Supplementary material

Associations of cortical SPP1 and ITGAX with cognition and common neuropathologies in older adults

Katia de Paiva Lopes^{1,2}, Lei Yu^{1,2}, Xianli Shen^{3,4}, Yiguo Qiu^{3,4}, Shinya Tasaki^{1,2}, Artemis Iatrou^{1,2,5}, Michal Schnaider Beeri^{6,7}, Nicholas T. Seyfried⁸, Vilas Menon⁹, Yanling Wang^{1,2}, Julie A. Schneider^{1,2,10}, Harvey Cantor^{3,4}, David A. Bennett^{1,2}

¹Rush Alzheimer's Disease Center, Rush University Medical Center; Chicago, IL, 60612, USA

² Department of Neurological Sciences, Rush University Medical Center; Chicago, IL, 60612, USA

³ Department of Cancer Immunology and Virology, Dana-Farber Cancer Institute, Boston, MA, 02215, USA

⁴Department of Immunology, Harvard Medical School, Boston, MA, 02115, USA

⁵ Department of Psychiatry, McLean Hospital, Harvard Medical School, Belmont, MA, 02114, USA

⁶ Joseph Sagol Neuroscience Center, Sheba Medical Center, Ramat Gan, 52621, Israel

⁷ Department of Psychiatry, Icahn School of Medicine at Mount Sinai, New York, NY, 10029, USA

⁸ Goizueta Alzheimer's Disease Research Center, Department of Neurology and Department of Biochemistry, Emory University School of Medicine, Atlanta, GA, 30322, USA

⁹ Center for Translational and Computational Neuroimmunology, Department of Neurology & Taub Institute for Research on Alzheimer's disease and the Aging Brain, Columbia University Irving Medical Center; New York, NY, 10032, USA

¹⁰ Department of Pathology, Rush University Medical Center; Chicago, IL, 60612, USA.

Corresponding author: Katia de Paiva Lopes, PhD Email: katia_d_lopes@rush.edu Rush Alzheimer's Disease Center 1750 W Harrison Street, Suite 1000 Chicago, IL 60612

List of figures and tables

Supplementary Figure 1 – The correlations of SPP1 and ITGAX expression from bulk RNASeq.

- Supplementary Figure 2 ITGAX and SPP1 expression in the snRNASeq data.
- Supplementary Figure 3 SPP1 and ITGAX expression in the microglial subpopulation.
- Supplementary Table 01 The associations of SPP1 and OPN with clinical diagnosis at death.
- Supplementary Table 02 Association analysis with the MSBB RNASeq dataset.
- Supplementary Table 03 Association analysis with the Mayo Clinic RNASeq dataset.
- Supplementary Table 04 Association analysis with TMT proteins from MSBB.

Supplementary Table 05 – Annotation of the microglial subpopulations.

							Scatter Plo	t M atrix	
Pe	arson Corr	elation Coeffi	cients			SPP1_MF	ITGAX_MF	P10451	P20702
Prob > r under H0: Rho=0 Number of Observations					1_MF				
	SPP1_MF	ITGAX_MF	P10451	P20702	g				
SPP1_MF	1.00000 1216	0.25473 <.0001 1216	0.48657 <.0001 541	0.07852 0.0887 471	AX_MF				
ITGAX_MF	0.25473 <.0001 1216	1.00000	0.08557 0.0467 541	0.16631 0.0003 471	ITG				0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
P10451	0.48657 <.0001 541	0.08557 0.0467 541	1.00000	0.26142 <.0001 489	P10451				
P20702	0.07852 0.0887 471	0.16631 0.0003 471	0.26142 <.0001 489	1.00000 505	P20702				

Supplementary Figure 1 - Correlations of *SPP1* **and** *ITGAX* **expression from bulk RNASeq.** The results are for RNA and protein levels. P10451 = OPN, P20702 = CD11c.



Supplementary Figure 2 - ITGAX and SPP1 expression in the snRNASeq data. A) *ITGAX* expression in the microglial subpopulation. B) *SPP1* expression in the microglial subpopulation. C) *SPP1* expression in the oligodendrocytes clusters. Cells nomenclature: Mic = microglia and Oli = oligodendrocytes.



Supplementary Figure 3 - *SPP1* and *ITGAX* expression in the microglial subpopulations. A) Microglial subclusters visualized in an UMAP reduction. Annotations from Green et al, 2023 and Fujita et al, 2022^{1,2}. B) Selected clusters associated with neuropathologic indices for better visualization. C) *SPP1* expression across the microglial sub-clusters. D) *ITGAX* surface protein expression across the microglial subpopulations. In these plots, each dot is a cell, so we can visualize the gene expression across the distinct cell clusters. Dark blue represents high expression, and gray no expression (C-D).

Supplementary Table 01 – Associations of SPP1 and OPN with clinical diagnosis at death.

Variables	SPP1 (N=1,205)	OPN (N=580)
Age at death,	1.0672 (1.0489,1.0857)	1.0932 (1.0653,1.1218)
Male sex	1.0330 (0.8160,1.3075)	1.0536 (0.7500,1.4801)
Educational	1.0087 (0.9781,1.0404)	1.0219 (0.9752,1.0708)
SPP1 expression	1.3629 (1.2072,1.5387)	
OPN expression		1.3012 (1.1101,1.5252)

The results for *SPP1*, and separately OPN, were obtained from a logistic regression model with a 3-level ordinal outcome of no cognitive impairment (reference), mild cognitive impairment and dementia. The statistics in each cell are odds ratio (95% confidence interval).

