nature genetics

Rare coding variants in *PLCG2*, *ABI3*, and *TREM2* implicate microglial-mediated innate immunity in Alzheimer's disease

We identified rare coding variants associated with Alzheimer's disease in a three-stage case–control study of 85,133 subjects. In stage 1, we genotyped 34,174 samples using a whole-exome microarray. In stage 2, we tested associated variants ($P < 1 \times 10^{-4}$) in 35,962 independent samples using *de novo* genotyping and imputed genotypes. In stage 3, we used an additional 14,997 samples to test the most significant stage 2 associations ($P < 5 \times 10^{-8}$) using imputed genotypes. We observed three new genome-wide significant nonsynonymous variants associated with Alzheimer's disease: a protective variant in *PLCG2* (rs72824905: p.Pro522Arg, $P = 5.38 \times 10^{-10}$, odds ratio (OR) = 0.68, minor allele frequency (MAF)$_{cases}$ = 0.0059, MAF$_{controls}$ = 0.0093), a risk variant in *ABI3* (rs616338: p.Ser209Phe, $P = 4.56 \times 10^{-10}$, OR = 1.43, MAF$_{cases}$ = 0.011, MAF$_{controls}$ = 0.008), and a new genome-wide significant variant in *TREM2* (rs143332484: p.Arg62His, $P = 1.55 \times 10^{-14}$, OR = 1.67, MAF$_{cases}$ = 0.0143, MAF$_{controls}$ = 0.0089), a known susceptibility gene for Alzheimer's disease. These protein-altering changes are in genes highly expressed in microglia and highlight an immune-related protein–protein interaction network enriched for previously identified risk genes in Alzheimer's disease. These genetic findings provide additional evidence that the microglia-mediated innate immune response contributes directly to the development of Alzheimer's disease.

Late-onset Alzheimer's disease (LOAD) has a substantial genetic component (h^2 = 58–79%)[1]. Nearly 30 LOAD susceptibility loci[2–12] are known, and risk is highly polygenic[13]. However, these loci explain only a proportion of disease heritability. Rare variants also contribute to disease risk[14–17]. Recent sequencing studies identified a number of genes that have rare variants associated with Alzheimer's disease[9–11,18–24]. Our approach to rare variant discovery is to genotype a large sample with microarrays targeting known exome variants with follow-up using genotyping and imputed genotypes in a large independent sample. This is a cost-effective alternative to *de novo* sequencing[25–29].

We applied a three-stage design (**Supplementary Fig. 1**) using subjects from the International Genomics of Alzheimer's Project (IGAP) (**Table 1** and **Supplementary Tables 1** and **2**). In stage 1, we genotyped 16,097 LOAD cases and 18,077 cognitively normal elderly controls using the Illumina HumanExome microarray. Data from multiple consortia were combined in a single-variant meta-analysis (Online Methods) assuming an additive model. In total, 241,551 variants passed quality control (**Supplementary Table 3**). Of these, 203,902 were polymorphic, 26,947 were common (MAF ≥ 5%), and 176,955 were low frequency or rare (MAF < 5%). We analyzed common variants using a logistic regression model in each sample cohort and combined data using METAL[30]. Rare and low-frequency variants were analyzed using the score test and data were combined with SeqMeta[31] (**Supplementary Fig. 2**).

We reviewed cluster plots for variants showing association ($P < 1 \times 10^{-4}$) and identified 43 candidate variants (**Supplementary Table 4**), excluding known risk loci (**Supplementary Table 5**). In stage 2, we tested these for association in 14,041 LOAD cases and 21,921 controls, using genotypes derived from *de novo* genotyping and imputation (Online Methods). We carried forward single-nucleotide variants (SNVs) with genome-wide significant associations and consistent directions of effect to stage 3 where genotypes for 6,652 independent cases and 8,345 controls were imputed using the Haplotype Reference Consortium resource[32,33] (Online Methods and **Supplementary Table 6**).

We identified four rare coding variants with genome-wide significant association signals with LOAD ($P < 5 \times 10^{-8}$) (**Table 2** and **Supplementary Tables 7 and 8**). The first is a missense variant p.Pro522Arg ($P = 5.38 \times 10^{-10}$, OR = 0.68) in *PLCG2* (phospholipase C γ2) (**Fig. 1a**, **Table 2**, **Supplementary Fig. 3**, and **Supplementary Table 9**). This variant is associated with decreased risk of LOAD, showing a MAF of 0.0059 in cases and 0.0093 in controls. The reference allele (Pro522) is conserved across several species (**Supplementary Fig. 4**). Gene-wide analysis showed nominal evidence for association at $P = 1.52 \times 10^{-4}$ (**Supplementary Tables 10** and **11**), and we found no other independent association at this gene (**Supplementary Fig. 5**).

The second new association is a missense change p.Ser209Phe ($P = 4.56 \times 10^{-10}$, OR = 1.43) in *ABI3* (B3-domain-containing transcription factor ABI3). The Phe209 allele showed consistent evidence for increasing LOAD risk across all stages, with a MAF of 0.011 in cases and 0.008 in controls (**Fig. 1b**, **Table 2**, **Supplementary Fig. 6**, and **Supplementary Table 12**). The reference allele is conserved across multiple species (**Supplementary Fig. 7**). Gene-wide analysis showed nominal evidence of association ($P = 5.22 \times 10^{-5}$) (**Supplementary**

A full list of authors and affiliations appears at the end of the paper.

Received 1 July 2016; accepted 16 June 2017; published online 17 July 2017; doi:10.1038/ng.3916

Table 1 Summary of the consortium data sets used for stages 1–3

	Consortium	*n* controls	*n* cases	*n* total
Stage 1	GERAD/PERADES	2,974	6,000	8,974
	ADGC	7,002	8,706	15,708
	CHARGE	8,101	1,391	9,492
Total		18,077	16,097	34,174
Stage 2	GERAD/PERADES genotype	5,049	4,049	9,098
	CHARGE, genotype	1,839	1,434	3,273
	CHARGE, *in silico*	3,246	722	3,968
	EADI, genotype	11,787	7,836	19,623
Total		21,921	14,041	35,962
Stage 3	ADGC, *in silico*	8,345	6,652	14,997
Stage 1–3 total		48,402	37,022	85,133

Data are from the Genetic and Environmental Risk for Alzheimer's Disease (GERAD)/Defining Genetic, Polygenic and Environmental Risk for Alzheimer's Disease (PERADES) Consortium, the Alzheimer's Disease Genetic Consortium (ADGC), the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE), and the European Alzheimer's disease Initiative (EADI) (**Supplementary Note**).

Tables 10 and **11**). The *B4GALNT2* gene, adjacent to *ABI3*, contained an independent suggestive association (**Supplementary Fig. 8**), but this failed to replicate in subsequent stages ($P_{combined} = 1.68 \times 10^{-4}$) (**Supplementary Table 7**).

Following reports of suggestive association with LOAD[34,35], we report the first evidence for genome-wide significant association at *TREM2* coding variant p.Arg62His ($P = 1.55 \times 10^{-14}$, OR = 1.67), with a MAF of 0.0143 in cases and 0.0089 in controls (**Fig. 1c**, **Table 2**, **Supplementary Figs. 9** and **10**, and **Supplementary Table 13**). We also observed evidence of association for the previously reported[9,11] *TREM2* rare variant p.Arg47His (**Table 2**). These variants are not in linkage disequilibrium (**Supplementary Table 14**), and conditional analyses confirmed that p.Arg62His and p.Arg47His are independent risk variants (**Supplementary Fig. 11**). Gene-wide analysis of *TREM2* showed a genome-wide significant association ($P_{SKAT} = 1.42 \times 10^{-15}$) (**Supplementary Tables 10** and **11**). Removal of p.Arg47His and the p.Arg62His variants from the analysis diminished the gene-wide association, but the signal remained interesting ($P_{SKAT\text{-}O} = 6.3 \times 10^{-3}$, $P_{Burden} = 4.1 \times 10^{-3}$). No single SNV was responsible for the remaining gene-wide association (**Supplementary Fig. 11** and **Supplementary Table 13**), suggesting that there are additional risk variants in *TREM2*. We previously reported a common variant association with LOAD near *TREM2*, in a genome-wide association study (GWAS) of cerebrospinal fluid tau and phosphorylated tau (P-tau)[36]. We also observed a different suggestive common variant signal in another LOAD case–control study ($P = 6.3 \times 10^{-7}$)[2].

We previously identified eight gene pathway clusters significantly enriched in common variants associated with Alzheimer's disease[36]. To test whether biological enrichments observed in common variants are also present in rare variants, we used the rare variant data (MAF < 1%) to reanalyze these eight Alzheimer's disease–associated pathway clusters (Online Methods and **Supplementary Table 15**). We used Fisher's method to combine gene-wide *P* values for all genes in each cluster. After correction for multiple testing, we observed enrichment for immune response ($P = 8.64 \times 10^{-3}$), cholesterol transport ($P = 3.84 \times 10^{-5}$), hemostasis ($P = 2.10 \times 10^{-3}$), clathrin–AP2 adaptor complex ($P = 9.20 \times 10^{-4}$), and protein folding ($P = 0.02$). We also performed pathway analyses on the rare variant data presented here using all 9,816 pathways used previously. The top pathways are related to lipoprotein particles, cholesterol efflux, B cell differentiation and immune response, areas of biology also enriched when common variants are analyzed[37] (**Supplementary Table 16**).

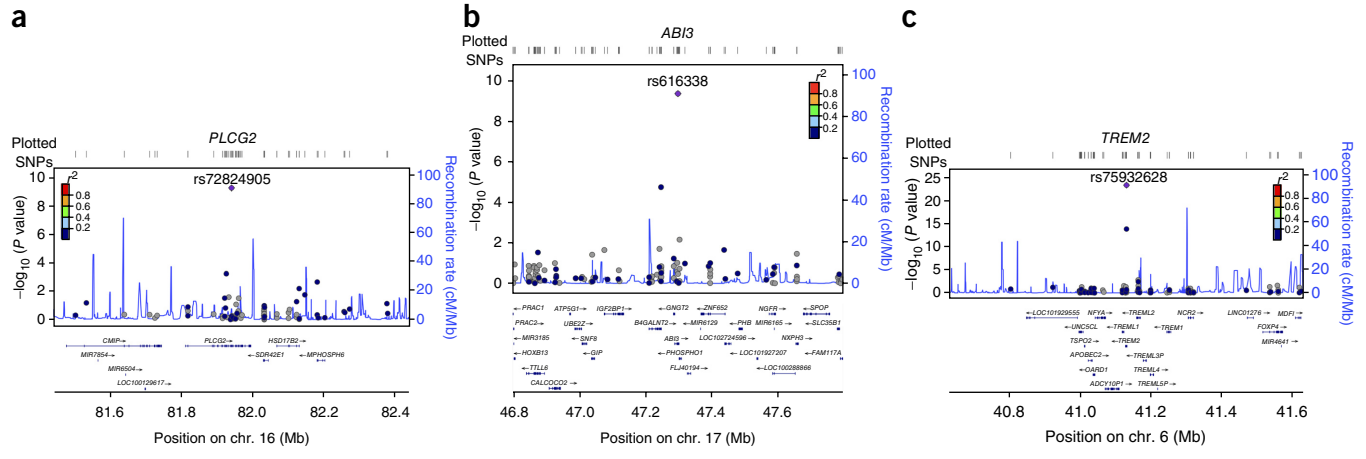

Figure 1 Association plots of *PLCG2*, *ABI3*, and *TREM2*. (**a**) Regional plot of identified association at the *PLCG2* locus. Top hit rs72824905 is indicated in purple. Data presented for rs72824905 include data from stage 1, stage 2, and stage 3 (*n* = 84,905). (**b**) Regional plot of identified association at the *ABI3* locus. Top hit rs616338 is indicated in purple. Data presented for rs616338 include data from stage 1, stage 2, and stage 3 (*n* = 84,493). (**c**) Regional plot of identified association at the *TREM2* locus. Top hit rs75932628 is indicated in purple. Data presented for rs75932628 and rs143332484 include data from stage 1, stage 2, and stage 3 (*n* = 80,733 and 53,042, respectively). SNVs with missing LD information are shown in gray.

