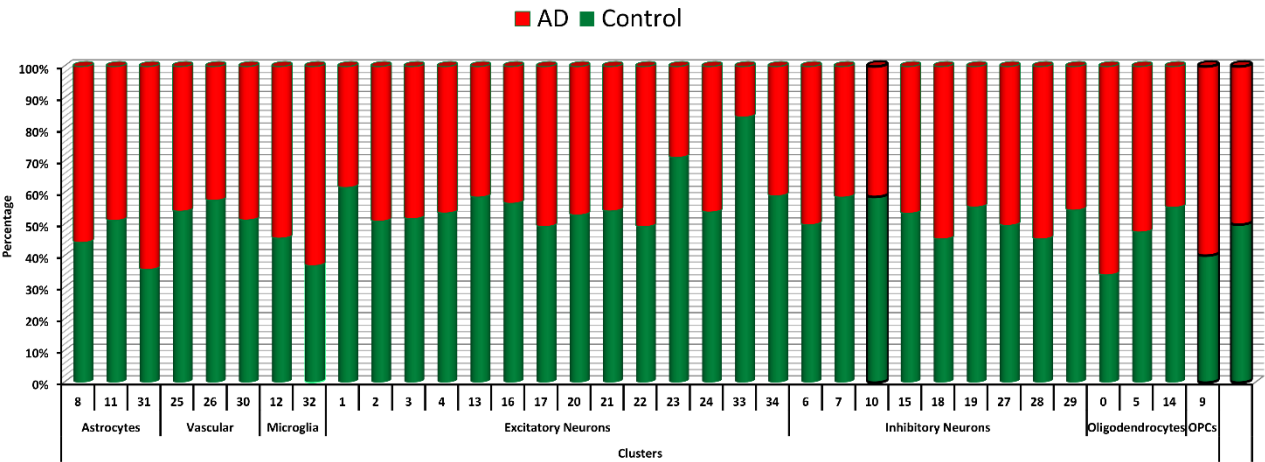
Supplementary Figure 5:



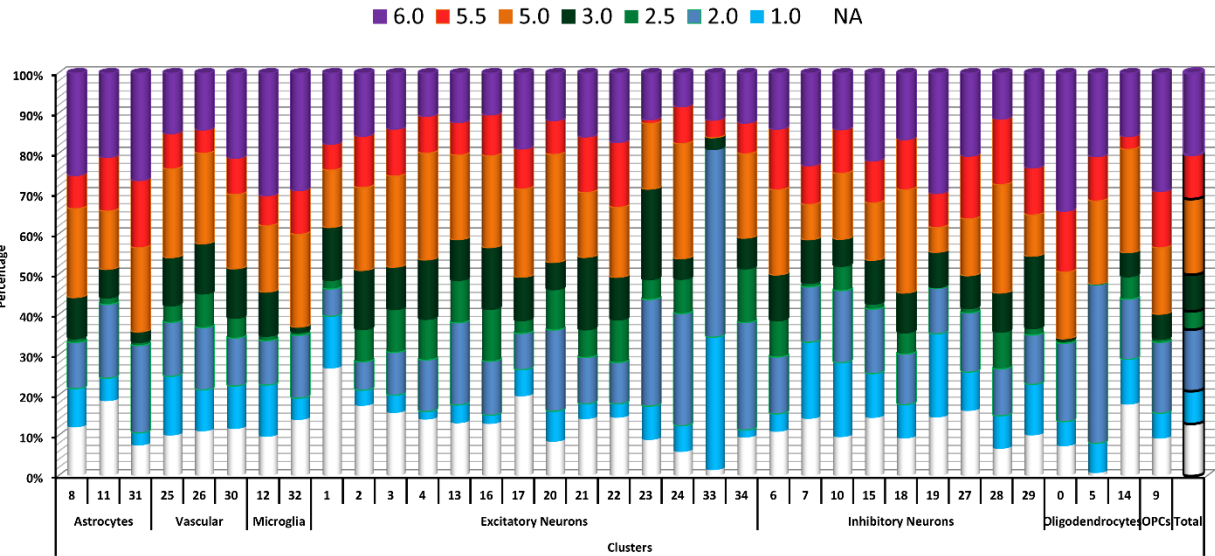
Supplementary Figure 5: snRNAseq nuclei clusters on UMAP by features:Top left: Nuclei clusters displayed on UMAP reduced dimension space, annotated as cluster number followed by cell type. Exc: excitatory neuron; Inh: inhibitory neuron; Oli: oligodendrocyte; OPC: oligodendrocyte progenitor cell; End: endothelia; Per: pericyte; Fib: fibroblast; Ast: astrocyte; Mic: microglia. Top right and bottom: Distributions are colored by variables. “APOE4 Yes” means either homozygotes or heterozygotes.

Supplementary Figure 6:

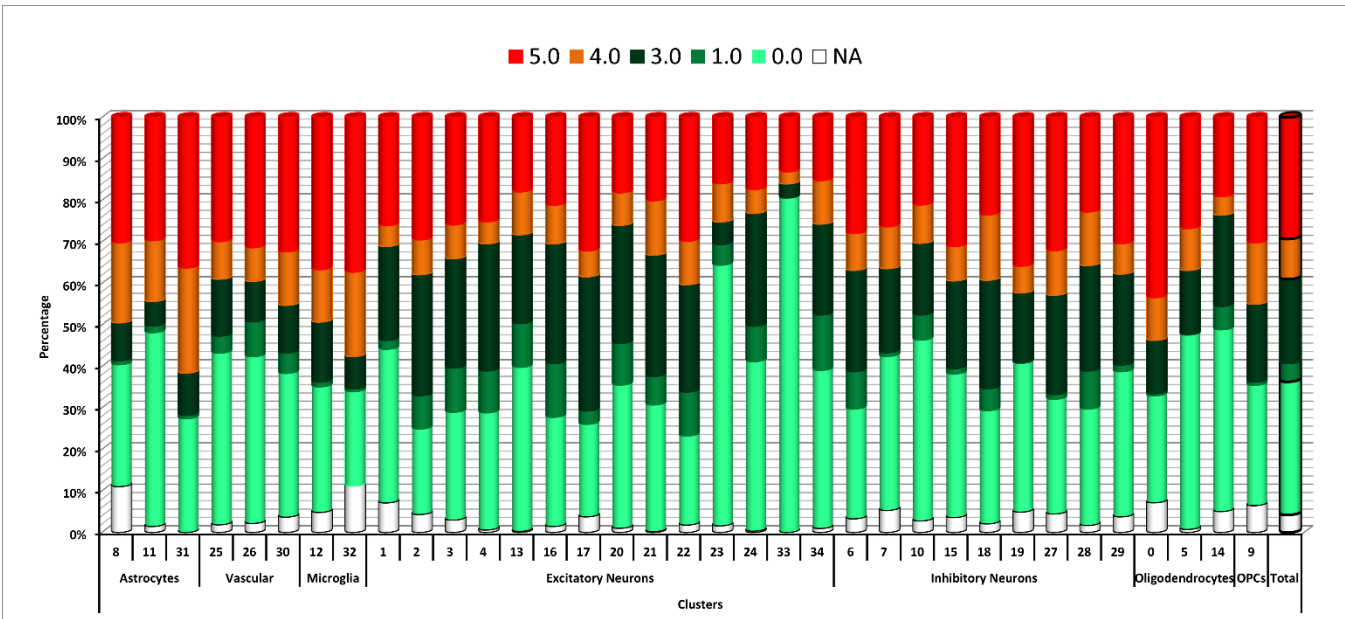
A. Cluster nuclei proportions by diagnosis



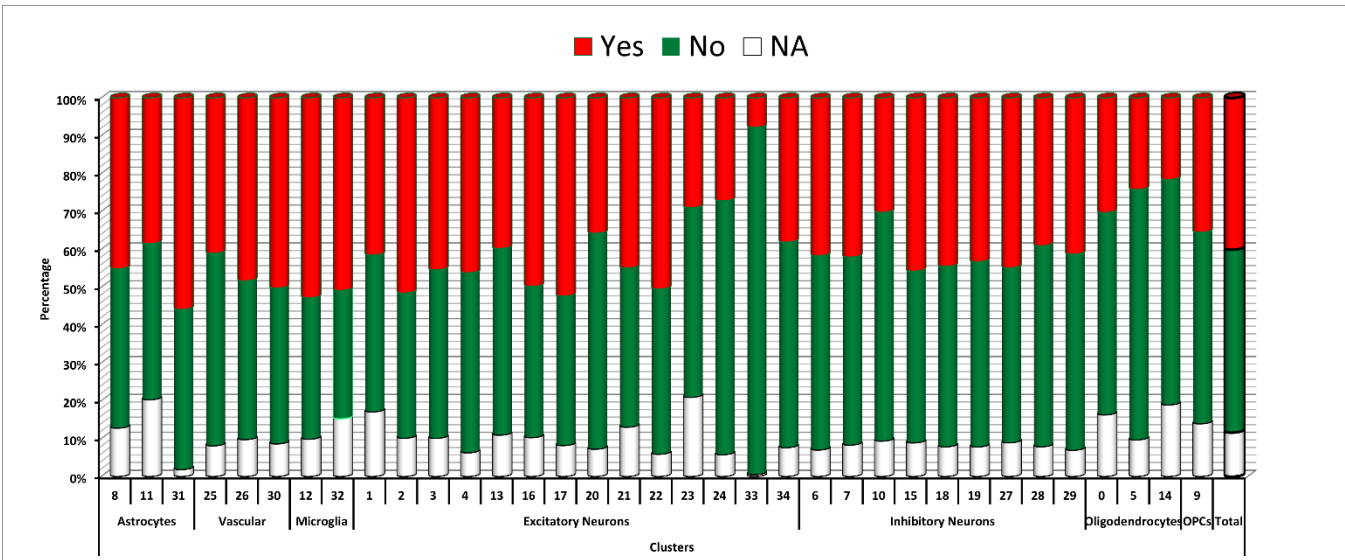
B. Cluster nuclei proportions by Braak stage



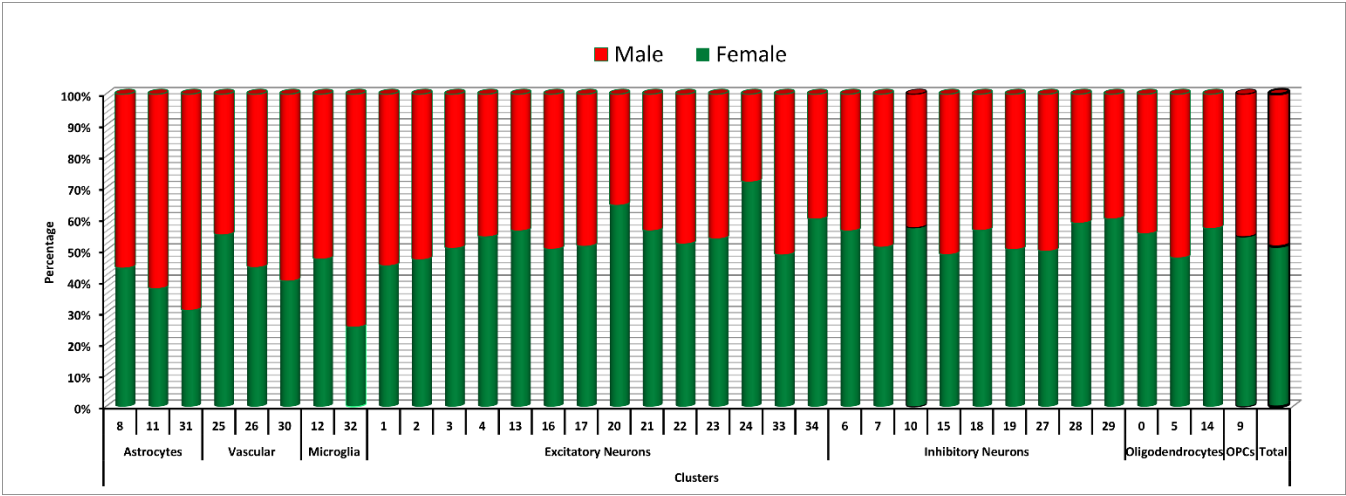
C. Cluster nuclei proportions by Thal phase



