

KATSUMATA ET AL, SUPPLEMENTAL MATERIAL

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Supplementary Table 1. Analytical sample size for each available neuropathology in three datasets

Neuropathology	ADRC		ROSMAP
	ADSP WGS	ADGC	
European ancestry ^a			
Braak NFT stage	1,026	2,191	1,266
Neocortical neuritic plaques	1,028	2,195	1,266
TDP-43 in any brain regions	364	797	1,176
Lewy bodies in any brain regions	1,023	2,185	1,225
Hippocampal sclerosis	478	1,109	1,244
Other ancestries			
Braak NFT stage	139	131	39
Neocortical neuritic plaques	140	134	39
TDP-43 in any brain regions	55	55	39
Lewy bodies in any brain regions	139	134	38
Hippocampal sclerosis	68	86	37

^a Cases who had at least one rare disease were excluded from people with European ancestry
 NFT = neurofibrillary tangle; TDP-43 = TAR DNA binding protein 43 kDa; ADRC = Alzheimer's Disease Research Center; ADSP = Alzheimer's Disease Sequencing Project; WGS = whole genome sequencing; ADGC = Alzheimer's Disease Genetics Consortium; ROSMAP = Religious Orders Study (ROS) and Memory and Aging Project (MAP)

Supplementary Table 2. Analytical sample size for each available neuropathology in sensitivity analysis

Neuropathology	ADRC	
	ADSP WGS	ADGC
European ancestry ^a		
Braak NFT stage	1,122	2,423
Neocortical neuritic plaques	1,126	2,446
TDP-43 in any brain regions	446	1,007
Lewy bodies in any brain regions	1,121	2,435
Hippocampal sclerosis	643	1,355

^a Cases who had rare disease were also included in people with European ancestry

NFT = neurofibrillary tangle; TDP-43 = TAR DNA binding protein 43 kDa; ADRC = Alzheimer's Disease Research Center; ADSP = Alzheimer's Disease Sequencing Project; WGS = whole genome sequencing; ADGC = Alzheimer's Disease Genetics Consortium

Supplementary Table 3. Characteristics in people with other ancestries

Characteristic	ADRC		ROSMAP (n = 39)
	ADSP WGS (n = 140)	ADGC (n = 134)	
Age at death, mean \pm SD	79.3 \pm 11.9	83.7 \pm 9.7	84.4 \pm 8.1
Years in education, mean \pm SD	15.6 \pm 10.7	15.3 \pm 13.4	13.6 \pm 4.6
Sex, n (%)			
Male	60 (42.9)	61 (45.5)	8 (20.5)
Female	80 (57.1)	73 (54.5)	31 (79.5)
APOE, n (%)			
-/-	58 (41.4)	77 (57.5)	27 (69.2)
-/ ϵ 4	63 (45)	51 (38.1)	11 (28.2)
ϵ 4/ ϵ 4	19 (13.6)	6 (4.5)	1 (2.6)
Braak NFT stage, n (%)			
0 – IV	47 (33.8)	64 (48.9)	27 (69.2)
V/VI	92 (66.2)	67 (51.1)	12 (30.8)
Neocortical neuritic plaques, n (%)			
No – moderate	52 (37.1)	74 (55.2)	26 (66.7)
Frequent	88 (62.9)	60 (44.8)	13 (33.3)
TDP-43 in any brain regions, n (%)			
No	37 (67.3)	39 (70.9)	27 (69.2)
Yes ^a	18 (32.7)	16 (29.1)	12 (30.8)
Lewy bodies in any brain regions, n (%)			
No	78 (56.1)	94 (70.1)	31 (81.6)
Yes ^b	61 (43.9)	40 (29.9)	7 (18.4)
Hippocampal sclerosis, n (%)			
No	57 (83.8)	69 (80.2)	35 (94.6)
Yes ^c	11 (16.2)	17 (19.8)	2 (5.4)

^a Observed in any regions including amygdala, hippocampus, entorhinal/inferior temporal cortex, and neocortex

^b Observed in any brain regions including brainstem-predominant, limbic, neocortical, amygdala predominant, and olfactory bulb

^c Observed in either unilateral or bilateral

SD = standard deviation; NFT = neurofibrillary tangle; TDP-43 = TAR DNA binding protein 43 kDa; ADRC = Alzheimer's Disease Research Center; ADSP = Alzheimer's Disease Sequencing Project; WGS = whole genome sequencing; ADGC = Alzheimer's Disease Genetics Consortium; ROSMAP = Religious Orders Study (ROS) and Memory and Aging Project (MAP)

Supplementary Table 4. List of Alzheimer's disease associated single nucleotide variants reported in Bellenguez et al. (2022)

Variant	Chr	Position ^a	Gene	Minor/Major	MAF ^b	
					EUR	Others
rs679515	1	207577223	<i>CR1</i>	T/C	0.17	0.039
rs6733839	2	127135234	<i>BIN1</i>	T/C	0.38	0.40
rs10933431	2	233117202	<i>INPP5D</i>	G/C	0.23	0.47
rs6846529	4	11023507	<i>CLNK</i>	C/T	0.28	0.29
rs6605556	6	32615322	<i>HLA-DQA1</i>	G/A	0.15	0.12
rs10947943	6	41036354	<i>UNC5CL</i>	A/G	0.11	0.11
rs143332484	6	41161469	<i>TREM2</i>	T/C	0.011	0.0035
rs75932628	6	41161514	<i>TREM2</i>	T/C	0.0050	0.0012
rs60755019	6	41181270	<i>TREML2</i>	G/A	0	0.093
rs7767350	6	47517390	<i>CD2AP</i>	T/C	0.25	0.17
rs6966331	7	37844191	<i>EPDR1</i>	T/C	0.35	0.42
rs7384878	7	100334426	<i>SPDYE3</i>	C/T	0.33	0.34
rs11771145	7	143413669	<i>EPHA1</i>	A/G	0.36	0.45
rs73223431	8	27362470	<i>PTK2B</i>	T/C	0.35	0.30
rs11787077	8	27607795	<i>CLU</i>	T/C	0.39	0.38
rs7912495	10	11676714	<i>USP6NL</i>	G/A	0.45	0.37
rs10437655	11	47370397	<i>SPI1</i>	A/G	0.38	0.36
rs1582763	11	60254475	<i>MS4A4A</i>	A/G	0.36	0.23
rs3851179	11	86157598	<i>EED</i>	T/C	0.37	0.30
rs74685827	11	121482368	<i>SORL1</i>	G/T	0.015	0.035
rs11218343	11	121564878	<i>SORL1</i>	C/T	0.043	0.13
rs17125924	14	52924962	<i>FERMT2</i>	G/A	0.080	0.13
rs7401792	14	92464917	<i>SLC24A4</i>	G/A	0.35	0.36
rs12590654	14	92472511	<i>SLC24A4</i>	A/G	0.34	0.41
rs8025980	15	50701814	<i>SPPL2A</i>	G/A	0.33	0.42
rs602602	15	58764824	<i>MINDY2</i>	A/T	0.31	0.47
rs117618017	15	63277703	<i>APH1B</i>	T/C	0.14	0.021
rs889555	16	31111250	<i>BCKDK</i>	T/C	0.28	0.41
rs4985556	16	70660097	<i>IL34</i>	A/C	0.10	0.049
rs12446759	16	81739398	<i>PLCG2</i>	G/A	0.38	0.49
rs72824905	16	81908423	<i>PLCG2</i>	G/C	0.011	0.00075
rs7225151	17	5233752	<i>SCIMP</i>	A/G	0.14	0.12
rs199515	17	46779275	<i>WNT3</i>	G/C	0.22	0.081
rs616338	17	49219935	<i>ABI3</i>	T/C	0.0070	0.00025
rs2526377	17	58332680	<i>TSPOAP1</i>	G/A	0.46	0.45
rs4277405	17	63471557	<i>ACE</i>	C/T	0.37	0.35
rs12151021	19	1050875	<i>ABCA7</i>	A/G	0.34	0.38
rs6014724	20	56423488	<i>CASS4</i>	G/A	0.089	0.18
rs2830489	21	26775872	<i>ADAMTS1</i>	T/C	0.30	0.088
rs141749679	1	109345810	<i>SORT1</i>	C/T	0	0.00050
rs72777026	2	9558882	<i>ADAM17</i>	G/A	0.13	0.22
rs17020490	2	37304796	<i>PRKD3</i>	C/T	0.16	0.37

rs143080277	2	105749599	<i>NCK2</i>	C/T	0.0050	0.00050
rs139643391	2	202878716	<i>WDR12</i>	T/TC	0.13	0.026
rs16824536	3	155069722	<i>MME</i>	A/G	0.032	0.12
rs61762319	3	155084189	<i>MME</i>	G/A	0.023	0.0032
rs3822030	4	993555	<i>IDUA</i>	G/T	0.40	0.46
rs2245466	4	40197226	<i>RHOH</i>	G/C	0.33	0.35
rs112403360	5	14724304	<i>ANKH</i>	A/T	0.075	0.058
rs62374257	5	86927378	<i>COX7C</i>	C/T	0.21	0.16
rs871269	5	151052827	<i>TNIP1</i>	T/C	0.34	0.47
rs113706587	5	180201150	<i>RASGEF1C</i>	A/G	0.10	0.056
rs785129	6	114291731	<i>HS3ST5</i>	T/C	0.34	0.40
rs6943429	7	7817263	<i>UMAD1</i>	T/C	0.42	0.47
rs10952097	7	8204382	<i>ICAI</i>	T/C	0.11	0.27
rs13237518	7	12229967	<i>TMEM106B</i>	A/C	0.40	0.34
rs1160871	7	28129126	<i>JAZF1</i>	G/GTCTT	0.24	0.28
rs76928645	7	54873635	<i>SEC61G</i>	T/C	0.13	0.016
rs1065712	8	11844613	<i>CTSB</i>	C/G	0.059	0.0047
rs34173062	8	144103704	<i>SHARPIN</i>	A/G	0.089	0.017
rs1800978	9	104903697	<i>ABCA1</i>	G/C	0.12	0.15
rs7068231	10	60025170	<i>ANK3</i>	T/G	0.40	0.46
rs6586028	10	80494228	<i>TSPAN14</i>	C/T	0.19	0.045
rs6584063	10	96266650	<i>BLNK</i>	G/A	0.029	0.033
rs7908662	10	122413396	<i>PLEKHA1</i>	G/A	0.47	0.49
rs6489896	12	113281983	<i>TPCN1</i>	C/T	0.094	0.15
rs7157106	14	105761758	<i>IGH</i> gene cluster	A/G	0.34	0.23
rs10131280	14	106665591	<i>IGH</i> gene cluster	A/G	0.14	0.18
rs3848143	15	64131307	<i>SNX1</i>	G/A	0.18	0.39
rs12592898	15	78936857	<i>CTSH</i>	A/G	0.13	0.15
rs1140239	16	30010081	<i>DOC2A</i>	T/C	0.38	0.31
rs450674	16	79574511	<i>MAF</i>	C/T	0.36	0.20
rs16941239	16	86420604	<i>FOXF1</i>	A/T	0.028	0.13
rs56407236	16	90103687	<i>PRDM7</i>	A/G	0.058	0.053
rs35048651	17	1728046	<i>WDR81</i>	T/TGAG	0.19	0.22
rs2242595	17	18156140	<i>MYO15A</i>	A/G	0.12	0.27
rs5848	17	44352876	<i>GRN</i>	T/C	0.30	0.46
rs149080927	19	1854254	<i>KLF16</i>	G/GC	0.49	0.26
rs9304690	19	49950060	<i>SIGLEC11</i>	T/C	0.24	0.20
rs587709	19	54267597	<i>LILRB2</i>	C/T	0.31	0.46
rs1358782	20	413334	<i>RBCK1</i>	A/G	0.27	0.14
rs6742	20	63743088	<i>SLC2A4RG</i>	T/C	0.21	0.21
rs2154481	21	26101558	<i>APP</i>	C/T	0.49	0.29

^a GRCh38 assembly

^b MAFs are calculated from 1000 genome phase 3 in Europeans (EUR) population and other populations (Africans, Admixed Americans, East Asians, and South Asians)

Chr = chromosome; MAF = minor allele frequency

Supplementary Table 5. Association with Braak neurofibrillary tangle stage in people with European ancestry

Variant	Gene	Effect allele	ADRC				ROSMAP (n = 1,266)	
			ADSP WGS (n = 1,028)		ADGC (n = 2,200)		OR	P-value
			OR	P-value	OR	P-value		
rs679515	<i>CR1</i>	T	1.25	0.071	1.27	0.0049	1.17	0.18
rs6733839	<i>BIN1</i>	T	1.42	5.6×10^{-4}	1.26	5.1×10^{-4}	1.30	0.0053
rs10933431	<i>INPP5D</i>	G	0.93	0.55	0.84	0.021	0.86	0.19
rs6846529	<i>CLNK</i>	C	1.00	0.99	1.10 ^a	0.20	1.21	0.065
drs6605556	<i>HLA-DQA1</i>	G	0.80 ^b	0.085	0.96	0.66	0.74	0.023
rs10947943	<i>UNC5CL</i>	A	1.02	0.90	0.87	0.14	0.83	0.16
rs143332484	<i>TREM2</i>	T	1.93	0.15	-	-	-	-
rs75932628	<i>TREM2</i>	T	1.00	1.00	-	-	-	-
rs60755019	<i>TREML2</i>	G	-	-	-	-	-	-
rs7767350	<i>CD2AP</i>	T	0.99	0.91	1.09	0.24	1.26	0.022
rs6966331	<i>EPDR1</i>	T	0.73	0.0036	1.07	0.32	0.93	0.48
rs7384878	<i>SPDYE3</i>	C	0.99	0.94	0.90	0.14	0.76	0.0073
rs11771145	<i>EPHA1</i>	A	0.96	0.70	0.91	0.16	0.92	0.42
rs73223431	<i>PTK2B</i>	T	0.98	0.86	1.10	0.17	1.25	0.015
rs11787077	<i>CLU</i>	T	0.87	0.17	0.98	0.80	0.93	0.41
rs7912495	<i>USP6NL</i>	G	1.04	0.72	1.07	0.32	1.07	0.46
rs10437655	<i>SPII</i>	A	1.11	0.31	1.10	0.14	1.23	0.023
rs1582763	<i>MS4A4A</i>	A	0.88	0.20	0.94	0.37	1.00	0.98
rs3851179	<i>EED</i>	T	0.84	0.083	0.89	0.075	0.91	0.31
rs74685827	<i>SORL1</i>	G	1.32	0.49	1.05	0.83	1.18	0.61
rs11218343	<i>SORL1</i>	C	1.08	0.73	0.69	0.028	1.06	0.81
rs17125924	<i>FERMT2</i>	G	0.86	0.41	1.21	0.11	1.22	0.17
rs7401792	<i>SLC24A4</i>	G	1.00	0.98	1.14	0.058	1.11	0.27
rs12590654	<i>SLC24A4</i>	A	0.88	0.25	0.98	0.77	0.92	0.39
rs8025980	<i>SPPL2A</i>	G	1.16	0.16	0.96 ^c	0.50	1.11	0.25
rs602602	<i>MINDY2</i>	A	-	-	0.93	0.28	1.09	0.41

rs117618017	<i>APH1B</i>	T	1.07	0.65	1.08	0.43	1.45	0.0042
rs889555	<i>BCKDK</i>	T	1.12	0.33	0.88	0.067	1.01	0.94
rs4985556	<i>IL34</i>	A	1.02	0.91	0.99	0.91	1.07	0.63
rs12446759	<i>PLCG2</i>	G	0.86	0.12	0.97	0.70	0.88	0.18
rs72824905	<i>PLCG2</i>	G	0.54	0.31	-	-	-	-
rs7225151	<i>SCIMP</i>	A	1.15	0.37	1.07	0.53	1.04	0.79
rs199515	<i>WNT3</i>	G	0.98	0.84	0.95	0.55	0.93	0.54
rs616338	<i>ABI3</i>	T	3.44	0.14	-	-	-	-
rs2526377	<i>TSPOAP1</i>	G	-	-	-	-	0.90	0.26
rs4277405	<i>ACE</i>	C	1.15	0.17	1.02	0.80	1.13	0.20
rs12151021	<i>ABCA7</i>	A	1.26	0.027	1.15	0.038	-	-
rs6014724	<i>CASS4</i>	G	1.13	0.52	0.82	0.072	1.19	0.27
rs2830489	<i>ADAMTS1</i>	T	1.04	0.71	1.03	0.72	0.89	0.24
rs141749679	<i>SORT1</i>	C	0.92	0.95				
rs72777026	<i>ADAM17</i>	G	0.99	0.91	1.04	0.66	1.22	0.13
rs17020490	<i>PRKD3</i>	C	0.87	0.29	0.98	0.86	1.09	0.50
rs143080277	<i>NCK2</i>	C	0.92	0.88	-	-	-	-
rs139643391	<i>WDR12</i>	T	1.06	0.72	0.99 ^d	0.96	0.81	0.14
rs16824536	<i>MME</i>	A	0.54	0.0088	0.65	0.0038	1.00	0.99
rs61762319	<i>MME</i>	G	1.21	0.54	1.18	0.44	-	-
rs3822030	<i>IDUA</i>	G	-	-	-	-	-	-
rs2245466	<i>RHOH</i>	G	1.05	0.63	1.00	0.99	0.94	0.52
rs112403360	<i>ANKH</i>	A	1.34	0.14	1.08	0.54	1.21	0.25
rs62374257	<i>COX7C</i>	C	1.13	0.32	1.21	0.013	1.24	0.047
rs871269	<i>TNIP1</i>	T	0.99	0.96	0.95	0.43	0.95	0.62
rs113706587	<i>RASGEF1C</i>	A	0.94	0.71	1.23	0.048	0.99	0.93
rs785129	<i>HS3ST5</i>	T	1.08	0.48	1.00	0.97	0.98	0.79
rs6943429	<i>UMAD1</i>	T	0.91	0.34	1.10	0.14	-	-
rs10952097	<i>ICA1</i>	T	1.16	0.36	1.06	0.61	-	-
rs13237518	<i>TMEM106B</i>	A	1.11	0.31	1.15	0.036	1.10	0.30
rs1160871	<i>JAZF1</i>	G	0.83	0.12	-	-	1.20	0.075