Table 2 Summary of stages 1, 2 and 3 and combined meta-analysis results for SNVs at $P < 5 \times 10^{-8}$

SNV	rs75932628	rs143332484	rs72824905	rs616338
Chr.	6	6	16	17
Position (bp)	41,129,252	41,129,207	81,942,028	47,297,297
Protein variation	Arg47His	Arg62His	Pro522Arg	Ser209Phe
Gene	*TREM2*	*TREM2*	*PLCG2*	*ABI3*
Effect allele	T	T	G	T
Stage 1				
P	3.02×10^{-12}	3.48×10^{-9}	1.19×10^{-5}	2.16×10^{-5}
OR	2.46	1.58	0.65	1.42
MAF_{cases}	0.003	0.015	0.006	0.013
$MAF_{controls}$	0.001	0.010	0.011	0.010
N	30,018	33,786	33,786	33,786
Stage 2				
P	4.38×10^{-8}	3.66×10^{-7}	1.35×10^{-4}	8.37×10^{-5}
OR	2.37	3.97	0.70	1.41
MAF_{cases}	0.004	0.014	0.006	0.010
$MAF_{controls}$	0.002	0.006	0.008	0.008
N	35,831	3,968	35,831	35,831
Stage 3				
P	1.23×10^{-6}	2.45×10^{-3}	2.48×10^{-2}	1.75×10^{-2}
OR	2.58	1.55	0.69	1.58
MAF_{cases}	0.006	0.012	0.006	0.010
$MAF_{controls}$	0.003	0.008	0.007	0.008
N	14,884	15,288	15,288	14,876
Stage 1–3 meta-analysis				
P	5.38×10^{-24}	1.55×10^{-14}	5.38×10^{-10}	4.56×10^{-10}
OR	2.46	1.67	0.68	1.43
MAF_{cases}	0.004	0.014	0.006	0.011
$MAF_{controls}$	0.002	0.009	0.009	0.008
N	80,733	53,042	84,905	84,493

Data include *P* value, odds ratios (OR), minor allele frequency (MAF) in cases and controls, and number of subjects included in each analytical stage. For OR 95% confidence intervals, see **Supplementary Table 7**. Concordance for alternate allele carrier genotypes between imputed versus called SNPs in stage 3 was 75.2% for rs75932628, 91.1% for rs143332484, 95.7% for rs72824905, and 81.9% for rs616338 (Online Methods and **Supplementary Table 6**). Chr., chromosome.

Previous analysis of normal brain coexpression networks identified four gene modules that are enriched for common variants associated with LOAD risk[2,3711]. These four modules are enriched for immune-response genes. We identified 151 genes present in two or more of these four modules, and these showed a strong enrichment for LOAD-associated common variants ($P = 4.0 \times 10^{-6}$)[36] and for rare variants described here (MAF < 1%) ($P = 1.17 \times 10^{-6}$; **Supplementary Table 15**). We then used a set of high-quality proteinprotein interactions[37] to construct, from these 151 genes, an interaction network containing 56 genes, including *PLCG2*, *ABI3*, and *TREM2* (**Fig. 2** and Online Methods). This subset is strongly enriched for association signals from both the previous common variant analysis ($P = 5.0 \times 10^{-6}$; **Supplementary Table 17**) and this rare variant gene set analysis ($P = 1.08 \times 10^{-7}$; **Supplementary Table 15**). The remaining 95 genes only have nominally significant enrichment for either common or rare variants (**Supplementary Tables 15** and **17**), suggesting that the 56-gene (**Supplementary Table 18**) network is driving the enrichment.

TREM2, *ABI3*, and *PLCG2* have a common expression pattern in human brain cortex, with high expression in microglia cells and limited expression in neurons, oligodendrocytes, astrocytes, and endothelial cells (**Supplementary Fig. 12**)[38]. Other known LOAD-associated loci with the same expression pattern included *SORL1*, the *MS4A* gene cluster, and *HLA-DRB1*. *PLCG2*, *ABI3*, and *TREM2* are upregulated in LOAD human cortex and in two amyloid precursor protein (APP) mouse models. However, when corrected for levels of other microglial genes, these changes in expression appeared to be related to microgliosis (**Supplementary Tables 19** and **20**).

PLCG2 (**Supplementary Fig. 13**) encodes a transmembrane signaling enzyme (PLCγ2) that hydrolyzes the membrane phospholipid PIP_2 (1-phosphatidyl-1D-myoinositol 4,5-bisphosphate) to secondary messengers IP_3 (myoinositol 1,4,5-trisphosphate) and DAG (diacylglycerol). IP_3 is released into the cytosol and acts at the endoplasmic reticulum where it binds to ligand-gated ion channels to increase cytoplasmic Ca^{2+}. DAG remains bound to the plasma membrane where it activates two major signaling molecules, protein kinase C (PKC) and Ras guanyl-nucleotide-releasing proteins (RasGRPs), which initiate the NF-κB and mitogen-activated protein kinase (MAPK) pathways. While the IP_3–DAG–Ca^{2+} signaling pathway is active in many cells and tissues, in brain *PLCG2* is primarily expressed in microglial cells. *PLCG2* variants also cause antibody deficiency and immune dysregulation (PLAID) and autoinflammation and PLAID (APLAID)[39]. Genomic deletions (PLAID) and missense mutations (APLAID) affect the cSH2 autoinhibitory regulatory region. The result is a complex mix of loss and gain of function in cellular signaling[39].

Functional annotation (**Supplementary Table 21**) suggests that *ABI3* (**Supplementary Fig. 14**) has a role in the innate immune response via interferon-mediated signaling[40]. *ABI3* is coexpressed with *INPP5D* ($P = 2.2 \times 10^{-10}$), a gene previously implicated in LOAD risk[2]. ABI3 has an important role in actin cytoskeleton organization through participation in the WAVE2 complex[41], a complex that regulates multiple pathways leading to T cell activation[42].

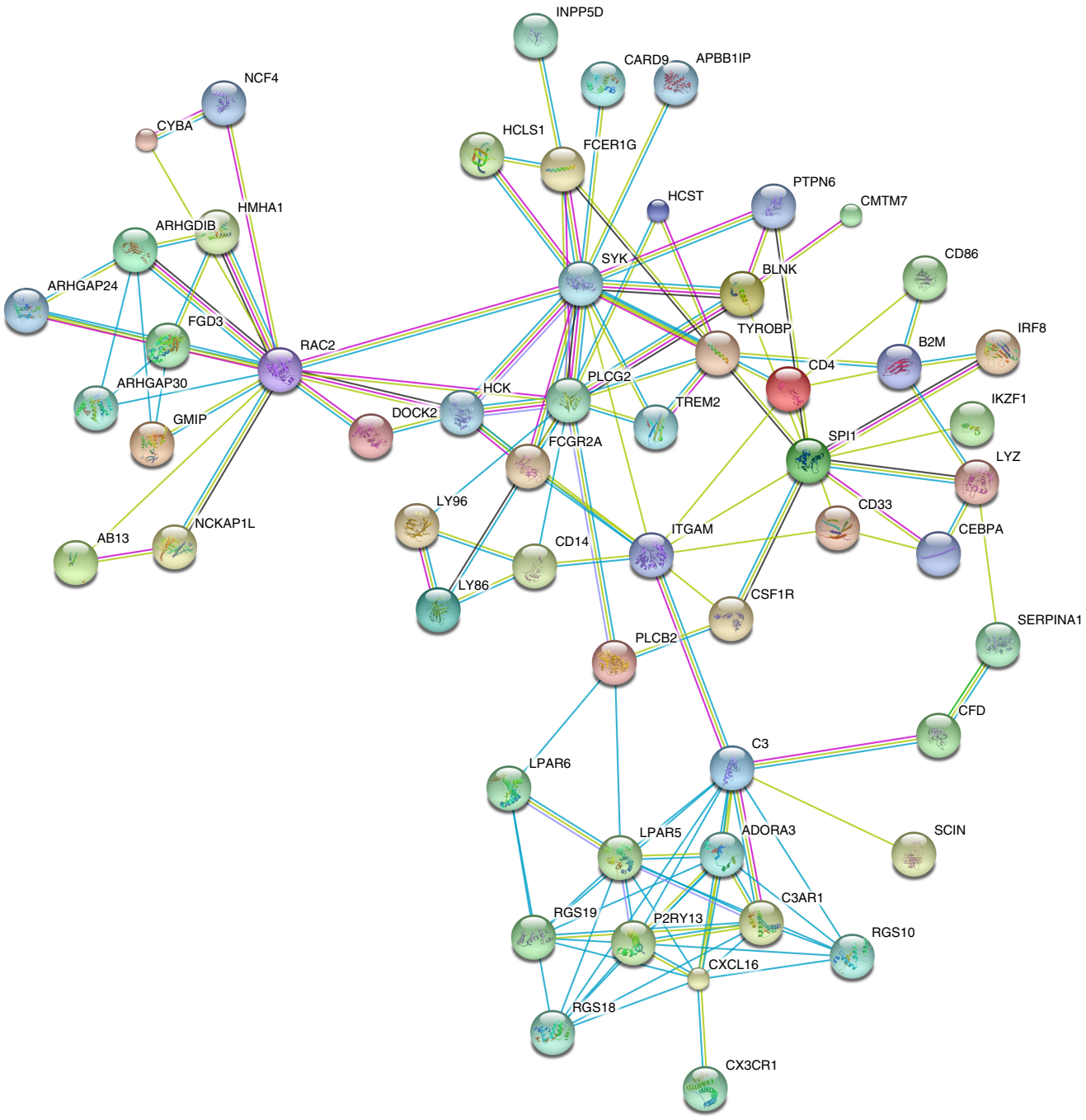

Figure 2 Protein–protein interaction network (using high-confidence human interactions from the STRING database) of 56 genes enriched for both common and rare variants associated with Alzheimer's disease risk. Colors of edges refer to the type of evidence linking the corresponding proteins: red, gene fusion; dark blue, co-occurrence; black, coexpression; magenta, experiments; cyan, databases; light green, text mining; mauve, homology. *TREM2*, *PLCG2*, and *ABI3* are highlighted by red circles, *SYK*, *CSF1R*, and *TYROBP* are highlighted by blue circles, and *INPP5D*, *SPI1*, and *CD33* identified as common variant risk loci[2,5–7] are highlighted by black circles.

TREM2 encodes a transmembrane receptor present in the plasma membrane of brain microglia (**Supplementary Fig. 15**). TREM2 protein forms an immune-receptor-signaling complex with DAP12. Receptor activation results in activation of Syk and ZAP70 signaling, which in turn activates PI3K activity and influences PLCγ2 activity[43]. In microglia, TREM2–DAP12 induces M2-like activation[44] and participates in recognition of membrane debris and amyloid deposits, resulting in microglial activation and proliferation[45–47]. When *Trem2*-homozygous-knockout or *Trem2*-heterozygous-knockout mice are crossed with *APP* transgenics that develop plaques, the size and number of microglia associated with plaques are markedly reduced[46,47].*TREM2* risk variants are located within exon 2, which is predicted to encode the conserved ligand-binding extracellular region of the protein. Any disruption in this region may attenuate or abolish TREM2 signaling, resulting in loss or decrease in TREM2 function[47].