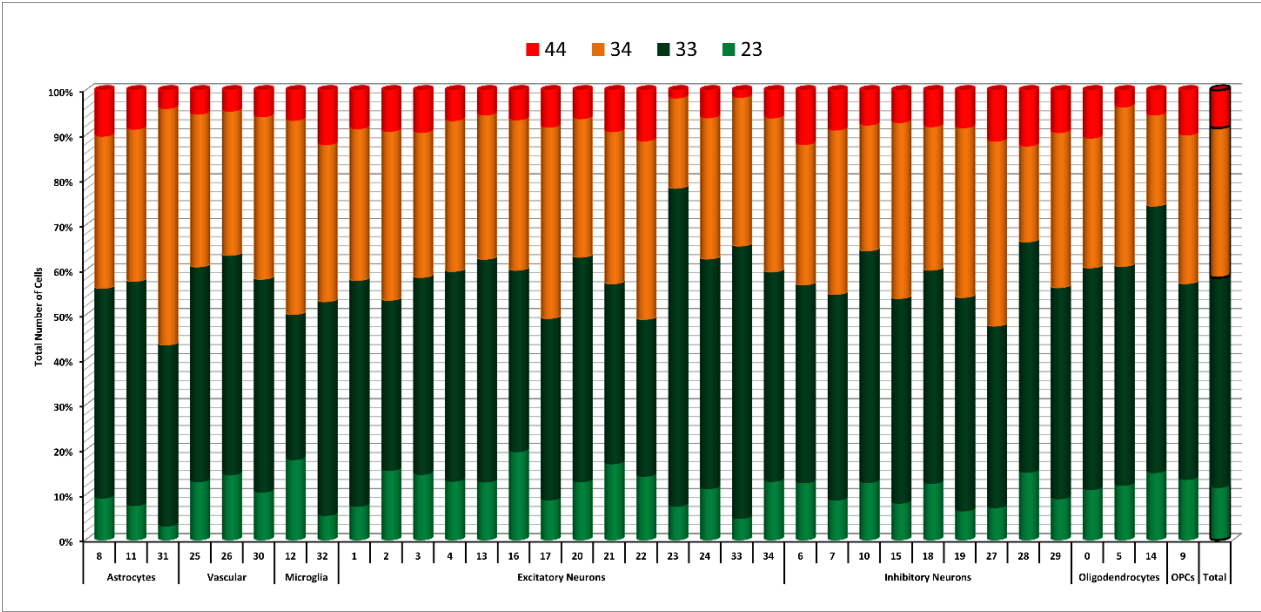
D. Cluster nuclei proportions by TDP43



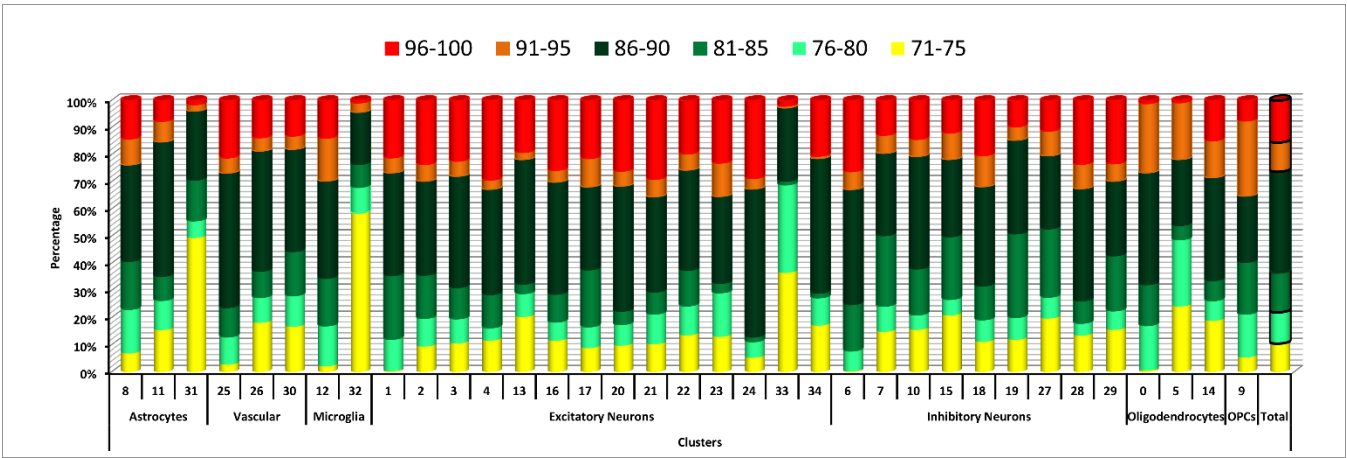
E. Cluster nuclei proportions by sex



F. Cluster nuclei proportions by APOE

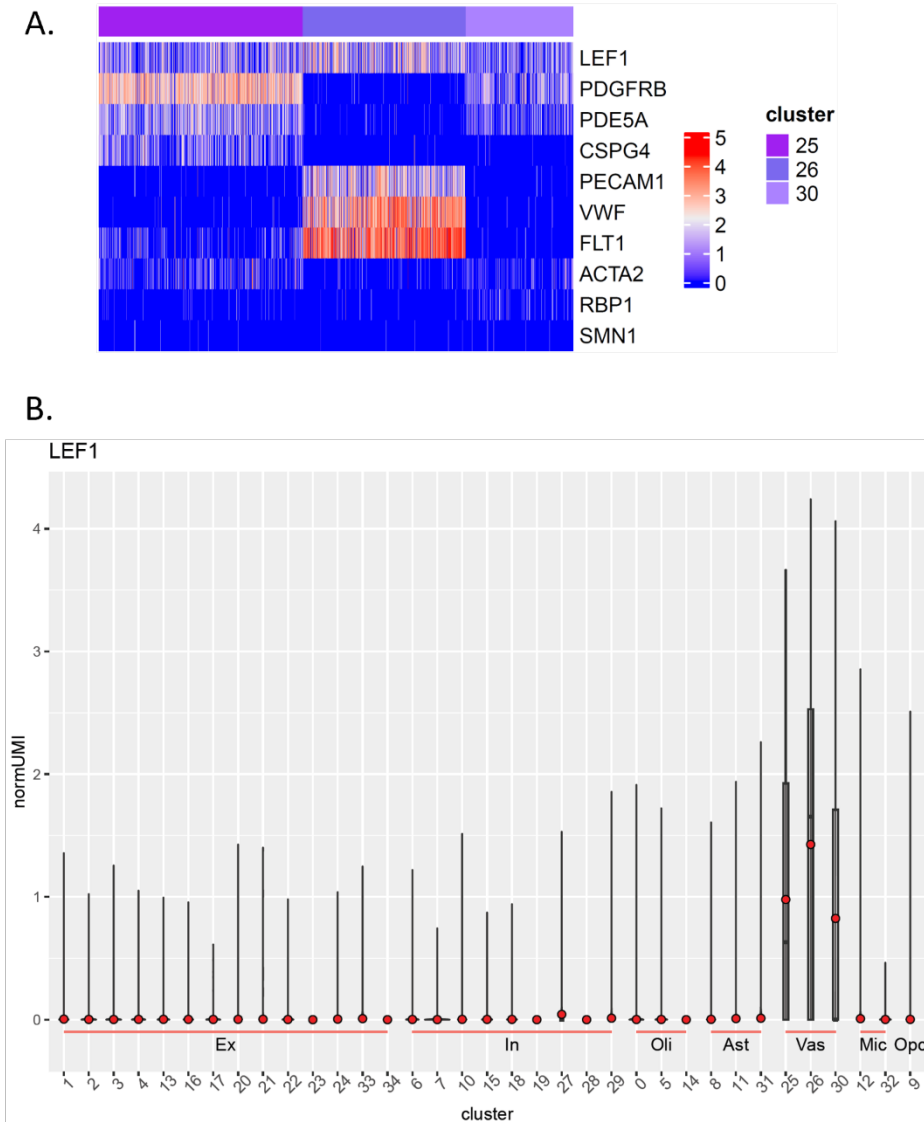


G. Cluster nuclei proportions by age



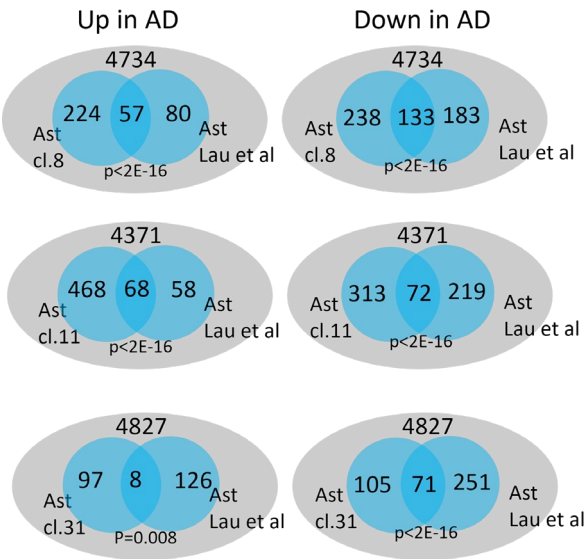
Supplementary Figure 6: snRNAseq cluster nuclei proportion distributions by A) diagnosis, B) Braak Stage, C) Thal phase, D) TDP-43, E) sex, F) *APOE* and G) age. Source data are provided as a Source Data file.

Supplementary Figure 7:



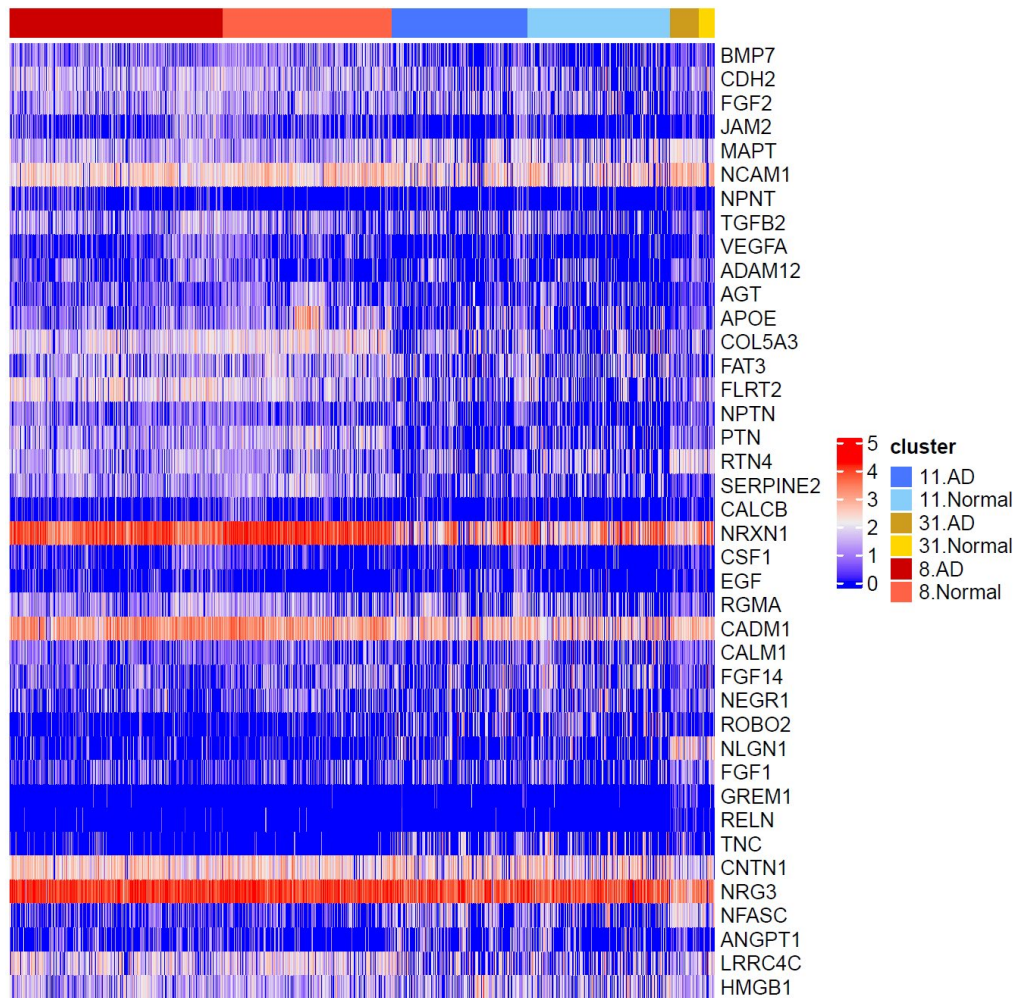
Supplementary Figure 7: Selected signature genes in brain vascular nuclei clusters. A. Expression of selected signature genes in vascular clusters. Cluster 25 (cl.25)=pericyte, cl.26=endothelia, cl.30=perivascular fibroblast. The scale bar indicates the mean log-normalized UMI counts. **B.** Only vascular nuclei clusters demonstrated expression of *LEF1*.

Supplementary Figure 8:



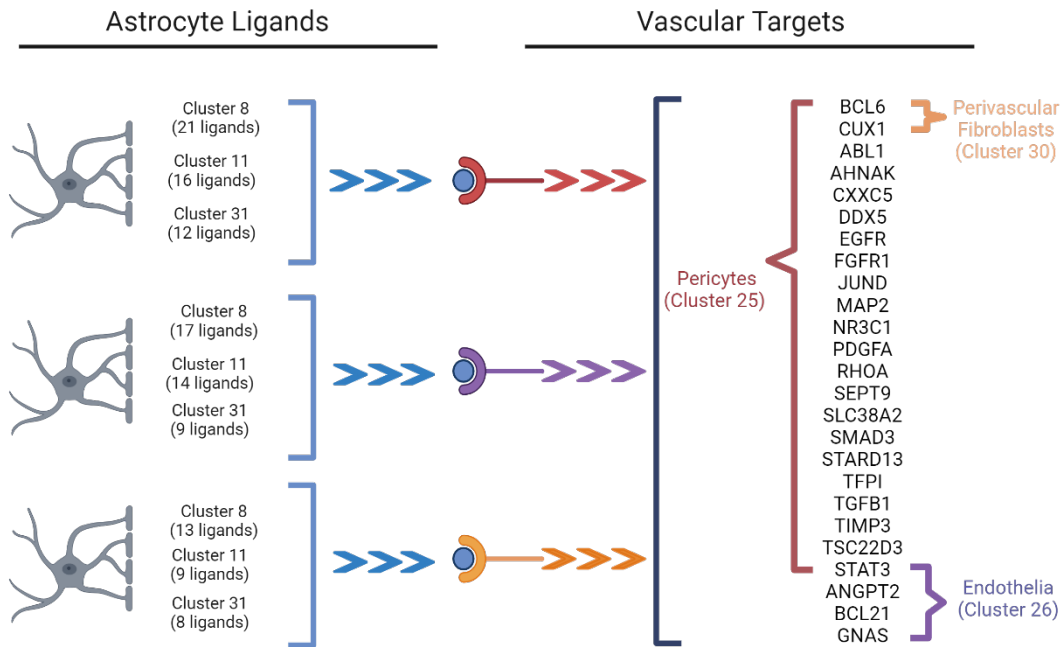
Supplementary Figure 8: Comparison of our study with previous study. Number of overlapping DEGs between astrocytic clusters in our study (cl.8, cl.112 and cl.31) and those from Lau et al. study⁴. The gray circles and the numbers indicate the detected genes in both Lau et al astrocyte cluster and our astrocytic clusters cl.8, cl.11 and cl.31 respectively. Enrichment p-value is from Fisher's exact test. Source data are provided as a Source Data file.