rs76928645	<i>SEC61G</i>	T	1.21	0.25	0.88	0.22	1.07	0.65
rs1065712	<i>CTSB</i>	C	-	-	0.94	0.66	0.77	0.21
rs34173062	<i>SHARPIN</i>	A	-	-	0.95	0.67	-	-
rs1800978	<i>ABCA1</i>	G	-	-	-	-	1.17	0.25
rs7068231	<i>ANK3</i>	T	1.03	0.79	0.95	0.45	0.92	0.36
rs6586028	<i>TSPAN14</i>	C	-	-	0.91	0.22	1.01	0.96
rs6584063	<i>BLNK</i>	G	1.30	0.37	0.94	0.71	1.32 ^e	0.18
rs7908662	<i>PLEKHA1</i>	G	0.98	0.87	0.99	0.86	-	-
rs6489896	<i>TPCN1</i>	C	1.31	0.21	1.03	0.79	1.17	0.38
rs7157106	<i>IGH</i> gene cluster	A	-	-	1.02	0.80	-	-
rs10131280	<i>IGH</i> gene cluster	A	0.80	0.13	0.97	0.71	1.12	0.41
rs3848143	<i>SNX1</i>	G	1.13	0.32	0.97	0.66	1.24	0.060
rs12592898	<i>CTSH</i>	A	0.83	0.20	0.91	0.34	0.88	0.37
rs1140239	<i>DOC2A</i>	T	0.96	0.70	0.90	0.10	-	-
rs450674	<i>MAF</i>	C	-	-	0.87	0.032	1.04	0.69
rs16941239	<i>FOXF1</i>	A	1.04	0.89	1.03	0.88	0.82	0.52
rs56407236	<i>PRDM7</i>	A	-	-	1.04	0.79	0.81	0.24
rs35048651	<i>WDR81</i>	T	1.05	0.69	-	-	0.89	0.32
rs2242595	<i>MYO15A</i>	A	0.87	0.36	0.81	0.033	0.95	0.70
rs5848	<i>GRN</i>	T	1.02	0.88	0.99	0.85	0.83	0.066
rs149080927	<i>KLF16</i>	G	0.91	0.34	-	-	1.10	0.32
rs9304690	<i>SIGLEC11</i>	T	0.94	0.62	1.00	0.99	0.99	0.91
rs587709	<i>LILRB2</i>	C	-	-	1.02	0.78	-	-
rs1358782	<i>RBCK1</i>	A	0.83	0.090	0.87	0.058	0.97	0.74
rs6742	<i>SLC2A4RG</i>	T	0.89	0.35	1.03	0.69	1.19	0.12
rs2154481	<i>APP</i>	C	-	-	0.92	0.16	1.04	0.67

^{a-d} OR and P-value were computed by the proxy which was in perfect linkage disequilibrium block (i.e., $r^2 = 1$ and $D' = 1$)

^a rs4351014, ^b rs6941385, ^c rs1291073, ^d rs6723704, ^e rs79663593

Supplementary Table 6. Association with neocortical neuritic plaques in people with European ancestry

Variant	Gene	Effect allele	ADRC				ROSMAP (n = 1,266)	
			ADSP WGS (n = 1,028)		ADGC (n = 2,200)		OR	P-value
			OR	P-value	OR	P-value		
rs679515	<i>CR1</i>	T	1.13	0.31	1.15	0.11	1.16	0.18
rs6733839	<i>BIN1</i>	T	1.13	0.21	1.23	0.0016	1.24	0.014
rs10933431	<i>INPP5D</i>	G	1.05	0.66	0.82	0.012	0.86	0.14
rs6846529	<i>CLNK</i>	C	1.11	0.33	1.04 ^a	0.56	0.96	0.68
rs6605556	<i>HLA-DQA1</i>	G	0.73 ^b	0.013	0.94	0.47	0.83	0.13
rs10947943	<i>UNC5CL</i>	A	0.99	0.96	0.89	0.23	0.77	0.032
rs143332484	<i>TREM2</i>	T	1.72	0.20	-	-	-	-
rs75932628	<i>TREM2</i>	T	1.51	0.36	-	-	-	-
rs60755019	<i>TREML2</i>	G	-	-	-	-	-	-
rs7767350	<i>CD2AP</i>	T	1.00	0.97	1.05	0.49	1.12	0.22
rs6966331	<i>EPDR1</i>	T	0.91	0.39	1.04	0.59	1.00	0.98
rs7384878	<i>SPDYE3</i>	C	1.01	0.95	0.87	0.047	0.82	0.043
rs11771145	<i>EPHA1</i>	A	1.00	0.97	0.90	0.14	1.08	0.38
rs73223431	<i>PTK2B</i>	T	1.14	0.20	1.09	0.23	1.21	0.029
rs11787077	<i>CLU</i>	T	0.99	0.90	0.98	0.75	1.01	0.88
rs7912495	<i>USP6NL</i>	G	0.96	0.65	0.93	0.30	1.09	0.33
rs10437655	<i>SPII</i>	A	1.09	0.37	1.09	0.20	1.02	0.84
rs1582763	<i>MS4A4A</i>	A	0.81	0.042	0.86	0.023	1.11	0.25
rs3851179	<i>EED</i>	T	0.81	0.039	0.93	0.27	0.77	0.0038
rs74685827	<i>SORL1</i>	G	1.35	0.44	1.14	0.57	1.07	0.82
rs11218343	<i>SORL1</i>	C	1.07	0.76	0.92	0.63	1.29	0.28
rs17125924	<i>FERMT2</i>	G	1.13	0.50	1.35	0.012	1.21	0.17
rs7401792	<i>SLC24A4</i>	G	1.08	0.43	1.00	1.00	0.97	0.77
rs12590654	<i>SLC24A4</i>	A	0.74	0.0047	1.04	0.53	1.19	0.047
rs8025980	<i>SPPL2A</i>	G	1.22	0.059	0.98 ^c	0.76	1.08	0.37
rs602602	<i>MINDY2</i>	A	-	-	0.87	0.051	1.08	0.45

rs117618017	<i>APH1B</i>	T	1.05	0.73	1.24	0.026	1.38	0.010
rs889555	<i>BCKDK</i>	T	1.18	0.13	0.86	0.044	1.16	0.12
rs4985556	<i>IL34</i>	A	1.06	0.73	0.85	0.12	0.95	0.70
rs12446759	<i>PLCG2</i>	G	0.74	0.0036	1.01	0.89	1.06	0.53
rs72824905	<i>PLCG2</i>	G	0.34	0.095	-	-	-	-
rs7225151	<i>SCIMP</i>	A	1.22	0.20	1.01	0.91	1.04	0.76
rs199515	<i>WNT3</i>	G	1.14	0.28	0.94	0.47	0.97	0.80
rs616338	<i>ABI3</i>	T	1.82	0.38	-	-	-	-
rs2526377	<i>TSPOAP1</i>	G	-	-	-	-	0.90	0.24
rs4277405	<i>ACE</i>	C	1.15	0.18	0.91	0.16	0.99	0.92
rs12151021	<i>ABCA7</i>	A	1.33	0.0059	1.12	0.091	-	-
rs6014724	<i>CASS4</i>	G	0.94	0.72	0.80	0.054	0.97	0.86
rs2830489	<i>ADAMTS1</i>	T	1.08	0.47	1.05	0.49	0.92	0.36
rs141749679	<i>SORT1</i>	C	1.31	0.83	-	-	-	-
rs72777026	<i>ADAM17</i>	G	1.07	0.64	1.19	0.072	1.25	0.070
rs17020490	<i>PRKD3</i>	C	0.77	0.051	1.00	0.99	1.27	0.055
rs143080277	<i>NCK2</i>	C	2.11	0.22	-	-	-	-
rs139643391	<i>WDR12</i>	T	1.14	0.37	1.01 ^d	0.91	0.83	0.15
rs16824536	<i>MME</i>	A	0.67	0.099	0.68	0.010	0.76	0.20
rs61762319	<i>MME</i>	G	1.56	0.15	1.29	0.22	-	-
rs3822030	<i>IDUA</i>	G	-	-	-	-	-	-
rs2245466	<i>RHOH</i>	G	1.16	0.15	0.97	0.66	0.96	0.63
rs112403360	<i>ANKH</i>	A	0.93	0.68	0.99	0.96	1.51	0.0078
rs62374257	<i>COX7C</i>	C	0.98	0.87	1.04	0.63	1.15	0.19
rs871269	<i>TNIP1</i>	T	0.99	0.93	0.98	0.74	1.02	0.83
rs113706587	<i>RASGEF1C</i>	A	1.10	0.54	1.18	0.12	0.77	0.076
rs785129	<i>HS3ST5</i>	T	0.85	0.13	0.98	0.83	0.92	0.35
rs6943429	<i>UMAD1</i>	T	0.90	0.31	0.98	0.75	-	-
rs10952097	<i>ICA1</i>	T	1.10	0.55	1.07	0.53	-	-
rs13237518	<i>TMEM106B</i>	A	1.07	0.49	1.00	0.95	0.92	0.35
rs1160871	<i>JAZF1</i>	G	0.89	0.35	-	-	1.04	0.73

rs76928645	<i>SEC61G</i>	T	0.94	0.72	0.95	0.66	1.12	0.42
rs1065712	<i>CTSB</i>	C	-	-	1.09	0.54	0.87	0.48
rs34173062	<i>SHARPIN</i>	A	-	-	0.94	0.57	-	-
rs1800978	<i>ABCA1</i>	G	-	-	-	-	1.29	0.048
rs7068231	<i>ANK3</i>	T	1.13	0.23	1.01	0.84	0.95	0.53
rs6586028	<i>TSPAN14</i>	C	-	-	0.91	0.27	0.95	0.61
rs6584063	<i>BLNK</i>	G	1.14	0.65	0.98	0.92	0.82 ^e	0.36
rs7908662	<i>PLEKHA1</i>	G	1.01	0.90	0.96	0.57	-	-
rs6489896	<i>TPCN1</i>	C	1.21	0.35	1.19	0.18	0.81	0.24
rs7157106	<i>IGH</i> gene cluster	A	-	-	1.21	0.0060	-	-
rs10131280	<i>IGH</i> gene cluster	A	0.97	0.82	1.00	0.99	1.01	0.92
rs3848143	<i>SNX1</i>	G	1.09	0.44	1.11	0.19	1.24	0.052
rs12592898	<i>CTSH</i>	A	1.12	0.44	0.95	0.59	0.70	0.0081
rs1140239	<i>DOC2A</i>	T	1.11	0.31	0.86	0.026	-	-
rs450674	<i>MAF</i>	C	-	-	0.87	0.035	0.93	0.40
rs16941239	<i>FOXF1</i>	A	0.78	0.40	0.92	0.68	1.05	0.87
rs56407236	<i>PRDM7</i>	A	-	-	0.94	0.64	0.93	0.67
rs35048651	<i>WDR81</i>	T	1.06	0.61	-	-	1.16	0.14
rs2242595	<i>MYO15A</i>	A	0.90	0.51	0.81	0.038	1.08	0.57
rs5848	<i>GRN</i>	T	1.02	0.84	0.94	0.39	0.99	0.89
rs149080927	<i>KLF16</i>	G	0.87	0.18	-	-	1.09	0.33
rs9304690	<i>SIGLEC11</i>	T	0.96	0.72	0.98	0.84	1.02	0.85
rs587709	<i>LILRB2</i>	C	-	-	0.99	0.88	-	-
rs1358782	<i>RBCK1</i>	A	0.87	0.23	0.86	0.044	0.81	0.044
rs6742	<i>SLC2A4RG</i>	T	1.04	0.72	1.03	0.73	1.06	0.57
rs2154481	<i>APP</i>	C	-	-	0.91	0.15	0.92	0.33

^{a-d} OR and P-value were computed by the proxy which was in perfect linkage disequilibrium block (i.e., $r^2 = 1$ and $D' = 1$)

^a rs4351014, ^b rs6941385, ^c rs1291073, ^d rs6723704, ^e rs79663593

Supplementary Table 7. Association with TDP-43 in any brain regions in people with European ancestry

Variant	Gene	Effect allele	ADRC				ROSMAP	
			ADSP WGS (n = 1,028)		ADGC (n = 2,200)		(n = 1,266)	
			OR	P-value	OR	P-value	OR	P-value
rs679515	<i>CR1</i>	T	0.98	0.93	1.27	0.080	1.18	0.14
rs6733839	<i>BIN1</i>	T	1.05	0.78	1.11	0.33	1.02	0.83
rs10933431	<i>INPP5D</i>	G	0.92	0.69	0.96	0.77	0.87	0.17
rs6846529	<i>CLNK</i>	C	1.19	0.37	1.03 ^a	0.81	1.13	0.22
rs6605556	<i>HLA-DQA1</i>	G	0.86 ^b	0.55	1.15	0.33	0.88	0.29
rs10947943	<i>UNC5CL</i>	A	0.69	0.15	0.99	0.94	0.93	0.53
rs143332484	<i>TREM2</i>	T	0.80	0.77	-	-	-	-
rs75932628	<i>TREM2</i>	T	0.48	0.51	-	-	-	-
rs60755019	<i>TREML2</i>	G	-	-	-	-	-	-
rs7767350	<i>CD2AP</i>	T	1.19	0.37	1.08	0.50	0.93	0.44
rs6966331	<i>EPDR1</i>	T	0.88	0.52	1.11	0.35	1.02	0.82
rs7384878	<i>SPDYE3</i>	C	0.78	0.22	1.07	0.59	1.02	0.85
rs11771145	<i>EPHA1</i>	A	0.99	0.96	1.16	0.20	0.90	0.27
rs73223431	<i>PTK2B</i>	T	1.02	0.91	0.87	0.21	1.14	0.15
rs11787077	<i>CLU</i>	T	0.93	0.68	1.03	0.79	1.07	0.44
rs7912495	<i>USP6NL</i>	G	0.86	0.44	1.01	0.91	0.93	0.41
rs10437655	<i>SPII</i>	A	0.93	0.68	1.13	0.27	0.91	0.25
rs1582763	<i>MS4A4A</i>	A	1.17	0.38	1.02	0.84	1.08	0.41
rs3851179	<i>EED</i>	T	1.11	0.57	0.98	0.84	1.10	0.28
rs74685827	<i>SORL1</i>	G	5.55	0.014	1.37	0.36	1.92	0.055
rs11218343	<i>SORL1</i>	C	1.06	0.88	0.56	0.053	1.11	0.67
rs17125924	<i>FERMT2</i>	G	1.55	0.18	0.93	0.71	1.03	0.83
rs7401792	<i>SLC24A4</i>	G	1.02	0.93	1.13	0.27	1.06	0.56
rs12590654	<i>SLC24A4</i>	A	1.07	0.71	1.12	0.30	1.17	0.080
rs8025980	<i>SPPL2A</i>	G	1.20	0.34	0.98 ^c	0.82	0.98	0.82
rs602602	<i>MINDY2</i>	A	-	-	1.08	0.53	1.01	0.90

rs117618017	<i>APH1B</i>	T	1.24	0.41	1.06	0.71	1.15	0.26
rs889555	<i>BCKDK</i>	T	1.22	0.31	0.81	0.094	0.99	0.93
rs4985556	<i>IL34</i>	A	0.69	0.22	0.93	0.69	1.05	0.72
rs12446759	<i>PLCG2</i>	G	0.83	0.33	0.97	0.77	1.07	0.46
rs72824905	<i>PLCG2</i>	G	1.61	0.61	-	-	-	-
rs7225151	<i>SCIMP</i>	A	1.61	0.072	1.01	0.95	1.11	0.45
rs199515	<i>WNT3</i>	G	0.91	0.68	0.74	0.031	0.90	0.32
rs616338	<i>ABI3</i>	T	1.10	0.95	-	-	-	-
rs2526377	<i>TSPOAP1</i>	G	-	-	-	-	0.98	0.78
rs4277405	<i>ACE</i>	C	0.86	0.43	0.78	0.026	1.07	0.43
rs12151021	<i>ABCA7</i>	A	1.25	0.24	1.34	0.010	-	-
rs6014724	<i>CASS4</i>	G	1.50	0.20	0.82	0.30	1.35	0.061
rs2830489	<i>ADAMTS1</i>	T	0.79	0.26	0.91	0.42	0.93	0.47
rs141749679	<i>SORT1</i>	C	1.34	0.81	-	-	-	-
rs72777026	<i>ADAM17</i>	G	0.88	0.60	1.06	0.71	1.13	0.33
rs17020490	<i>PRKD3</i>	C	1.24	0.35	1.13	0.42	1.07	0.57
rs143080277	<i>NCK2</i>	C	-	-	-	-	-	-
rs139643391	<i>WDR12</i>	T	1.03	0.92	1.06 ^d	0.71	1.02	0.89
rs16824536	<i>MME</i>	A	0.39	0.14	0.81	0.44	1.15	0.50
rs61762319	<i>MME</i>	G	0.91	0.83	1.53	0.17	-	-
rs3822030	<i>IDUA</i>	G	-	-	-	-	-	-
rs2245466	<i>RHOH</i>	G	1.13	0.52	1.05	0.66	1.10	0.33
rs112403360	<i>ANKH</i>	A	0.98	0.94	0.88	0.52	0.70	0.024
rs62374257	<i>COX7C</i>	C	0.84	0.44	1.11	0.39	1.19	0.095
rs871269	<i>TNIP1</i>	T	0.86	0.41	0.80	0.055	0.99	0.93
rs113706587	<i>RASGEF1C</i>	A	1.49	0.16	1.13	0.49	0.97	0.82
rs785129	<i>HS3ST5</i>	T	0.99	0.98	0.83	0.099	1.02	0.79
rs6943429	<i>UMAD1</i>	T	0.90	0.58	1.17	0.17	-	-
rs10952097	<i>ICA1</i>	T	1.26	0.37	0.85	0.40	-	-
rs13237518	<i>TMEM106B</i>	A	0.71	0.058	0.67	3.2×10^{-4}	0.88	0.15
rs1160871	<i>JAZF1</i>	G	0.65	0.064	-	-	0.85	0.11