The 56-gene interaction network identified here is enriched in immune-response genes and includes *TREM2*, *PLCG2*, *ABI3*, *SPI1*,

INPP5D, *CSF1R*, *SYK*, and *TYROBP* (**Fig. 2**). *SPI1* is a central transcription factor in microglial activation state that has a significant gene-wide association with Alzheimer's disease[5] and is in the proximity of genome-wide significant signals identified by IGAP[2]. Loss-of-function mutations in *CSF1R* cause hereditary diffuse leukoencephalopathy with spheroids, a white matter disease related to microglial dysfunction[48]. Activated microglial cells surround plaques[49,50], a finding consistently observed in Alzheimer's disease brain in humans and transgenic mouse models of Alzheimer's disease[51]. In the brains of mouse models of Alzheimer's disease, synaptic pruning associates with activated microglial signaling[52]. Pharmacological targeting of CSF1R inhibits microglial proliferation and shifts the microglial inflammatory profile to an anti-inflammatory phenotype in mouse models[53]. SYK regulates amyloid-β production and tau hyperphosphorylation[54], is affected by the INPP5D–CD2AP complex[55] encoded by two LOAD-associated genes[2], and mediates phosphorylation of PLCγ2 (ref. 56). Notably, the antihypertensive drug nilvadipine, currently in a phase 3 Alzheimer's disease clinical trial, targets *SYK* as well as *TYROBP*, a hub gene in an Alzheimer's disease–related brain expression network[38] that encodes the TREM2 complex protein DAP12.

We identified three rare coding variants in *PLCG2*, *ABI3*, and *TREM2* with genome-wide significant associations with LOAD that are part of a common innate immune response. This work provides additional evidence that the microglial response in LOAD is directly part of a causal pathway leading to disease and is not simply a downstream consequence of neurodegeneration[46,47,57,58]. Our network analysis supports this conclusion. In addition, PLCγ2, as an enzyme, represents the first classically druggable target, to our knowledge, to emerge from LOAD genetic studies. The variants described here account for a small portion of the 'missing heritability' of Alzheimer's disease. The remaining heritability may be due to a large number of common variants of small effect. For rare variants, there may be additional exonic sites with lower MAF or effect size, and/or intronic and intergenic sites. Complete resolution of the heritability for Alzheimer's disease will be facilitated by larger sample sizes and more comprehensive sequence data.

METHODS

Methods, including statements of data availability and any associated accession codes and references, are available in the online version of the paper.

Note: Any Supplementary Information and Source Data files are available in the online version of the paper.

ACKNOWLEDGMENTS

GERAD/PERADES. We thank all individuals who participated in this study. Cardiff University was supported by the Alzheimer's Society (AS; grant RF014/164) and the Medical Research Council (MRC; grants G0801418/1, MR/K013041/1, MR/L023784/1) (R. Sims is an AS Research Fellow). Cardiff University was also supported by the European Joint Programme for Neurodegenerative Disease (JPND; grant MR/L501517/1), Alzheimer's Research UK (ARUK; grant ARUK-PG2014-1), the Welsh Assembly Government (grant SGR544:CADR), and a donation from the Moondance Charitable Foundation. Cardiff University acknowledges the support of the UK Dementia Research Institute, of which J. Williams is an associate director. Cambridge University acknowledges support from the MRC. Patient recruitment for the MRC Prion Unit/UCL Department of Neurodegenerative Disease collection was supported by the UCLH/UCL Biomedical Centre and NIHR Queen Square Dementia Biomedical Research Unit. The University of Southampton acknowledges support from the AS. King's College London was supported by the NIHR Biomedical Research Centre for Mental Health and the Biomedical Research Unit for Dementia at the South London and Maudsley NHS Foundation Trust and by King's College London and the MRC. ARUK and the Big Lottery Fund provided support to Nottingham University. Ulster Garden Villages, AS, ARUK, the American Federation for Aging Research, and the Northern Ireland R&D Office provided support for Queen's University, Belfast. The Centro de Biología Molecular Severo Ochoa (CSIS-UAM), CIBERNED, Instituto de Investigación Sanitaria la Paz, University Hospital La Paz, and the Universidad Autónoma de Madrid were supported by grants from the Ministerio de Educación y Ciencia and the Ministerio de Sanidad y Consumo (Instituto de Salud Carlos III) and by an institutional grant of the Fundación Ramón Areces to the CMBSO. We thank I. Sastre and A. Martinez-Garcia for DNA preparation, and P. Gil and P. Coria for their recruitment efforts. The Department of Neurology, University Hospital Mútua de Terrassa, was supported by CIBERNED, Instituto de Salud Carlos III, Madrid, Spain, and acknowledges M.A. Pastor (University of Navarra Medical School and Center for Applied Medical Research), M. Seijo-Martinez (Hospital do Salnes), and R. Rene, J. Gascon, and J. Campdelacreu (Hospital de Bellvitage) for providing DNA samples. The Hospital de la Sant Pau, Universitat Autònoma de Barcelona, acknowledges support from the Spanish Ministry of Economy and Competitiveness (grant PI12/01311) and from the Generalitat de Catalunya (2014SGR-235). The Santa Lucia Foundation and the Fondazione Ca' Granda IRCCS Ospedale Policlinico, Italy, acknowledge the Italian Ministry of Health (grant RC 10.11.12.13/A). The Bonn samples are part of the German Dementia Competence Network (DCN) and the German Research Network on Degenerative Dementia (KNDD), which are funded by the German Federal Ministry of Education and Research (grants KND: 01G10102, 01GI0420, 01GI0422, 01GI0423, 01GI0429, 01GI0431, 01GI0433, 04GI0434; grants KNDD: 01GI1007A, 01GI0710, 01GI0711, 01GI0712, 01GI0713, 01GI0714, 01GI0715, 01GI0716, 01ET1006B). M.M.N. is a member of the German Research Foundation (DFG) cluster of excellence ImmunoSensation. Funding for Saarland University was provided by the German Federal Ministry of Education and Research (BMBF), grant 01GS08125, to M. Riemenschneider. The University of Washington was supported by grants from the US National Institutes of Health (R01-NS085419 and R01-AG044546), the Alzheimer's Association (NIRG-11-200110), and the American Federation for Aging Research (C. Cruchaga was recipient of a New Investigator Award in Alzheimer's disease). Brigham Young University was supported by the Alzheimer's Association (MNIRG-11-205368), the BYU Gerontology Program, and the US National Institutes of Health (R01-AG11380, R01-AG021136, P30-S069329-01, R01-AG042611). We also acknowledge funding from the Institute of Neurology, UCL, London, who was supported in part by ARUK via an anonymous donor, and by a fellowship to R.G. The participation of D.S., M.U., and C. Masullo in the study was completely supported by Ministero della Salute, IRCCS Research Program, Ricerca Corrente 2015–2017, Linea 2 'Malattiecomplesse e Terapie Innovative' and by the '5 × 1000' voluntary contribution. AddNeuromed is supported by InnoMed, an Integrated Project funded by the European Union's Sixth Framework Programme priority FP6-2004-LIFESCIHEALTH-5, Life Sciences, Genomics, and Biotechnology for Health. We are grateful to the Wellcome Trust for awarding a Principal Research Fellowship to D.C.R. (095317/Z/11/Z). M. Riemenschneider was funded by BMBF NGFN grant 01GS08125. B.N. was supported by the Fondazione Cassa di Risparmio di Pistoia e Pescia (grants 2014.0365, 2011.0264, 2013.0347). H. Hampel is supported by the AXA Research Fund, the Fondation Universite Pierre et Marie Curie, and the 'Fondation pour la Recherche sur Alzheimer', Paris, France. The research leading to these results has received funding from the program 'Investissements d'Avenir', ANR-10-IAIHU-06 (Agence Nationale de la Recherche-10-IA Agence Institut Hospitalo-Universitaire-6.
CHARGE. Infrastructure for the CHARGE Consortium is supported in part by National Heart, Lung, and Blood Institute grant HL105756 and for the neurology working group by AG033193 and AG049505.
Rotterdam (RS). The Rotterdam Study is funded by Erasmus Medical Center and Erasmus University, Rotterdam, the Netherlands Organization for Health Research and Development (ZonMw), the Research Institute for Diseases in the Elderly (RIDE), the Ministry of Education, Culture and Science, the Ministry for Health, Welfare and Sports, the European Commission (DG XII), and the municipality of Rotterdam. The authors are grateful to the study participants, the staff from the Rotterdam Study, and the participating general practitioners and pharmacists. Generation and management of the Illumina exome chip v1.0 array data for the Rotterdam Study (RS-I) was executed by the Human Genotyping Facility of the Genetic Laboratory of the Department of Internal Medicine (http://www.glimdna.org/), Erasmus MC, Rotterdam, the Netherlands. The Exome chip array data set was funded by the Genetic Laboratory of the Department of Internal Medicine, Erasmus MC, from the Netherlands Genomics Initiative (NGI)/Netherlands Organization for Scientific Research (NWO)-sponsored Netherlands Consortium for Healthy Aging (NCHA; project 050-060-810); the Netherlands Organization for Scientific Research (NWO; project 184021007); and by the Rainbow Project (RP10; Netherlands Exome Chip Project) of Biobanking and Biomolecular Research Infrastructure Netherlands (BBMRI-NL; http://www.bbmri.nl). Generation and management of GWAS genotype data for the Rotterdam Study (RS-I, RS-II, RS-III) was executed by the Human Genotyping Facility of the Genetic

Laboratory of the Department of Internal Medicine, Erasmus MC, Rotterdam, the Netherlands. The GWAS data sets are supported by the Netherlands Organization of Scientific Research NWO Investments (175.010.2005.011, 911-03-012), the Genetic Laboratory of the Department of Internal Medicine, Erasmus MC, the Research Institute for Diseases in the Elderly (014-93-015; RIDE2), and the Netherlands Genomics Initiative (NGI)/Netherlands Organization for Scientific Research (NWO) Netherlands Consortium for Healthy Aging (NCHA), project 050-060-810. This study makes use of an extended data set of RS-II and RS-III samples based on Illumina Omni 2.5 and 5.0 GWAS genotype data. This data set was funded by the Genetic Laboratory of the Department of Internal Medicine, the Department of Forensic Molecular Biology, and the Department of Dermatology, Erasmus MC, Rotterdam, the Netherlands. We thank M. Jhamai, S. Higgins, and M. Verkerk for their help in creating the exome chip database; C. Medina-Gomez, L. Karsten, and L. Broer for quality control and variant calling; M. Jhamai, M. Verkerk, L. Herrera, M. Peters, and C. Medina-Gomez for their help in creating the GWAS database; and L. Broer for the creation of the HRC-imputed data. Variants were called using the best practice protocol developed by M.L. Grove and colleagues as part of the CHARGE Consortium Exome Chip central calling effort. The work for this manuscript was further supported by ADAPTED: Alzheimer's Disease Apolipoprotein Pathology for Treatment Elucidation and Development (115975); the CoSTREAM project (http://www.costream.eu/); and funding from the European Union's Horizon 2020 research and innovation programme under grant agreement 667375.

AGES. The AGES study has been funded by NIA contracts N01-AG-12100 and HHSN271201200022C with contributions from NEI, NIDCD, and NHLBI, the NIA Intramural Research Program, Hjartavernd (the Icelandic Heart Association), and the Althingi (the Icelandic Parliament).

Cardiovascular Health Study (CHS). This research was supported by contracts HHSN268201200036C, HHSN268200800007C, N01HC55222, N01HC85079, N01HC85080, N01HC85081, N01HC85082, N01HC85083, and N01HC85086 and grant U01HL080295 from the National Heart, Lung, and Blood Institute (NHLBI), with additional contribution from the National Institute of Neurological Disorders and Stroke (NINDS). Additional support was provided by R01AG033193, R01AG023629, R01AG15928, and R01AG20098 and by U01AG049505 from the National Institute on Aging (NIA). The provision of genotyping data was supported in part by the National Center for Advancing Translational Sciences, CTSI grant UL1TR000124, and National Institute of Diabetes and Digestive and Kidney Disease Diabetes Research Center (DRC) grant DK063491 to the Southern California Diabetes Endocrinology Research Center. A full list of CHS principal investigators and institutions can be found at https://chs-nhlbi.org/.
The content is solely the responsibility of the authors and does not necessarily represent the official views of the US National Institutes of Health.

