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 |
| NPPDXA | Pigment-spheroid degeneration/NBIA |

Ordinal results

| 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 |
| 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. | | | | | | | | |

Gene-based analysis results

| 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. | | | |