Supplementary Tables and Figures

National Alzheimer's Coordinating Center (NACC) participants were excluded if they had any of the following conditions noted in the NACC Neuropathology Data Set. Variable names and descriptions are taken from https://files.alz.washington.edu/documentation/rdd-np.pdf. Variable descriptions may be lightly edited. Participants were not excluding for missing data in any of these fields.

Table S1: NACC Exclusion Criteria

NACC variable	Description
NACCDOWN	Down syndrom
NPPDXB	Multiple system atrophy
NPPDXE	Malformation of cortical development
NPPDXD	Trinucleotide disease (Huntington disease, SCA, other)
NPPDXF	Metabolic/storage disorder of any type
NPPDXG	White matter disease, leukodystrophy
NPPDXH	White matter disease, multiple sclerosis or other demyelinating disease
NPPDXI	Contusion/traumatic brain injury of any type, acute
NPPDXJ	Contusion/traumatic brain injury of any type, chronic
NPPDXK	Neoplasm, primary
NPPDXL	Neoplasm, metastatic
NPPDXM	Infectious process of any type (encephalitis, abscess, etc.)
NPPDXN	Herniation, any site
NACCPRIO	Prion disease
NPPATH10	CADASIL (hereditary stroke disorder)
NPALSMND	ALS/motor neuron disease (MND)
NPFTDTAU	FTLD with tau pathology (FTLD-tau) or other tauopathy
NPFTDTDP	FTLD with TDP- 43 pathology (FTLD-TDP)
NPOFTD	Other FTLD

Table S1: NACC Exclusion Criteria

NACC variable	Description
NPPDXA	Pigment-spheroid degeneration/NBIA

Supplementary Table S2: Stage 1 Ordinal Regression Results

SNP	CHR	BP	Gene	A1/A2	NACC OR [95% CI]	NACC P	ROSMAP OR [95% CI]	ROSMAP P
rs11691214	2	59,435,619	*FANCL*	A/T	1.27 [1.14-1.4]	9.6e-06	0.95 [0.8-1.13]	0.61
rs34349961	2	65,535,731	*SPRED2*	G/A	1.32 [1.17-1.48]	3.1e-06	1.16 [0.96-1.4]	0.13
rs56366943	2	126,891,098	*GYPC*	G/A	1.35 [1.18-1.54]	6.9e-06	1.01 [0.81-1.26]	0.94
rs10049413	3	49,892,896	*TRAIP*	A/G	1.25 [1.13-1.38]	7.6e-06	0.97 [0.83-1.14]	0.75
rs76172105	4	21,674,745	*KCNIP4*	A/G	1.43 [1.23-1.66]	4.6e-06	1.03 [0.81-1.31]	0.8
rs3774902	4	23,890,782	*PPARGC1A*	A/G	1.6 [1.32-1.95]	2.1e-06	-	-
rs4596251	4	124,472,197	*SPRY1*	A/G	1.32 [1.17-1.49]	5.9e-06	0.94 [0.77-1.14]	0.54
rs9392767	6	6,342,851	*F13A1*	C/T	1.23 [1.12-1.35]	8.4e-06	1.17 [1-1.37]	0.042
rs2603462	6	81,418,667	*BCKDHB*	C/A	1.32 [1.18-1.48]	2.5e-06	1.05 [0.86-1.28]	0.63

Supplementary Table S2: Stage 1 Ordinal Regression Results

SNP	CHR	BP	Gene	A1/A2	NACC OR [95% CI]	NACC P	ROSMAP OR [95% CI]	ROSMAP P
rs6574718	14	26,395,832	*NOVA1*	C/T	1.25 [1.14-1.37]	4.1e-06	-	-
rs11644522	16	6,686,023	*RBFOX1*	G/A	1.25 [1.14-1.37]	2.4e-06	1 [0.86-1.16]	0.99
rs112700375	18	33,834,804	*MOCOS*	T/G	1.54 [1.28-1.85]	4.1e-06	0.68 [0.51-0.92]	0.014
rs387083	19	35,847,115	*FFAR3*	G/A	1.23 [1.13-1.35]	3.9e-06	0.98 [0.84-1.14]	0.85
rs116881820	19	45,397,952	*TOMM40*	C/T	1.6 [1.3-1.96]	5.9e-06	-	-
rs6081741	20	19,744,341	*SLC24A3*	G/A	1.26 [1.14-1.39]	2.7e-06	1.06 [0.89-1.26]	0.49
rs11204484	22	49,218,823	*FAM19A5*	G/T	1.24 [1.13-1.36]	2.1e-06	-	-

Key: SNP, single nucleotide polymorphism; CHR, Chromosome; BP, base pair; Gene, closest protein-coding gene; A1/A2, effect/non-effect allele; OR, odds ratio; 95% CI, 95% confidence interval. A1 set so that NACC OR >= 1.