Framingham Heart Study. This work was supported by the National Heart, Lung, and Blood Institute's Framingham Heart Study (contracts N01-HC-25195 and HHSN268201500001I). This study was also supported by grants from the National Institute on Aging: AG033193, U01-AG049505, and AG008122 (S. Seshadri). S. Seshadri and A.L.D. were also supported by additional grants from the National Institute on Aging (R01AG049607) and the National Institute of Neurological Disorders and Stroke (R01-NS017950).

Fundació ACE. We sincerely acknowledge the collaboration of S. Ruiz, M. Rosende-Roca, A. Mauleon, L. Vargas, O. Rodriguez-Gomez, M. Alegret, A. Espinosa, G. Ortega, M. Tarragona, C. Abdelnour, and D. Sanchez. We thank all patients for their participation in this project. We are obliged to T. Port-Carbo and her family for their support of the Fundació ACE research programs. Fundació ACE collaborates with CIBERNED and is one of the participating centers of Dementia Genetics Spanish Consortium 430 (DEGESCO). CIBERNED is an Instituto de Salud Carlos III Project. A. Ruiz is supported by grant PI13/02434 (Acción Estratégica en Salud, Instituto de Salud Carlos III, Ministerio de Economía y Competitividad, Spain) and Obra Social 'La Caixa' (Barcelona, Spain).

ADGC. The US National Institutes of Health, National Institute on Aging (NIH-NIA) supported this work through the following grants: ADGC, U01 AG032984, and RC2 AG036528. Samples from the National Cell Repository for Alzheimer's Disease (NCRAD), which receives government support under a cooperative agreement grant (U24 AG21886) awarded by the National Institute on Aging (NIA), were used in this study. We thank the contributors who collected samples used in this study, as well as the patients and their families, whose help and participation made this work possible. Data for this study were prepared, archived, and distributed by the National Institute on Aging Alzheimer's Disease Data Storage Site (NIAGADS) at the University of Pennsylvania (U24-AG041689-01), NACC (U01 AG016976), NIA LOAD (Columbia University) (U24 AG026395, R01AG041797), Banner Sun Health Research Institute (P30 AG019610), Boston University (P30 AG013846, U01 AG10483, R01 CA129769, R01 MH080295, R01 AG017173, R01 AG025259, R01 AG048927, R01AG33193), Columbia University (P50 AG008702, R37 AG015473), Duke University (P30 AG028377, AG05128), Emory University (AG025688), Group Health Research Institute (UO1 AG006781, UO1 HG004610, UO1 HG006375), Indiana University (P30 AG10133), Johns Hopkins University (P50 AG005146, R01 AG020688), Massachusetts General Hospital (P50 AG005134), Mayo Clinic (P50 AG016574), Mount Sinai School of Medicine (P50 AG005138, P01 AG002219), New York University (P30 AG08051, UL1 RR029893, 5R01AG012101, 5R01AG022374, 5R01AG013616, 1RC2AG036502, 1R01AG035137), Northwestern University (P30 AG013854), Oregon Health & Science University (P30 AG008017, R01 AG026916), Rush University (P30 AG010161, R01 AG019085, R01 AG15819, R01 AG17917, R01 AG30146), TGen (R01 NS059873), University of Alabama at Birmingham (P50 AG016582), University of Arizona (R01 AG031581), University of California, Davis (P30 AG010129), University of California, Irvine (P50 AG016573), University of California, Los Angeles (P50 AG016570), University of California, San Diego (P50 AG005131), University of California, San Francisco (P50 AG023501, P01 AG019724), University of Kentucky (P30 AG028383, AG05144), University of Michigan (P50 AG008671), University of Pennsylvania (P30 AG010124), University of Pittsburgh (P50 AG005133, AG030653, AG041718, AG07562, AG02365), University of Southern California (P50 AG005142), University of Texas Southwestern (P30 AG012300), University of Miami (R01 AG027944, AG010491, AG027944, AG021547, AG019757), University of Washington (P50 AG005136), University of Wisconsin (P50 AG033514), Vanderbilt University (R01 AG019085), and Washington University (P50 AG005681, P01 AG03991). The Kathleen Price Bryan Brain Bank at Duke University Medical Center is funded by NINDS grant NS39764, NIMH MH60451, and by GlaxoSmithKline. Support was also provided by the Alzheimer's Association (L.A.F., IIRG-08-89720; M.P.-V., IIRG-05-14147), the US Department of Veterans Affairs Administration, the Office of Research and Development, the Biomedical Laboratory Research Program, and the BrightFocus Foundation (M.P.-V., A2111048). P.S.G.-H. is supported by the Wellcome Trust, the Howard Hughes Medical Institute, and the Canadian Institutes of Health Research. Genotyping of the TGEN2 cohort was supported by Kronos Science. The TGen series was also funded by NIA grant AG041232 to A.J.M. and M.J.H., the Banner Alzheimer's Foundation, the Johnnie B. Byrd Sr. Alzheimer's Institute, the Medical Research Council, and the state of Arizona and also includes samples from the following sites: the Newcastle Brain Tissue Resource (funding via the Medical Research Council, local NHS trusts, and Newcastle University), the MRC London Brain Bank for Neurodegenerative Diseases (funding via the Medical Research Council), the South West Dementia Brain Bank (funding via numerous sources including the Higher Education Funding Council for England (HEFCE), Alzheimer's Research UK (ARUK), and BRACE as well as the North Bristol NHS Trust Research and Innovation Department and DeNDRoN), the Netherlands Brain Bank (funding via numerous sources including Stichting MS Research, Brain Net Europe, Hersenstichting Nederland Breinbrekend Werk, International Parkinson Fonds, Internationale Stiching Alzheimer Onderzoek), and the Institut de Neuropatologia, Servei Anatomia Patologica, Universitat de Barcelona. ADNI data collection and sharing were funded by US National Institutes of Health grant U01 AG024904 and Department of Defense award W81XWH-12-2-0012. ADNI is funded by the National Institute on Aging, the National Institute of Biomedical Imaging and Bioengineering, and through generous contributions from the following: AbbVie, Alzheimer's Association; the Alzheimer's Drug Discovery Foundation; Araclon Biotech; BioClinica, Inc.; Biogen; Bristol-Myers Squibb Company; CereSpir, Inc.; Eisai, Inc.; Elan Pharmaceuticals, Inc.; Eli Lilly and Company; EuroImmun; F. Hoffmann-La Roche, Ltd., and its affiliated company Genentech, Inc.; Fujirebio; GE Healthcare; IXICO, Ltd.; Janssen Alzheimer Immunotherapy Research & Development, LLC.; Johnson & Johnson Pharmaceutical Research & Development, LLC.; Lumosity; Lundbeck; Merck & Co., Inc.; Meso Scale Diagnostics, LLC.; NeuroRx Research; Neurotrack Technologies; Novartis Pharmaceuticals Corporation; Pfizer, Inc.; Piramal Imaging; Servier; Takeda Pharmaceutical Company; and Transition Therapeutics. The Canadian Institutes of Health Research provide funds to support ADNI clinical sites in Canada. Private sector contributions are facilitated by the Foundation for the National Institutes of Health (http://www.fnih.org/). The grantee organization is the Northern California Institute for Research and Education, and the study is coordinated by the Alzheimer's Disease Cooperative Study at the University of California, San Diego. ADNI data are disseminated by the Laboratory for Neuro Imaging at the University of Southern California. We thank D.S. Snyder and M. Miller from the NIA who are ex-officio ADGC members.

EADI. This work was supported by INSERM, the National Foundation for Alzheimer's Disease and Related Disorders, the Institut Pasteur de Lille, and the Centre National de Génotypage. This work has been developed and supported by the LABEX (Laboratory of Excellence Program Investment for the Future) DISTALZ grant (Development of Innovative Strategies for a Transdisciplinary Approach to Alzheimer's Disease) including funding from MEL (Métropole Européenne de Lille), ERDF (European Regional Development Fund), and the Conseil Régional du Nord-Pas-de-Calais. The Three-City Study was performed

as part of collaboration between INSERM, Victor Segalen Bordeaux II University, and Sanofi-Synthelabo. The Fondation pour la Recherche Médicale funded the preparation and initiation of the study. The 3C Study was also funded by the Caisse Nationale Maladie des Travailleurs Salaries, Direction Générale de la Santé, MGEN, Institut de la Longévité, Agence Française de Sécurité Sanitaire des Produits de Santé, the Aquitaine and Bourgogne regional councils, Agence Nationale de la Recherche (ANR supported the COGINUT and COVADIS projects), Fondation de France, and the joint French Ministry of Research/INSERM 'Cohortes et Collections de Données Biologiques' program. The Lille Genopole received an unconditional grant from Eisai and was supported by the European Joint Programme for Neurodegenerative Disease (JPND: grant MR/L501517/1). The Three-City Biological Bank was developed and maintained by the Laboratory for Genomic Analysis LAG-BRC, Institut Pasteur de Lille.

Belgium sample collection. Research at the Antwerp site is funded in part by the Interuniversity Attraction Poles program of the Belgian Science Policy Office, the Foundation for Alzheimer Research (SAO-FRA), a Methusalem Excellence Grant of the Flemish Government, the Research Foundation Flanders (FWO), and the Special Research Fund of the University of Antwerp, Belgium. Authors from the Antwerp site thank the personnel of the VIB Genetic Service Facility, the Biobank of the Institute Born-Bunge, and the Departments of Neurology and Memory Clinics at the Hospital Network Antwerp and University Hospitals Leuven.

Finnish sample collection. Financial support for this project was provided by the Health Research Council of the Academy of Finland, EVO grant 5772708 of Kuopio University Hospital, and the Nordic Center of Excellence in Neurodegeneration.

Swedish sample collection. Sample collection was financially supported in part by the Swedish Brain Power network, the Marianne and Marcus Wallenberg Foundation, the Swedish Research Council (521-2010-3134), King Gustaf V and Queen Victoria's Foundation of Freemasons, the Regional Agreement on Medical Training and Clinical Research (ALF) between the Stockholm County Council and the Karolinska Institutet, the Swedish Brain Foundation, and the Swedish Alzheimer Foundation.

AMP AD University of Florida/Mayo Clinic/Institutes of Systems Biology. For human brain donations, we thank all patients and their families, without whom this work would not have been possible. This work was supported by NIH/NIA AG046139-01 (T.E.G., N.E.-T., N.P., S.G.Y.). We thank T.G. Beach (Banner Sun Health Institute) for sharing human tissue.

The Mayo Clinic Brain Bank. Data collection was supported through funding by NIA grants P50 AG016574, R01 AG032990, U01 AG046139, R01 AG018023, U01 AG006576, U01 AG006786, R01 AG025711, R01 AG017216, and R01 AG003949, NINDS grant R01 NS080820, the CurePSP Foundation, and support from the Mayo Foundation.

Sun Health Research Institute Brain and Body Donation Program of Sun City, Arizona. The Brain and Body Donation Program is supported by the National Institute of Neurological Disorders and Stroke (U24 NS072026 National Brain and Tissue Resource for Parkinson's Disease and Related Disorders), the National Institute on Aging (P30 AG19610 Arizona Alzheimer's Disease Core Center), the Arizona Department of Health Services (contract 211002, Arizona Alzheimer's Research Center), the Arizona Biomedical Research Commission (contracts 4001, 0011, 05-901, and 1001 to the Arizona Parkinson's Disease Consortium), and the Michael J. Fox Foundation for Parkinson's Research.