rs76928645	<i>SEC61G</i>	T	1.09	0.77	1.09	0.63	1.02	0.89
rs1065712	<i>CTSB</i>	C	-	-	1.20	0.43	1.24	0.26
rs34173062	<i>SHARPIN</i>	A	-	-	1.76	0.0029	-	-
rs1800978	<i>ABCA1</i>	G	-	-	-	-	1.22	0.13
rs7068231	<i>ANK3</i>	T	1.19	0.37	0.92	0.42	0.96	0.60
rs6586028	<i>TSPAN14</i>	C	-	-	0.94	0.66	0.91	0.41
rs6584063	<i>BLNK</i>	G	1.13	0.78	1.23	0.47	1.09 ^e	0.70
rs7908662	<i>PLEKHA1</i>	G	0.88	0.45	0.97	0.79	-	-
rs6489896	<i>TPCN1</i>	C	1.72	0.094	1.05	0.84	1.63	0.0069
rs7157106	<i>IGH</i> gene cluster	A	-	-	1.02	0.90	-	-
rs10131280	<i>IGH</i> gene cluster	A	1.26	0.34	0.74	0.075	0.77	0.050
rs3848143	<i>SNX1</i>	G	1.50	0.054	0.97	0.81	1.10	0.39
rs12592898	<i>CTSH</i>	A	1.08	0.77	1.06	0.73	0.78	0.059
rs1140239	<i>DOC2A</i>	T	0.94	0.75	0.95	0.61	-	-
rs450674	<i>MAF</i>	C	-	-	0.91	0.40	1.10	0.28
rs16941239	<i>FOXF1</i>	A	1.61	0.35	1.08	0.81	1.42	0.22
rs56407236	<i>PRDM7</i>	A	-	-	0.45	9.3 × 10 ⁻⁴	1.14	0.42
rs35048651	<i>WDR81</i>	T	0.66	0.072	-	-	0.85	0.12
rs2242595	<i>MYO15A</i>	A	1.30	0.36	1.23	0.23	0.95	0.68
rs5848	<i>GRN</i>	T	1.12	0.56	1.11	0.37	1.33	0.0035
rs149080927	<i>KLF16</i>	G	1.05	0.80	-	-	0.97	0.70
rs9304690	<i>SIGLEC11</i>	T	0.75	0.22	1.07	0.62	1.04	0.68
rs587709	<i>LILRB2</i>	C	-	-	1.02	0.85	-	-
rs1358782	<i>RBCK1</i>	A	1.01	0.98	1.06	0.63	0.92	0.40
rs6742	<i>SLC2A4RG</i>	T	1.39	0.13	0.97	0.83	1.19	0.099
rs2154481	<i>APP</i>	C	-	-	0.88	0.21	1.07	0.45

^{a-d} OR and P-value were computed by the proxy which was in perfect linkage disequilibrium block (i.e., $r^2 = 1$ and $D' = 1$)

^a rs4351014, ^b rs6941385, ^c rs1291073, ^d rs6723704, ^e rs79663593

Supplementary Table 8. Association with Lewy bodies in any brain regions in people with European ancestry

Variant	Gene	Effect allele	ADRC				ROSMAP (n = 1,266)	
			ADSP WGS (n = 1,028)		ADGC (n = 2,200)		OR	P-value
			OR	P-value	OR	P-value		
rs679515	<i>CR1</i>	T	1.05	0.68	1.08	0.37	0.93	0.56
rs6733839	<i>BINI</i>	T	1.24	0.023	1.13	0.054	1.16	0.13
rs10933431	<i>INPP5D</i>	G	1.03	0.81	1.10	0.20	1.05	0.67
rs6846529	<i>CLNK</i>	C	0.97	0.75	1.04 ^a	0.62	1.09	0.43
rs6605556	<i>HLA-DQA1</i>	G	0.83 ^b	0.14	1.01	0.96	0.92	0.56
rs10947943	<i>UNC5CL</i>	A	1.16	0.28	0.96	0.69	0.88	0.35
rs143332484	<i>TREM2</i>	T	1.95	0.079	-	-	-	-
rs75932628	<i>TREM2</i>	T	0.55	0.17	-	-	-	-
rs60755019	<i>TREML2</i>	G	2.02	0.45	-	-	-	-
rs7767350	<i>CD2AP</i>	T	1.04	0.70	1.06	0.39	0.88	0.25
rs6966331	<i>EPDR1</i>	T	1.11	0.32	0.99	0.89	1.24	0.031
rs7384878	<i>SPDYE3</i>	C	1.07	0.51	0.98	0.79	1.02	0.84
rs11771145	<i>EPHA1</i>	A	0.97	0.79	0.97	0.68	1.14	0.18
rs73223431	<i>PTK2B</i>	T	1.15	0.15	0.94	0.34	1.03	0.74
rs11787077	<i>CLU</i>	T	0.88	0.18	1.03	0.64	0.90	0.27
rs7912495	<i>USP6NL</i>	G	1.08	0.45	1.12	0.069	1.26	0.021
rs10437655	<i>SPII</i>	A	1.06	0.55	0.95	0.39	1.18	0.077
rs1582763	<i>MS4A4A</i>	A	0.92	0.38	1.07	0.31	0.94	0.55
rs3851179	<i>EED</i>	T	0.97	0.77	0.92	0.20	1.00	0.99
rs74685827	<i>SORL1</i>	G	1.43	0.32	0.92	0.70	0.98	0.95
rs11218343	<i>SORL1</i>	C	1.07	0.77	0.98	0.90	1.43	0.15
rs17125924	<i>FERMT2</i>	G	1.02	0.88	0.96	0.74	1.00	0.98
rs7401792	<i>SLC24A4</i>	G	1.10	0.32	1.00	0.97	0.85	0.12
rs12590654	<i>SLC24A4</i>	A	1.02	0.89	0.96	0.60	0.96	0.70
rs8025980	<i>SPPL2A</i>	G	1.08	0.46	1.00 ^c	1.00	1.06	0.52
rs602602	<i>MINDY2</i>	A	-	-	1.14	0.057	1.16	0.16

rs117618017	<i>APH1B</i>	T	1.20	0.16	1.02	0.86	1.09	0.53
rs889555	<i>BCKDK</i>	T	0.96	0.73	1.05	0.47	0.82	0.061
rs4985556	<i>IL34</i>	A	0.98	0.87	1.23	0.031	1.08	0.59
rs12446759	<i>PLCG2</i>	G	0.92	0.38	0.89	0.091	1.14	0.19
rs72824905	<i>PLCG2</i>	G	1.46	0.49	-	-	-	-
rs7225151	<i>SCIMP</i>	A	1.10	0.49	1.26	0.017	0.95	0.75
rs199515	<i>WNT3</i>	G	1.13	0.28	1.01	0.90	0.85	0.16
rs616338	<i>ABI3</i>	T	1.68	0.35	-	-	-	-
rs2526377	<i>TSPOAP1</i>	G	-	-	-	-	1.03	0.73
rs4277405	<i>ACE</i>	C	0.89	0.22	1.04	0.60	1.05	0.62
rs12151021	<i>ABCA7</i>	A	1.13	0.23	1.03	0.72	-	-
rs6014724	<i>CASS4</i>	G	0.92	0.65	0.85	0.16	1.27	0.15
rs2830489	<i>ADAMTS1</i>	T	1.12	0.30	1.04	0.63	0.84	0.10
rs141749679	<i>SORT1</i>	C	4.74	0.19	-	-	-	-
rs72777026	<i>ADAM17</i>	G	1.10	0.48	1.07	0.47	1.30	0.050
rs17020490	<i>PRKD3</i>	C	1.14	0.29	0.97	0.71	0.90	0.44
rs143080277	<i>NCK2</i>	C	0.27	0.088	-	-	-	-
rs139643391	<i>WDR12</i>	T	0.80	0.12	1.07 ^d	0.47	1.22	0.15
rs16824536	<i>MME</i>	A	0.86	0.51	0.92	0.59	1.26	0.29
rs61762319	<i>MME</i>	G	1.05	0.87	0.92	0.71	-	-
rs3822030	<i>IDUA</i>	G	-	-	-	-	-	-
rs2245466	<i>RHOH</i>	G	0.94	0.52	1.16	0.030	0.96	0.69
rs112403360	<i>ANKH</i>	A	1.06	0.72	1.06	0.62	0.82	0.27
rs62374257	<i>COX7C</i>	C	0.84	0.13	0.94	0.39	1.13	0.30
rs871269	<i>TNIP1</i>	T	0.83	0.066	1.07	0.33	1.02	0.87
rs113706587	<i>RASGEF1C</i>	A	0.93	0.65	1.09	0.40	0.97	0.86
rs785129	<i>HS3ST5</i>	T	1.10	0.33	1.02	0.80	1.08	0.42
rs6943429	<i>UMAD1</i>	T	0.84	0.079	0.99	0.93	-	-
rs10952097	<i>ICA1</i>	T	0.83	0.22	0.82	0.074	-	-
rs13237518	<i>TMEM106B</i>	A	1.15	0.16	1.08	0.25	1.17	0.10
rs1160871	<i>JAZF1</i>	G	1.06	0.59	-	-	0.78	0.035

rs76928645	<i>SEC61G</i>	T	0.80	0.17	1.24	0.042	0.97	0.86
rs1065712	<i>CTSB</i>	C	-	-	0.94	0.67	1.32	0.16
rs34173062	<i>SHARPIN</i>	A	-	-	1.07	0.54	-	-
rs1800978	<i>ABCA1</i>	G	-	-	-	-	0.89	0.42
rs7068231	<i>ANK3</i>	T	1.00	0.98	0.96	0.51	0.88	0.17
rs6586028	<i>TSPAN14</i>	C	-	-	1.05	0.53	0.88	0.31
rs6584063	<i>BLNK</i>	G	1.16	0.55	1.21	0.26	0.79 ^e	0.33
rs7908662	<i>PLEKHA1</i>	G	0.96	0.67	0.93	0.25	-	-
rs6489896	<i>TPCN1</i>	C	0.88	0.51	1.01	0.94	1.39	0.081
rs7157106	<i>IGH</i> gene cluster	A	-	-	0.98	0.75	-	-
rs10131280	<i>IGH</i> gene cluster	A	0.96	0.77	0.83	0.058	1.05	0.72
rs3848143	<i>SNX1</i>	G	1.12	0.31	0.86	0.060	1.02	0.86
rs12592898	<i>CTSH</i>	A	0.96	0.76	1.00	0.98	0.85	0.27
rs1140239	<i>DOC2A</i>	T	0.94	0.54	0.98	0.77	-	-
rs450674	<i>MAF</i>	C	-	-	0.85	0.019	1.15	0.16
rs16941239	<i>FOXF1</i>	A	1.08	0.78	1.09	0.68	0.78	0.46
rs56407236	<i>PRDM7</i>	A	-	-	1.12	0.37	0.96	0.84
rs35048651	<i>WDR81</i>	T	1.06	0.60	-	-	0.97	0.82
rs2242595	<i>MYO15A</i>	A	0.92	0.58	0.81	0.041	0.78	0.12
rs5848	<i>GRN</i>	T	1.18	0.11	0.96	0.54	0.98	0.85
rs149080927	<i>KLF16</i>	G	0.99	0.92	-	-	0.87	0.13
rs9304690	<i>SIGLEC11</i>	T	0.68	0.0013	1.00	0.96	1.27	0.022
rs587709	<i>LILRB2</i>	C	-	-	1.09	0.24	-	-
rs1358782	<i>RBCK1</i>	A	1.24	0.042	0.96	0.55	0.94	0.56
rs6742	<i>SLC2A4RG</i>	T	0.98	0.89	1.03	0.73	1.02	0.89
rs2154481	<i>APP</i>	C	-	-	0.98	0.70	1.14	0.17

^{a-d} OR and P-value were computed by the proxy which was in perfect linkage disequilibrium block (i.e., $r^2 = 1$ and $D' = 1$)

^a rs4351014, ^b rs6941385, ^c rs1291073, ^d rs6723704, ^e rs79663593

Supplementary Table 9. Association with hippocampal sclerosis in people with European ancestry

Variant	Gene	Effect allele	ADRC				ROSMAP (n = 1,266)	
			ADSP WGS (n = 1,028)		ADGC (n = 2,200)		OR	P-value
			OR	P-value	OR	P-value		
rs679515	<i>CR1</i>	T	0.86	0.56	1.31	0.089	1.01	0.97
rs6733839	<i>BIN1</i>	T	0.87	0.47	0.93	0.57	1.16	0.33
rs10933431	<i>INPP5D</i>	G	0.81	0.40	0.77	0.094	1.04	0.82
rs6846529	<i>CLNK</i>	C	1.09	0.67	0.90 ^a	0.46	1.08	0.62
rs6605556	<i>HLA-DQA1</i>	G	0.68 ^b	0.19	0.87	0.44	0.79	0.28
rs10947943	<i>UNC5CL</i>	A	0.68	0.20	0.73	0.12	1.34	0.12
rs143332484	<i>TREM2</i>	T	3.71	0.037	-	-	-	-
rs75932628	<i>TREM2</i>	T	-	-	-	-	-	-
rs60755019	<i>TREML2</i>	G	-	-	-	-	-	-
rs7767350	<i>CD2AP</i>	T	1.31	0.21	0.93	0.59	0.88	0.41
rs6966331	<i>EPDR1</i>	T	0.68	0.092	1.35	0.021	1.06	0.69
rs7384878	<i>SPDYE3</i>	C	0.98	0.92	0.89	0.38	0.98	0.89
rs11771145	<i>EPHA1</i>	A	1.17	0.44	1.02	0.89	1.08	0.62
rs73223431	<i>PTK2B</i>	T	1.31	0.18	0.84	0.21	0.88	0.39
rs11787077	<i>CLU</i>	T	1.10	0.64	1.19	0.17	0.80	0.15
rs7912495	<i>USP6NL</i>	G	0.93	0.71	1.13	0.33	1.24	0.15
rs10437655	<i>SPII</i>	A	1.14	0.53	1.14	0.30	0.78	0.10
rs1582763	<i>MS4A4A</i>	A	0.87	0.50	1.12	0.41	0.86	0.34
rs3851179	<i>EED</i>	T	1.02	0.91	0.98	0.86	1.00	0.99
rs74685827	<i>SORL1</i>	G	1.75	0.40	1.63	0.18	2.06	0.070
rs11218343	<i>SORL1</i>	C	1.23	0.61	0.75	0.44	0.70	0.45
rs17125924	<i>FERMT2</i>	G	1.27	0.49	1.16	0.49	1.07	0.79
rs7401792	<i>SLC24A4</i>	G	0.81	0.32	1.13	0.37	1.20	0.24
rs12590654	<i>SLC24A4</i>	A	1.10	0.66	1.34	0.027	1.05	0.73
rs8025980	<i>SPPL2A</i>	G	1.04	0.84	0.98 ^c	0.88	0.88	0.40
rs602602	<i>MINDY2</i>	A	-	-	0.85	0.27	0.86	0.36