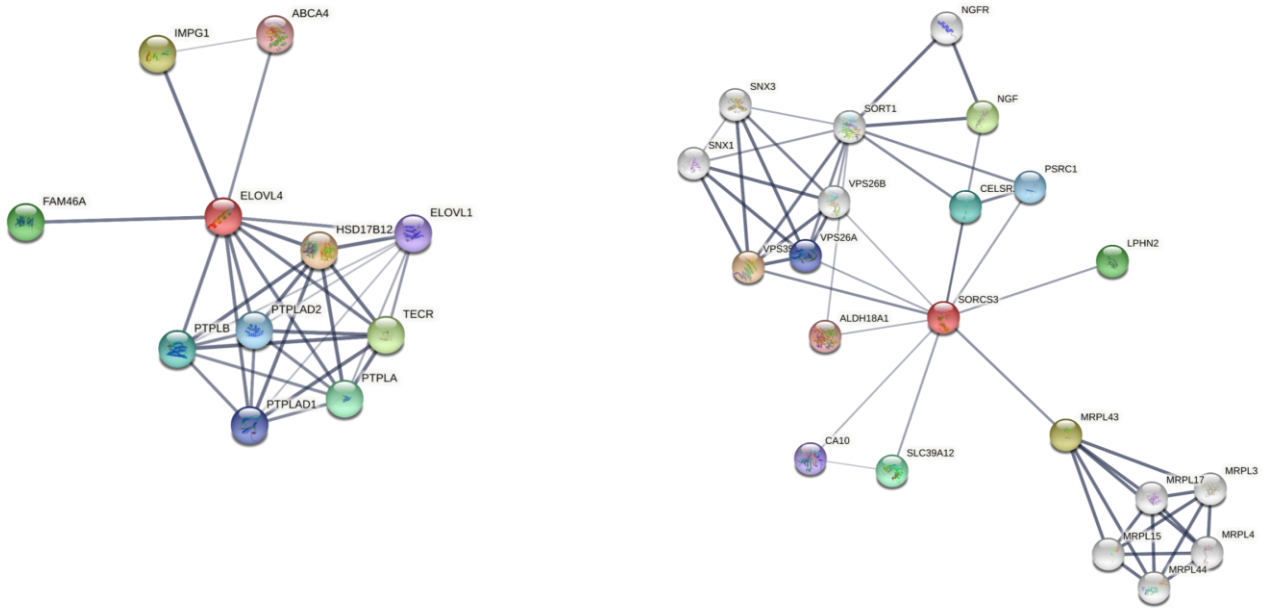

Figure S1: *ELOVL4* and *SORCS3* Gene Networks. Left: *ELOVL4* gene network. Right: *SORCS3* gene network. Confidence of association denoted by line thickness. Generated using STRING (https://string-db.org/).

Supplementary Table S3: Stage 3 Gene-Based Analysis Results

Gene	CHR	Start-Stop	P

Supplementary Table S3: Stage 3 Gene-Based Analysis Results

Gene	CHR	Start-Stop	P
SORCS1	10	107,333,421 - 109,924,466	5.5e-05
ADAM28	8	23,151,553 - 25,212,726	6.0e-04
OR1K1	9	124,562,402 - 126,563,352	6.2e-04
OR5C1	9	124,551,212 - 126,552,174	6.4e-04
OR1L6	9	124,512,127 - 126,513,062	6.4e-04
OR1L4	9	124,486,269 - 126,487,204	6.5e-04
PDCL	9	124,580,376 - 126,590,935	8.9e-04
OR1L3	9	124,437,409 - 126,438,383	1.0e-03

Key: CHR, Chromosome; Start-Stop, start and end positions of region mapped to gene.

All genes with $p < 0.0001$ included.