AUTHOR CONTRIBUTIONS

GERAD/PERADES. *Study design or conception:* R. Sims, V.E.-P., M.C.O'D., M.J.O., P.A.H., J. Williams. *Sample contribution:* M.M.N., W.M., S. Herms, A.J.F., J. Williams, A. Ramirez, M.K.L., C. Medway, K. Brown, B.M., P. Proitsi, P. Pastor, A.F.-G., I.G., H. Hampel, P.M., V.B., M. Scherer, M.L., S.R.-H., A. Braae, C. Masullo, G. Spalletta, P. Bossù, E. Sacchinelli, P.S.-J., F.J., J. Morris, C. Corcoran, J. Tschanz, M.N., R. Munger, M.J.B., E.C., V.A., M. Gallo, A.C.B., M. Dichgans, D.G., E. Scarpini, M. Mancuso, U.B., A.D., O.P., B.N., M. Riemenschneider, R.H., C. Brayne, D.C.R., A.A., C.E.S., J. Collinge, D.M., M.T., J. Clarimón, R. Sussams, S. Lovestone, S. Mead, C.H., J.P., K.M., P. Passmore, D.R., S.O.-C., J. Kauwe, M. Dunstan, A. Braddel, C. Thomas, A.M., R. Marshall, M.D.F., A. Hodges, B.V., H. Soininen, I.K., M. Daniilidou, J.U., Y.P., J.T.H., J.L., J. Turton, A.M.H., M. Aguilar, R.C., C. Fenoglio, M. Serpente, M. Arcaro, C. Caltagirone, M.D.O., A.C., S.P., M. Mayhaus, W.G., A. Lleó, J.F., R. Blesa, I.S.B., K. Brookes, C. Cupidi, R.G.M., D. Carrell, S. Sorbi, S. Moebus, M.U., A. Pilotto, J. Kornhuber, P. Bosco, S. Todd, D. Craig, J. Johnston, M. Gill, B.L., A. Lynch, N.C.F., D.S., ARUK Consortium. *Data generation:* R. Sims, R.R., S.H.-H., P.H., R.T., T.M., N.D., A. Ramirez, J. Williams, J. B., R.G., J. Hardy, A.G., J. Chapman, M. Hill. *Analysis:* R. Sims, N.B., M.V., D. Harold, E. Majounie, P.A.H. *Manuscript preparation:* R. Sims, S. Taylor, L.J., P.A.H., J. Williams. *Study supervision/management:* R. Sims, A. Ramirez, J. Williams.
ADGC. *Study design or conception:* L.A.F., J. Haines, R. Mayeux, M.A.P.-V., L.-S.W., G.D.S. *Sample contribution:* A.R.W., S. Mukherjee, P.K.C., R.C.B., P.M.A., M.S.A., D. Blacker, R.S.D., T.J.F., M.P.F., B.G., R.M.H., M.I.K., M.J.K., C.D.K., E.B.L., R.B.L., T.J.M., R.C.P., E.M.R., J.S.R., D.R.R., M. Sano, P.S.G.-H., D.W.T., C.-K.W., A.M.G., C. Cruchaga, S.G.Y., D.W.D., W.A.K., N.E.-T., R.L.A., L.G.A., S.E.A., S. Asthana, C.S.A., L.L.B., T.G.B., J.T.B., E.H.B., T.D.B., B.F.B., J.D.Bowen, A. Boxer, J.R.B., J.M.B., J.D.Buxbaum, N.J.C., C. Cao, C.S.C., C.M.C., M.M.C., S.L.C., H.C.C., D.G.C., D.H.C., C. DeCarli, M. Dick, R.D., D.A.E., K.M.F., K.B.F., D.W.F., M.R.F., S.F., T.M.F., D.R.G., M. Gearing, D.H.G., N.R.G.-R., R.C.G., J.H.G., R.L.H., L.E.H., L.S.H., M.J.H., C.M.H., B.T.H., G.P.J., E.A., L.-W.J., A. K., J.A.K., R.K., N.W.K., J.H.K., F.M.L., J.J.L., J.B.L., A.I.L., G.L., A.P.L., C.G.L., D.C.Marson, F.M., E. Masliah, W.C.M., S.M.M., A.N.M., A.C.M., M. Mesulam, B.L.M., C.A.M., J.W.M., J.C.M., J.R.M., A.J.M., S.O'B., J.M.O., V.S.P., J.E.P., H.L.P., E.P., A. Pierce, W.W.P., H.P., J.F.Q., A. Raj, M. Raskind, B.R., J.M.R., E.D.R., E.R., H.J.R., R.N.R., M.A.S., A.J.S., J.A. Schneider, L.S.S., W.W.S., A.G.S., J.A. Sonnen, S. Spina, R.A.S., R.H.S., R.E.T., J.Q.T., J.C.T., V.M.V.D., L.J.V.E., H.V.V., J.P.V., S.W., K.A.W.-B., K.C.W., J. Williamson, T.S.W., R.L.W., C.-E.Y., L.Y. *Data generation:* O.V., L.Q., Y.Z., J. Malamon, C.C.F., H. Li, J.D.Burgess, M. Allen, N.D.P., P. Chakrabarty, X.W., T.E.G., H. Hakonarson, T.W.B., B. Dombroski, W.A.K., N.E.-T., L.B.C., D. Beekly, P.W., C.T.B., R.M.C., C.C.D., E.A.C., J.R.G., D.C.Marsh, W.P., T.A.T.-W., C.B.W. *Analysis:* A.C.N., B.W.K., E.R.M., A.B.K., R.R.G., B.N.V., K.L.H.-N., G.W.B., S.B., G.J., K.L.L., C.R. *Manuscript preparation:* A.C.N., G.D.S. *Study supervision/management:* L.A.F., J.L.H., R. Mayeux, M.A.P.-V., L.-S.W., G.D.S.
CHARGE. *Study design or conception:* S.J.v.d.L., J.C.B., P.L.D.J., V. Gudnason, A.L.D., L.J.L., N.A., C.M.v.D., S. Seshadri. *Sample contribution:* J.C.B., A. Ruiz, M.L.G., C.L.S., F.J.W., T.H.M., A.S.B., M.E.G., G.E., R. Schmidt, H. Schmidt, W.T.L., O.L.L., J.J.H., A.L.F., A. Hofman, D.A.B., P.L.D.J., B.M.P., V. Gudnason, M.B., M.A.I., L.J.L. *Data generation:* S.J.v.d.L., A. Ruiz, F.R., A.G.U., J.C.B., M.L.G., H. Schmidt, J. Jakobsdottir, A.V.S., J.A.B., M.F., X.J., H. Lin, L.A.C., D.L., Q.Y., T.A., E.B., C.J.O'D., M.B., S. Ahmad, S.M.-G., H.H.A., I.H., L.T., O.S.-G., N.A., V.E., *Analysis:* S.J.v.d.L., A. Ruiz, J.C.B., M.L.G., H. Schmidt, J. Jakobsdottir, A.V.S., S.M.-G., N.A., V.C., C.C.W., S.-H.C., J.D., Y.C., S. Li, A.L.D. *Manuscript preparation:* S.J.v.d.L., A. Ruiz, J.C.B., J. Jakobsdottir, V.C., C.C.W., C.M.v.D., S. Seshadri. *Study supervision/management:* C.M.v.D., S. Seshadri, M.A.I.
EADI. *Study design or conception:* P.A., J.-C.L. *Sample contribution:* J.E., D.W., D. Hannequin, F. Pasquier, C. Berr, J.-F. Dartigues, D. Campion, C. Tzourio, P.A., J.-C.L., V.D., N.F., O.H., C. Dufouil, A. Brice, K.R., B. Dubois, K.S., M. Hiltunen, F.S.G., M.C.D.N., L.F., L. Keller, F. Panza, P. Caffarra, L. Lannfelt, M.I., C.G., O.C., C.V.B., S.E., R.V., P.P.D.D., A.S., P.S.-J., C.M.F., Y.A.B., H.T., C. Forsell, L. Lilius, A.K.-S., V. Giedraitis, L. Kilander, R. Brundin, L.C., S. Helisalmi, A.M.K., A. Haapasalo, V.S. *Data generation:* A. Boland, C. Dulary, C. Derbois, D. Bacq, J.-F. Deleuze, F. Garzia, F. Golamaully, G. Septier., R.O *Analysis:* C. Bellenguez, B.G.-B., P.A., J.-C.L. *Manuscript preparation:* C. Bellenguez, J.-C.L. *Study supervision/management:* P.A., J.-C.L.

COMPETING FINANCIAL INTERESTS

The authors declare competing financial interests: details are available in the online version of the paper.

1. Gatz, M. *et al.* Role of genes and environments for explaining Alzheimer disease. *Arch. Gen. Psychiatry* **63**, 168–174 (2006).
2. Lambert, J.-C. *et al.* Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci for Alzheimer's disease. *Nat. Genet.* **45**, 1452–1458 (2013).
3. Harold, D. *et al.* Genome-wide association study identifies variants at *CLU* and *PICALM* associated with Alzheimer's disease. *Nat. Genet.* **41**, 1088–1093 (2009).
4. Lambert, J.-C. *et al.* Genome-wide association study identifies variants at *CLU* and *CR1* associated with Alzheimer's disease. *Nat. Genet.* **41**, 1094–1099 (2009).
5. Escott-Price, V. *et al.* Gene-wide analysis detects two new susceptibility genes for Alzheimer's disease. *PLoS One* **9**, e94661 (2014).
6. Hollingworth, P. *et al.* Common variants at *ABCA7*, *MS4A6A*/*MS4A4E*, *EPHA1*, *CD33* and *CD2AP* are associated with Alzheimer's disease. *Nat. Genet.* **43**, 429–435 (2011).
7. Naj, A.C. *et al.* Common variants at *MS4A4*/*MS4A6E*, *CD2AP*, *CD33* and *EPHA1* are associated with late-onset Alzheimer's disease. *Nat. Genet.* **43**, 436–441 (2011).
8. Ruiz, A. *et al.* Toward fine mapping and functional characterization of genome-wide association study–identified locus rs74615166 (*TRIP4*) for Alzheimer's disease. *Alzheimers Dement.* **10**, 257–P258 (2014).
9. Jonsson, T. *et al.* Variant of *TREM2* associated with the risk of Alzheimer's disease. *N. Engl. J. Med.* **368**, 107–116 (2013).
10. Jonsson, T. *et al.* A mutation in *APP* protects against Alzheimer's disease and age-related cognitive decline. *Nature* **488**, 96–99 (2012).
11. Guerreiro, R. *et al. TREM2* variants in Alzheimer's disease. *N. Engl. J. Med.* **368**, 117–127 (2013).

