

Supplementary Materials for

Integrative glycoproteomics reveals protein N-glycosylation aberrations and glycoproteomic network alterations in Alzheimer's disease

Qi Zhang, Cheng Ma, Lih-Shen Chin*, Lian Li*

*Corresponding author. Email: lli5@emory.edu (L.L.); lchin@emory.edu (L.-S.C.)

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Other Supplementary Material for this manuscript includes the following:

(available at advances.sciencemag.org/cgi/content/full/6/40/eabc5802/DC1)

Tables S2 to S7

SUPPLEMENTARY TABLES

Table S1. Demographics and phenotypic traits of human AD and control cases

Case	Sex	Age at death (yr)	Age at onset (yr)	Disease duration (yr)	PMI (hr)	Braak stage	CERAD score	ApoE genotype
Control								
CT1	Male	65			6	0	Sparse	E3/3
CT2	Female	75			6	I	None	E3/3
CT3	Male	61			<12	II	None	E3/4
CT4	Female	74			7	II	None	E3/3
CT5	Male	59			6	I	None	E2/3
CT6	Female	78			11.5	II	None	E3/3
CT7	Male	94			5.5	II	None	E3/3
CT8	Female	61			6	II	None	n.d.
Mean ± SEM		70.88 ± 4.19			7.5 ± 0.94			
Alzheimer's disease								
AD1	Male	79	73	6	6	V-VI	Frequent	E4/4
AD2	Female	72	59	13	7	VI	Frequent	E3/4
AD3	Male	67	56	11	6.5	VI	Frequent	E2/3
AD4	Male	77	70	7	12	VI	Frequent	E3/4
AD5	Male	74	60	14	2.5	VI	Frequent	E3/3
AD6	Male	68	60	8	14.5	VI	Frequent	E3/3
AD7	Female	61	51	10	6	VI	Frequent	E3/3
AD8	Male	69	59	10	3.5	VI	Frequent	E3/4
Mean ± SEM		70.88 ± 2.07	61 ± 2.54	9.88 ± 0.99	7.25 ± 1.44			