rs117618017	<i>APH1B</i>	T	0.75	0.38	0.88	0.48	1.05	0.84
rs889555	<i>BCKDK</i>	T	0.77	0.26	0.89	0.43	0.91	0.56
rs4985556	<i>IL34</i>	A	1.59	0.096	0.61	0.027	0.82	0.40
rs12446759	<i>PLCG2</i>	G	0.68	0.072	1.03	0.81	1.03	0.84
rs72824905	<i>PLCG2</i>	G	-	-	-	-	-	-
rs7225151	<i>SCIMP</i>	A	1.65	0.064	1.14	0.49	1.54	0.035
rs199515	<i>WNT3</i>	G	0.71	0.20	0.66	0.018	0.71	0.075
rs616338	<i>ABI3</i>	T	1.43	0.75	-	-	-	-
rs2526377	<i>TSPOAP1</i>	G	-	-	-	-	0.99	0.92
rs4277405	<i>ACE</i>	C	0.98	0.90	1.24	0.095	1.44	0.013
rs12151021	<i>ABCA7</i>	A	1.16	0.48	1.05	0.71	-	-
rs6014724	<i>CASS4</i>	G	0.92	0.83	1.40	0.087	0.87	0.61
rs2830489	<i>ADAMTS1</i>	T	0.54	0.015	0.94	0.66	0.92	0.60
rs141749679	<i>SORT1</i>	C	-	-	-	-	-	-
rs72777026	<i>ADAM17</i>	G	0.81	0.46	1.04	0.85	0.87	0.52
rs17020490	<i>PRKD3</i>	C	0.82	0.50	1.22	0.26	1.21	0.35
rs143080277	<i>NCK2</i>	C	1.78	0.61	-	-	-	-
rs139643391	<i>WDR12</i>	T	1.06	0.83	0.62 ^d	0.035	0.77	0.27
rs16824536	<i>MME</i>	A	0.40	0.22	0.59	0.15	1.49	0.19
rs61762319	<i>MME</i>	G	1.56	0.34	1.31	0.47	-	-
rs3822030	<i>IDUA</i>	G	-	-	-	-	-	-
rs2245466	<i>RHOH</i>	G	1.52	0.038	0.88	0.35	0.86	0.35
rs112403360	<i>ANKH</i>	A	1.02	0.95	0.71	0.21	0.99	0.96
rs62374257	<i>COX7C</i>	C	1.03	0.91	0.85	0.27	0.93	0.67
rs871269	<i>TNIP1</i>	T	0.79	0.27	0.82	0.15	0.64	0.0073
rs113706587	<i>RASGEF1C</i>	A	0.97	0.93	1.48	0.042	0.92	0.74
rs785129	<i>HS3ST5</i>	T	0.91	0.65	1.10	0.46	1.27	0.10
rs6943429	<i>UMAD1</i>	T	0.99	0.95	0.94	0.62	-	-
rs10952097	<i>ICA1</i>	T	1.44	0.18	0.93	0.74	-	-
rs13237518	<i>TMEM106B</i>	A	0.51	0.0019	0.64	8.5×10^{-4}	0.71	0.021
rs1160871	<i>JAZF1</i>	G	0.56	0.033	-	-	0.83	0.29

rs76928645	<i>SEC61G</i>	T	0.96	0.91	1.19	0.39	0.72	0.21
rs1065712	<i>CTSB</i>	C	-	-	1.01	0.97	1.17	0.60
rs34173062	<i>SHARPIN</i>	A	-	-	0.95	0.81	-	-
rs1800978	<i>ABCA1</i>	G	-	-	-	-	1.41	0.097
rs7068231	<i>ANK3</i>	T	1.02	0.91	0.91	0.46	0.96	0.80
rs6586028	<i>TSPAN14</i>	C	-	-	1.19	0.27	1.15	0.44
rs6584063	<i>BLNK</i>	G	1.02	0.97	1.06	0.85	0.71 ^e	0.35
rs7908662	<i>PLEKHA1</i>	G	0.89	0.54	1.42	0.0052	-	-
rs6489896	<i>TPCN1</i>	C	1.01	0.99	1.33	0.24	1.14	0.66
rs7157106	<i>IGH</i> gene cluster	A	-	-	1.11	0.42	-	-
rs10131280	<i>IGH</i> gene cluster	A	0.65	0.19	0.86	0.43	0.88	0.59
rs3848143	<i>SNX1</i>	G	1.39	0.14	1.00	0.97	1.05	0.78
rs12592898	<i>CTSH</i>	A	1.27	0.39	1.10	0.60	0.83	0.44
rs1140239	<i>DOC2A</i>	T	0.79	0.25	1.17	0.21	-	-
rs450674	<i>MAF</i>	C	-	-	0.79	0.083	1.08	0.62
rs16941239	<i>FOXF1</i>	A	1.87	0.20	1.10	0.79	1.22	0.63
rs56407236	<i>PRDM7</i>	A	-	-	1.01	0.96	0.69	0.27
rs35048651	<i>WDR81</i>	T	0.95	0.82	-	-	1.01	0.94
rs2242595	<i>MYO15A</i>	A	1.33	0.32	1.07	0.73	0.84	0.45
rs5848	<i>GRN</i>	T	1.75	0.0072	1.40	0.012	1.61	0.0019
rs149080927	<i>KLF16</i>	G	0.95	0.80	-	-	1.07	0.64
rs9304690	<i>SIGLEC11</i>	T	0.87	0.58	0.92	0.57	0.87	0.42
rs587709	<i>LILRB2</i>	C	-	-	1.11	0.46	-	-
rs1358782	<i>RBCK1</i>	A	0.71	0.14	1.08	0.61	0.86	0.37
rs6742	<i>SLC2A4RG</i>	T	1.05	0.84	1.05	0.73	1.02	0.90
rs2154481	<i>APP</i>	C	-	-	0.99	0.95	1.01	0.97

^{a-d} OR and P-value were computed by the proxy which was in perfect linkage disequilibrium block (i.e., $r^2 = 1$ and $D' = 1$)

^a rs4351014, ^b rs6941385, ^c rs1291073, ^d rs6723704, ^e rs79663593

Supplementary Table 10. Association results from meta-analysis in people with European ancestry

Variant	Gene	Braak NFT stage		Neocortical neuritic plaques		TDP-43 in any brain regions		Lewy bodies in any brain regions		Hippocampal sclerosis	
		OR	P-value	OR	P-value	OR	P-value	OR	P-value	OR	P-value
rs679515	<i>CRI</i>	1.24	3.8×10^{-4}	1.15	0.020	1.19	0.041	1.03	0.60	1.11	0.39
rs6733839	<i>BIN1</i>	1.30	2.6×10^{-8}	1.21	3.9×10^{-5}	1.05	0.41	1.16	0.0012	0.99	1.00
rs10933431	<i>INPP5D</i>	0.86	0.0094	0.88	0.021	0.90	0.20	1.07	0.22	0.87	0.21
rs6846529	<i>CLNK</i>	1.11	0.17	1.03	0.73	1.14	0.13	1.02	0.72	1.09	0.52
rs6605556	<i>HLA-DQA1</i>	0.89	0.086	0.90	0.13	0.98	0.85	0.98	0.76	0.81	0.082
rs10947943	<i>UNC5CL</i>	0.89	0.087	0.87	0.046	0.92	0.30	0.99	0.80	0.95	0.64
rs7767350	<i>CD2AP</i>	1.11	0.046	1.06	0.25	1.01	0.84	1.01	0.85	0.97	0.72
rs6966331	<i>EPDR1</i>	0.95	0.28	1.00	0.97	1.03	0.65	1.07	0.13	1.11	0.31
rs7384878	<i>SPDYE3</i>	0.88	0.013	0.88	0.015	1.00	0.97	1.01	0.81	0.94	0.50
rs11771145	<i>EPHA1</i>	0.92	0.11	0.97	0.59	1.00	0.98	1.01	0.79	1.07	0.46
rs73223431	<i>PTK2B</i>	1.11	0.030	1.13	0.0088	1.03	0.74	1.01	0.84	0.93	0.42
rs11787077	<i>CLU</i>	0.94	0.21	0.99	0.84	1.04	0.58	0.96	0.37	1.03	0.91
rs7912495	<i>USP6NL</i>	1.06	0.21	0.98	0.67	0.95	0.41	1.14	0.0043	1.13	0.15
rs10437655	<i>SPI1</i>	1.13	0.0064	1.07	0.15	0.98	0.74	1.03	0.54	1.00	0.86
rs1582763	<i>MS4A4A</i>	0.94	0.22	0.91	0.048	1.07	0.30	1.00	0.99	0.97	0.70
rs3851179	<i>EED</i>	0.88	0.0089	0.85	1.0E-03	1.06	0.39	0.95	0.30	1.00	0.96
rs74685827	<i>SORL1</i>	1.13	0.45	1.15	0.37	1.85	0.0042	1.02	0.86	1.81	0.017
rs11218343	<i>SORL1</i>	0.86	0.21	1.05	0.70	0.89	0.44	1.10	0.42	0.87	0.44
rs17125924	<i>FERMT2</i>	1.13	0.15	1.25	0.0047	1.04	0.64	0.99	0.88	1.14	0.37
rs7401792	<i>SLC24A4</i>	1.10	0.057	1.01	0.83	1.08	0.27	0.99	0.71	1.08	0.36
rs12590654	<i>SLC24A4</i>	0.94	0.22	1.01	0.89	1.14	0.047	0.98	0.61	1.18	0.072
rs8025980	<i>SPPL2A</i>	1.13	0.072	1.14	0.053	1.02	0.79	1.07	0.33	0.93	0.54
rs117618017	<i>APH1B</i>	1.17	0.022	1.23	0.0020	1.13	0.18	1.08	0.26	0.91	0.50
rs889555	<i>BCKDK</i>	0.96	0.44	1.01	0.89	0.95	0.52	0.97	0.52	0.88	0.18
rs4985556	<i>IL34</i>	1.02	0.81	0.92	0.25	0.96	0.64	1.14	0.086	0.86	0.21
rs12446759	<i>PLCG2</i>	0.92	0.084	0.96	0.33	1.00	0.97	0.95	0.35	0.96	0.65
rs7225151	<i>SCIMP</i>	1.08	0.31	1.06	0.39	1.13	0.20	1.15	0.066	1.36	0.0095

rs199515	<i>WNT3</i>	0.95	0.40	0.99	0.90	0.85	0.033	1.00	0.90	0.69	0.0014
rs4277405	<i>ACE</i>	1.07	0.13	0.98	0.69	0.94	0.29	1.00	0.97	1.25	0.0082
rs6014724	<i>CASS4</i>	0.96	0.71	0.87	0.11	1.15	0.22	0.96	0.65	1.14	0.52
rs2830489	<i>ADAMTS1</i>	0.99	0.86	1.02	0.73	0.91	0.15	1.00	0.99	0.86	0.10
rs72777026	<i>ADAM17</i>	1.07	0.29	1.17	0.015	1.07	0.48	1.13	0.062	0.93	0.54
rs17020490	<i>PRKD3</i>	0.98	0.78	1.01	0.93	1.12	0.21	0.99	0.87	1.13	0.30
rs139643391	<i>WDR12</i>	0.92	0.40	0.96	0.64	1.02	0.87	1.00	1.00	0.88	0.41
rs16824536	<i>MME</i>	0.70	9.8×10^{-4}	0.70	0.0011	0.95	0.57	0.98	0.88	0.94	0.58
rs2245466	<i>RHOH</i>	0.99	0.90	1.01	0.90	1.08	0.23	1.05	0.32	0.98	0.72
rs112403360	<i>ANKH</i>	1.16	0.081	1.11	0.24	0.79	0.045	1.00	0.96	0.87	0.42
rs62374257	<i>COX7C</i>	1.20	0.0011	1.05	0.34	1.12	0.17	0.95	0.42	0.91	0.35
rs871269	<i>TNIP1</i>	0.96	0.40	0.99	0.87	0.91	0.13	0.99	0.91	0.75	0.0018
rs113706587	<i>RASGEF1C</i>	1.09	0.25	1.04	0.66	1.08	0.43	1.02	0.78	1.18	0.31
rs785129	<i>HS3ST5</i>	1.01	0.83	0.94	0.17	0.95	0.43	1.05	0.28	1.13	0.17
rs13237518	<i>TMEM106B</i>	1.12	0.013	0.99	0.84	0.78	1.0×10^{-4}	1.11	0.019	0.64	9.3×10^{-7}
rs76928645	<i>SEC61G</i>	0.99	0.94	1.00	0.96	1.05	0.62	1.06	0.50	0.98	0.73
rs7068231	<i>ANK3</i>	0.96	0.37	1.02	0.71	0.97	0.63	0.95	0.24	0.95	0.55
rs6584063	<i>BLNK</i>	1.11	0.37	0.95	0.74	1.13	0.42	1.08	0.57	0.91	0.62
rs6489896	<i>TPCN1</i>	1.12	0.21	1.08	0.44	1.42	0.0071	1.06	0.51	1.20	0.30
rs10131280	<i>IGH</i> gene cluster	0.96	0.58	1.00	0.96	0.82	0.041	0.91	0.20	0.82	0.16
rs3848143	<i>SNX1</i>	1.06	0.25	1.14	0.021	1.10	0.22	0.96	0.46	1.09	0.44
rs12592898	<i>CTSH</i>	0.89	0.079	0.91	0.16	0.91	0.31	0.95	0.46	1.05	0.87
rs16941239	<i>FOXF1</i>	0.98	0.87	0.92	0.54	1.31	0.17	1.02	0.97	1.29	0.31
rs2242595	<i>MYO15A</i>	0.85	0.032	0.90	0.14	1.07	0.44	0.83	0.012	1.04	0.90
rs5848	<i>GRN</i>	0.95	0.31	0.97	0.56	1.22	0.0049	1.01	0.80	1.53	2.1×10^{-6}
rs9304690	<i>SIGLEC11</i>	0.98	0.76	0.99	0.83	1.02	0.92	0.98	0.69	0.89	0.26
rs1358782	<i>RBCK1</i>	0.88	0.021	0.85	0.0023	0.98	0.76	1.02	0.80	0.92	0.38
rs6742	<i>SLC2A4RG</i>	1.04	0.51	1.04	0.47	1.13	0.099	1.01	0.80	1.04	0.70

NFT = neurofibrillary tangle; TDP-43 = TAR DNA binding protein 43 kDa

Supplementary Table 11. Association with Braak neurofibrillary tangle stage in people with other ancestries

Variant	Gene	Effect allele	ADRC			
			ADSP WGS (n = 140)		ADGC (n = 134)	
			OR	P-value	OR	P-value
rs679515	<i>CRI</i>	T	1.23	0.73	0.66	0.43
rs6733839	<i>BINI</i>	T	1.52	0.15	1.47	0.17
rs10933431	<i>INPP5D</i>	G	0.74	0.26	1.38	0.24
rs6846529	<i>CLNK</i>	C	0.48	0.0066	-	-
rs6605556	<i>HLA-DQA1</i>	G	-	-	0.56	0.12
rs10947943	<i>UNC5CL</i>	A	1.61	0.53	0.82	0.63
rs143332484	<i>TREM2</i>	T	-	-	-	-
rs75932628	<i>TREM2</i>	T	-	-	-	-
rs60755019	<i>TREML2</i>	G	1.08	0.82	1.14	0.80
rs7767350	<i>CD2AP</i>	T	1.72	0.12	1.03	0.92
rs6966331	<i>EPDR1</i>	T	1.15	0.63	0.71	0.25
rs7384878	<i>SPDYE3</i>	C	1.26	0.55	0.67	0.22
rs11771145	<i>EPHA1</i>	A	0.85	0.53	1.11	0.69
rs73223431	<i>PTK2B</i>	T	0.90	0.72	1.37	0.26
rs11787077	<i>CLU</i>	T	1.11	0.69	1.02	0.95
rs7912495	<i>USP6NL</i>	G	1.45	0.20	1.50	0.13
rs10437655	<i>SPI1</i>	A	1.09	0.77	1.14	0.64
rs1582763	<i>MS4A4A</i>	A	1.57	0.30	1.00	1.00
rs3851179	<i>EED</i>	T	0.73	0.36	1.67	0.099
rs74685827	<i>SORL1</i>	G	1.80	0.62	2.13	0.59
rs11218343	<i>SORL1</i>	C	1.19	0.74	0.74	0.57
rs17125924	<i>FERMT2</i>	G	0.99	0.99	0.82	0.66
rs7401792	<i>SLC24A4</i>	G	0.63	0.15	1.10	0.74
rs12590654	<i>SLC24A4</i>	A	1.08	0.80	0.74	0.30
rs8025980	<i>SPPL2A</i>	G	1.71	0.058	-	-
rs602602	<i>MINDY2</i>	A	-	-	1.81	0.037
rs117618017	<i>APH1B</i>	T	1.63	0.57	2.22	0.16
rs889555	<i>BCKDK</i>	T	0.91	0.72	1.23	0.47
rs4985556	<i>IL34</i>	A	0.58	0.38	0.91	0.87
rs12446759	<i>PLCG2</i>	G	0.92	0.79	1.38	0.25
rs72824905	<i>PLCG2</i>	G	-	-	-	-
rs7225151	<i>SCIMP</i>	A	0.86	0.67	0.44	0.057
rs199515	<i>WNT3</i>	G	0.97	0.93	1.21	0.66
rs616338	<i>ABI3</i>	T	-	-	-	-
rs2526377	<i>TSPOAP1</i>	G	-	-	-	-
rs4277405	<i>ACE</i>	C	1.39	0.23	0.57	0.065
rs12151021	<i>ABCA7</i>	A	1.88	0.024	1.52	0.13
rs6014724	<i>CASS4</i>	G	1.21	0.69	0.91	0.79
rs2830489	<i>ADAMTS1</i>	T	1.32	0.59	0.85	0.70
rs141749679	<i>SORT1</i>	C	-	-	-	-

rs72777026	<i>ADAM17</i>	G	1.46	0.22	0.98	0.95
rs17020490	<i>PRKD3</i>	C	1.47	0.28	0.97	0.93
rs143080277	<i>NCK2</i>	C	0.65	0.77	-	-
rs139643391	<i>WDR12</i>	T	3.31	0.17	1.08	0.92 ^a
rs16824536	<i>MME</i>	A	0.48	0.014	0.71	0.43
rs61762319	<i>MME</i>	G	0.65	0.77	-	-
rs3822030	<i>IDUA</i>	G	-	-	-	-
rs2245466	<i>RHOH</i>	G	1.43	0.27	1.57	0.11
rs112403360	<i>ANKH</i>	A	2.03	0.20	2.08	0.21
rs62374257	<i>COX7C</i>	C	1.17	0.77	1.59	0.17
rs871269	<i>TNIP1</i>	T	0.70	0.22	0.81	0.45
rs113706587	<i>RASGEF1C</i>	A	1.68	0.41	0.95	0.92
rs785129	<i>HS3ST5</i>	T	0.95	0.87	0.64	0.11
rs6943429	<i>UMAD1</i>	T	1.08	0.79	1.16	0.55
rs10952097	<i>ICAI</i>	T	1.86	0.050	0.93	0.81
rs13237518	<i>TMEM106B</i>	A	1.28	0.38	0.89	0.67
rs1160871	<i>JAZF1</i>	G	0.59	0.092	-	-
rs76928645	<i>SEC61G</i>	T	1.93	0.60	1.09	0.88
rs1065712	<i>CTSB</i>	C	-	-	-	-
rs34173062	<i>SHARPIN</i>	A	-	-	0.44	0.29
rs1800978	<i>ABCA1</i>	G	-	-	-	-
rs7068231	<i>ANK3</i>	T	0.69	0.23	0.75	0.29
rs6586028	<i>TSPAN14</i>	C	-	-	0.39	0.055
rs6584063	<i>BLNK</i>	G	1.45	0.66	0.73	0.61
rs7908662	<i>PLEKHA1</i>	G	0.57	0.050	1.06	0.82
rs6489896	<i>TPCN1</i>	C	0.71	0.33	1.25	0.54
rs7157106	<i>IGH</i> gene cluster	A	-	-	1.42	0.24
rs10131280	<i>IGH</i> gene cluster	A	1.04	0.92	1.14	0.73
rs3848143	<i>SNX1</i>	G	0.99	0.97	1.61	0.10
rs12592898	<i>CTSH</i>	A	0.53	0.041	0.84	0.69
rs1140239	<i>DOC2A</i>	T	1.00	0.99	1.23	0.47
rs450674	<i>MAF</i>	C	-	-	0.84	0.59
rs16941239	<i>FOXF1</i>	A	0.62	0.16	1.17	0.70
rs56407236	<i>PRDM7</i>	A	-	-	1.90	0.34
rs35048651	<i>WDR81</i>	T	1.70	0.19	-	-
rs2242595	<i>MYO15A</i>	A	0.73	0.42	0.90	0.76
rs5848	<i>GRN</i>	T	0.85	0.60	1.57	0.16
rs149080927	<i>KLF16</i>	G	0.59	0.18	-	-
rs9304690	<i>SIGLEC11</i>	T	0.87	0.70	2.13	0.036
rs587709	<i>LILRB2</i>	C	-	-	0.95	0.86
rs1358782	<i>RBCK1</i>	A	0.75	0.40	0.44	0.023
rs6742	<i>SLC2A4RG</i>	T	1.12	0.73	0.85	0.63
rs2154481	<i>APP</i>	C	-	-	1.23	0.51