12. Seshadri, S. *et al.* Genome-wide analysis of genetic loci associated with Alzheimer disease. *J. Am. Med. Assoc.* **303**, 1832–1840 (2010).
13. Escott-Price, V. *et al.* Common polygenic variation enhances risk prediction for Alzheimer's disease. *Brain* **138**, 3673–3684 (2015).
14. Bodmer, W. & Bonilla, C. Common and rare variants in multifactorial susceptibility to common diseases. *Nat. Genet.* **40**, 695–701 (2008).
15. Pritchard, J.K. Are rare variants responsible for susceptibility to complex diseases? *Am. J. Hum. Genet.* **69**, 124–137 (2001).
16. Schork, N.J., Murray, S.S., Frazer, K.A. & Topol, E.J. Common vs. rare allele hypotheses for complex diseases. *Curr. Opin. Genet. Dev.* **19**, 212–219 (2009).
17. Surakka, I. *et al.* The impact of low-frequency and rare variants on lipid levels. *Nat. Genet.* **47**, 589–597 (2015).
18. Vardarajan, B.N. *et al.* Coding mutations in *SORL1* and Alzheimer disease. *Ann. Neurol.* **77**, 215–227 (2015).
19. Vardarajan, B.N. *et al.* Rare coding mutations identified by sequencing of Alzheimer disease genome-wide association studies loci. *Ann. Neurol.* **78**, 487–498 (2015).
20. Steinberg, S. *et al.* Loss-of-function variants in *ABCA7* confer risk of Alzheimer's disease. *Nat. Genet.* **47**, 445–447 (2015).
21. Logue, M.W. *et al.* Two rare *AKAP9* variants are associated with Alzheimer's disease in African Americans. *Alzheimers Dement.* **10**, 609–618 (2014).
22. Jun, G. *et al. PLXNA4* is associated with Alzheimer disease and modulates tau phosphorylation. *Ann. Neurol.* **76**, 379–392 (2014).
23. Hunkapiller, J. *et al.* A rare coding variant alters *UNC5C* function and predisposes to Alzheimer's disease. *Alzheimers Dement.* **9**, 853 (2013).
24. Wetzel-Smith, M.K. *et al.* A rare mutation in *UNC5C* predisposes to late-onset Alzheimer's disease and increases neuronal cell death. *Nat. Med.* **20**, 1452–1457 (2014).
25. Richards, A.L. *et al.* Exome arrays capture polygenic rare variant contributions to schizophrenia. *Hum. Mol. Genet.* **25**, 1001–1007 (2016).
26. Wessel, J. *et al.* Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. *Nat. Commun.* **6**, 5897 (2015).
27. Igartua, C. *et al.* Ethnic-specific associations of rare and low-frequency DNA sequence variants with asthma. *Nat. Commun.* **6**, 5965 (2015).
28. Tachmazidou, I. *et al.* A rare functional cardioprotective *APOC3* variant has risen in frequency in distinct population isolates. *Nat. Commun.* **4**, 2872 (2013).
29. Huyghe, J.R. *et al.* Exome array analysis identifies new loci and low-frequency variants influencing insulin processing and secretion. *Nat. Genet.* **45**, 197–201 (2013).
30. Willer, C.J., Li, Y. & Abecasis, G.R. METAL: fast and efficient meta-analysis of genomewide association scans. *Bioinformatics* **26**, 2190–2191 (2010).
31. R Development Core Team. *R: A Language and Environment for Statistical Computing* (R Foundation for Statistical Computing, 2014).
32. Das, S. *et al.* Next-generation genotype imputation service and methods. *Nat. Genet.* **48**, 1284–1287 (2016).
33. McCarthy, S. *et al.* A reference panel of 64,976 haplotypes for genotype imputation. *Nat. Genet.* **48**, 1279–1283 (2016).
34. Jin, S.C. *et al.* Coding variants in *TREM2* increase risk for Alzheimer's disease. *Hum. Mol. Genet.* **23**, 5838–5846 (2014).
35. Lu, Y., Liu, W. & Wang, X. *TREM2* variants and risk of Alzheimer's disease: a meta-analysis. *Neurol. Sci.* **36**, 1881–1888 (2015).
36. Cruchaga, C. *et al.* GWAS of cerebrospinal fluid tau levels identifies risk variants for Alzheimer's disease. *Neuron* **78**, 256–268 (2013).
37. International Genomics of Alzheimer's Disease Consortium (IGAP).. Convergent genetic and expression data implicate immunity in Alzheimer's disease. *Alzheimers Dement.* **11**, 658–671 (2015).
38. Zhang, Y. *et al.* Purification and characterization of progenitor and mature human astrocytes reveals transcriptional and functional differences with mouse. *Neuron* **89**, 37–53 (2016).
39. Milner, J.D. PLAID: a syndrome of complex patterns of disease and unique phenotypes. *J. Clin. Immunol.* **35**, 527–530 (2015).
40. Fairfax, B.P. *et al.* Innate immune activity conditions the effect of regulatory variants upon monocyte gene expression. *Science* **343**, 1246949 (2014).
41. Sekino, S. *et al.* The NESH/Abi-3-based WAVE2 complex is functionally distinct from the Abi-1-based WAVE2 complex. *Cell Commun. Signal.* **13**, 41 (2015).
42. Nolz, J.C. *et al.* The WAVE2 complex regulates actin cytoskeletal reorganization and CRAC-mediated calcium entry during T cell activation. *Curr. Biol.* **16**, 24–34 (2006).
43. Xing, J., Titus, A.R. & Humphrey, M.B. The TREM2–DAP12 signaling pathway in Nasu–Hakola disease: a molecular genetics perspective. *Res. Rep. Biochem.* **5**, 89–100 (2015).
44. Neumann, H. & Takahashi, K. Essential role of the microglial triggering receptor expressed on myeloid cells-2 (TREM2) for central nervous tissue immune homeostasis. *J. Neuroimmunol.* **184**, 92–99 (2007).
45. Painter, M.M. *et al.* TREM2 in CNS homeostasis and neurodegenerative disease. *Mol. Neurodegener.* **10**, 43 (2015).
46. Ulrich, J.D. *et al. In vivo* measurement of apolipoprotein E from the brain interstitial fluid using microdialysis. *Mol. Neurodegener.* **8**, 13 (2013).
47. Wang, Y. *et al.* TREM2 lipid sensing sustains the microglial response in an Alzheimer's disease model. *Cell* **160**, 1061–1071 (2015).
48. Rademakers, R. *et al.* Mutations in the colony stimulating factor 1 receptor (*CSF1R*) gene cause hereditary diffuse leukoencephalopathy with spheroids. *Nat. Genet.* **44**, 200–205 (2011).
49. Perlmutter, L.S., Barron, E. & Chui, H.C. Morphologic association between microglia and senile plaque amyloid in Alzheimer's disease. *Neurosci. Lett.* **119**, 32–36 (1990).
50. Wisniewski, H.M., Wegiel, J., Wang, K.C. & Lach, B. Ultrastructural studies of the cells forming amyloid in the cortical vessel wall in Alzheimer's disease. *Acta Neuropathol.* **84**, 117–127 (1992).
51. Schwab, C., Klegeris, A. & McGeer, P.L. Inflammation in transgenic mouse models of neurodegenerative disorders. *Biochim. Biophys. Acta* **1802**, 889–902 (2010).
52. Hong, S. *et al.* Complement and microglia mediate early synapse loss in Alzheimer mouse models. *Science* **352**, 712–716 (2016).
53. Olmos-Alonso, A. *et al.* Pharmacological targeting of CSF1R inhibits microglial proliferation and prevents the progression of Alzheimer's-like pathology. *Brain* **139**, 891–907 (2016).
54. Paris, D. *et al.* The spleen tyrosine kinase (Syk) regulates Alzheimer amyloid-β production and tau hyperphosphorylation. *J. Biol. Chem.* **289**, 33927–33944 (2014).
55. Bao, M. *et al.* CD2AP/SHIP1 complex positively regulates plasmacytoid dendritic cell receptor signaling by inhibiting the E3 ubiquitin ligase Cbl. *J. Immunol.* **189**, 786–792 (2012).
56. Kurosaki, T. & Tsukada, S. BLNK: connecting Syk and Btk to calcium signals. *Immunity* **12**, 1–5 (2000).
57. Wang, Y. *et al.* TREM2-mediated early microglial response limits diffusion and toxicity of amyloid plaques. *J. Exp. Med.* **213**, 667–675 (2016).
58. Yuan, P. *et al.* TREM2 haplodeficiency in mice and humans impairs the microglia barrier function leading to decreased amyloid compaction and severe axonal dystrophy. *Neuron* **90**, 724–739 (2016).

Rebecca Sims[1,281], Sven J van der Lee[2,281], Adam C Naj[3,281], Céline Bellenguez[4,5,6,281], Nandini Badarinarayan[1], Johanna Jakobsdottir[7], Brian W Kunkle[8], Anne Boland[9], Rachel Raybould[1], Joshua C Bis[10], Eden R Martin[8,11], Benjamin Grenier-Boley[4,5,6], Stefanie Heilmann-Heimbach[12,13], Vincent Chouraki[14,15], Amanda B Kuzma[16], Kristel Sleegers[17,18], Maria Vronskaya[1], Agustin Ruiz[19], Robert R Graham[20], Robert Olaso[9], Per Hoffmann[12,13,21], Megan L Grove[22], Badri N Vardarajan[23–25], Mikko Hiltunen[26,27], Markus M Nöthen[12,13], Charles C White[28], Kara L Hamilton-Nelson[8], Jacques Epelbaum[29], Wolfgang Maier[30,31], Seung-Hoan Choi[14,32], Gary W Beecham[8,11], Cécile Dulary[9], Stefan Herms[12,13,21], Albert V Smith[7,33], Cory C Funk[34], Céline Derbois[9], Andreas J Forstner[12,13], Shahzad Ahmad[2], Hongdong Li[34], Delphine Bacq[9], Denise Harold[35], Claudia L Satizabal[14,15], Otto Valladares[16], Alessio Squassina[36], Rhodri Thomas[1], Jennifer A Brody[10], Liming Qu[16], Pascual Sánchez-Juan[37], Taniesha Morgan[1], Frank J Wolters[2], Yi Zhao[16], Florentino Sanchez Garcia[38], Nicola Denning[1], Myriam Fornage[39], John Malamon[16], Maria Candida Deniz Naranjo[38], Elisa Majounie[1], Thomas H Mosley[40], Beth Dombroski[16], David Wallon[41,42], Michelle K Lupton[43,44], Josée Dupuis[32], Patrice Whitehead[8], Laura Fratiglioni[45,46], Christopher Medway[47], Xueqiu Jian[39], Shubhabrata Mukherjee[48], Lina Keller[46], Kristelle Brown[47], Honghuang Lin[49], Laura B Cantwell[16], Francesco Panza[50], Bernadette McGuinness[51],