Supplementary Figure 9:



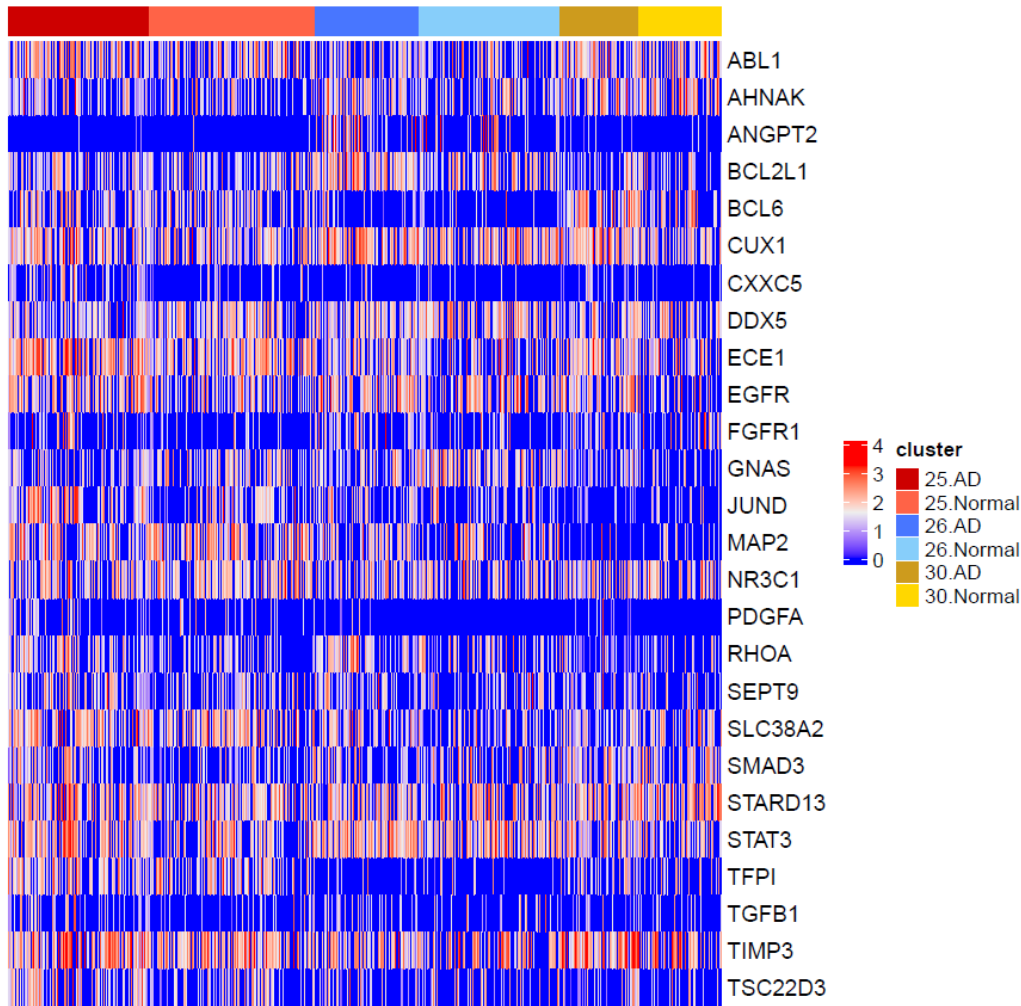
Supplementary Figure 9: Heatmap of 40 astrocyte ligand genes identified through ligand-target interaction analysis platform Nichenet⁵. This analysis used significant DEGs between AD and control tissue identified in astrocyte clusters (cl.8, cl.11 and cl.31) as ligands and those in endothelial clusters (cl.25, cl.26 and cl.30) as potential targets. For more detailed description of this analysis, please see main text and method. Columns are cells arranged by clusters and diagnosis. Values shown in the heatmap are normalized expression.

Supplementary Figure 10:



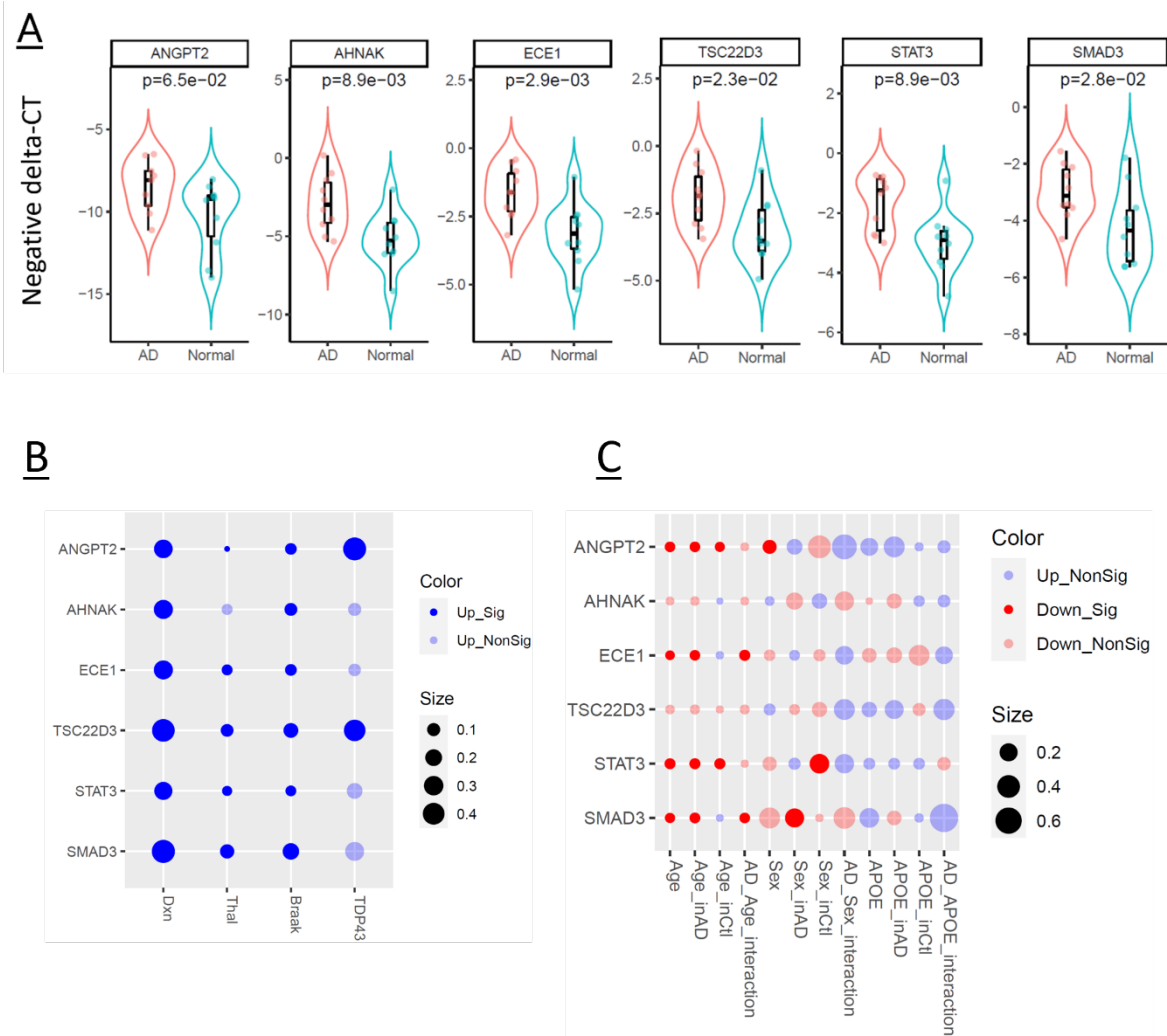
Supplementary Figure 10: Astrocyte ligands and vascular targets. Using NicheNet⁵ and focusing on significant DEGs in astrocytic clusters, we identified a combined pool of 40 unique potential ligand genes that have corresponding targets in one or more of the vascular clusters. There were 22, 4 and 2 predicted vascular targets in the pericyte cl.25 (red), endothelial cluster cl.26 (purple) and perivascular fibroblasts cluster cl.30 (orange), respectively, comprising 26 unique target genes (Supplementary Figure 10 Created with BioRender.com released under a Creative Commons Attribution-NonCommercial-NoDerivs license).

Supplementary Figure 11:



Supplementary Figure 11: Heatmap of 26 vascular target genes identified through ligand-target interaction analysis platform Nichenet⁵. This analysis used DEGs between AD and control tissue identified in astrocyte clusters (cl.8, cl.11 and cl.31) as ligands and those in endothelial clusters (cl.25, cl.26 and cl.30) as potential targets. For more detailed description of this analysis, please see main text and method. Columns are cells arranged by clusters and diagnosis. Values shown in the heatmap are normalized expression.

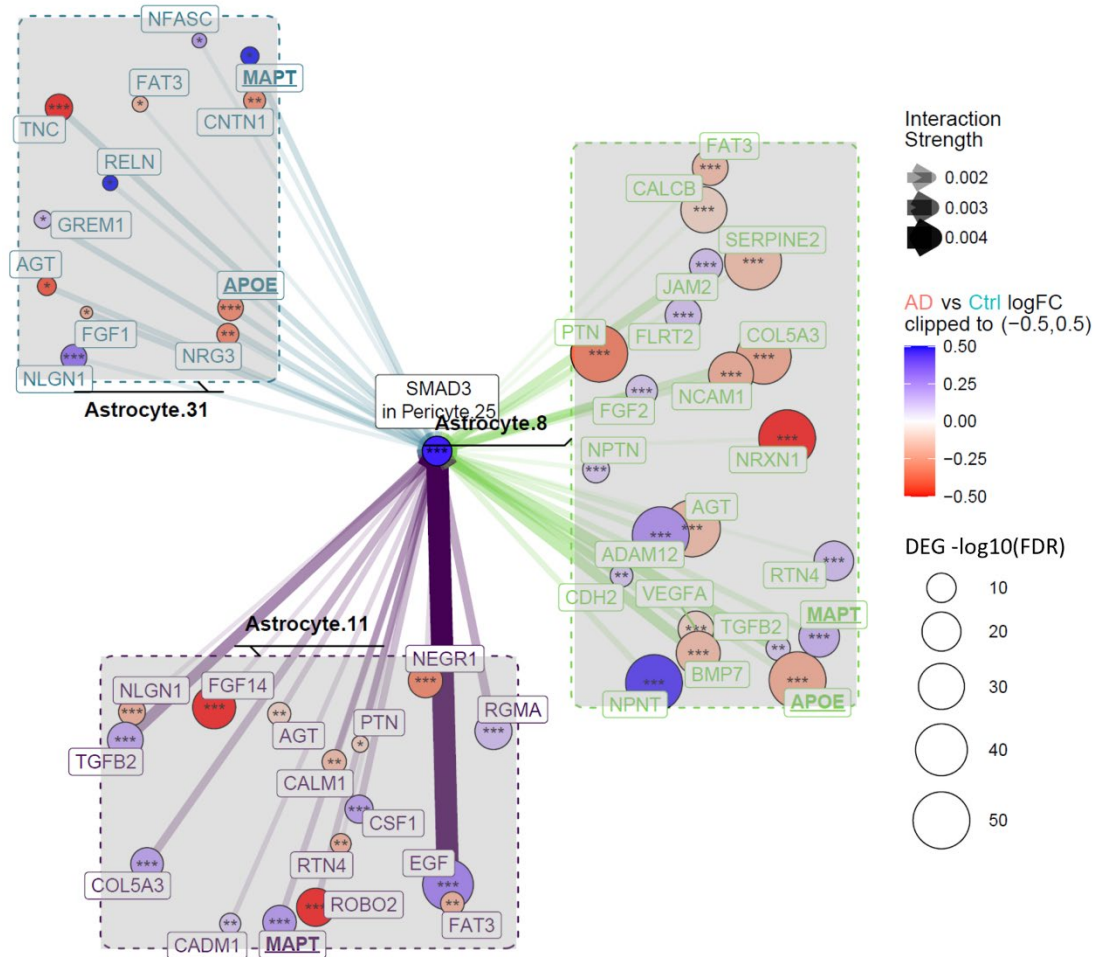
Supplementary Figure 12:



Supplementary Figure 12: Validation of six vascular prioritized genes. Expression of six prioritized vascular target genes were validated via qPCR from nuclear fractions. A) Distribution of negative delta-CT from qPCR experiment of six prioritized vascular target genes, which reflect the expression of these gene. Two-sided Wilcoxon rank sum tests were performed to test whether these genes were expressed higher in AD compared to control nuclei, as observed from snRNAseq. B) The association between AD-related pathologies and snRNAseq expression of six vascular genes. Blue bubble: significant positive association with pathologies at $q\text{-value} \leq 0.05$. Red bubble: significant negative association with pathologies at $q\text{-value} \leq 0.05$. Gray-masked bubble: not significant. Size of the bubble reflects the association coefficient. C) The association between age at death, sex and *APOEε4* and expression of six prioritized vascular genes in combined AD and controls, ADs only and controls only, respectively, as shown in the first three columns for each association. The fourth column for each association shows the interaction effects between age, sex or *APOEε4* with diagnosis on gene expression. A significant interaction effect indicates that the association between the risk factor and gene expression is dependent on disease status. Blue bubble: significant positive association at $q\text{-value} \leq 0.05$. Red bubble:

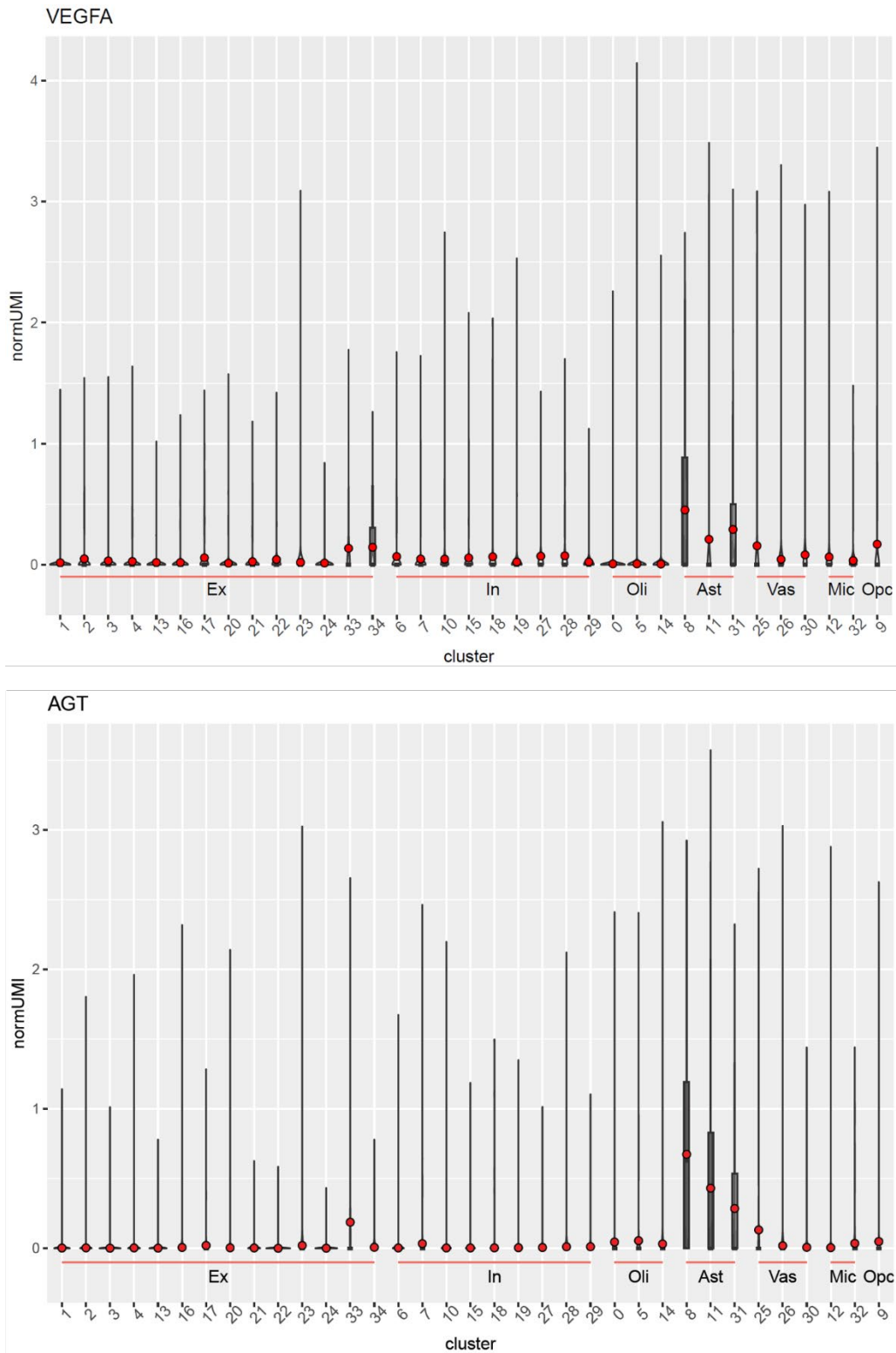
337 significant negative association at $q\text{-value} \leq 0.05$. As males or *APOE* $\epsilon 4$ carriers were denoted as 1 whereas
338 females or *APOE* $\epsilon 4$ non-carriers as 0, blue means higher in males or *APOE* $\epsilon 4$ carriers and red means
339 lower in males or *APOE* $\epsilon 4$ carriers. Gray-masked bubble: not significant. Size of the bubble reflects the
340 association coefficient. Source data are provided as a Source Data file.
341

Supplementary Figure 13:



Supplementary Figure 13: SMAD3 is a predicted target for multiple astrocytic ligands in AD from NicheNet. DEG (differentially expressed gene) is from comparing AD and control nuclei using MAST. The figure outlines the connections between astrocytic ligand genes to SMAD3 based on the interaction strengths in three astrocytic clusters. SMAD3 ligands include well-known AD genes in astrocytes such as APOE, MAPT, PSEN1, and APP. Line thickness: the Astrocytic gene's connection strength to SMAD3; Red Blue gradient heatmap: Fold change of differential expressed gene expression in AD vs control (downregulated (blue) and upregulated (red)); Radius of circle: FDR corrected significance between AD vs controls. Source data are provided as a Source Data file.

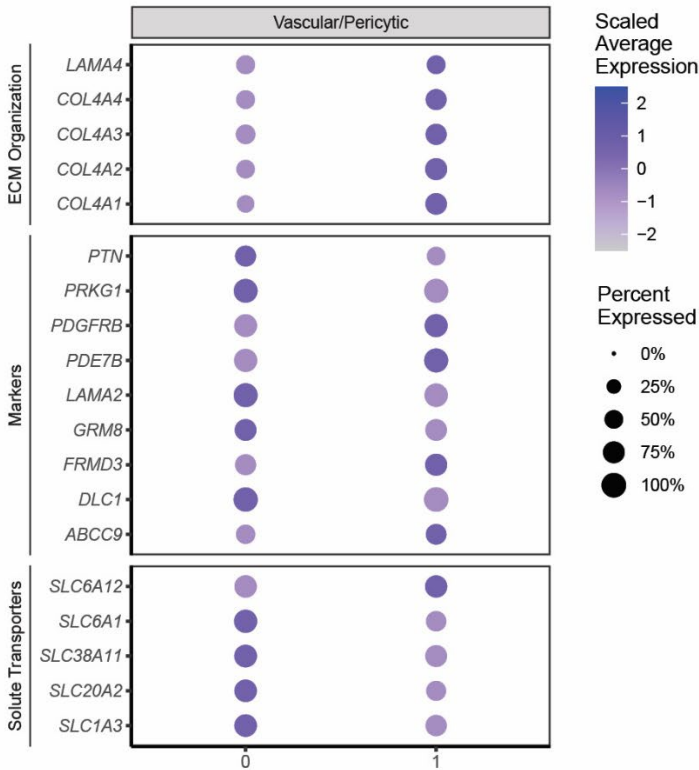
Supplementary Figure 14



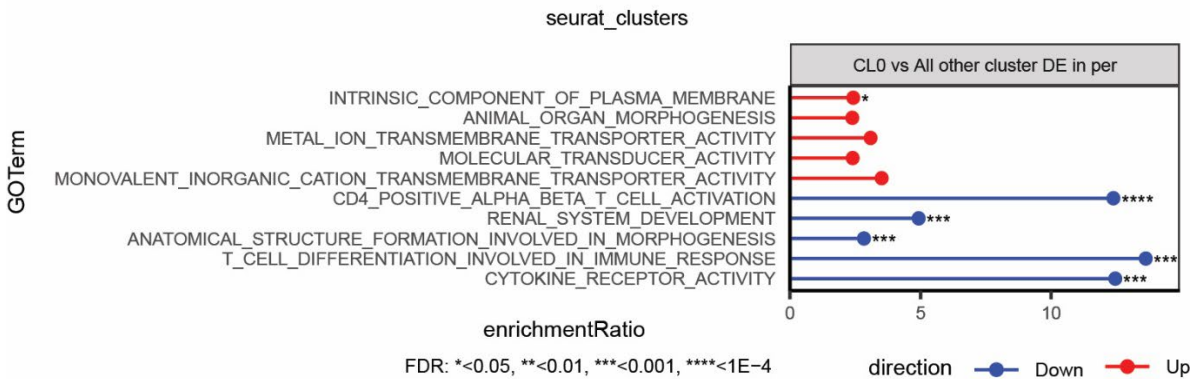
Supplementary Figure 14: High expression of *VEGFA* is detected in astrocytes. In human temporal cortex, *AGT* expression is restricted to astrocytes.

Supplementary Figure 15

A



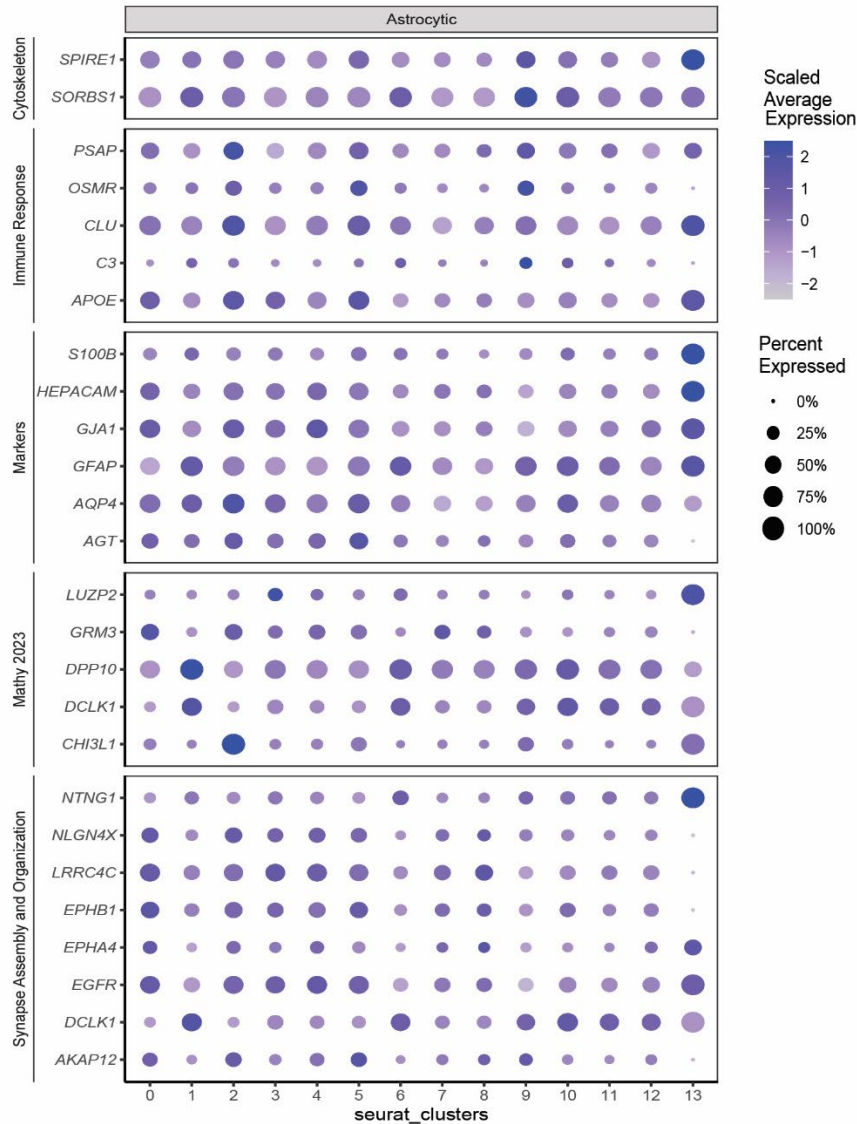
B



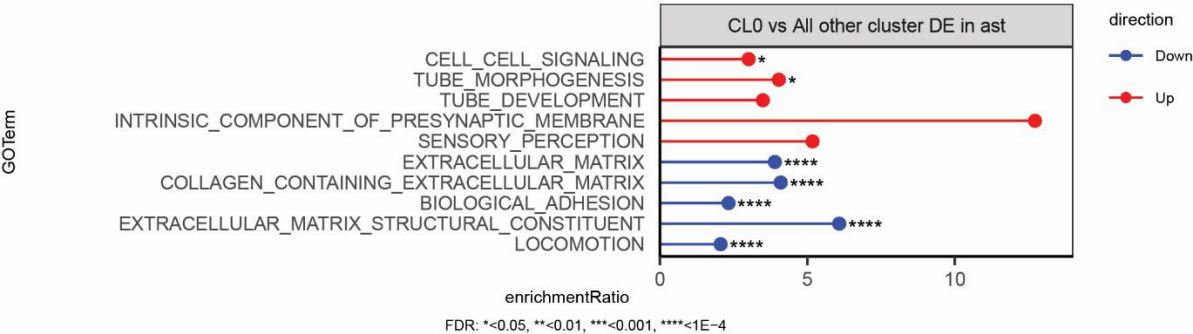
Supplementary Figure 15: Marker gene expression profile of pericytes in integrated datasets. A) Despite highly similar transcription profile, pericyte cluster 0 showed slight upregulation in the genes that regulate solute transporters. **B)** GO Term pathway analysis in pericyte cluster 0 displayed downregulation in the genes that regulate immune functions. Source data are provided as a Source Data file.