^a OR and P-value were computed by the proxy (rs72934704) which was in perfect linkage disequilibrium block (i.e., $r^2 = 1$ and $D' = 1$)

Supplementary Table 12. Association with neocortical neuritic plaques in people with other ancestries

Variant	Gene	Effect allele	ADRC			
			ADSP WGS (n = 140)		ADGC (n = 134)	
			OR	P-value	OR	P-value
rs679515	<i>CR1</i>	T	0.56	0.29	0.52	0.23
rs6733839	<i>BIN1</i>	T	1.72	0.059	1.77	0.048
rs10933431	<i>INPP5D</i>	G	0.67	0.13	1.44	0.21
rs6846529	<i>CLNK</i>	C	0.64	0.091	-	-
rs6605556	<i>HLA-DQA1</i>	G	-	-	1.00	0.99
rs10947943	<i>UNC5CL</i>	A	0.75	0.67	1.23	0.62
rs143332484	<i>TREM2</i>	T	-	-	-	-
rs75932628	<i>TREM2</i>	T	-	-	-	-
rs60755019	<i>TREML2</i>	G	0.99	0.98	0.73	0.56
rs7767350	<i>CD2AP</i>	T	1.22	0.54	1.31	0.39
rs6966331	<i>EPDR1</i>	T	1.05	0.87	0.90	0.73
rs7384878	<i>SPDYE3</i>	C	1.45	0.35	0.90	0.76
rs11771145	<i>EPHA1</i>	A	1.08	0.77	1.25	0.40
rs73223431	<i>PTK2B</i>	T	1.13	0.68	1.89	0.033
rs11787077	<i>CLU</i>	T	1.09	0.74	0.81	0.48
rs7912495	<i>USP6NL</i>	G	1.29	0.37	1.46	0.16
rs10437655	<i>SPI1</i>	A	0.91	0.75	1.08	0.80
rs1582763	<i>MS4A4A</i>	A	1.38	0.44	1.38	0.41
rs3851179	<i>EED</i>	T	0.69	0.28	1.50	0.19
rs74685827	<i>SORL1</i>	G	2.30	0.49	3.27	0.43
rs11218343	<i>SORL1</i>	C	1.02	0.98	0.27	0.047
rs17125924	<i>FERMT2</i>	G	1.23	0.71	1.54	0.36
rs7401792	<i>SLC24A4</i>	G	0.79	0.41	1.32	0.35
rs12590654	<i>SLC24A4</i>	A	1.28	0.38	0.75	0.32
rs8025980	<i>SPPL2A</i>	G	1.05	0.84	-	-
rs602602	<i>MINDY2</i>	A	-	-	1.48	0.16
rs117618017	<i>APH1B</i>	T	1.70	0.54	2.07	0.17
rs889555	<i>BCKDK</i>	T	0.92	0.76	1.07	0.83
rs4985556	<i>IL34</i>	A	0.46	0.22	0.86	0.81
rs12446759	<i>PLCG2</i>	G	1.02	0.95	0.94	0.82
rs72824905	<i>PLCG2</i>	G	-	-	-	-
rs7225151	<i>SCIMP</i>	A	1.19	0.61	0.36	0.029
rs199515	<i>WNT3</i>	G	1.04	0.91	2.00	0.12
rs616338	<i>ABI3</i>	T	-	-	-	-
rs2526377	<i>TSPOAP1</i>	G	-	-	-	-
rs4277405	<i>ACE</i>	C	1.28	0.36	0.89	0.71
rs12151021	<i>ABCA7</i>	A	1.61	0.076	1.87	0.025
rs6014724	<i>CASS4</i>	G	1.11	0.82	1.25	0.56
rs2830489	<i>ADAMTS1</i>	T	1.29	0.62	0.92	0.85
rs141749679	<i>SORT1</i>	C	-	-	-	-

rs72777026	<i>ADAM17</i>	G	1.48	0.20	1.13	0.72
rs17020490	<i>PRKD3</i>	C	1.35	0.38	0.83	0.57
rs143080277	<i>NCK2</i>	C	-	-	-	-
rs139643391	<i>WDR12</i>	T	3.05	0.20	0.50	0.35 ^a
rs16824536	<i>MME</i>	A	0.83	0.53	0.78	0.57
rs61762319	<i>MME</i>	G	0.83	0.90	-	-
rs3822030	<i>IDUA</i>	G	-	-	-	-
rs2245466	<i>RHOH</i>	G	0.87	0.64	1.11	0.70
rs112403360	<i>ANKH</i>	A	1.55	0.40	1.11	0.85
rs62374257	<i>COX7C</i>	C	1.21	0.73	1.51	0.23
rs871269	<i>TNIP1</i>	T	1.04	0.89	0.81	0.46
rs113706587	<i>RASGEF1C</i>	A	1.90	0.31	0.93	0.88
rs785129	<i>HS3ST5</i>	T	1.00	0.99	0.78	0.37
rs6943429	<i>UMAD1</i>	T	1.30	0.34	1.02	0.93
rs10952097	<i>ICA1</i>	T	1.28	0.41	0.82	0.53
rs13237518	<i>TMEM106B</i>	A	0.85	0.58	1.55	0.12
rs1160871	<i>JAZF1</i>	G	0.93	0.79	-	-
rs76928645	<i>SEC61G</i>	T	2.22	0.52	1.66	0.38
rs1065712	<i>CTSB</i>	C	-	-	-	-
rs34173062	<i>SHARPIN</i>	A	-	-	1.02	0.98
rs1800978	<i>ABCA1</i>	G	-	-	-	-
rs7068231	<i>ANK3</i>	T	0.60	0.093	0.58	0.059
rs6586028	<i>TSPAN14</i>	C	-	-	0.96	0.93
rs6584063	<i>BLNK</i>	G	3.81	0.22	0.30	0.13
rs7908662	<i>PLEKHA1</i>	G	0.84	0.53	0.73	0.26
rs6489896	<i>TPCN1</i>	C	1.18	0.64	1.61	0.20
rs7157106	<i>IGH</i> gene cluster	A	-	-	0.76	0.36
rs10131280	<i>IGH</i> gene cluster	A	1.08	0.82	0.92	0.82
rs3848143	<i>SNX1</i>	G	0.72	0.24	1.35	0.30
rs12592898	<i>CTSH</i>	A	0.82	0.51	1.71	0.23
rs1140239	<i>DOC2A</i>	T	1.13	0.69	1.11	0.71
rs450674	<i>MAF</i>	C	-	-	0.82	0.55
rs16941239	<i>FOXF1</i>	A	0.80	0.50	0.83	0.66
rs56407236	<i>PRDM7</i>	A	-	-	5.15	0.026
rs35048651	<i>WDR81</i>	T	1.68	0.19	-	-
rs2242595	<i>MYO15A</i>	A	0.77	0.52	1.73	0.13
rs5848	<i>GRN</i>	T	0.82	0.50	1.66	0.13
rs149080927	<i>KLF16</i>	G	0.85	0.66	-	-
rs9304690	<i>SIGLEC11</i>	T	0.86	0.67	1.53	0.23
rs587709	<i>LILRB2</i>	C	-	-	1.01	0.97
rs1358782	<i>RBCK1</i>	A	0.89	0.73	0.46	0.043
rs6742	<i>SLC2A4RG</i>	T	1.24	0.50	1.05	0.90
rs2154481	<i>APP</i>	C	-	-	1.14	0.68

^a OR and P-value were computed by the proxy (rs72934704) which was in perfect linkage disequilibrium block (i.e., $r^2 = 1$ and $D' = 1$)

Supplementary Table 13. Association with TDP-43 in any brain regions in people with other ancestries

Variant	Gene	Effect allele	ADRC			
			ADSP WGS (n = 140)		ADGC (n = 134)	
			OR	P-value	OR	P-value
rs679515	<i>CRI</i>	T	1.28	0.91	0.89	0.93
rs6733839	<i>BIN1</i>	T	0.55	0.25	2.14	0.11
rs10933431	<i>INPP5D</i>	G	1.04	0.94	1.20	0.70
rs6846529	<i>CLNK</i>	C	0.46	0.18	-	-
rs6605556	<i>HLA-DQA1</i>	G	-	-	0.58	0.42
rs10947943	<i>UNC5CL</i>	A	-	-	1.89	0.37
rs143332484	<i>TREM2</i>	T	-	-	-	-
rs75932628	<i>TREM2</i>	T	-	-	-	-
rs60755019	<i>TREML2</i>	G	0.73	0.56	0.69	0.65
rs7767350	<i>CD2AP</i>	T	0.78	0.67	3.71	0.044
rs6966331	<i>EPDR1</i>	T	0.76	0.61	0.58	0.42
rs7384878	<i>SPDYE3</i>	C	0.87	0.84	0.82	0.72
rs11771145	<i>EPHA1</i>	A	0.61	0.35	2.50	0.071
rs73223431	<i>PTK2B</i>	T	1.31	0.63	0.71	0.50
rs11787077	<i>CLU</i>	T	0.89	0.81	1.01	0.98
rs7912495	<i>USP6NL</i>	G	0.91	0.88	0.75	0.58
rs10437655	<i>SPI1</i>	A	1.03	0.96	0.87	0.79
rs1582763	<i>MS4A4A</i>	A	0.09	0.16	0.90	0.89
rs3851179	<i>EED</i>	T	1.30	0.67	0.43	0.14
rs74685827	<i>SORL1</i>	G	-	-	-	-
rs11218343	<i>SORL1</i>	C	0.63	0.61	0.36	0.31
rs17125924	<i>FERMT2</i>	G	1.56	0.64	0.53	0.47
rs7401792	<i>SLC24A4</i>	G	1.13	0.81	0.75	0.60
rs12590654	<i>SLC24A4</i>	A	0.65	0.42	0.47	0.14
rs8025980	<i>SPPL2A</i>	G	1.56	0.35	-	-
rs602602	<i>MINDY2</i>	A	-	-	0.78	0.62
rs117618017	<i>APH1B</i>	T	1.93	0.67	1.14	0.88
rs889555	<i>BCKDK</i>	T	2.45	0.083	1.61	0.34
rs4985556	<i>IL34</i>	A	0.64	0.73	1.23	0.84
rs12446759	<i>PLCG2</i>	G	0.13	0.0031	0.58	0.28
rs72824905	<i>PLCG2</i>	G	-	-	-	-
rs7225151	<i>SCIMP</i>	A	1.93	0.26	0.67	0.64
rs199515	<i>WNT3</i>	G	1.13	0.84	0.88	0.87
rs616338	<i>ABI3</i>	T	-	-	-	-
rs2526377	<i>TSPOAP1</i>	G	-	-	-	-
rs4277405	<i>ACE</i>	C	0.33	0.026	1.12	0.83
rs12151021	<i>ABCA7</i>	A	1.27	0.59	0.57	0.23
rs6014724	<i>CASS4</i>	G	0.01	0.11	1.58	0.48
rs2830489	<i>ADAMTS1</i>	T	1.21	0.90	1.93	0.36
rs141749679	<i>SORT1</i>	C	-	-	-	-

rs72777026	<i>ADAM17</i>	G	0.89	0.82	0.58	0.30
rs17020490	<i>PRKD3</i>	C	0.68	0.59	2.50	0.15
rs143080277	<i>NCK2</i>	C	-	-	-	-
rs139643391	<i>WDR12</i>	T	-	-	0.83 ^a	0.89
rs16824536	<i>MME</i>	A	0.85	0.76	0.36	0.15
rs61762319	<i>MME</i>	G	-	-	-	-
rs3822030	<i>IDUA</i>	G	-	-	-	-
rs2245466	<i>RHOH</i>	G	2.03	0.21	1.48	0.39
rs112403360	<i>ANKH</i>	A	0.28	0.24	6.92	0.041
rs62374257	<i>COX7C</i>	C	0.36	0.33	1.10	0.86
rs871269	<i>TNIP1</i>	T	0.43	0.17	1.00	0.99
rs113706587	<i>RASGEF1C</i>	A	0.94	0.96	1.32	0.76
rs785129	<i>HS3ST5</i>	T	0.94	0.91	1.12	0.81
rs6943429	<i>UMAD1</i>	T	2.81	0.074	0.88	0.79
rs10952097	<i>ICAI</i>	T	0.90	0.84	0.76	0.61
rs13237518	<i>TMEM106B</i>	A	1.02	0.97	1.05	0.92
rs1160871	<i>JAZF1</i>	G	0.23	0.018	-	-
rs76928645	<i>SEC61G</i>	T	-	-	-	-
rs1065712	<i>CTSB</i>	C	-	-	-	-
rs34173062	<i>SHARPIN</i>	A	-	-	3.07	0.47
rs1800978	<i>ABCA1</i>	G	-	-	-	-
rs7068231	<i>ANK3</i>	T	0.75	0.67	1.24	0.63
rs6586028	<i>TSPAN14</i>	C	-	-	0.52	0.46
rs6584063	<i>BLNK</i>	G	1.13	0.93	0.86	0.86
rs7908662	<i>PLEKHA1</i>	G	0.91	0.87	0.46	0.11
rs6489896	<i>TPCN1</i>	C	0.92	0.91	0.37	0.23
rs7157106	<i>IGH</i> gene cluster	A	-	-	1.50	0.46
rs10131280	<i>IGH</i> gene cluster	A	0.52	0.36	3.21	0.10
rs3848143	<i>SNX1</i>	G	1.09	0.85	2.12	0.12
rs12592898	<i>CTSH</i>	A	0.79	0.66	0.49	0.36
rs1140239	<i>DOC2A</i>	T	0.96	0.95	1.04	0.94
rs450674	<i>MAF</i>	C	-	-	0.60	0.36
rs16941239	<i>FOXF1</i>	A	0.55	0.34	1.46	0.50
rs56407236	<i>PRDM7</i>	A	-	-	5.56	0.074
rs35048651	<i>WDR81</i>	T	0.89	0.88	-	-
rs2242595	<i>MYO15A</i>	A	2.63	0.21	1.64	0.42
rs5848	<i>GRN</i>	T	1.47	0.48	2.36	0.14
rs149080927	<i>KLF16</i>	G	0.41	0.24	-	-
rs9304690	<i>SIGLEC11</i>	T	0.69	0.60	2.37	0.18
rs587709	<i>LILRB2</i>	C	-	-	2.33	0.14
rs1358782	<i>RBCK1</i>	A	0.68	0.63	0.90	0.85
rs6742	<i>SLC2A4RG</i>	T	1.02	0.97	2.44	0.12
rs2154481	<i>APP</i>	C	-	-	1.56	0.44

^a OR and P-value were computed by the proxy (rs72934704) which was in perfect linkage disequilibrium block (i.e., $r^2 = 1$ and $D' = 1$)

Supplementary Table 14. Association with Lewy bodies in any brain regions in people with other ancestries