Sonia Moreno-Grau[19], Jeremy D Burgess[52], Vincenzo Solfrizzi[53], Petra Proitsi[43], Hieab H Adams[2], Mariet Allen[52], Davide Seripa[54], Pau Pastor[55], L Adrienne Cupples[15,32], Nathan D Price[34], Didier Hannequin[42,56], Ana Frank-García[57,58,59], Daniel Levy[14,15,60], Paramita Chakrabarty[61], Paolo Caffarra[62,63], Ina Giegling[64], Alexa S Beiser[15,32], Vilmantas Giedraitis[65], Harald Hampel[66–68], Melissa E Garcia[69], Xue Wang[52], Lars Lannfelt[65], Patrizia Mecocci[55], Gudny Eiriksdottir[7], Paul K Crane[48], Florence Pasquier[70,71], Virginia Boccardi[55], Isabel Henández[19], Robert C Barber[72], Martin Scherer[73], Lluis Tarraga[19], Perrie M Adams[74], Markus Leber[75], Yuning Chen[32], Marilyn S Albert[76], Steffi Riedel-Heller[77], Valur Emilsson[7,78], Duane Beekly[79], Anne Braae[80], Reinhold Schmidt[81], Deborah Blacker[82,83], Carlo Masullo[84], Helena Schmidt[85], Rachelle S Doody[86], Gianfranco Spalletta[87], W T Longstreth Jr[88,89], Thomas J Fairchild[90], Paola Bossù[87], Oscar L Lopez[91,92], Matthew P Frosch[93], Eleonora Sacchinelli[87], Bernardino Ghetti[94], Qiong Yang[32], Ryan M Huebinger[95], Frank Jessen[30,31,75], Shuo Li[32], M Ilyas Kamboh[96,97], John Morris[98,99], Oscar Sotolongo-Grau[19], Mindy J Katz[100], Chris Corcoran[101], Melanie Dunstan[1], Amy Braddel[1], Charlene Thomas[1], Alun Meggy[1], Rachel Marshall[1], Amy Gerrish[1], Jade Chapman[1], Miquel Aguilar[102,103], Sarah Taylor[1], Matt Hill[1], Mònica Díez Fairén[59,102], Angela Hodges[104], Bruno Vellas[105], Hilkka Soininen[27], Iwona Kloszewska[106], Makrina Daniilidou[107], James Uphill[108], Yogen Patel[43], Joseph T Hughes[43], Jenny Lord[47], James Turton[47], Annette M Hartmann[64], Roberta Cecchetti[55], Chiara Fenoglio[109], Maria Serpente[109], Marina Arcaro[109], Carlo Caltagirone[87], Maria Donata Orfei[87], Antonio Ciaramella[87], Sabrina Pichler[110], Manuel Mayhaus[110], Wei Gu[110], Alberto Lleó[59,111], Juan Fortea[59,111], Rafael Blesa[59,111], Imelda S Barber[80], Keeley Brookes[80], Chiara Cupidi[112], Raffaele Giovanni Maletta[112], David Carrell[113], Sandro Sorbi[114,115], Susanne Moebus[116], Maria Urbano[54], Alberto Pilotto[54], Johannes Kornhuber[117], Paolo Bosco[118], Stephen Todd[51], David Craig[51], Janet Johnston[51], Michael Gill[119], Brian Lawlor[119], Aoibhinn Lynch[119], Nick C Fox[120], John Hardy[120], ARUKConsortium, Roger L Albin[121–123], Liana G Apostolova[124–127], Steven E Arnold[128], Sanjay Asthana[129–131], Craig S Atwood[129–131], Clinton T Baldwin[132], Lisa L Barnes[133–135], Sandra Barral[23–25], Thomas G Beach[136], James T Becker[137], Eileen H Bigio[138,139], Thomas D Bird[88,140], Bradley F Boeve[141], James D Bowen[142], Adam Boxer[143], James R Burke[144], Jeffrey M Burns[145], Joseph D Buxbaum[146–148], Nigel J Cairns[149], Chuanhai Cao[150], Chris S Carlson[151], Cynthia M Carlsson[130,131], Regina M Carney[152], Minerva M Carrasquillo[52], Steven L Carroll[153], Carolina Ceballos Diaz[61], Helena C Chui[154], David G Clark[155,156], David H Cribbs[157], Elizabeth A Crocco[152], Charles DeCarli[158], Malcolm Dick[159], Ranjan Duara[160], Denis A Evans[161], Kelley M Faber[125], Kenneth B Fallon[162], David W Fardo[163], Martin R Farlow[126], Steven Ferris[164], Tatiana M Foroud[125], Douglas R Galasko[165], Marla Gearing[166,167], Daniel H Geschwind[168], John R Gilbert[8,11], Neill R Graff-Radford[52,169], Robert C Green[170], John H Growdon[171], Ronald L Hamilton[172], Lindy E Harrell[173], Lawrence S Honig[23], Matthew J Huentelman[174], Christine M Hulette[175], Bradley T Hyman[171], Gail P Jarvik[176,177], Erin Abner[178], Lee-Way Jin[179], Gyungah Jun[132,180,181], Anna Karydas[143], Jeffrey A Kaye[182,183], Ronald Kim[184], Neil W Kowall[185,186], Joel H Kramer[187], Frank M LaFerla[188], James J Lah[189], James B Leverenz[190], Allan I Levey[189], Ge Li[113,140], Andrew P Lieberman[191], Kathryn L Lunetta[180], Constantine G Lyketsos[192], Daniel C Marson[173], Frank Martiniuk[193], Deborah C Mash[194], Eliezer Masliah[165,195], Wayne C McCormick[48], Susan M McCurry[196], Andrew N McDavid[151], Ann C McKee[185,186], Marsel Mesulam[139,197], Bruce L Miller[143], Carol A Miller[198], Joshua W Miller[179], John C Morris[149,199], Jill R Murrell[94,125], Amanda J Myers[152], Sid O'Bryant[200], John M Olichney[158], Vernon S Pankratz[201], Joseph E Parisi[202], Henry L Paulson[121,123], William Perry[8], Elaine Peskind[113], Aimee Pierce[157], Wayne W Poon[159], Huntington Potter[203], Joseph F Quinn[182,183], Ashok Raj[150], Murray Raskind[113], Barry Reisberg[164,204], Christiane Reitz[24,25,205], John M Ringman[206], Erik D Roberson[173], Ekaterina Rogaeva[207], Howard J Rosen[143], Roger N Rosenberg[208], Mark A Sager[130], Andrew J Saykin[125,127], Julie A Schneider[133,135,209], Lon S Schneider[154,210], William W Seeley[143], Amanda G Smith[150], Joshua A Sonnen[211], Salvatore Spina[94], Robert A Stern[185], Russell H Swerdlow[145], Rudolph E Tanzi[171], Tricia A Thornton-Wells[212], John Q Trojanowski[213], Juan C Troncoso[214], Vivianna M Van Deerlin[213], Linda J Van Eldik[215], Harry V Vinters[206,216], Jean Paul Vonsattel[217], Sandra Weintraub[139,218], Kathleen A Welsh-Bohmer[144,219], Kirk C Wilhelmsen[220], Jennifer Williamson[23], Thomas S Wingo[189], Randall L Woltjer[221], Clinton B Wright[222], Chang-En Yu[48], Lei Yu[133,135], Fabienne Garzia[9], Feroze Golamaully[9], Gislain Septier[9], Sebastien Engelborghs[18,223], Rik Vandenberghe[223,224], Peter P De Deyn[18,223], Carmen Muñoz Fernadez[38], Yoland Aladro Benito[38], Hakan Thonberg[225,226], Charlotte Forsell[225,226], Lena Lilius[225,226], Anne Kinhult-Stählbom[225,226], Lena Kilander[65],

RoseMarie Brundin[65], Letizia Concari[62,63], Seppo Helisalmi[27,227], Anne Maria Koivisto[27,227], Annakaisa Haapasalo[27,227], Vincent Dermecourt[228], Nathalie Fievet[4–6,229], Olivier Hanon[229], Carole Dufouil[230,231], Alexis Brice[232,233], Karen Ritchie[234], Bruno Dubois[235–238], Jayanadra J Himali[14], C Dirk Keene[211], JoAnn Tschanz[101], Annette L Fitzpatrick[89,239], Walter A Kukull[89], Maria Norton[101], Thor Aspelund[7,240], Eric B Larson[48,241], Ron Munger[101], Jerome I Rotter[242], Richard B Lipton[100], María J Bullido[58,59,243], Albert Hofman[2], Thomas J Montine[211], Eliecer Coto[244], Eric Boerwinkle[22,245], Ronald C Petersen[141], Victoria Alvarez[244], Fernando Rivadeneira[2,246,247], Eric M Reiman[174,248–250], Maura Gallo[112], Christopher J O'Donnell[15], Joan S Reisch[251], Amalia Cecilia Bruni[112], Donald R Royall[252], Martin Dichgans[253,254], Mary Sano[148], Daniela Galimberti[109], Peter St George-Hyslop[207,255], Elio Scarpini[109], Debby W Tsuang[113,140], Michelangelo Mancuso[256], Ubaldo Bonuccelli[256], Ashley R Winslow[257], Antonio Daniele[258], Chuang-Kuo Wu[259], GERAD/PERADES, CHARGE, ADGC, EADI, Oliver Peters[260], Benedetta Nacmias[114,115], Matthias Riemenschneider[110], Reinhard Heun[31], Carol Brayne[261], David C Rubinsztein[255], Jose Bras[120,262], Rita Guerreiro[120,262], Ammar Al-Chalabi[263], Christopher E Shaw[263], John Collinge[108], David Mann[264], Magda Tsolaki[265], Jordi Clarimón[59,111], Rebecca Sussams[266], Simon Lovestone[267], Michael C O'Donovan[1], Michael J Owen[1], Timothy W Behrens[20], Simon Mead[108], Alison M Goate[147], Andre G Uitterlinden[2,108,109], Clive Holmes[140], Carlos Cruchaga[98,99], Martin Ingelsson[65], David A Bennett[133,135], John Powell[43], Todd E Golde[61,268], Caroline Graff[45,226], Philip L De Jager[269], Kevin Morgan[47], Nilufer Ertekin-Taner[52,169], Onofre Combarros[37], Bruce M Psaty[10,59,89,270], Peter Passmore[51], Steven G Younkin[52,169], Claudine Berr[235,271,272], Vilmundur Gudnason[7,33], Dan Rujescu[64], Dennis W Dickson[52], Jean-François Dartigues[273], Anita L DeStefano[15,32], Sara Ortega-Cubero[59,274,275], Hakon Hakonarson[276], Dominique Campion[41,42], Merce Boada[19], John Keoni Kauwe[277], Lindsay A Farrer[14,132,180,181,185], Christine Van Broeckhoven[17,18], M Arfan Ikram[2,278], Lesley Jones[1], Jonathan L Haines[279], Christophe Tzourio[232,280], Lenore J Launer[69], Valentina Escott-Price[1], Richard Mayeux[23–25], Jean-François Deleuze[9], Najaf Amin[2], Peter A Holmans[1], Margaret A Pericak-Vance[8,11], Philippe Amouyel[4–6,70,283], Cornelia M van Duijn[2,282], Alfredo Ramirez[12,31,75,282], Li-San Wang[16,282], Jean-Charles Lambert[4–6,282], Sudha Seshadri[14,15,282], Julie Williams[1,282] & Gerard D Schellenberg[16,282]