Supplementary Figure 16

A



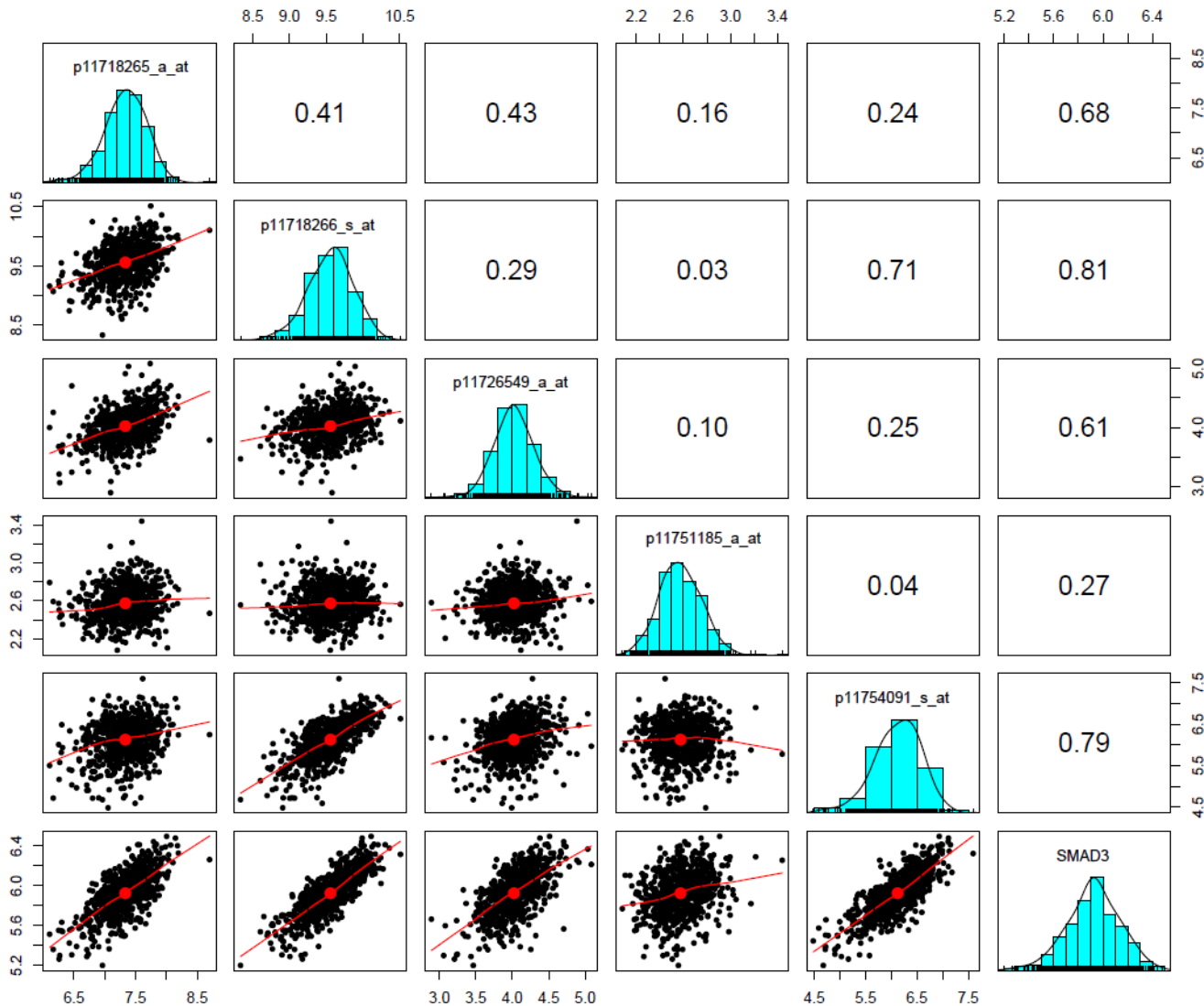
B



Supplementary Figure 16: Marker gene expression profile of astrocytes in integrated datasets. A) Despite highly similar transcription profile, astrocyte cluster 0 showed slight upregulation in the genes that regulate synapse assembly and organization. B) Top Enriched GO terms of signature genes in Ast.0 compared to all other astrocyte clusters are displayed. Upregulated genes are enriched in cell signalling

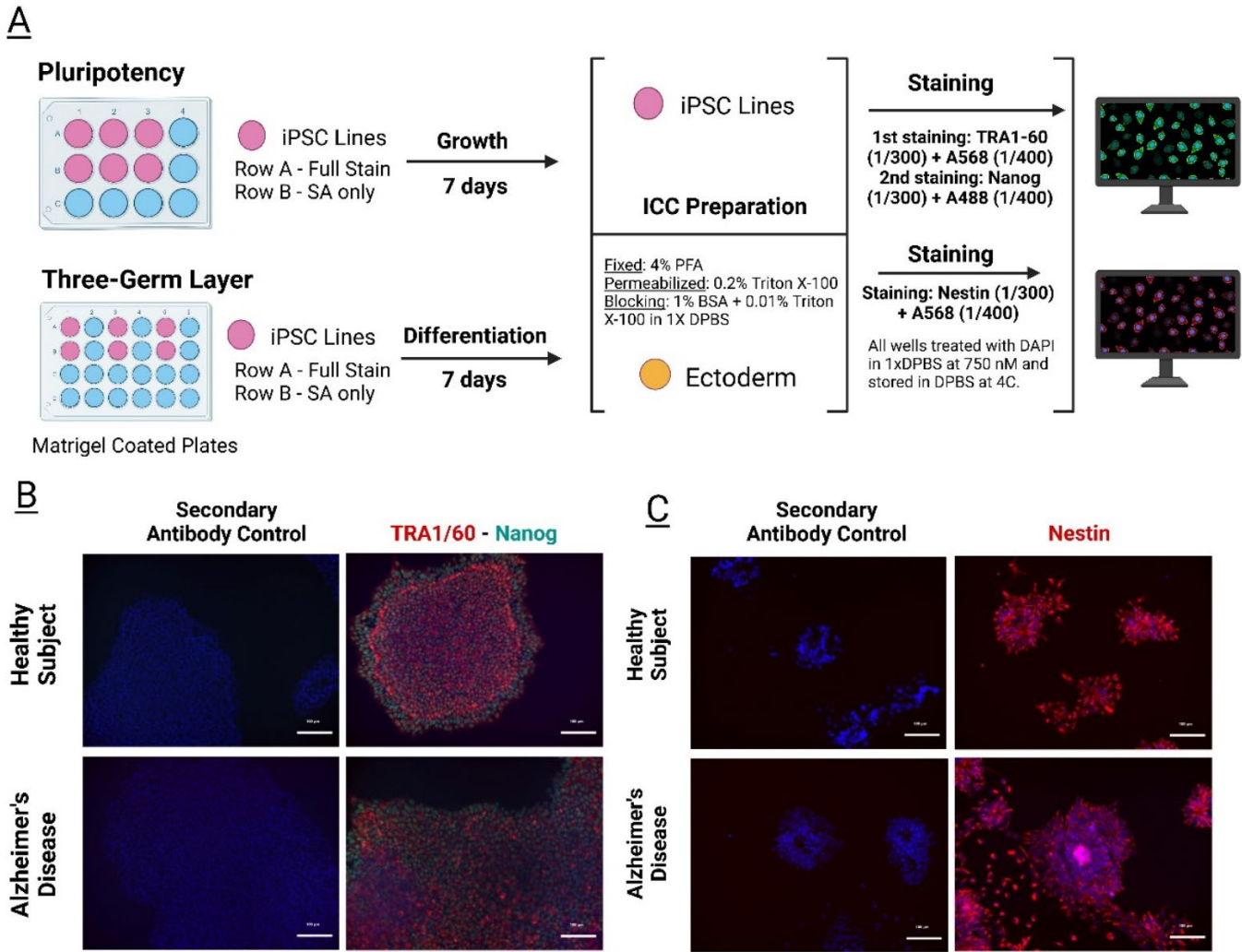
380 and tube morphogenesis and downregulated genes are enriched in the extracellular matrix related
381 pathways. Source data are provided as a Source Data file.
382

Supplementary Figure 17



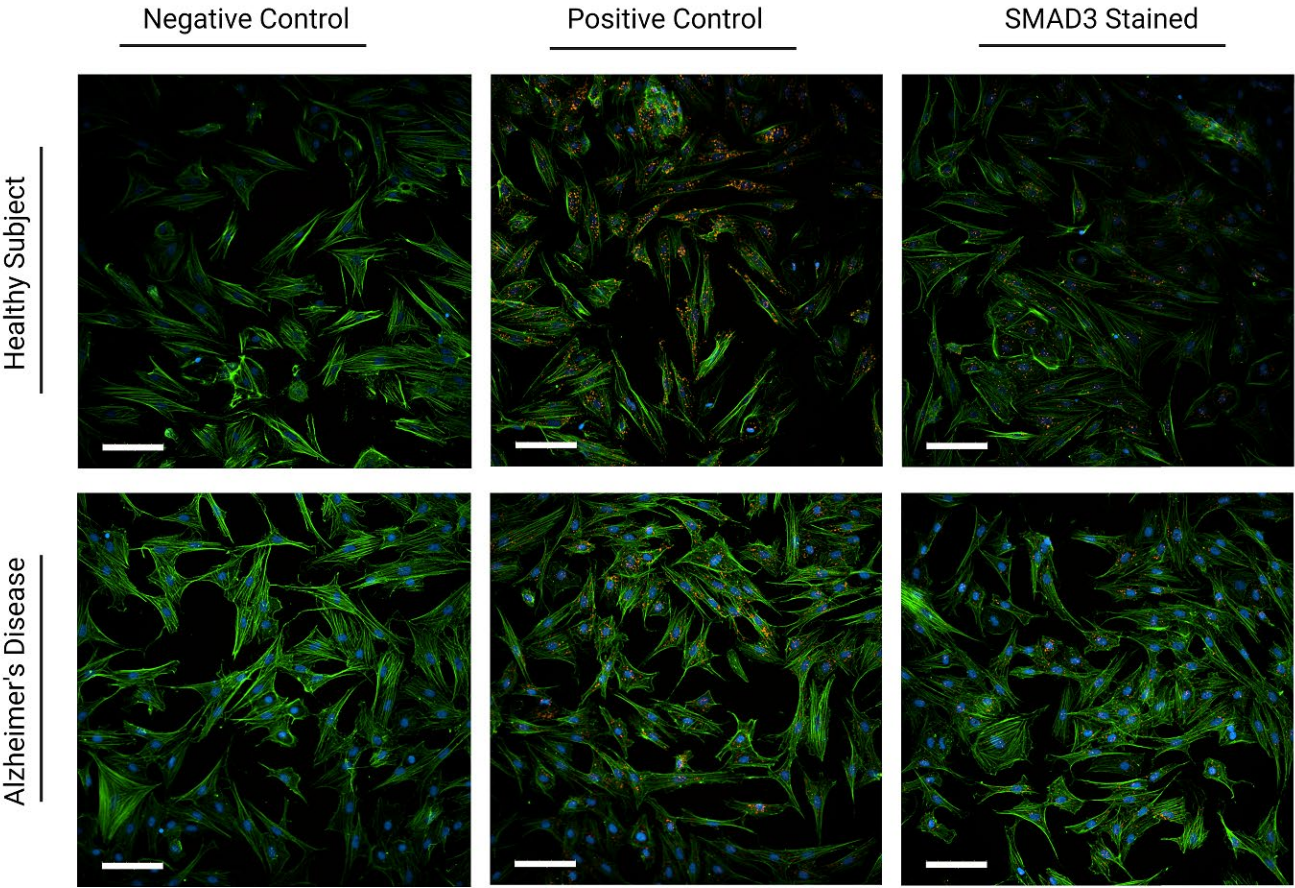
Supplementary Figure 17: Correlation amongst *SMAD3* probes. To evaluate the association of genetic variants with *SMAD3* gene expression, blood RNA expression quantified using Affymetrix Human Genome U219 Array (Affymetrix, Santa Clara, CA) for 5 *SMAD3* probes was obtained from 645 ADNI participants⁶. Histograms (teal) showing the distribution of expression quantified by each probe ('p11718265_a_at', 'p11718266_s_at', 'p11726549_a_at', 'p11751185_a_at', 'p11754091_s_at') as well the distribution of the average expression across all probes ('SMAD3') is shown across the diagonal in the figure. Pearson correlation coefficients are shown above the diagonal and scatter plots comparing expression values are shown below. Source data are provided as a Source Data file.

Supplementary Figure 18



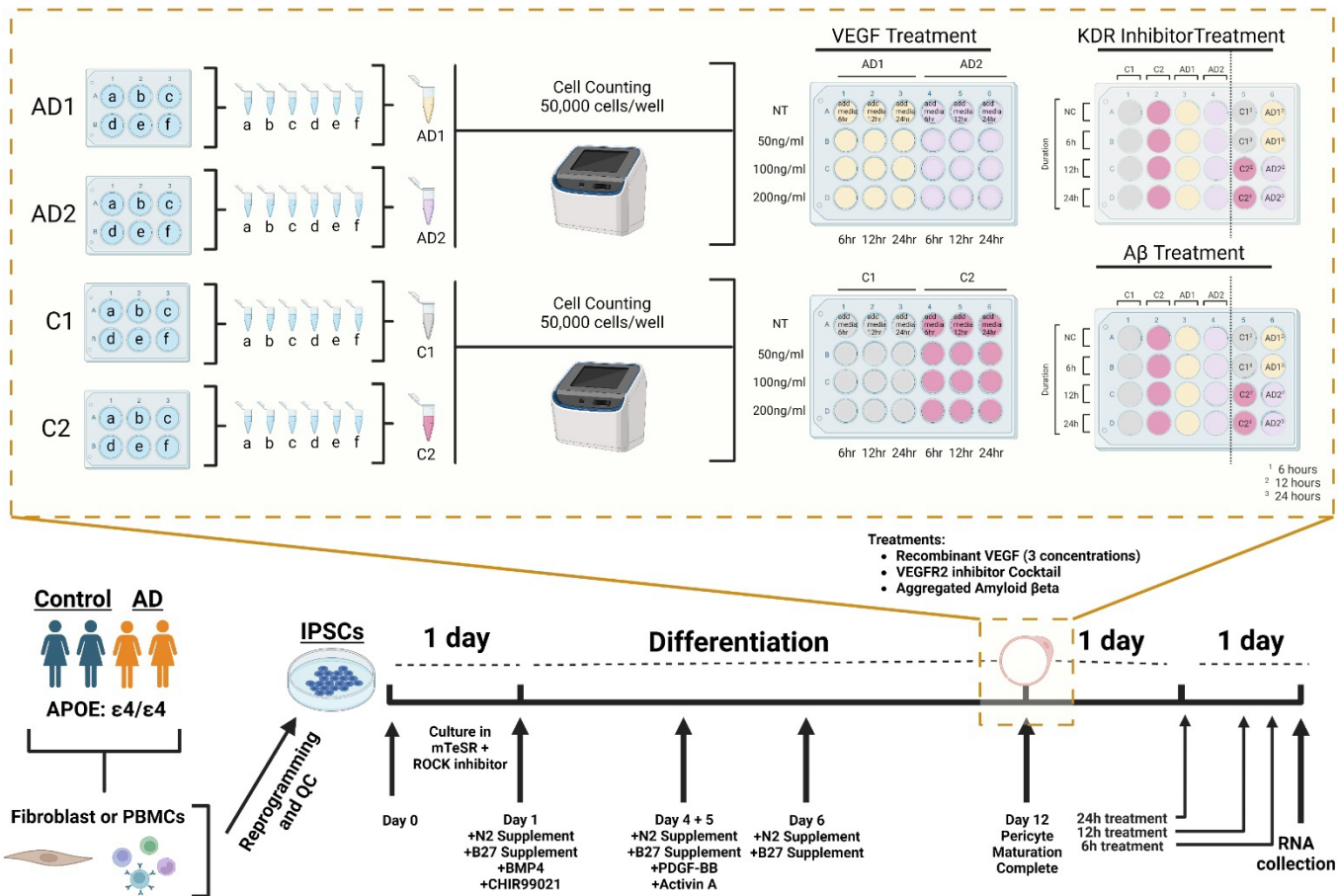
Supplementary Figure 18: QC of utilized iPSCs. A) Depiction of experimental paradigm to validate the pluripotency and ectodermal differentiating capability of iPSCs. This experiment was completed once for each IPSC lines, in a total of 4 cell lines (n=4). **B)** We stained iPSCs for TRA1/60 and Nanog. **C)** We stained differentiated IPSCs with Nestin. (Supplementary Figure 18/panel A Created with BioRender.com released under a Creative Commons Attribution-NonCommercial-NoDerivs license).