Variant	Gene	Effect allele	ADRC			
			ADSP WGS (n = 140)		ADGC (n = 134)	
			OR	P-value	OR	P-value
rs679515	<i>CR1</i>	T	2.45	0.11	0.84	0.76
rs6733839	<i>BIN1</i>	T	1.63	0.071	1.56	0.14
rs10933431	<i>INPP5D</i>	G	1.07	0.78	1.01	0.97
rs6846529	<i>CLNK</i>	C	1.08	0.77	-	-
rs6605556	<i>HLA-DQA1</i>	G	-	-	0.91	0.81
rs10947943	<i>UNC5CL</i>	A	1.61	0.47	1.90	0.14
rs143332484	<i>TREM2</i>	T	-	-	-	-
rs75932628	<i>TREM2</i>	T	-	-	-	-
rs60755019	<i>TREML2</i>	G	1.45	0.22	1.46	0.47
rs7767350	<i>CD2AP</i>	T	1.75	0.072	0.92	0.81
rs6966331	<i>EPDR1</i>	T	0.65	0.12	1.19	0.60
rs7384878	<i>SPDYE3</i>	C	1.17	0.67	1.00	0.99
rs11771145	<i>EPHA1</i>	A	1.11	0.66	1.48	0.17
rs73223431	<i>PTK2B</i>	T	0.99	0.96	0.88	0.67
rs11787077	<i>CLU</i>	T	0.85	0.52	0.76	0.38
rs7912495	<i>USP6NL</i>	G	1.40	0.21	0.75	0.31
rs10437655	<i>SPI1</i>	A	1.48	0.16	1.02	0.95
rs1582763	<i>MS4A4A</i>	A	0.57	0.17	0.33	0.017
rs3851179	<i>EED</i>	T	0.50	0.060	1.12	0.72
rs74685827	<i>SORL1</i>	G	1.25	0.83	8.87	0.13
rs11218343	<i>SORL1</i>	C	0.64	0.37	0.55	0.34
rs17125924	<i>FERMT2</i>	G	1.10	0.85	1.04	0.94
rs7401792	<i>SLC24A4</i>	G	1.43	0.20	1.20	0.57
rs12590654	<i>SLC24A4</i>	A	0.96	0.87	0.89	0.71
rs8025980	<i>SPPL2A</i>	G	0.44	0.0026	-	-
rs602602	<i>MINDY2</i>	A	-	-	1.17	0.59
rs117618017	<i>APH1B</i>	T	0.74	0.69	1.50	0.42
rs889555	<i>BCKDK</i>	T	1.28	0.32	0.69	0.24
rs4985556	<i>IL34</i>	A	0.32	0.11	0.96	0.95
rs12446759	<i>PLCG2</i>	G	0.94	0.82	1.02	0.96
rs72824905	<i>PLCG2</i>	G	-	-	-	-
rs7225151	<i>SCIMP</i>	A	0.92	0.80	0.68	0.40
rs199515	<i>WNT3</i>	G	1.39	0.34	0.93	0.87
rs616338	<i>ABI3</i>	T	-	-	-	-
rs2526377	<i>TSPOAP1</i>	G	-	-	-	-
rs4277405	<i>ACE</i>	C	0.92	0.75	1.08	0.81
rs12151021	<i>ABCA7</i>	A	1.49	0.11	1.35	0.28
rs6014724	<i>CASS4</i>	G	1.34	0.49	0.81	0.61
rs2830489	<i>ADAMTS1</i>	T	0.81	0.67	0.52	0.18
rs141749679	<i>SORT1</i>	C	-	-	-	-

rs72777026	<i>ADAM17</i>	G	0.93	0.81	1.14	0.70
rs17020490	<i>PRKD3</i>	C	0.90	0.74	1.07	0.84
rs143080277	<i>NCK2</i>	C	-	-	-	-
rs139643391	<i>WDR12</i>	T	0.53	0.39	2.11	0.27 ^a
rs16824536	<i>MME</i>	A	1.00	0.99	1.51	0.34
rs61762319	<i>MME</i>	G	1.13	0.93	-	-
rs3822030	<i>IDUA</i>	G	-	-	-	-
rs2245466	<i>RHOH</i>	G	1.34	0.31	1.17	0.59
rs112403360	<i>ANKH</i>	A	0.58	0.27	1.76	0.31
rs62374257	<i>COX7C</i>	C	0.71	0.51	1.61	0.16
rs871269	<i>TNIP1</i>	T	0.95	0.85	0.81	0.48
rs113706587	<i>RASGEF1C</i>	A	0.89	0.83	1.44	0.47
rs785129	<i>HS3ST5</i>	T	1.38	0.24	0.87	0.65
rs6943429	<i>UMAD1</i>	T	1.16	0.57	1.51	0.15
rs10952097	<i>ICAI</i>	T	1.21	0.52	1.54	0.20
rs13237518	<i>TMEM106B</i>	A	1.07	0.81	1.42	0.23
rs1160871	<i>JAZF1</i>	G	0.46	0.0061	-	-
rs76928645	<i>SEC61G</i>	T	1.39	0.76	2.31	0.17
rs1065712	<i>CTSB</i>	C	-	-	-	-
rs34173062	<i>SHARPIN</i>	A	-	-	0.56	0.51
rs1800978	<i>ABCA1</i>	G	-	-	-	-
rs7068231	<i>ANK3</i>	T	1.12	0.69	0.48	0.017
rs6586028	<i>TSPAN14</i>	C	-	-	1.22	0.69
rs6584063	<i>BLNK</i>	G	3.59	0.14	1.46	0.54
rs7908662	<i>PLEKHA1</i>	G	1.02	0.93	1.08	0.78
rs6489896	<i>TPCN1</i>	C	1.83	0.074	0.94	0.87
rs7157106	<i>IGH</i> gene cluster	A	-	-	1.33	0.37
rs10131280	<i>IGH</i> gene cluster	A	1.47	0.22	0.73	0.45
rs3848143	<i>SNX1</i>	G	1.11	0.69	1.49	0.19
rs12592898	<i>CTSH</i>	A	0.63	0.13	0.94	0.90
rs1140239	<i>DOC2A</i>	T	1.02	0.96	1.43	0.23
rs450674	<i>MAF</i>	C	-	-	0.70	0.33
rs16941239	<i>FOXF1</i>	A	0.62	0.16	2.15	0.074
rs56407236	<i>PRDM7</i>	A	-	-	2.24	0.22
rs35048651	<i>WDR81</i>	T	1.34	0.42	-	-
rs2242595	<i>MYO15A</i>	A	0.74	0.43	1.99	0.067
rs5848	<i>GRN</i>	T	0.77	0.35	1.62	0.16
rs149080927	<i>KLF16</i>	G	0.88	0.71	-	-
rs9304690	<i>SIGLEC11</i>	T	0.52	0.077	2.21	0.029
rs587709	<i>LILRB2</i>	C	-	-	0.71	0.28
rs1358782	<i>RBCK1</i>	A	1.23	0.53	0.85	0.65
rs6742	<i>SLC2A4RG</i>	T	0.71	0.26	1.25	0.55
rs2154481	<i>APP</i>	C	-	-	0.50	0.037

^a OR and P-value were computed by the proxy (rs72934704) which was in perfect linkage disequilibrium block (i.e., $r^2 = 1$ and $D' = 1$)

Supplementary Table 15. Association with hippocampal sclerosis in people with other ancestries

Variant	Gene	Effect allele	ADRC			
			ADSP WGS (n = 140)		ADGC (n = 134)	
			OR	P-value	OR	P-value
rs679515	<i>CR1</i>	T	2.12	0.59	0.48	0.54
rs6733839	<i>BIN1</i>	T	1.25	0.71	1.64	0.25
rs10933431	<i>INPP5D</i>	G	0.71	0.52	0.78	0.58
rs6846529	<i>CLNK</i>	C	3.77	0.042	-	-
rs6605556	<i>HLA-DQA1</i>	G	-	-	0.58	0.42
rs10947943	<i>UNC5CL</i>	A	-	-	2.94	0.069
rs143332484	<i>TREM2</i>	T	-	-	-	-
rs75932628	<i>TREM2</i>	T	-	-	-	-
rs60755019	<i>TREML2</i>	G	-	-	2.24	0.32
rs7767350	<i>CD2AP</i>	T	3.39	0.084	0.87	0.80
rs6966331	<i>EPDR1</i>	T	0.69	0.50	1.38	0.52
rs7384878	<i>SPDYE3</i>	C	0.50	0.41	0.37	0.10
rs11771145	<i>EPHA1</i>	A	1.19	0.74	1.20	0.68
rs73223431	<i>PTK2B</i>	T	0.49	0.36	0.60	0.31
rs11787077	<i>CLU</i>	T	5.24	0.020	2.00	0.16
rs7912495	<i>USP6NL</i>	G	0.41	0.20	1.25	0.63
rs10437655	<i>SPI1</i>	A	0.24	0.086	1.28	0.61
rs1582763	<i>MS4A4A</i>	A	0.33	0.34	4.32	0.014
rs3851179	<i>EED</i>	T	1.44	0.58	0.63	0.36
rs74685827	<i>SORL1</i>	G	-	-	1.66	0.73
rs11218343	<i>SORL1</i>	C	17.34	0.0046	0.40	0.32
rs17125924	<i>FERMT2</i>	G	2.86	0.30	1.02	0.98
rs7401792	<i>SLC24A4</i>	G	0.68	0.50	1.03	0.94
rs12590654	<i>SLC24A4</i>	A	-	-	0.78	0.59
rs8025980	<i>SPPL2A</i>	G	0.75	0.61	-	-
rs602602	<i>MINDY2</i>	A	-	-	1.05	0.92
rs117618017	<i>APH1B</i>	T	-	-	0.40	0.43
rs889555	<i>BCKDK</i>	T	1.06	0.91	1.26	0.65
rs4985556	<i>IL34</i>	A	1.40	0.79	1.27	0.78
rs12446759	<i>PLCG2</i>	G	0.83	0.76	0.43	0.077
rs72824905	<i>PLCG2</i>	G	-	-	-	-
rs7225151	<i>SCIMP</i>	A	1.92	0.27	0.79	0.76
rs199515	<i>WNT3</i>	G	0.91	0.89	1.16	0.83
rs616338	<i>ABI3</i>	T	-	-	-	-
rs2526377	<i>TSPOAP1</i>	G	-	-	-	-
rs4277405	<i>ACE</i>	C	0.62	0.36	1.72	0.31
rs12151021	<i>ABCA7</i>	A	1.43	0.49	1.75	0.19
rs6014724	<i>CASS4</i>	G	1.40	0.71	1.24	0.72
rs2830489	<i>ADAMTS1</i>	T	4.66	0.15	1.77	0.39
rs141749679	<i>SORT1</i>	C	-	-	-	-

rs72777026	<i>ADAM17</i>	G	0.54	0.35	0.43	0.17
rs17020490	<i>PRKD3</i>	C	0.40	0.31	1.96	0.20
rs143080277	<i>NCK2</i>	C	-	-	-	-
rs139643391	<i>WDR12</i>	T	-	-	0.62	0.71 ^a
rs16824536	<i>MME</i>	A	0.54	0.39	0.59	0.45
rs61762319	<i>MME</i>	G	-	-	-	-
rs3822030	<i>IDUA</i>	G	-	-	-	-
rs2245466	<i>RHOH</i>	G	2.38	0.17	0.48	0.12
rs112403360	<i>ANKH</i>	A	1.87	0.51	13.25	0.0014
rs62374257	<i>COX7C</i>	C	0.76	0.82	0.92	0.88
rs871269	<i>TNIP1</i>	T	1.05	0.94	0.50	0.16
rs113706587	<i>RASGEF1C</i>	A	1.43	0.71	3.53	0.11
rs785129	<i>HS3ST5</i>	T	0.86	0.79	0.50	0.14
rs6943429	<i>UMAD1</i>	T	0.62	0.45	1.75	0.22
rs10952097	<i>ICA1</i>	T	0.63	0.44	0.75	0.53
rs13237518	<i>TMEM106B</i>	A	3.83	0.075	1.25	0.65
rs1160871	<i>JAZF1</i>	G	-	-	-	-
rs76928645	<i>SEC61G</i>	T	-	-	-	-
rs1065712	<i>CTSB</i>	C	-	-	-	-
rs34173062	<i>SHARPIN</i>	A	-	-	-	-
rs1800978	<i>ABCA1</i>	G	-	-	-	-
rs7068231	<i>ANK3</i>	T	1.11	0.88	0.89	0.80
rs6586028	<i>TSPAN14</i>	C	-	-	0.42	0.44
rs6584063	<i>BLNK</i>	G	3.81	0.34	0.36	0.38
rs7908662	<i>PLEKHA1</i>	G	1.37	0.62	0.78	0.56
rs6489896	<i>TPCN1</i>	C	1.10	0.89	0.97	0.96
rs7157106	<i>IGH</i> gene cluster	A	-	-	2.39	0.13
rs10131280	<i>IGH</i> gene cluster	A	0.35	0.21	0.78	0.71
rs3848143	<i>SNX1</i>	G	0.59	0.33	2.21	0.093
rs12592898	<i>CTSH</i>	A	0.40	0.22	1.47	0.54
rs1140239	<i>DOC2A</i>	T	1.24	0.77	2.00	0.10
rs450674	<i>MAF</i>	C	-	-	0.99	0.98
rs16941239	<i>FOXF1</i>	A	0.97	0.97	1.12	0.86
rs56407236	<i>PRDM7</i>	A	-	-	2.36	0.36
rs35048651	<i>WDR81</i>	T	-	-	-	-
rs2242595	<i>MYO15A</i>	A	2.18	0.38	0.92	0.88
rs5848	<i>GRN</i>	T	1.94	0.30	1.48	0.47
rs149080927	<i>KLF16</i>	G	0.25	0.082	-	-
rs9304690	<i>SIGLEC11</i>	T	1.17	0.83	1.71	0.35
rs587709	<i>LILRB2</i>	C	-	-	0.92	0.85
rs1358782	<i>RBCK1</i>	A	3.05	0.11	0.54	0.33
rs6742	<i>SLC2A4RG</i>	T	0.87	0.85	1.35	0.57
rs2154481	<i>APP</i>	C	-	-	0.67	0.43

^a OR and P-value were computed by the proxy (rs72934704) which was in perfect linkage disequilibrium block (i.e., $r^2 = 1$ and $D' = 1$)

Supplementary Table 16. Association results from meta-analysis (ADSP WGS and ADGC) in people with other ancestries

Variant	Gene	Braak NFT stage		Neocortical neuritic plaques		TDP-43 in any brain regions		Lewy bodies in any brain regions		Hippocampal sclerosis	
		OR	P-value	OR	P-value	OR	P-value	OR	P-value	OR	P-value
rs679515	<i>CRI</i>	0.87	0.76	0.54	0.11	0.99	0.98	1.41	0.36	0.90	0.92
rs6733839	<i>BIN1</i>	1.49	0.046	1.74	0.0063	1.14	0.76	1.60	0.020	1.50	0.27
rs10933431	<i>INPP5D</i>	1.00	1.00	0.95	0.84	1.12	0.75	1.05	0.82	0.75	0.40
rs10947943	<i>UNC5CL</i>	0.96	0.91	1.07	0.96	1.35	0.66	1.81	0.12	2.21	0.26
rs60755019	<i>TREML2</i>	1.09	0.73	0.92	0.68	0.71	0.46	1.45	0.16	-	-
rs7767350	<i>CD2AP</i>	1.29	0.23	1.27	0.30	1.56	0.26	1.29	0.27	1.48	0.34
rs6966331	<i>EPDR1</i>	0.91	0.65	0.98	0.90	0.69	0.35	0.84	0.46	1.01	0.98
rs7384878	<i>SPDYE3</i>	0.87	0.67	1.10	0.65	0.84	0.69	1.07	0.77	0.41	0.077
rs11771145	<i>EPHA1</i>	0.97	0.86	1.16	0.43	1.27	0.53	1.25	0.21	1.19	0.60
rs73223431	<i>PTK2B</i>	1.12	0.60	1.46	0.073	0.93	0.89	0.94	0.74	0.57	0.17
rs11787077	<i>CLU</i>	1.07	0.74	0.96	0.80	0.95	0.88	0.81	0.28	2.74	0.010
rs7912495	<i>USP6NL</i>	1.48	0.049	1.37	0.10	0.82	0.62	1.04	0.86	0.88	0.61
rs10437655	<i>SPII</i>	1.12	0.59	0.99	0.97	0.95	0.87	1.24	0.31	0.83	0.45
rs1582763	<i>MS4A4A</i>	1.21	0.46	1.38	0.26	0.64	0.28	0.45	0.0078	2.53	0.23
rs3851179	<i>EED</i>	1.15	0.62	1.06	0.89	0.72	0.46	0.78	0.27	0.86	0.75
rs74685827	<i>SORL1</i>	1.93	0.47	2.63	0.30	-	-	2.38	0.27	1.66	0.79
rs11218343	<i>SORL1</i>	0.95	0.88	0.63	0.17	0.49	0.28	0.60	0.19	2.20	0.26
rs17125924	<i>FERMT2</i>	0.89	0.75	1.40	0.37	0.87	0.86	1.07	0.85	1.50	0.47
rs7401792	<i>SLC24A4</i>	0.86	0.42	1.02	0.95	0.93	0.84	1.32	0.19	0.88	0.69
rs12590654	<i>SLC24A4</i>	0.90	0.59	0.99	0.95	0.55	0.10	0.93	0.70	0.62	0.17
rs117618017	<i>APH1B</i>	2.02	0.17	1.96	0.16	1.30	0.68	1.21	0.78	0.40	0.51
rs889555	<i>BCKDK</i>	1.04	0.80	0.98	0.95	1.98	0.057	1.01	0.91	1.17	0.68
rs4985556	<i>IL34</i>	0.73	0.46	0.63	0.29	0.96	0.92	0.58	0.24	1.31	0.70
rs12446759	<i>PLCG2</i>	1.14	0.54	0.98	0.91	0.35	0.0042	0.97	0.90	0.55	0.13
rs7225151	<i>SCIMP</i>	0.66	0.10	0.78	0.24	1.38	0.64	0.83	0.44	1.39	0.61
rs199515	<i>WNT3</i>	1.06	0.81	1.34	0.24	1.03	0.98	1.20	0.57	1.02	0.95
rs4277405	<i>ACE</i>	0.94	0.67	1.10	0.69	0.59	0.16	0.98	0.95	1.02	0.88
rs12151021	<i>ABCA7</i>	1.68	0.0072	1.73	0.0046	0.86	0.63	1.43	0.057	1.61	0.15
rs6014724	<i>CASS4</i>	1.01	0.93	1.19	0.57	1.22	0.54	1.03	0.90	1.28	0.61