Supplementary Table 02 – The associations with the MSBB RNASeq dataset. CERAD = Test from the Consortium to Establish a Registry for Alzheimer's Disease, Braak refers to the AD score for progression of neurofibrillary pathology, CDR = Clinical dementia rating scale, plaqueMean = density of neuritic plaques ³.

pheno	Estimate	Std. Error	df	t value	Pr(> t)	gene
CERAD	0.037653501	0.0614423	299.7822056	0.612826969	0.540455366	SPP1
Braak	0.099004344	0.03015903	302.9530329	3.282742649	0.001148289	SPP1
CDR	0.125009888	0.03435023	306.0363784	3.639273326	0.000320839	SPP1
plaqueMean	0.017723861	0.00818247	213.7553285	2.166076854	0.031411825	SPP1
CERAD	-0.035957882	0.03909985	297.5154299	-0.919642513	0.35850462	ITGAX
Braak	0.125168845	0.01824624	304.0141866	6.859981894	3.86093E-11	ITGAX
CDR	0.123132451	0.02131791	308.0457942	5.776008856	1.86966E-08	ITGAX
plaqueMean	0.023543896	0.00493446	208.5736712	4.7713196	3.43755E-06	ITGAX

Supplementary Table 03 – The associations with the Mayo Clinic RNASeq dataset. Braak refers to the AD score for progression of neurofibrillary pathology, PSP = progressive supranuclear palsy ⁴.

pheno	Estimate	Std. Error	df	t value	Pr(> t)	gene
AD diagnosis	0.307570139	0.185600408	499	1.657163056	0.098115056	SPP1
Pathological aging						
diagnosis	0.190206151	0.256856691	499	0.740514682	0.459336043	SPP1
PSP diagnosis	-0.236916037	0.2004781	499	-1.181755198	0.237865712	SPP1
Braak	0.106960571	0.044332514	364	2.412689043	0.016328988	SPP1
Thal	0.091376596	0.044360377	284	2.059869686	0.040322097	SPP1
AD diagnosis	-0.138084235	0.131774779	499	-1.047880603	0.295200896	ITGAX
Pathological aging						
diagnosis	0.295747153	0.18236616	499	1.62172167	0.105494592	ITGAX
PSP diagnosis	-0.443004548	0.142337819	499	-3.112346047	0.001962499	ITGAX
Braak	0.061267428	0.030956667	364	1.979135143	0.048553966	ITGAX
Thal	0.075218418	0.030707532	284	2.449510383	0.014909154	ITGAX

Supplementary Table 04 – The associations with the TMT proteins from MSBB. CERAD = Test from the Consortium to Establish a Registry for Alzheimer's Disease, Braak refers to the AD score for progression of neurofibrillary pathology, CDR = Clinical dementia rating scale, plaqueMean = density of neuritic plaques ⁵

pheno	Estimate	Std. Error	t value	Pr(> t)	protein
CERAD	0.009657771	0.024736194	0.390430767	0.696682279	ITGAX_P20702
Braak	0.084896821	0.011311835	7.505132235	2.77835E-12	ITGAX_P20702
CDR	0.082060625	0.013610941	6.029019336	9.20806E-09	ITGAX_P20702
plaqueMean	0.0217182	0.003276788	6.627893605	7.76197E-10	ITGAX_P20702
CERAD	0.050384217	0.035962956	1.401003238	0.16294438	SPP1_P10451
Braak	0.058424912	0.01844173	3.168081899	0.001804642	SPP1_P10451
CDR	0.046929212	0.021530326	2.179679607	0.030586966	SPP1_P10451
plaqueMean	0.012752548	0.005189532	2.457360098	0.015283687	SPP1_P10451

Supplementary Table 05 - Annotation of the microglial subpopulations. Annotation from Fujita et al, 2022 and Gilad Green et al, 2023. In bold, the clusters associated with neuropathologic indices, in our study.

State	Description
Mic.1	Proliferating
Mic.2	Homeostatic
Mic.3	Homeostatic/ tau-associated
Mic.4	Homeostatic
Mic.5	Homeostatic
Mic.6	Reactive
Mic.7	Reactive
Mic.8	Reactive
Mic.9	Homeostatic-Redox
Mic.10	Reactive-Redox
Mic.11	Stress-Response
Mic.12	Disease-Elevated/ lipid-associated
Mic.13	Disease-Elevated/ lipid-associated
Mic.14	Interferon-Response
Mic.15	Mic.15
Mic.16	Mic.16

REFERENCES

- 1. Fujita M, Gao Z, Zeng L, et al. Cell-subtype specific effects of genetic variation in the aging and Alzheimer cortex. *bioRxivorg*. Published online November 8, 2022. doi:10.1101/2022.11.07.515446
- 2. Green GS, Fujita M, Yang HS, et al. Cellular dynamics across aged human brains uncover a multicellular cascade leading to Alzheimer's disease. *bioRxivorg*. Published online March 9, 2023. doi:10.1101/2023.03.07.531493
- 3. Wang M, Beckmann ND, Roussos P, et al. The Mount Sinai cohort of large-scale genomic, transcriptomic and proteomic data in Alzheimer's disease. *Sci Data*. 2018;5(1):180185.
- 4. Allen M, Carrasquillo MM, Funk C, et al. Human whole genome genotype and transcriptome data for Alzheimer's and other neurodegenerative diseases. *Sci Data*. 2016;3:160089.
- 5. Bai B, Wang X, Li Y, et al. Deep multilayer brain proteomics identifies molecular networks in Alzheimer's disease progression. *Neuron*. 2020;106(4):700.