Supplementary Figure 19



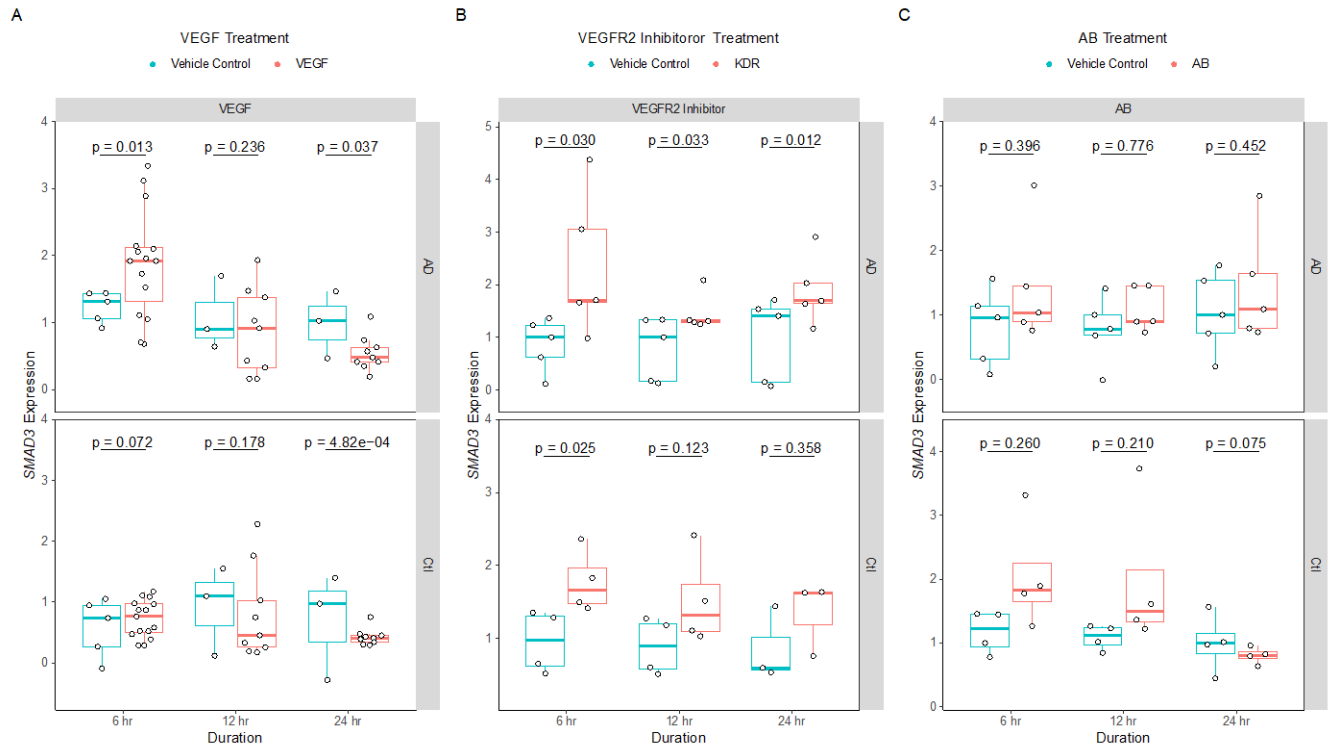
Supplementary Figure 19: Validation of *SMAD3* gene expression through RNAscope at iPSC derived pericytes. Negative Control: Bacterial *dapb*, Positive Control: *PPIB*, Orange: *SMAD3*, Green: Actin, Blue: Nuclei (DAPI). The white scale bar in each panel equals 100 μ m.

Supplementary Figure 20



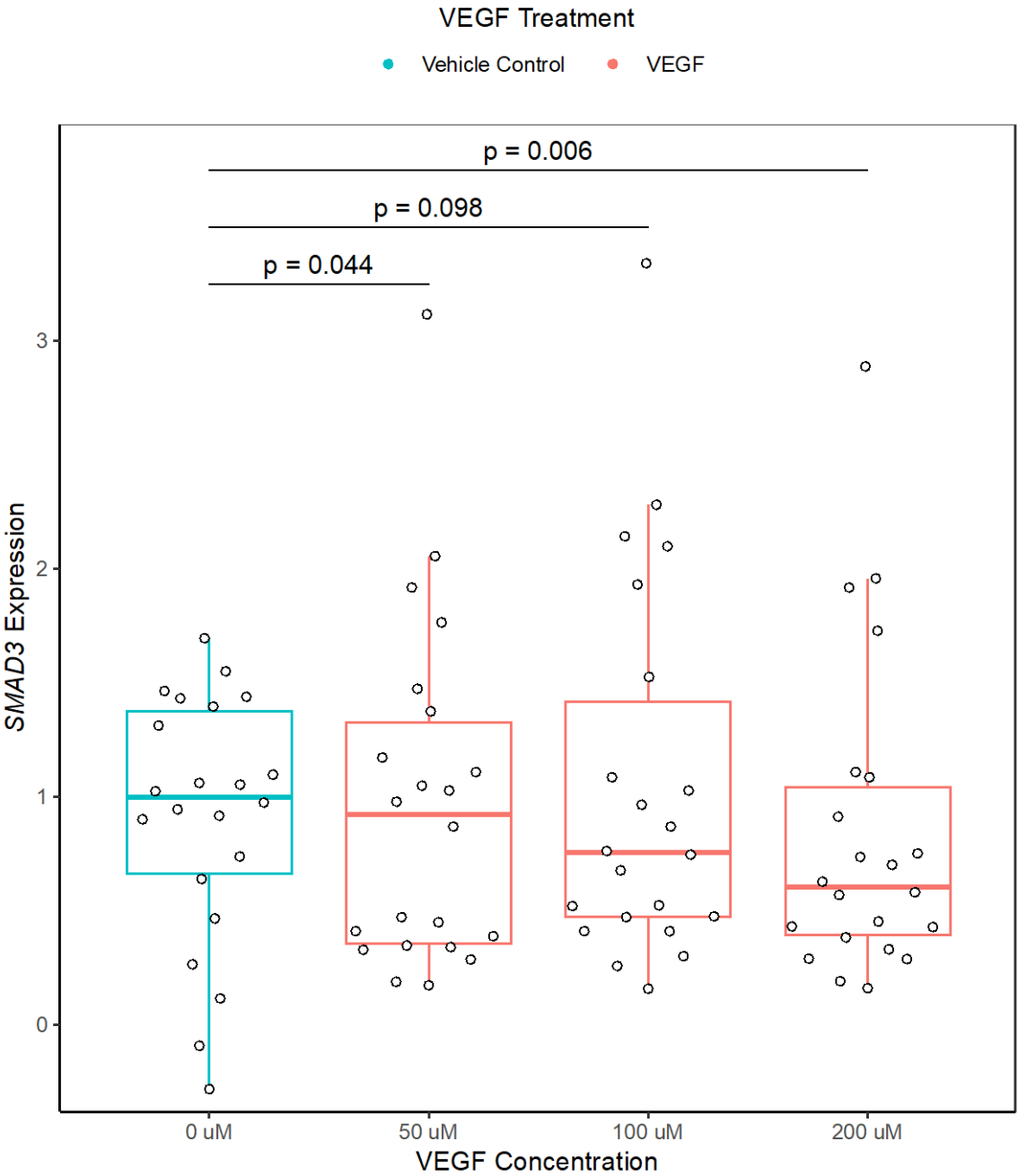
Supplementary Figure 20: Experimental design for the treatment of iPSC derived pericytes. The flowchart outlines the iPSC experimental design. Four patient-derived iPSC lines ($n_{AD}=2$, $n_{CONTROL}=2$) were used to differentiate into pericytes. Each patient derived iPSC was seeded on all wells of a 6 well plate. Seeded cells were differentiated into pericytes using established protocols as depicted. Cells in each well is accounted as one technical replicate and merged into one single tube to a total of 6 tubes. Collected cells were reseeded onto a 24 well plate for treatment experiments. Concentrations that were used for each stimulant were as follows: 50 ng/mL, 100 ng/mL, 200 ng/mL recombinant VEGF; 250 nM aggregated Aβ; and VEGFR2 inhibitor cocktail that contains (Semaxanib SU5416 (10 uM, SelleckChem S2845), Tivozanib AV- 951 (10 uM, SelleckChem S1207), and ZM 306416 (10 uM, SelleckChem, S2897). Treatment durations were as follows for each treatment: 6 hours, 12 hours, and 24 hours. Following treatment, RNA was collected and expression of selected genes were checked via qPCR. (Supplementary Figure 20 Created with BioRender.com released under a Creative Commons Attribution-NonCommercial-NoDerivs license)).

Supplementary Figure 21



Supplementary Figure 21: Diagnosis stratified response of iPSC derived pericytes towards A) VEGF, B) VEGFR2 inhibitor and C) aggregated A β . Source data are provided as a Source Data file.

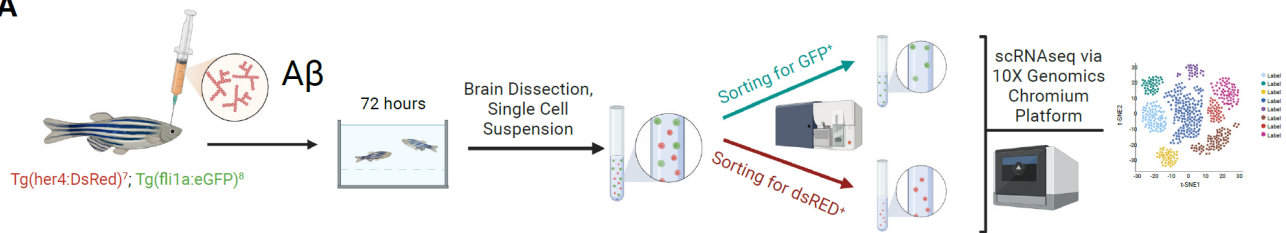
Supplementary Figure 22



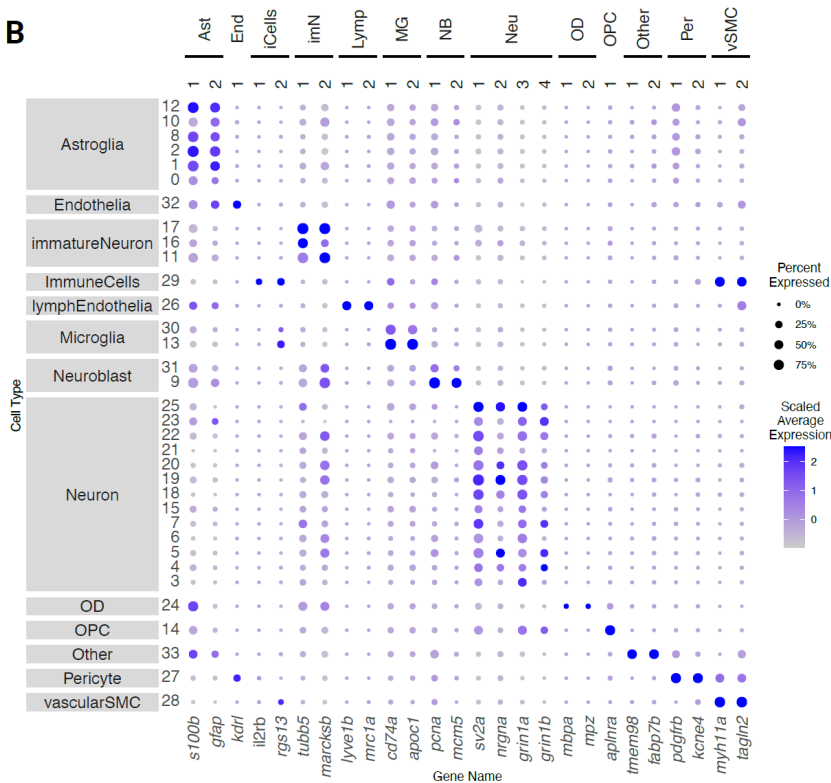
Supplementary Figure 22: Pericyte SMAD3 levels at different VEGF treatment concentrations. All timepoints from treatment with VEGF are compiled together and checked against untreated controls. 50 ng/mL and 100 ng/mL VEGF treatment caused significant downregulation of SMAD3 expression in iPSC derived pericytes compared to control conditions ($p < 0.05$). Source data are provided as a Source Data file.