rs2830489	<i>ADAMTS1</i>	1.01	0.91	1.06	0.82	1.78	0.46	0.65	0.21	2.32	0.11
rs72777026	<i>ADAM17</i>	1.22	0.40	1.31	0.24	0.73	0.37	1.01	0.92	0.48	0.098
rs17020490	<i>PRKD3</i>	1.16	0.48	1.04	0.83	1.40	0.53	0.98	0.92	1.31	0.79
rs139643391	<i>WDR12</i>	1.68	0.29	1.08	0.79	-	-	1.12	0.87	-	-
rs16824536	<i>MME</i>	0.54	0.021	0.82	0.40	0.63	0.22	1.13	0.51	0.56	0.26
rs2245466	<i>RHOH</i>	1.51	0.055	0.99	0.95	1.68	0.13	1.25	0.27	0.85	0.80
rs112403360	<i>ANKH</i>	2.05	0.074	1.32	0.47	1.70	0.54	0.95	0.95	5.82	0.0048
rs62374257	<i>COX7C</i>	1.46	0.25	1.42	0.28	0.86	0.57	1.26	0.61	0.89	0.79
rs871269	<i>TNIP1</i>	0.76	0.16	0.92	0.68	0.75	0.34	0.88	0.53	0.65	0.31
rs113706587	<i>RASGEF1C</i>	1.18	0.60	1.22	0.54	1.15	0.86	1.17	0.72	2.41	0.15
rs785129	<i>HS3ST5</i>	0.78	0.22	0.88	0.54	1.04	0.93	1.12	0.60	0.62	0.20
rs6943429	<i>UMAD1</i>	1.12	0.54	1.15	0.46	1.39	0.28	1.31	0.15	1.23	0.68
rs10952097	<i>ICAI</i>	1.30	0.22	1.04	0.88	0.82	0.62	1.34	0.17	0.70	0.33
rs13237518	<i>TMEM106B</i>	1.06	0.75	1.15	0.49	1.04	0.92	1.22	0.31	1.73	0.13
rs76928645	<i>SEC61G</i>	1.20	0.62	1.75	0.29	-	-	2.04	0.25	-	-
rs7068231	<i>ANK3</i>	0.72	0.11	0.59	0.012	1.06	0.97	0.75	0.16	0.95	0.92
rs6584063	<i>BLNK</i>	0.93	0.97	0.71	0.84	0.93	0.95	1.99	0.14	0.97	0.99
rs7908662	<i>PLEKHA1</i>	0.80	0.21	0.78	0.21	0.62	0.21	1.05	0.80	0.93	0.91
rs6489896	<i>TPCNI</i>	0.93	0.79	1.36	0.22	0.64	0.35	1.37	0.25	1.03	0.96
rs10131280	<i>IGH</i> gene cluster	1.08	0.76	1.00	1.00	1.31	0.61	1.14	0.73	0.57	0.26
rs3848143	<i>SNX1</i>	1.25	0.26	0.97	0.92	1.52	0.21	1.26	0.23	1.24	0.54
rs12592898	<i>CTSH</i>	0.62	0.081	1.03	0.71	0.69	0.34	0.71	0.25	0.86	0.72
rs1140239	<i>DOC2A</i>	1.12	0.61	1.12	0.58	1.01	0.99	1.21	0.38	1.77	0.16
rs16941239	<i>FOXF1</i>	0.81	0.46	0.81	0.43	0.94	0.84	1.00	0.81	1.05	0.92
rs2242595	<i>MYO15A</i>	0.82	0.43	1.20	0.55	1.97	0.15	1.23	0.47	1.18	0.64
rs5848	<i>GRN</i>	1.14	0.54	1.13	0.56	1.84	0.12	1.04	0.76	1.66	0.22
rs9304690	<i>SIGLEC11</i>	1.37	0.24	1.15	0.59	1.37	0.56	1.08	0.78	1.49	0.40
rs1358782	<i>RBCK1</i>	0.58	0.029	0.66	0.097	0.82	0.63	1.04	0.89	1.20	0.72
rs6742	<i>SLC2A4RG</i>	0.98	0.92	1.15	0.57	1.64	0.25	0.89	0.71	1.16	0.76

NFT = neurofibrillary tangle; TDP-43 = TAR DNA binding protein 43 kDa; ADSP = Alzheimer's Disease Sequencing Project; WGS = whole genome sequencing; ADGC = Alzheimer's Disease Genetics Consortium;

Supplementary Table 17. Summary of association from sensitivity analysis in people with European ancestry including cases with rare disease

Gene	Variant	Meta-analysis	
		NP-OR	P-value
Braak NFT stage			
<i>BIN1</i>	rs6733839	1.33	5.8×10^{-10}
<i>CR1</i>	rs679515	1.20	0.0012
<i>MME</i>	rs16824536	0.74	0.0030
<i>COX7C</i>	rs62374257	1.19	7.9×10^{-4}
<i>SPI1</i>	rs10437655	1.13	0.0054
<i>EED/PICALM</i>	rs3851179	0.88	0.0045
<i>INPP5D</i>	rs10933431	0.85	0.0024
Neocortical neuritic plaques			
<i>BIN1</i>	rs6733839	1.22	5.7×10^{-6}
<i>EED/PICALM</i>	rs3851179	0.85	2.9×10^{-4}
<i>MME</i>	rs16824536	0.73	0.0020
<i>APH1B</i>	rs117618017	1.25	5.8×10^{-4}
<i>RBCK1</i>	rs1358782	0.86	0.0033
<i>FERMT2</i>	rs17125924	1.28	0.0014
<i>PTK2B</i>	rs73223431	1.11	0.024
TDP-43 in any brain regions			
<i>TMEM106B</i>	rs13237518	0.75	8.1×10^{-7}
<i>SORL1</i>	rs74685827	1.72	0.0061
<i>GRN</i>	rs5848	1.27	1.6×10^{-4}
<i>TPCN1</i>	rs6489896	1.42	0.0033
Lewy bodies in any brain regions			
<i>BIN1</i>	rs6733839	1.16	9.2×10^{-4}
<i>USP6NL</i>	rs7912495	1.14	0.0031
Hippocampal sclerosis			
<i>TMEM106B</i>	rs13237518	0.61	7.3×10^{-9}
<i>GRN</i>	rs5848	1.57	4.3×10^{-8}
<i>WNT3</i>	rs199515	0.74	0.0032
<i>TNIP1</i>	rs871269	0.78	0.0026
<i>ACE</i>	rs4277405	1.18	0.029
<i>SCIMP</i>	rs7225151	1.38	0.0028

NP = neuropathology; OR = odds ratio; NFT = neurofibrillary tangle; TDP-43 = TAR DNA binding protein 43 kDa

Supplementary Table 18. Summary of association from sensitivity analysis for different dichotomized neuropathologies

Gene	Variant	Meta-analysis	
		NP-OR	P-value
Braak NFT stage IV-VI vs. 0-III			
<i>BIN1</i>	rs6733839	1.38	1.3×10^{-10}
<i>CR1</i>	rs679515	1.14	0.038
<i>MME</i>	rs16824536	0.74	0.0040
<i>COX7C</i>	rs62374257	1.21	0.0017
<i>SPI1</i>	rs10437655	1.16	0.0023
<i>EED/PICALM</i>	rs3851179	0.96	0.41
<i>INPP5D</i>	rs10933431	0.79	5.8×10^{-5}
<i>ADAM17</i>	rs72777026	1.24	0.0038
<i>TMEM106B</i>	rs13237518	1.16	0.0025
Neocortical neuritic plaques moderate/frequent vs. no/sparse ^a			
<i>BIN1</i>	rs6733839	1.29	2.8×10^{-7}
<i>EED/PICALM</i>	rs3851179	0.88	0.014
<i>MME</i>	rs16824536	0.68	2.7×10^{-4}
<i>APH1B</i>	rs117618017	1.15	0.045
<i>RBCK1</i>	rs1358782	0.95	0.37
<i>FERMT2</i>	rs17125924	1.16	0.11
<i>PTK2B</i>	rs73223431	1.11	0.026
<i>CR1</i>	rs679515	1.25	5.3×10^{-4}
<i>INPP5D</i>	rs10933431	0.82	7.6×10^{-4}
<i>SPDYE3</i>	rs7384878	0.83	4.7×10^{-4}
<i>TPCN1</i>	rs6489896	1.33	0.0062
TDP-43 in hippocampus/entorhinal or inferior temporal cortex/neocortex vs. no/amygdala ^b			
<i>TMEM106B</i>	rs13237518	0.66	7.4×10^{-10}
<i>SORL1</i>	rs74685827	2.14	6.0×10^{-4}
<i>GRN</i>	rs5848	1.29	3.6×10^{-4}
<i>TPCN1</i>	rs6489896	1.20	0.18
<i>IGH gene cluster</i>	rs10131280	0.77	0.0090
Lewy bodies in neocortical vs. no/other regions ^c			
<i>BIN1</i>	rs6733839	1.14	0.038
<i>USP6NL</i>	rs7912495	1.09	0.16

Bold results indicate the additional SNVs that were associated with the different operationalization for severities in neuropathologies.

^a Probable/definite vs. no AD/possible in ROSMAP

^b Amygdala + limbic/amygdala + limbic + neocortical vs. no/amygdala in ROSMAP/

^c Neocortical-type vs. not present/nigral-predominant/limbic-type in ROSMAP

NP = neuropathology; OR = odds ratio; NFT = neurofibrillary tangle; TDP-43 = TAR DNA binding protein 43 kDa; ROSMAP = Religious Orders Study (ROS) and Memory and Aging Project (MAP)

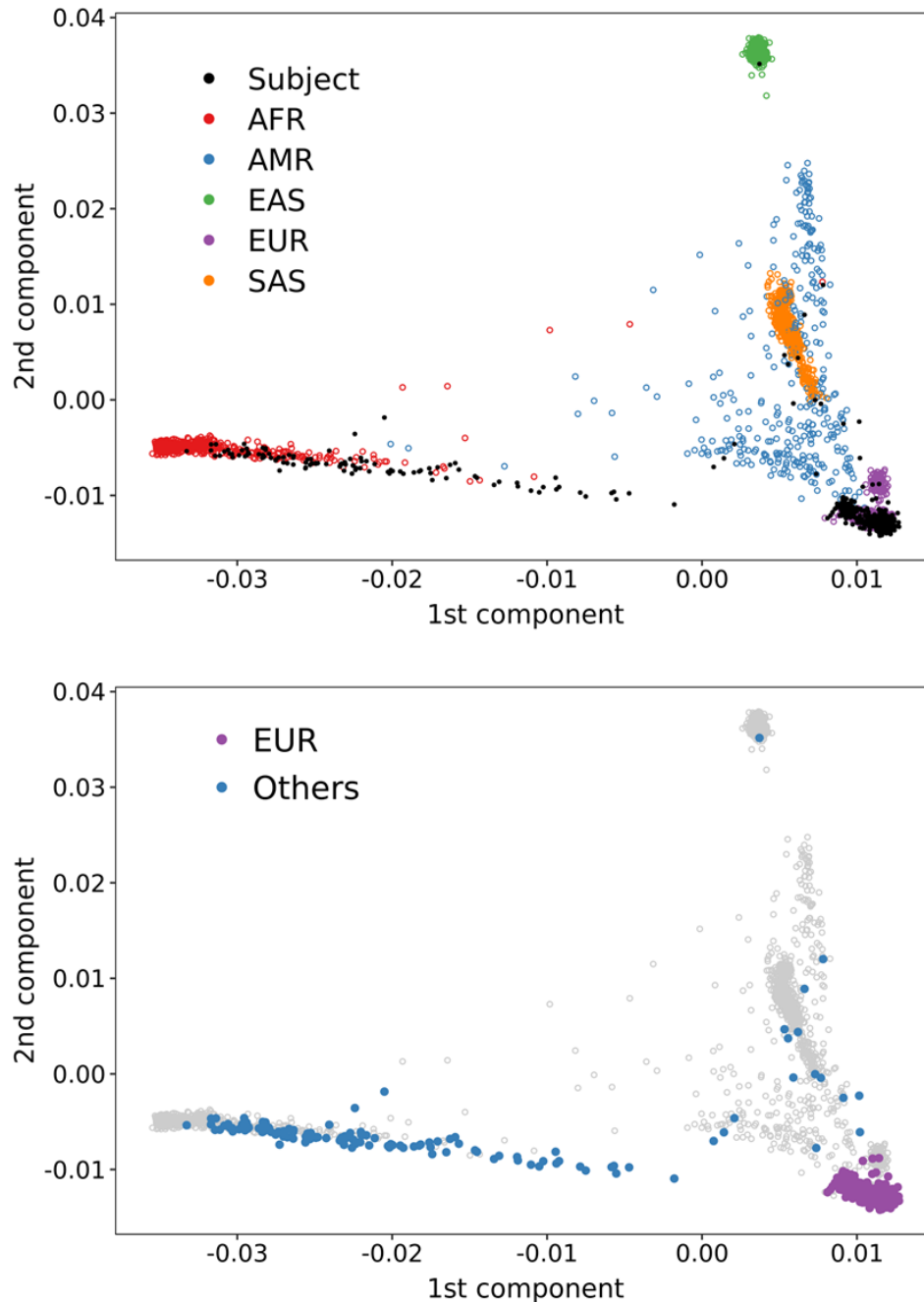
Supplementary Table 19. Association of *APOE* diplotype from meta-analysis in people with European ancestry and other ancestries

<i>APOE</i> diplotype ^a	Meta-analysis			
	European ancestry		Other ancestries	
	NP-OR ^b	P-value	NP-OR ^b	P-value
Braak NFT stage				
ε2/ε3	0.45	5.2 × 10 ⁻⁸	0.35	0.085
ε2/ε4	1.51	0.045	1.89	0.41
ε3/ε4	2.54	7.4 × 10 ⁻³⁴	4.11	3.7 × 10 ⁻⁵
ε4/ε4	5.89	9.0 × 10 ⁻²⁴	9.09	0.067
Neocortical neuritic plaques				
ε2/ε3	0.47	9.2 × 10 ⁻⁷	0.63	0.44
ε2/ε4	1.60	0.018	1.22	0.83
ε3/ε4	2.47	4.6 × 10 ⁻³³	5.72	5.7 × 10 ⁻⁷
ε4/ε4	3.88	1.95 × 10 ⁻¹⁹	7.44	0.0019
TDP-43 in any brain regions				
ε2/ε3	0.89	0.51	-	-
ε2/ε4	1.09	0.80	1.93	0.59
ε3/ε4	1.97	3.9 × 10 ⁻¹⁰	1.30	0.80
ε4/ε4	2.85	1.6 × 10 ⁻⁵	4.93	0.45
Lewy bodies in any brain regions				
ε2/ε3	0.89	0.47	0.72	0.50
ε2/ε4	1.05	0.63	2.62	0.27
ε3/ε4	1.63	2.6 × 10 ⁻¹⁰	2.02	0.028
ε4/ε4	2.13	1.0 × 10 ⁻⁶	3.42	0.035
Hippocampal sclerosis				
ε2/ε3	0.96	0.94	1.19	0.85
ε2/ε4	1.06	0.86	7.85	0.40
ε3/ε4	1.83	1.1 × 10 ⁻⁵	1.26	0.99
ε4/ε4	2.22	0.0027	2.46	0.67

^a *APOE* diplotype was determined with rs429358 and rs7412. Because nobody has ε2/ε2 in ADSP WGS, we removed people with ε2/ε2 from ROSMAP and ADGC.