SUPPLEMENTARY FIGURES

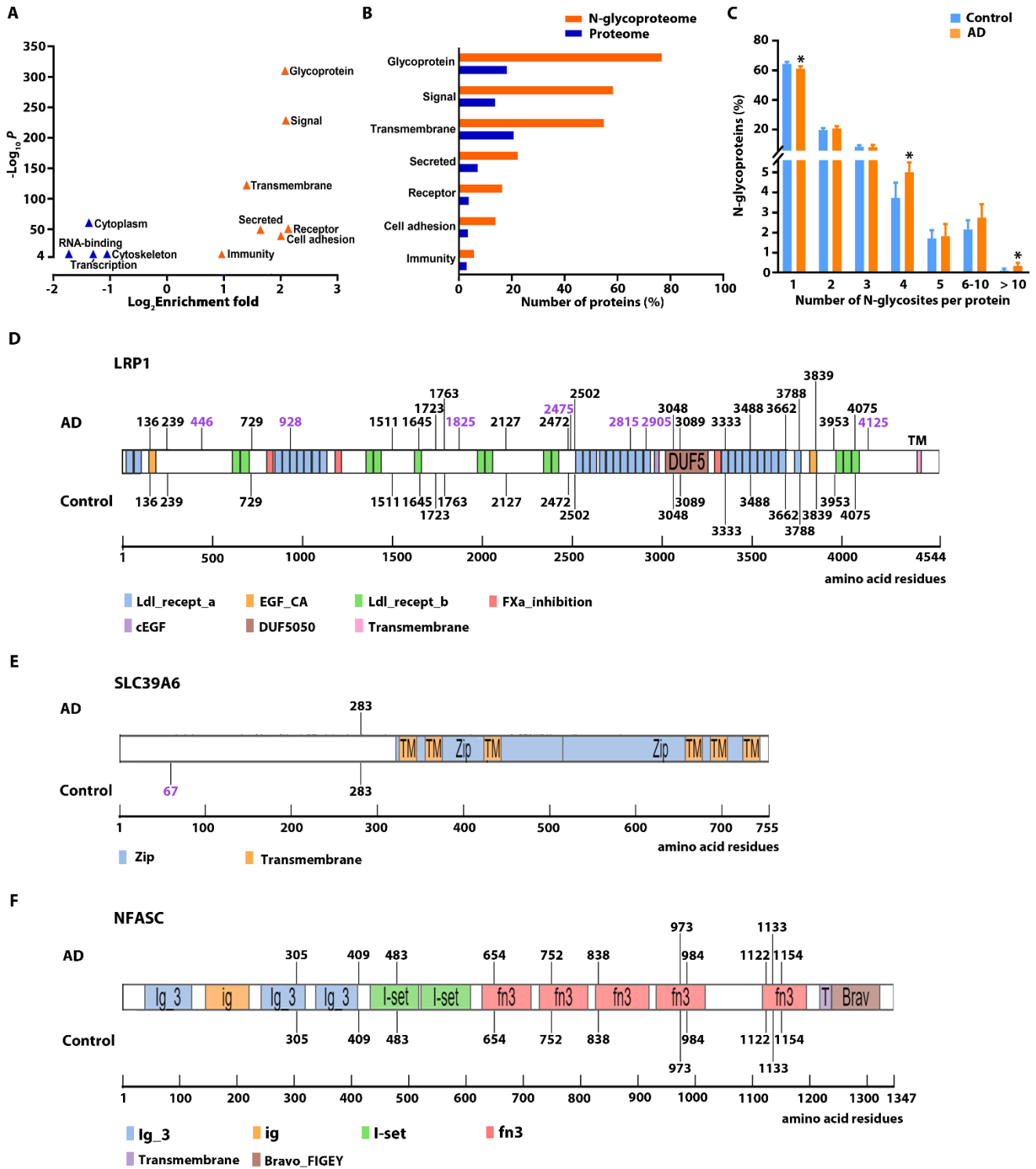


Fig. S1. UniProt keyword enrichment analysis and examples of *in vivo* N-glycosylation site changes in AD. (A) UniProt keywords enriched or underrepresented in the brain N-glycoproteome

compared to the brain proteome with Benjamini-Hochberg FDR-corrected $P < 0.0001$. **(B)** Percentages of proteins in the brain N-glycoproteome and proteome with each enriched UniProt keywords. **(C)** Distribution of the identified N-glycoproteins with the indicated number of *in vivo* N-glycosites per protein in AD and control brains is shown as mean \pm SD (n = 8 cases per AD or control group). * $P < 0.01$ versus the control. **(D-F)** Examples of N-glycoproteins with increased (D), reduced (E), or unaltered (F) number of *in vivo* N-glycosylation sites in AD compared to control brains. The asparagine residue positions of the N-glycosites of LRP1, SLC39A6, NFASC identified in AD or controls are indicated by the numbers flanking the protein domain diagram, with the purple numbers denoting the N-glycosites gained (D) or lost (E) in AD. Domain diagram for each protein is derived from PhosphoSitePlus[®] (www.phosphosite.org) with the names of color-coded domains shown below the diagram.