Supplementary Figure 23

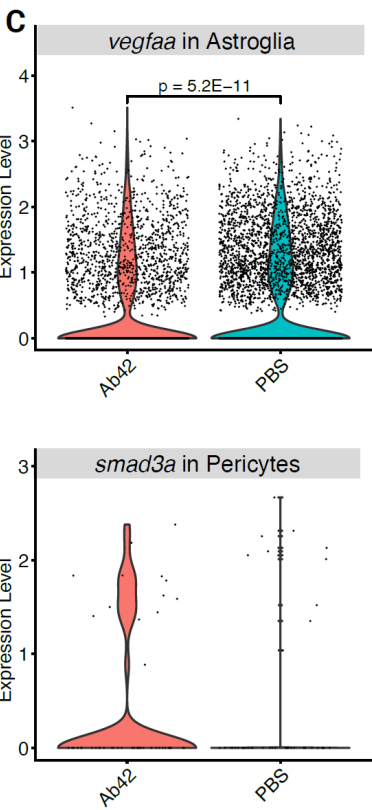
A



B

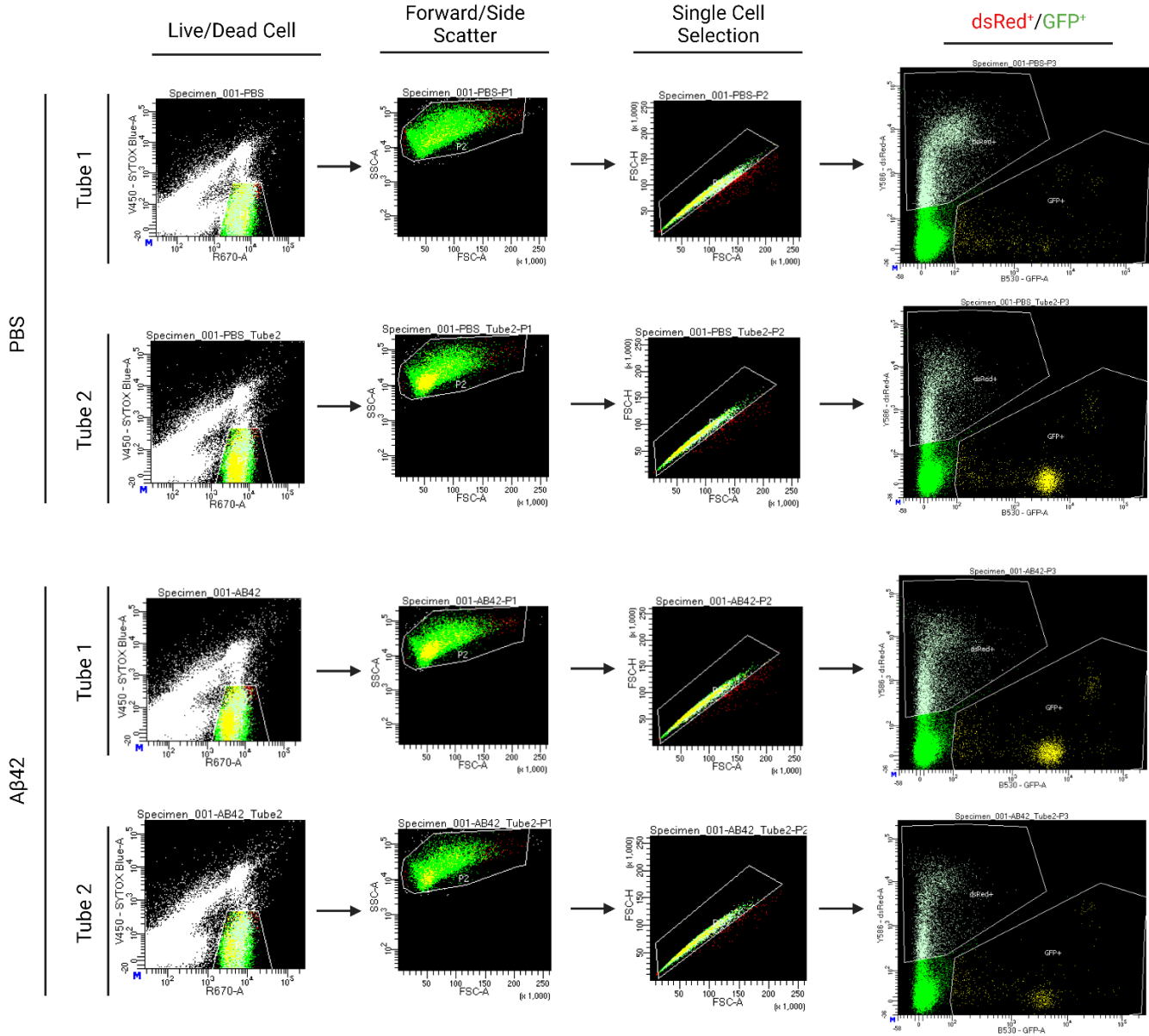


C



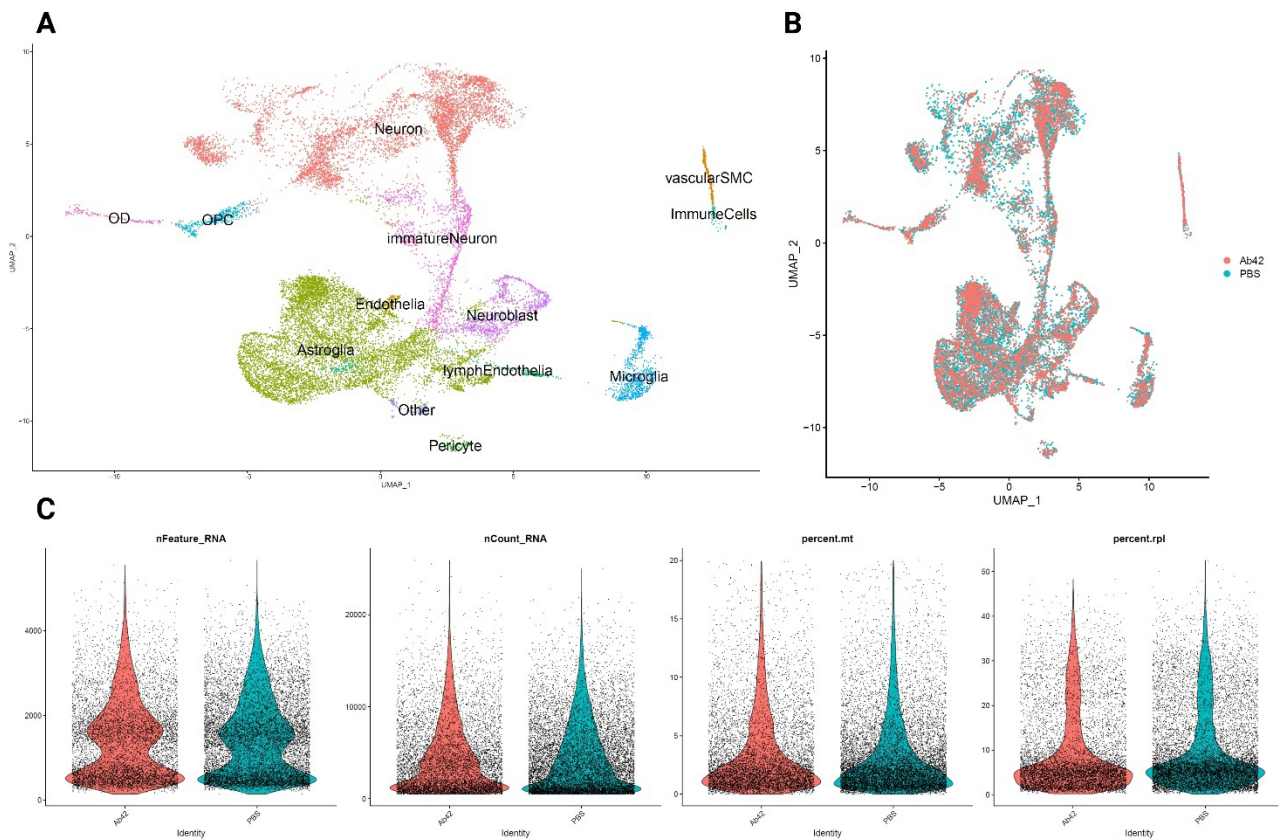
Supplementary Figure 23: Validation of human snRNAseq results on transgenic zebrafish. We confirmed that VEGF regulates SMAD3 and this signaling is altered in zebrafish AD model. A) Amyloid toxicity was induced in the adult telencephalon of double reporter transgenic zebrafish line – Tg(*her4*:dsRED) and Tg(*fli1*:EGFP) as established. B) Single cell clusters were clustered on UMAP and annotated based on marker gene expression. C) Injection of amyloid caused increased expression of *smad3a* in pericytes and decreased expression in astroglia cluster through scRNAseq. (Supplementary Figure 23/Panel A Created with BioRender.com released under a Creative Commons Attribution-NonCommercial-NoDerivs license).

459 **Supplementary Figure 24**



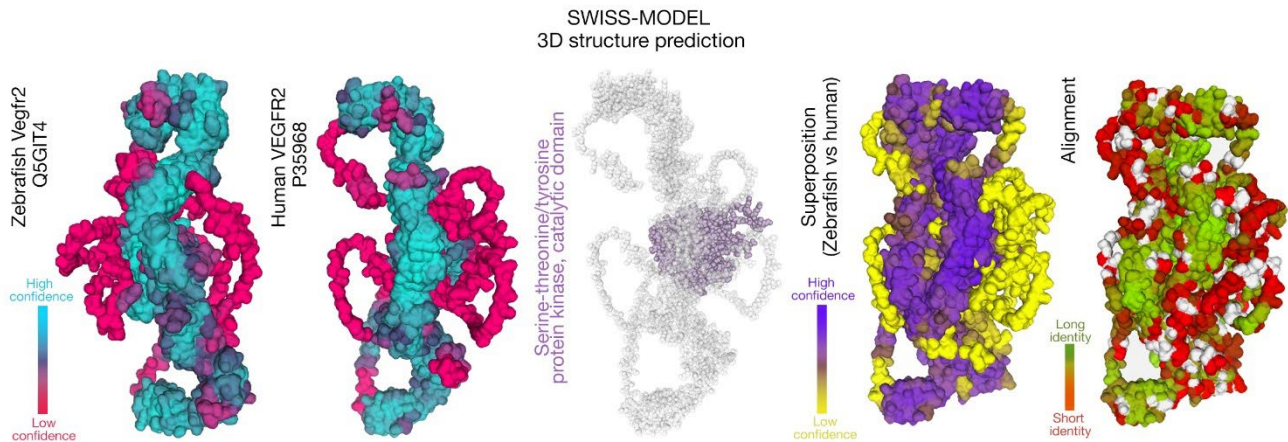
Supplementary Figure 24: FACS Gating strategy of zebrafish brain cells. Dot plots demonstrate gating strategy to obtain GFP⁺ and dsRED⁺ populations from PBS and Aβ₄₂ injected Tg(*her4*:dsRED) and Tg(*fl1*:EGFP) zebrafish model. These cells were used to obtain scRNAseq profile from zebrafish brain cells.

Supplementary Figure 25



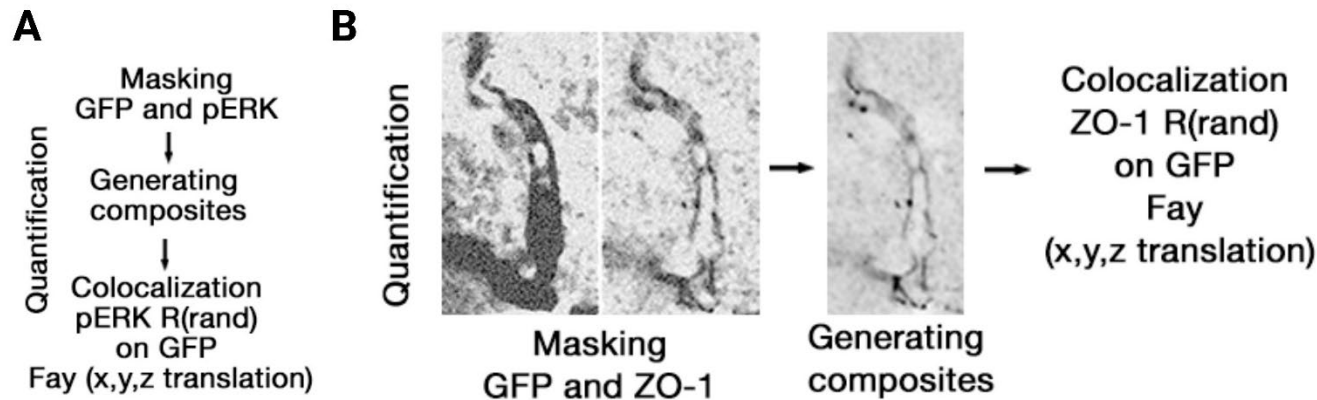
Supplementary Figure 25: QC Results of Aβ and PBS treated transgenic zebrafish results. A) Cell clusters displayed on UMAP reduced dimension space, annotated as brain cell types. Transcriptomic profile of major and minor brain cell types was obtained: Neurons, immature neurons, neuroblast, oligodendrocytes (OD), oligodendrocyte precursor cells (OPCs), endothelia, astroglia, microglia, and pericytes. **B)** Distribution of cell types according to treatment status (Aβ42 or PBS as vehicle) on UMAP reduced dimension space. **C)** Density plots demonstrate cell distributions in two treatment groups according to single cell transcriptomic parameters (nFeature_RNA: the number of genes detected in each cell; nCount_RNA: Total number of molecules detected within a cell; percent.mt: The percentage of reads that map to the mitochondrial genome; percent.rpl: The percentage of reads that map to the ribosomal protein L (rpl) genes).