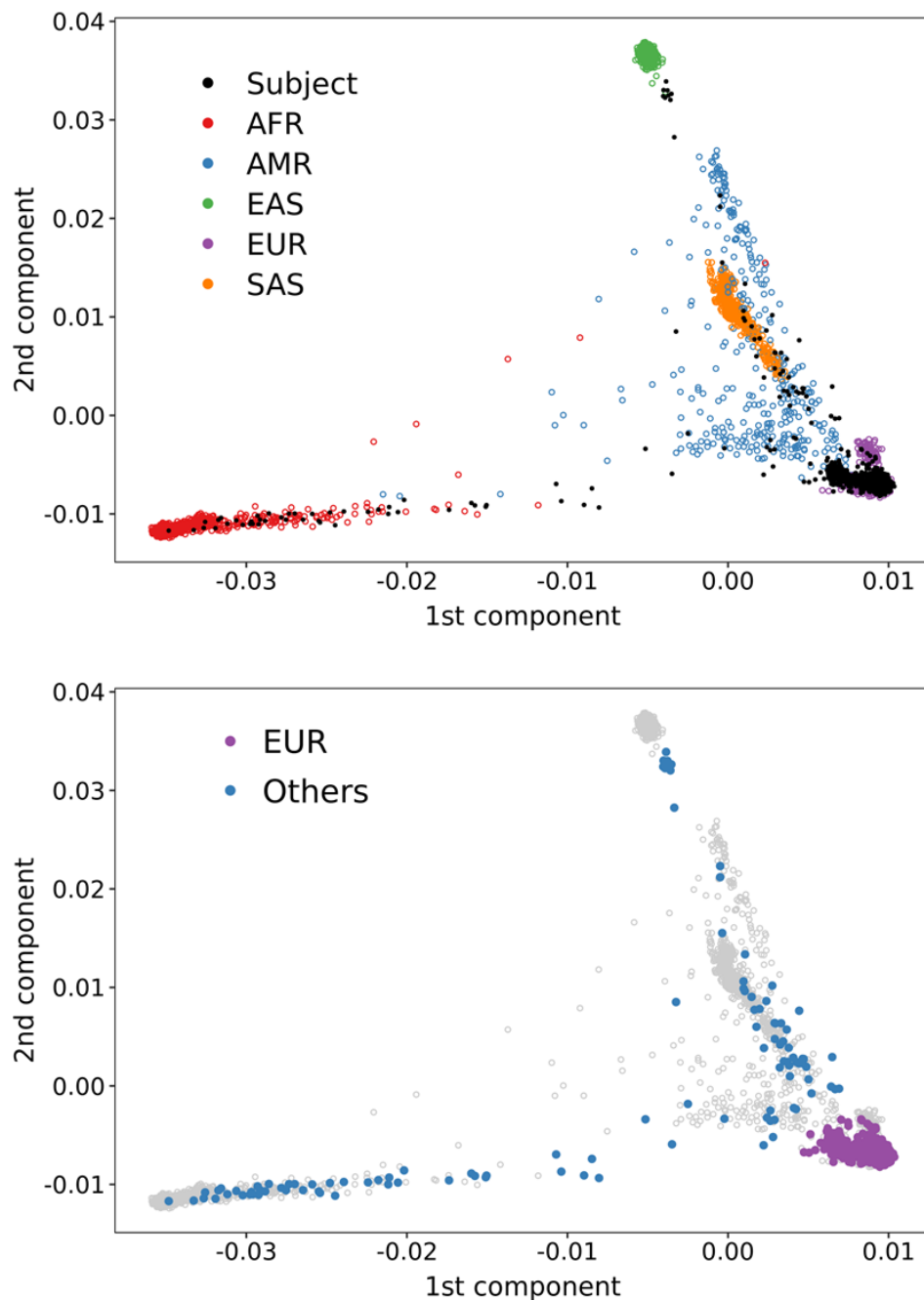
^b The reference group is ε3/ε3.

Abbreviations: NFT = neurofibrillary tangle; NP = neuropathology; OR = odds ratio; TDP-43 = TAR DNA binding protein 43 kDa



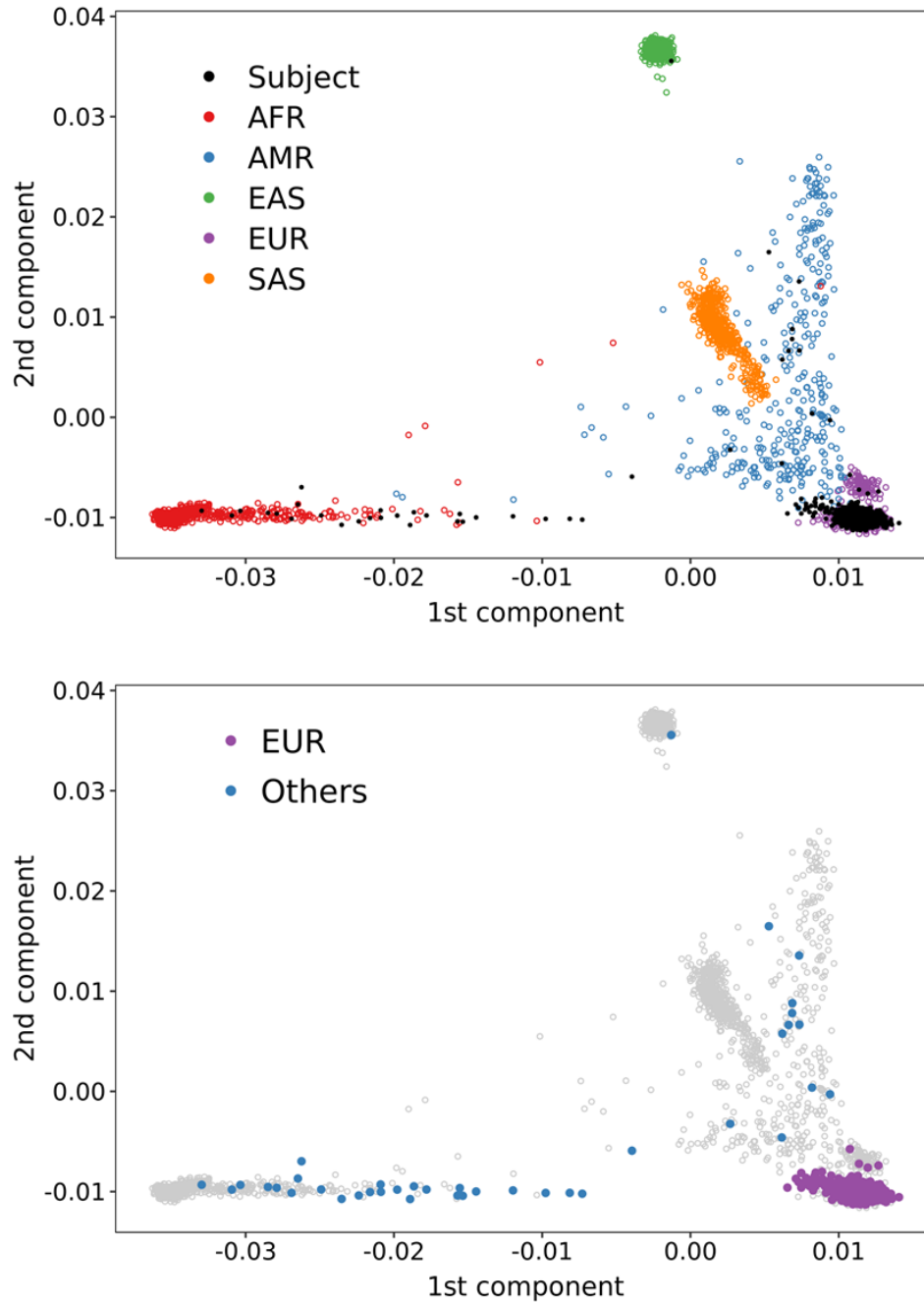
Supplementary Figure 1. First and second principal components plots along with 1000 genome reference samples. Block dots indicate individuals in the ADSP WGS dataset. The upper plot represents the entire sample and the lower plot shows split participants into European ancestry and other ancestries.

AFR = African; AMR = Admixed American; EAS = East Asian; EUR = European; SAS = South Asian; ADSP = Alzheimer's Disease Sequencing Project; WGS = whole genome sequencing



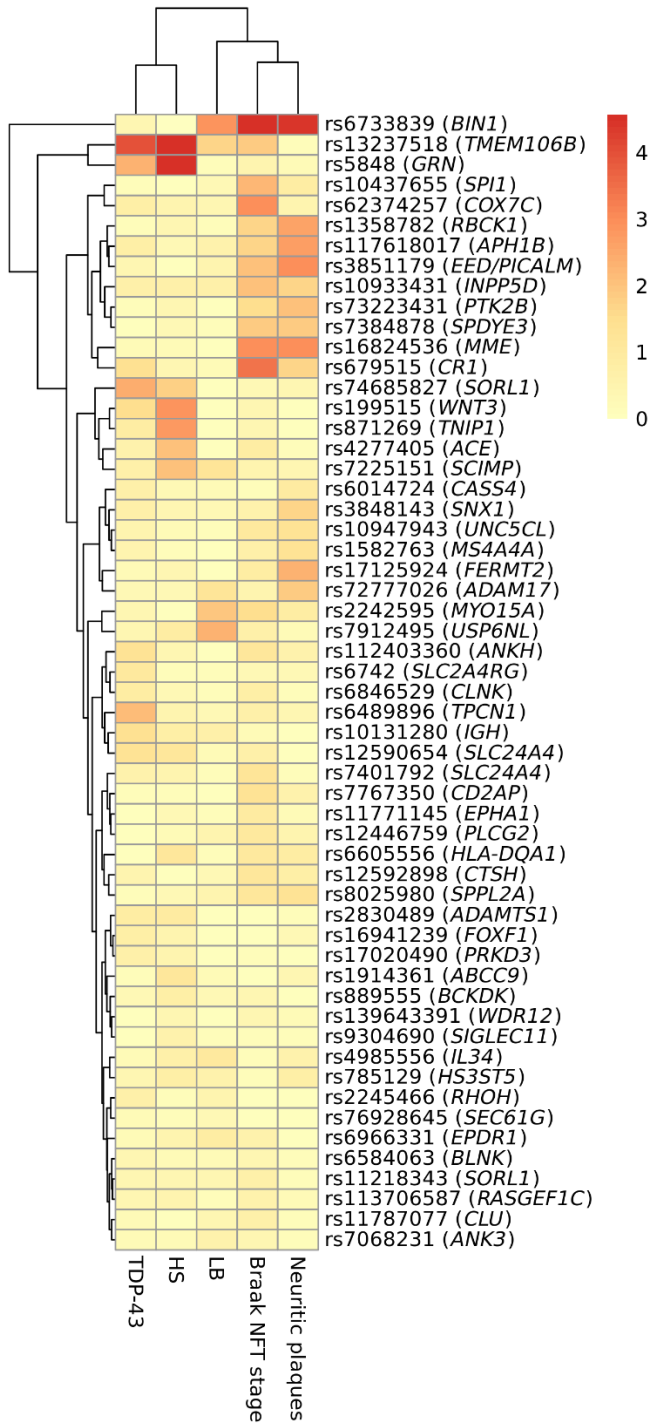
Supplementary Figure 2. First and second principal components plots along with 1000 genome reference samples. Block dots indicate individuals in the ADGC dataset. The upper plot represents the entire sample and the lower plot shows split participants into European ancestry and other ancestries.

AFR = African; AMR = Admixed American; EAS = East Asian; EUR = European; SAS = South Asian; ADGC = Alzheimer's Disease Genetics Consortium

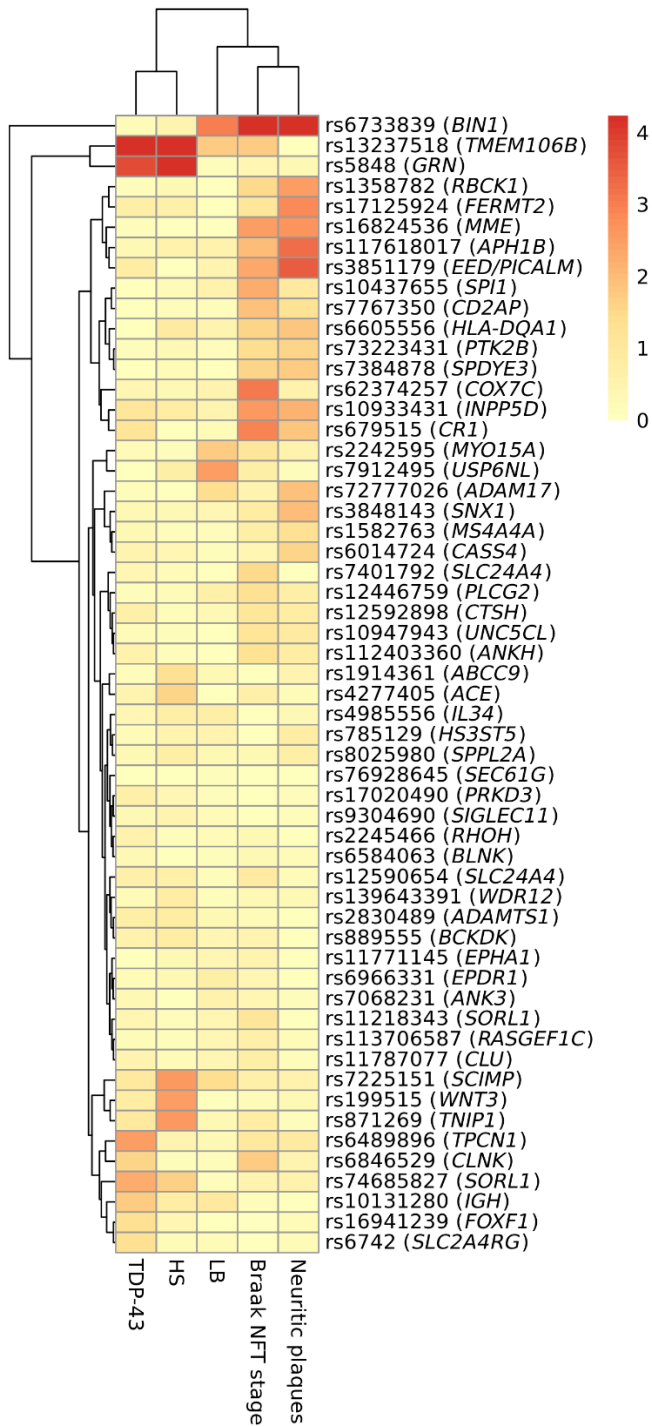


Supplementary Figure 3. First and second principal components plots along with 1000 genome reference samples. Block dots indicate individuals in the ROSMAP dataset. The upper plot represents the entire sample and the lower plot shows split participants into European ancestry and other ancestries.

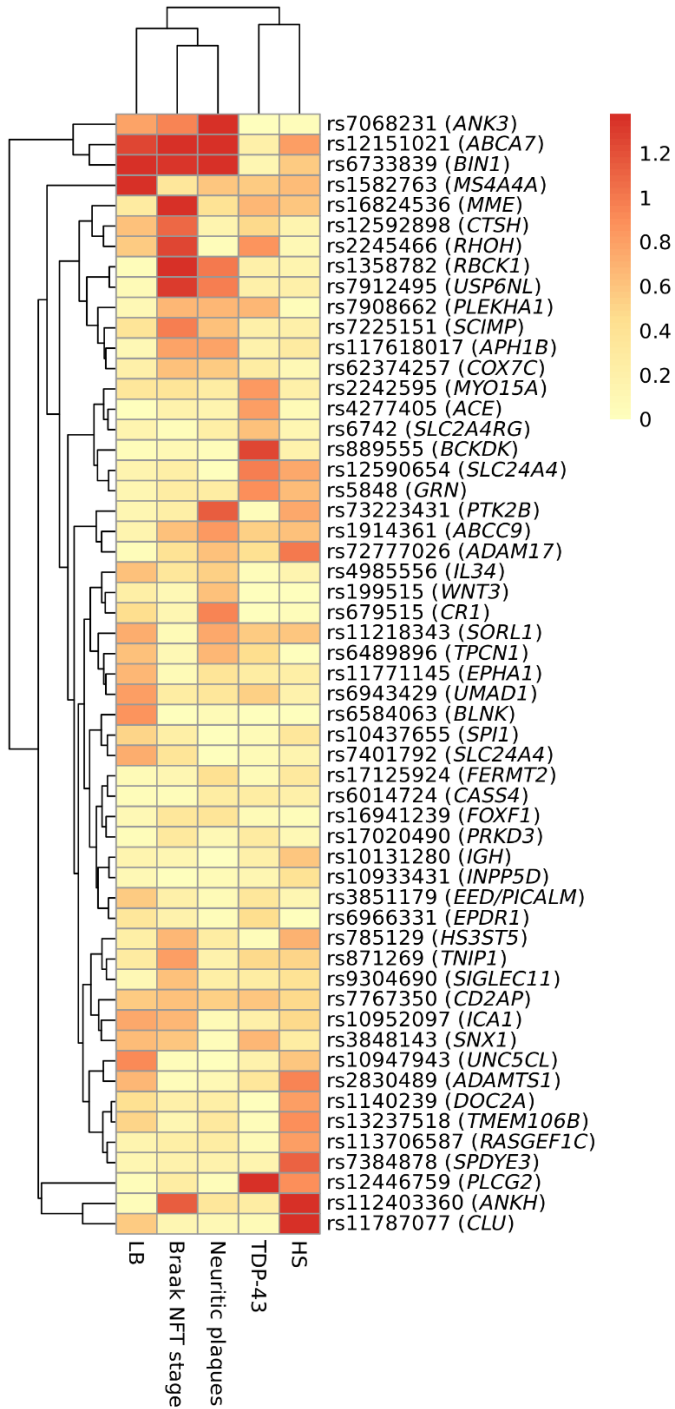
AFR = African; AMR = Admixed American; EAS = East Asian; EUR = European; SAS = South Asian; ROSMAP = Religious Orders Study (ROS) and Memory and Aging Project (MAP)



Supplementary Figure 4. Heatmap for $-\log_{10}$ transformed p-values of all single nucleotide variants in people with European ancestry (excluding cases who had at least one rare disease) TDP-43 = TAR DNA binding protein 43 kDa; HS = hippocampal sclerosis; LB = Lewy bodies; NFT = neurofibrillary tangle



Supplementary Figure 5. Heatmap for $-\log_{10}$ transformed p-values of all single nucleotide variants in people with European ancestry (including people with or without rare disease) TDP-43 = TAR DNA binding protein 43 kDa; HS = hippocampal sclerosis; LB = Lewy bodies; NFT = neurofibrillary tangle



Supplementary Figure 6. Heatmap for $-\log_{10}$ transformed p-values of all single nucleotide variants in people with other ancestries
TDP-43 = TAR DNA binding protein 43 kDa; HS = hippocampal sclerosis; LB = Lewy bodies;
NFT = neurofibrillary tangle