Alzheimer's Research & Therapy

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Correction to: Exploring the potential of the platelet membrane proteome as a source of peripheral biomarkers for Alzheimer's disease

Laura E. Donovan[1], Eric B. Dammer[2], Duc M. Duong[3], John J. Hanfelt[4], Allan I. Levey[1], Nicholas T. Seyfried[1,3*] and James J. Lah[1*]

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It has recently come to our attention that a paper we published in 2013 in Alzheimer's Research & Therapy never included the tables (Tables 1, 2 and 3) and supplemental tables (Additional file 1) in the published manuscript [1]. This must have been an oversight at the proof or production stage.

Tables 1, 2 and 3 are shown below.

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s13195-021-00839-y.

Additional file 1: Supplementary Table S1. 1009 proteins identified by unique peptides (top group members) identified in platelet membrane proteome from either a probable AD pool or a cognitive normal pool. **Supplementary Table S2.** 1957 total proteins (all potential group members) identified in platelet membrane proteome from either a probable AD pool or a cognitive normal pool. **Supplementary Table S3.** 144 potential marker proteins identified in platelet membrane proteome from a probable AD pool (FDR < 7%). **Supplementary Table 4.** 10 Classes incorporating 97 potentially novel AD biomarkers quantified in platelet membrane pools.

Author details
[1]Department of Neurology and Center for Neurodegenerative Disease, Emory University School of Medicine, 615 Michael Street NE, Atlanta, GA 30322, USA. [2]Department of Human Genetics, Emory University School ofMedicine, 615 Michael Street NE, Atlanta, GA 30322, USA. [3]Departmentof Biochemistry, Emory University School of Medicine, 1510 Clifton Road NE, Atlanta, GA 30322, USA. [4]Department of Biostatistics and Bioinformatics, Emory University School of Medicine, 1518 Clifton Road NE, Atlanta, GA 30322, USA.

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* Correspondence: nseyfri@emory.edu; jlah@emory.edu
[1]Department of Neurology and Center for Neurodegenerative Disease, Emory University School of Medicine, 615 Michael Street NE, Atlanta, GA 30322, USA
Full list of author information is available at the end of the article

Table 1 Participants

Controls			Probable Alzheimer's Disease (AD)		
Case #	**Age**	**MMSE[a]**	**Case #**	**Age**	**MMSE[a]**
1	75	28	**1**	**83**	**20**
2	**72**	**29**	**2**	**77**	**18**
3	**74**	**30**	**3**	**90**	**11**
4	**67**	**29**	**4**	**83**	**20**
5	**73**	**29**	**5**	**82**	**24**
6	**60**	**30**	6	61	12
7	69	30	7	55	25
AVERAGES:	70.00	29.3		75.86	18.6

Cases in bold were pooled for proteomic analysis
Bold type-face indicates cases pooled for proteomic analysis
[a]*MMSE* mini mental status exam, clinical measurement of cognitive function

Table 2 DAVID analysis of changes in proteins associated with platelet-specific secretion

Mean log_2 (AD/CT)	R1 vs R2 CV, SD%	Symbol	Protein Name	Ontology Groups
−1.70	**0.6%**	FGA	fibrinogen alpha chain	A, B, C, E, F
−2.03	**7.5%**	FGB	fibrinogen beta chain	A, B, C, E, F
−1.69	**1.5%**	FGG	fibrinogen gamma chain	A, B, C, E, F
−2.02	**1.9%**	VWF	von Willebrand factor	A, B, C, E
−1.23	**39%**	PROS1	protein S (alpha)	B, C, E, F
−1.19	**59%**	FN1	fibronectin 1	B, C, D, F
−1.19	**41%**	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	B, C, E
−1.47	**31%**	SPARC	secreted protein, acidic, cysteine-rich (osteonectin)	B, C, F
−2.05	**0.9%**	THBS1	thrombospondin 1	B, C, F
1.47	**1.2%**	GP9	glycoprotein IX (platelet)	B, C
−2.82	**2.9%**	C4BPA	complement component 4 binding protein, alpha	D, E
−1.24	**94%**	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	E, F
−1.83	**66%**	TF	transferrin	C
−1.65	**10%**	HP	haptoglobin-related protein; haptoglobin	D
−1.33	**31%**	SUSD1	sushi domain containing 1	D

Table 3 Overlap of AD platelet membrane protein changes with previously proposed mechanistic and diagnostic biomarkers

Mean log_2 (AD/CT)	R1 vs R2 CV, SD%	Symbol	Protein Name
2.46	14%	MGAT4B	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme B
−1.23	52%	VPS13C	vacuolar protein sorting 13 homolog C (*S. cerevisiae*)
−1.24	20%	AGPS	alkylglycerone phosphate synthase
−1.92	15%	FTL	ferritin, light polypeptide
−1.97	7.0%	IGF1R	insulin-like growth factor 1 receptor