Supplementary Figure 26



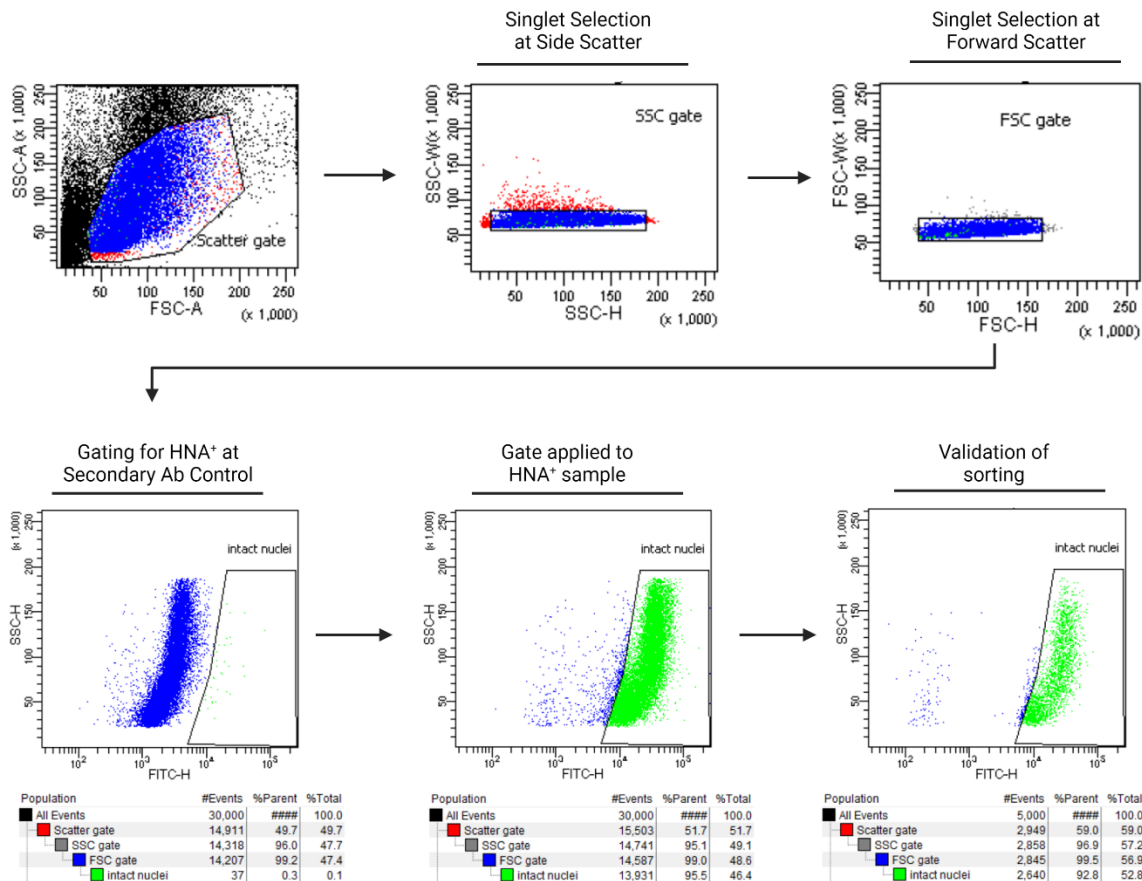
Supplementary Figure 26: Structural comparison of VEGFR2 in human and zebrafish. We made a structural comparison of human VEGFR2 with zebrafish vegfr2 using Swiss 3D Model prediction algorithm. Our *in silico* analysis predicts that the catalytic domain is highly conserved in 3D and drugs targeting this domain would be effective for both species.

Supplementary Figure 27



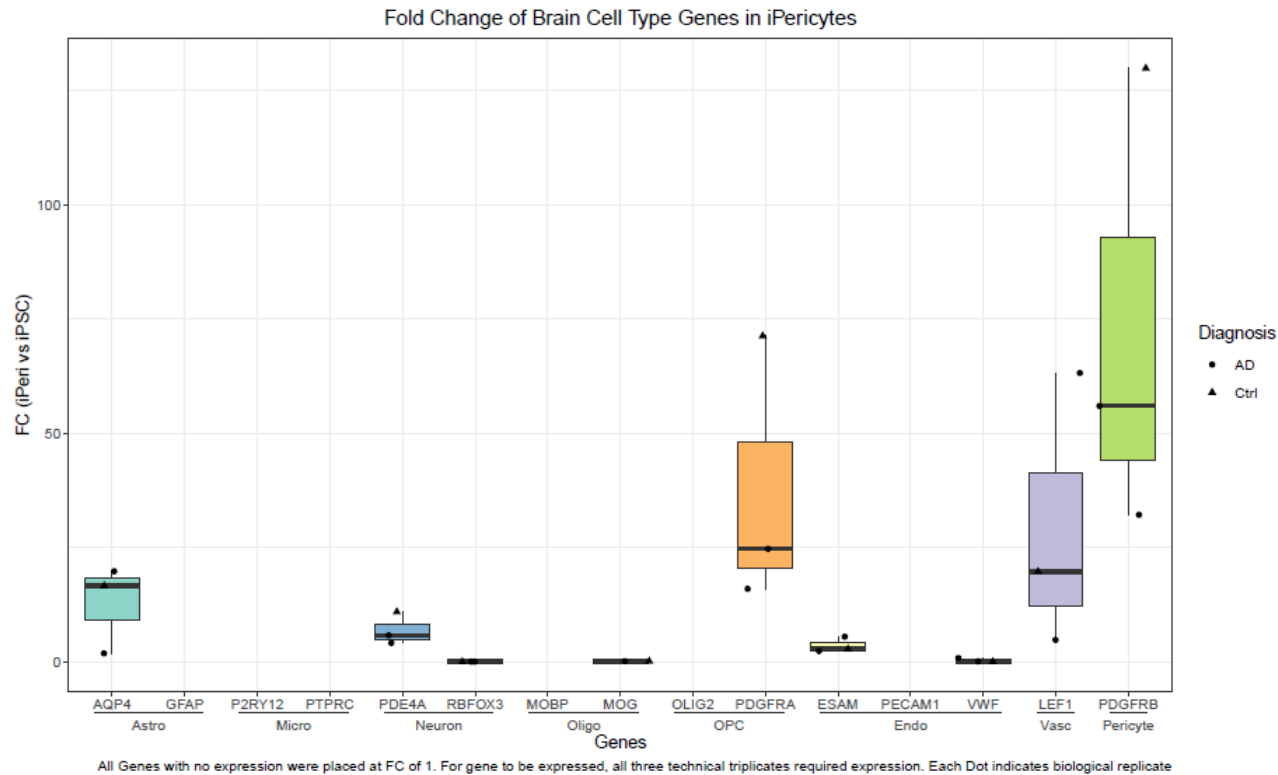
Supplementary Figure 27: Colocalization of A) pERK and B) ZO-1 on GFP fay is visualized. In order to quantify the colocalization of markers, ImageJ software's colocalization module was used to generate two-channel composites, R(and) colocalization analyses, and Fay translation into correlation values. Pairwise comparisons were performed with unpaired parametric t test with Welch's correction.

Supplementary Figure 28



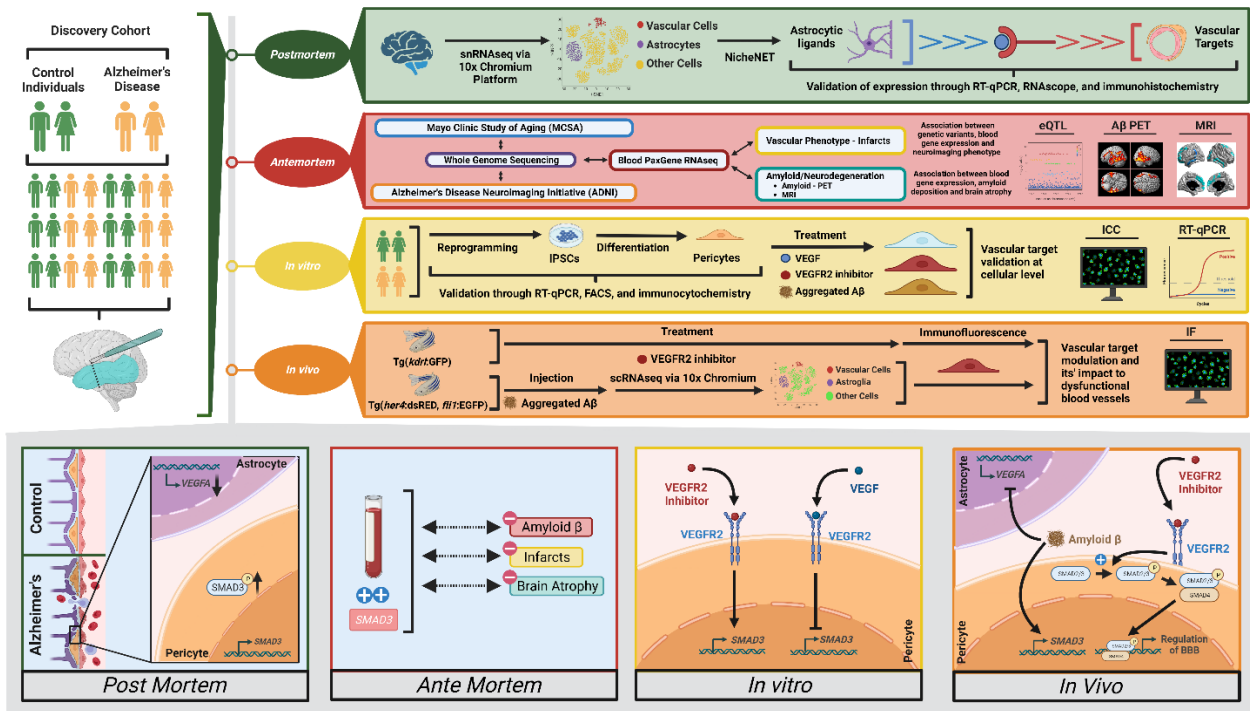
Supplementary Figure 28: FANS Gating strategy of intact nuclei from frozen human brain. Dot plots demonstrate gating strategy to obtain HNA⁺ population from nuclear samples. Isolation of nuclei were performed as previously established and purified via FANS as depicted. Sorted nuclei were directly used to generate snRNAseq data, or to seed for validation experiments such as RNAscope and qPCR.

Supplementary Figure 29



Supplementary Figure 29: Fold change in gene expression profile of iPSC-derived pericytes. To confirm the identity of differentiated cells' profile, expression of brain cell type marker genes was analyzed via qPCR: *AQP4* and *GFAP* for astrocytes; *P2RY12* and *PTPRC* for microglia; *PDE4A* and *RBFOX3* for neurons; *MOBP* and *MOG* for oligodendrocytes; *OLIG2* and *PDGFRA* for OPCs; *ESAM*, *PECAM1* and *VWF* for endothelia; *PDGFRB* for pericytes; and *LEF1* for vascular cells. Source data are provided as a Source Data file.

Supplementary Figure 30



Supplementary Figure 30: Graphical Abstract. Using single nucleus transcriptome from brain tissue of donors with Alzheimer's disease (AD) and elderly controls, we dissected the transcriptional landscape of vascular cells (red) and astrocytes (purple) that form the gliovascular unit (GVU) at the blood brain barrier (BBB) which is disrupted in AD. We performed tiered complementary studies to discover and validate astrocytic ligand – vascular target pairs that contribute to this BBB disruption in AD. Postmortem: Our human brain snRNAseq study discovered perturbed vascular and astrocytic transcript pairs, of which pericytic *SMAD3* (up in AD) and astrocytic *VEGFA* (down in AD) were prioritized. These findings were validated with orthogonal quantitative PCR, RNAscope and immunohistochemistry studies and replicated in external human brain snRNAseq data. Antemortem: Using *SMAD3* locus genetic variants, we performed expression QTL (eQTL) with blood *SMAD3* levels and associations with neuroimaging phenotypes relevant to AD. Genetic variants associated with higher blood *SMAD3* levels also associated with lower brain infarcts. Further, higher blood *SMAD3* levels associated with less amyloid and cortical atrophy on antemortem imaging. In Vitro: We validated *VEGFA-SMAD3* interactions in human iPSC-derived pericytes. Treatment of human pericytes with VEGF (encoded by *VEGFA*) reduces *SMAD3*, and blocking VEGF signalling increases *SMAD3*. In Vivo: To determine impact of *VEGFA-SMAD3* interactions on the blood-brain-barrier experimentally, we utilized a well-established zebrafish model. Injection of amyloid β 42 in this model decreased *vegfaa* (zebrafish ortholog to human *VEGFA*) expression in astroglia. Blocking *vegfaa* signaling pharmacologically increased phosphorylated Smad3, the active form of this signalling molecule and importantly also impaired blood-brain-barrier integrity. Collectively, our findings highlight the vast transcriptome changes in AD at the GVU, prioritize perturbed pericytic *SMAD3*-astrocytic *VEGFA* interactions with cross species experimental validations that provide a mechanistic avenue that contributes to BBB disintegration in AD. (Supplementary Figure 30 Created with BioRender.com released under a Creative Commons Attribution-NonCommercial-NoDerivs license).

543

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II. DOD ADNI

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Principal Investigator

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ATRI PI and Director of Coordinating Center Clinical Core

Paul Aisen, MD	University of Southern California
Co Director Clinical Core Ron Petersen	Mayo Clinic

Executive Committee

Michael W. Weiner, MD	University of California, San Francisco
Paul Aisen, MD	University of Southern California
Ronald Petersen, MD, PhD	Mayo Clinic, Rochester
Robert C. Green, MD, MPH	Brigham and Women's Hospital/ Harvard Medical School
Danielle Harvey, PhD	University of California, Davis
Clifford R. Jack, Jr., MD	Mayo Clinic, Rochester
William Jagust, MD	University of California, Berkeley
John C. Morris, MD	Washington University St. Louis
Andrew J. Saykin, PsyD	Indiana University
Leslie M. Shaw, PhD	Perelman School of Medicine, University of Pennsylvania
Arthur W. Toga, PhD	University of Southern California
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Psychological Evaluation/PTSD Core

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Traumatic Brain Injury/TBI Core

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Data and Publication Committee (DPC)

Robert C. Green, MD, MPH	BWH/HMS (Chair)
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Resource Allocation Review Committee

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Jennifer Salazar, MBS	University of Southern California
Caileigh Zimmerman, MS	University of Southern California
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Payam Mahboubi, MPH	University of Southern California



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Matthew Bernstein, PhD	Mayo Clinic, Rochester
Bret Borowski, RT	Mayo Clinic
Jeff Gunter, PhD	Mayo Clinic
Matt Senjem, MS	Mayo Clinic
Kejal Kantarci	Mayo Clinic
Chad Ward	Mayo Clinic
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III. ADNI Depression

Part A: Leadership and Infrastructure

Principal Investigator

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Caileigh Zimmerman, MS	University of Southern California
Sarah Walter, MSc	University of Southern California
Olusegun Adegoke, MSc	University of Southern California
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Michael W. Weiner, MD	University of California, San Francisco
Paul Aisen, MD	University of Southern California
Rema Raman, PhD	University of Southern California
Clifford R. Jack, Jr., MD	Mayo Clinic, Rochester
Susan Landau, PhD	University of California, Berkeley
Andrew J. Saykin, PsyD	Indiana University
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Robert A. Koeppe, PhD	University of Michigan

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