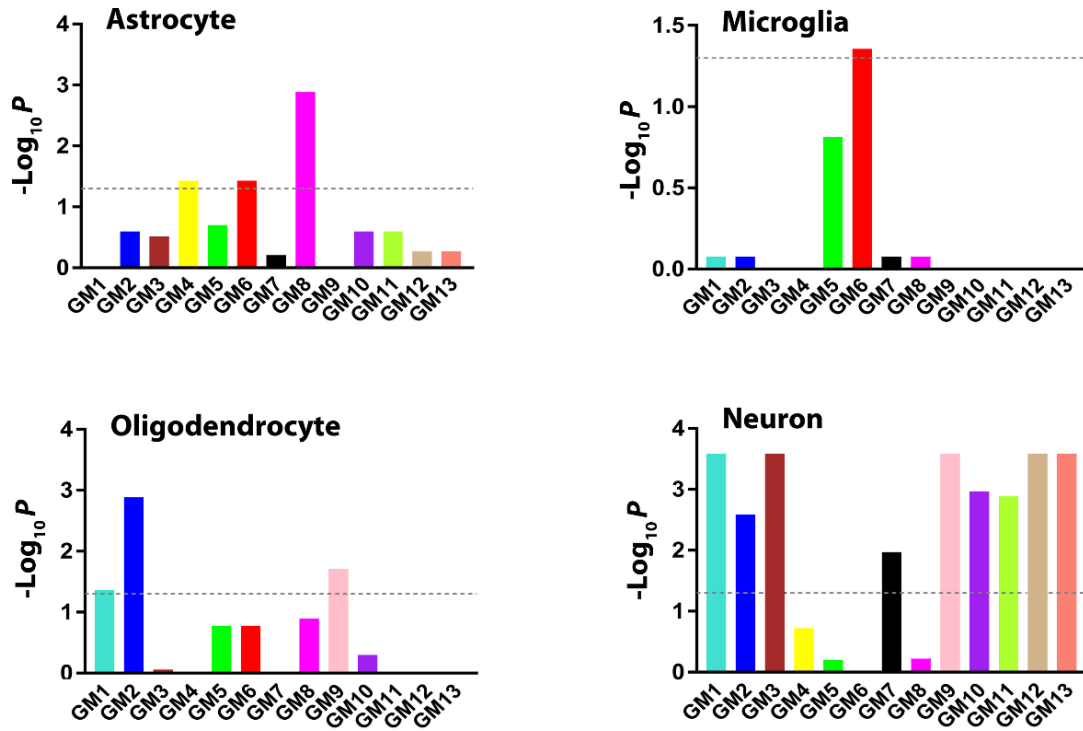


Fig. S2. Enrichment analysis for cell-type markers in glyco-network modules. Enrichment for markers of astrocyte, microglia, oligodendrocyte, or neuron in each module was assessed using one-sided Fisher's exact test P value followed by Benjamini-Hochberg FDR correction. Enrichment with FDR-corrected $P < 0.05$ (above the dashed line) is considered significant.

Module-trait relationships

	Age	Sex	AD status	Plaque	Braak	ApoE	PMI
GM8	0.27 (0.3)	-0.43 (0.1)	0.53 (0.03)	0.55 (0.03)	0.46 (0.08)	0.67 (0.004)	-0.34 (0.2)
GM6	0.15 (0.6)	-0.22 (0.4)	0.88 (6x10 ⁻⁶)	0.88 (8x10 ⁻⁶)	0.87 (9x10 ⁻⁶)	0.41 (0.1)	-0.31 (0.2)
GM4	-0.092 (0.7)	-0.3 (0.3)	0.71 (0.002)	0.62 (0.01)	0.68 (0.004)	-0.11 (0.7)	-0.28 (0.3)
GM2	-0.27 (0.3)	-0.32 (0.2)	-0.3 (0.3)	-0.29 (0.3)	-0.38 (0.1)	-0.069 (0.8)	-0.22 (0.4)
GM5	-0.14 (0.6)	-0.14 (0.6)	-0.36 (0.2)	-0.35 (0.2)	-0.41 (0.1)	-0.033 (0.9)	-0.0016 (1)
GM9	-0.26 (0.3)	-0.22 (0.4)	-0.54 (0.03)	-0.53 (0.03)	-0.57 (0.02)	-0.13 (0.6)	-0.019 (0.9)
GM7	-0.17 (0.5)	-0.21 (0.4)	0.14 (0.6)	0.15 (0.6)	0.08 (0.8)	-0.29 (0.3)	-0.23 (0.4)
GM3	-0.2 (0.5)	-0.52 (0.04)	-0.15 (0.6)	-0.13 (0.6)	-0.22 (0.4)	-0.066 (0.8)	-0.28 (0.3)
GM1	-0.025 (0.9)	-0.13 (0.6)	-0.61 (0.01)	-0.58 (0.02)	-0.62 (0.01)	-0.36 (0.2)	0.088 (0.7)
GM10	-5x10 ⁻⁴ (1)	-0.29 (0.3)	-0.064 (0.8)	-0.086 (0.8)	-0.097 (0.7)	0.051 (0.9)	-0.14 (0.6)
GM13	0.13 (0.6)	-0.2 (0.5)	-0.26 (0.3)	-0.16 (0.6)	-0.23 (0.4)	-0.2 (0.5)	-0.2 (0.5)
GM11	0.081 (0.8)	-0.21 (0.4)	0.27 (0.3)	0.2 (0.5)	0.3 (0.3)	-0.081 (0.8)	-0.2 (0.4)
GM12	0.08 (0.8)	-0.38 (0.1)	0.65 (0.006)	0.62 (0.01)	0.66 (0.005)	0.26 (0.3)	-0.17 (0.5)

Fig. S3. Module-trait relationships of glyco-network modules to clinical or neuro-pathological traits. The relationship between each module to each trait was assessed by biweight midcorrelation between the module eigenglycopeptide and the indicated trait, with the correlation coefficient (bicor r -value) shown on the top and P value in the bracket below. Significant positive correlations ($r > 0.50$, $P < 0.05$) are highlighted in *Orange*, and significant negative correlations ($r < -0.50$, $P < 0.05$) in *Blue*. PMI, postmortem interval.