[1]Institute of Psychological Medicine and Clinical Neurosciences, MRC Centre for Neuropsychiatric Genetics and Genomics, Cardiff University, Cardiff, UK. [2]Department of Epidemiology, Erasmus Medical Center, Rotterdam, the Netherlands. [3]Department of Biostatistics and Epidemiology/Center for Clinical Epidemiology and Biostatistics, University of Pennsylvania Perelman School of Medicine, Philadelphia, Pennsylvania, USA. [4]INSERM, U1167, RID-AGE–Risk Factors and Molecular Determinants of Aging-Related Diseases, Lille, France. [5]Institut Pasteur de Lille, Lille, France. [6]University Lille, U1167–Excellence Laboratory LabEx DISTALZ, Lille, France. [7]Icelandic Heart Association, Kopavogur, Iceland. [8]John P. Hussman Institute for Human Genomics, University of Miami, Miami, Florida, USA. [9]CEA/Institut de Génomique, Centre National de Génotypage, Evry, France. [10]Cardiovascular Health Research Unit, Department of Medicine, University of Washington, Seattle, Washington, USA. [11]Dr. John T. Macdonald Foundation, Department of Human Genetics, University of Miami, Miami, Florida, USA. [12]Institute of Human Genetics, University of Bonn, Bonn, Germany. [13]Department of Genomics, Life & Brain Center, University of Bonn, Bonn, Germany. [14]Boston University School of Medicine, Boston, Massachusetts, USA. [15]Framingham Heart Study, Framingham, Massachusetts, USA. [16]Penn Neurodegeneration Genomics Center, Department of Pathology and Laboratory Medicine, University of Pennsylvania Perelman School of Medicine, Philadelphia, Pennsylvania, USA. [17]Neurodegenerative Brain Diseases Group, Department of Molecular Genetics, VIB, Antwerp, Belgium. [18]Institute Born-Bunge, University of Antwerp, Antwerp, Belgium. [19]Research Center and Memory Clinic of Fundació ACE, Institut Català de Neurociències Aplicades, Barcelona, Spain. [20]Immunology Biomarkers Group, Genentech, South San Francisco, California, USA. [21]Division of Medical Genetics, University Hospital and Department of Biomedicine, University of Basel, Basel, Switzerland. [22]School of Public Health, Human Genetics Center, University of Texas Health Science Center at Houston, Houston, Texas, USA. [23]Taub Institute on Alzheimer's Disease and the Aging Brain, Department of Neurology, Columbia University, New York, New York, USA. [24]Gertrude H. Sergievsky Center, Columbia University, New York, New York, USA. [25]Department of Neurology, Columbia University, New York, New York, USA. [26]Institute of Biomedicine, University of Eastern Finland, Kuopio, Finland. [27]Department of Neurology, Kuopio University Hospital, Kuopio, Finland. [28]Program in Translational NeuroPsychiatric Genomics, Institute for the Neurosciences, Departments of Neurology and Psychiatry, Brigham and Women's Hospital, Boston, Massachusetts, USA. [29]UMR 894, Center for Psychiatry and Neuroscience, INSERM, Université Paris Descartes, Paris, France. [30]German Center for Neurodegenerative Diseases (DZNE), Bonn, Germany. [31]Department of Psychiatry and Psychotherapy, University of Bonn, Bonn, Germany. [32]Department of Biostatistics, Boston University School of Public Health, Boston, Massachusetts, USA. [33]Faculty of Medicine, University of Iceland, Reykjavik, Iceland. [34]Institute for Systems Biology, Seattle, Washington, USA. [35]School of Biotechnology, Dublin City University, Dublin, Ireland. [36]Section of Neuroscience and Clinical Pharmacology, Department of Biomedical Sciences, University of Cagliari, Cagliari, Italy. [37]Neurology Service and CIBERNED, 'Marqués de Valdecilla' University Hospital (University of Cantabria and IFIMAV), Santander, Spain. [38]Department of Immunology, Hospital Universitario Doctor Negrín, Las Palmas de Gran Canaria, Spain. [39]Brown Foundation Institute of Molecular Medicine, University of Texas Health Sciences Center at Houston, Houston, Texas, USA. [40]Departments of Medicine, Geriatrics, Gerontology and Neurology, University of Mississippi Medical Center, Jackson, Mississippi, USA. [41]Centre Hospitalier du Rouvray, Sotteville les Rouen, France. [42]INSERM U1079, Rouen University, IRIB, Normandy University, Rouen, France. [43]Department of Basic and Clinical Neuroscience, Institute of Psychiatry, Psychology and Neuroscience, King's College London, London, UK. [44]Genetic Epidemiology, QIMR Berghofer Medical Research Institute, Herston, Queensland, Australia. [45]Department of Geriatric Medicine, Karolinska University Hospital Huddinge, Stockholm, Sweden. [46]Aging Research Center, Department of Neurobiology, Care Sciences and Society, Karolinska Institutet and Stockholm University, Stockholm, Sweden. [47]Institute of Genetics, Queen's Medical Centre, University of Nottingham, Nottingham, UK. [48]Department of Medicine, University of Washington, Seattle, Washington, USA. [49]Section of Computational Biomedicine, Department of Medicine, Boston University School of Medicine, Boston, Massachusetts, USA. [50]Neurodegenerative Disease Unit, Department of Basic Medicine, Neuroscience, and Sense Organs, University of Bari Aldo Moro, Bari, Italy. [51]Centre for Public Health, School of Medicine, Dentistry and Biomedical Sciences, Queen's University, Belfast, UK. [52]Department of Neuroscience, Mayo Clinic, Jacksonville, Florida, USA. [53]Geriatric Medicine–Memory Unit and Rare Disease Centre, University of Bari Aldo Moro, Bari, Italy. [54]Geriatric Unit and Gerontology–Geriatrics Research Laboratory, Department of Medical Sciences,

IRCCS Casa Sollievo della Sofferenza, San Giovanni Rotondo, Italy. [55]Section of Gerontology and Geriatrics, Department of Medicine, University of Perugia, Perugia, Italy. [56]Department of Neurology, Rouen University Hospital, Rouen, France. [57]Department of Neurology, University Hospital La Paz, Universidad Autónoma de Madrid, Madrid, Spain. [58]Instituto de Investigación Sanitaria Hospital la Paz (IdiPAZ), Madrid, Spain. [59]Centro de Investigación Biomédica en Red de Enfermedades Neurodegenerativas (CIBERNED), Instituto de Salud Carlos III, Madrid, Spain. [60]National Heart, Lung, and Blood Institute, Bethesda, Maryland, USA. [61]Center for Translational Research in Neurodegenerative Disease, Department of Neuroscience, University of Florida, Gainesville, Florida, USA. [62]Department of Neuroscience, University of Parma, Parma, Italy. [63]Center for Cognitive Disorders AUSL, Parma, Italy. [64]Department of Psychiatry, Martin Luther University Halle-Wittenberg, Halle, Germany. [65]Department of Public Health/Geriatrics, Uppsala University, Uppsala, Sweden. [66]AXA Research Fund and UPMC Chair, Paris, France. [67]Sorbonne Universités, Université Pierre et Marie Curie, Paris, France. [68]Institut de la Mémoire et de la Maladie d'Alzheimer (IM2A) and Institut du Cerveau et de la Moelle Épinière (ICM), Département de Neurologie, Hôpital de la Pitié-Salpêtrière, Paris, France. [69]Laboratory of Epidemiology and Population Sciences, National Institute on Aging, Bethesda, Maryland, USA. [70]Centre Hospitalier Universitaire de Lille, Epidemiology and Public Health Department, Lille, France. [71]INSERM UMRS 1171, CNR-Maj, Lille, France. [72]Department of Pharmacology and Neuroscience, University of North Texas Health Science Center, Fort Worth, Texas, USA. [73]Department of Primary Medical Care, University Medical Centre Hamburg-Eppendorf, Hamburg, Germany. [74]Department of Psychiatry, University of Texas Southwestern Medical Center, Dallas, Texas, USA. [75]Department of Psychiatry and Psychotherapy, University of Cologne, Cologne, Germany. [76]Department of Neurology, Johns Hopkins University, Baltimore, Maryland, USA. [77]Institute of Social Medicine, Occupational Health and Public Health, University of Leipzig, Leipzig, Germany. [78]Faculty of Pharmaceutical Sciences, University of Iceland, Reykjavik, Iceland. [79]National Alzheimer's Coordinating Center, University of Washington, Seattle, Washington, USA. [80]Schools of Life Sciences and Medicine, University of Nottingham, Nottingham, UK. [81]Department of Neurology, Clinical Division of Neurogeriatrics, Medical University Graz, Graz, Austria. [82]Department of Epidemiology, Harvard School of Public Health, Boston, Massachusetts, USA. [83]Department of Psychiatry, Massachusetts General Hospital/Harvard Medical School, Boston, Massachusetts, USA. [84]Department of Neurology, Catholic University of Rome, Rome, Italy. [85]Institute of Molecular Biology and Biochemistry, Medical University Graz, Graz, Austria. [86]Alzheimer's Disease and Memory Disorders Center, Baylor College of Medicine, Houston, Texas, USA. [87]Experimental Neuropsychiatry Laboratory, IRCCS Santa Lucia Foundation, Department of Clinical and Behavioural Neurology, Rome, Italy. [88]Department of Neurology, University of Washington, Seattle, Washington, USA. [89]Department of Epidemiology, University of Washington, Seattle, Washington, USA. [90]Office of Strategy and Measurement, University of North Texas Health Science Center, Fort Worth, Texas, USA. [91]Department of Psychiatry, University of Pittsburgh, Pittsburgh, Pennsylvania, USA. [92]Department of Neurology, University of Pittsburgh, Pittsburgh, Pennsylvania, USA. [93]C.S. Kubik Laboratory for Neuropathology, Massachusetts General Hospital, Charlestown, Massachusetts, USA. [94]Department of Pathology and Laboratory Medicine, Indiana University, Indianapolis, Indiana, USA. [95]Department of Surgery, University of Texas Southwestern Medical Center, Dallas, Texas, USA. [96]Alzheimer's Disease Research Center, University of Pittsburgh, Pittsburgh, Pennsylvania, USA. [97]Department of Human Genetics, University of Pittsburgh, Pittsburgh, Pennsylvania, USA. [98]Department of Psychiatry, Washington University School of Medicine, St. Louis, Missouri, USA. [99]Hope Center Program on Protein Aggregation and Neurodegeneration, Washington University School of Medicine, St. Louis, Missouri, USA. [100]Department of Neurology, Albert Einstein College of Medicine, Bronx, New York, USA. [101]Department of Mathematics and Statistics, Utah State University, Logan, Utah, USA. [102]Fundació per la Recerca Biomèdica i Social Mútua Terrassa, Terrassa, Barcelona, Spain. [103]Memory Unit, Department of Neurology, Hospital Universitario Mútua Terrassa, Terrassa, Barcelona, Spain. [104]Department of Old Age Psychiatry, Institute of Psychiatry, Psychology and Neuroscience, King's College London, London, UK. [105]INSERM U558, University of Toulouse, Toulouse, France. [106]Elderly and Psychiatric Disorders Department, Medical University of Lodz, Lodz, Poland. [107]Department of Health Sciences, Psychiatry for the Elderly, University of Leicester, Leicester, UK. [108]Department of Neurodegenerative Disease, MRC Prion Unit, UCL Institute of Neurology, London, UK. [109]Department of Pathophysiology and Transplantation, University of Milan, Fondazione Ca' Granda, IRCCS Ospedale Policlinico, Milan, Italy. [110]Department of Psychiatry and Psychotherapy, University Hospital, Saarland, Germany. [111]Memory Unit, Neurology Department and Sant Pau Biomedical Research Institute, Hospital de la Santa Creu i Sant Pau, Autonomous University of Barcelona, Barcelona, Spain. [112]Regional Neurogenetic Centre (CRN), ASP Catanzaro, Lamezia Terme, Italy. [113]Department of Psychiatry and Behavioral Sciences, University of Washington School of Medicine, Seattle, Washington, USA. [114]NEUROFARBA (Department of Neuroscience, Psychology, Drug Research and Child Health), University of Florence, Florence, Italy. [115]IRCCS 'Don Carlo Gnocchi', Florence, Italy. [116]Institute for Medical Informatics, Biometry and Epidemiology, University Hospital of Essen, University Duisburg-Essen, Essen, Germany. [117]Department of Psychiatry and Psychotherapy, University of Erlangen-Nuremberg, Erlangen, Germany. [118]Istituto di Ricovero e Cura a Carattere Scientifico (IRCCS) Associazione Oasi Maria Santissima Srl, Troina, Italy. [119]Mercers Institute for Research on Aging, St. James Hospital and Trinity College, Dublin, Ireland. [120]Department of Molecular Neuroscience, UCL, Institute of Neurology, London, UK. [121]Department of Neurology, University of Michigan, Ann Arbor, Michigan, USA. [122]Geriatric Research, Education and Clinical Center (GRECC), VA Ann Arbor Healthcare System (VAAAHS), Ann Arbor, Michigan, USA. [123]Michigan Alzheimer Disease Center, Ann Arbor, Michigan, USA. [124]Indiana Alzheimer's Disease Center, Indiana University School of Medicine, Indianapolis, Indiana, USA. [125]Department of Medical and Molecular Genetics, Indiana University, Indianapolis, Indiana, USA. [126]Department of Neurology, Indiana University, Indianapolis, Indiana, USA. [127]Department of Radiology and Imaging Sciences, Indiana University, Indianapolis, Indiana, USA. [128]Department of Psychiatry, University of Pennsylvania Perelman School of Medicine, Philadelphia, Pennsylvania, USA. [129]Geriatric Research, Education and Clinical Center (GRECC), University of Wisconsin, Madison, Wisconsin, USA. [130]Department of Medicine, University of Wisconsin, Madison, Wisconsin, USA. [131]Wisconsin Alzheimer's Disease Research Center, Madison, Wisconsin, USA. [132]Department of Medicine (Genetics Program), Boston University, Boston, Massachusetts, USA. [133]Department of Neurological Sciences, Rush University Medical Center, Chicago, Illinois, USA. [134]Department of Behavioral Sciences, Rush University Medical Center, Chicago, Illinois, USA. [135]Rush Alzheimer's Disease Center, Rush University Medical Center, Chicago, Illinois, USA. [136]Civin Laboratory for Neuropathology, Banner Sun Health Research Institute, Phoenix, Arizona, USA. [137]Departments of Psychiatry, Neurology, and Psychology, University of Pittsburgh School of Medicine, Pittsburgh, Pennsylvania, USA. [138]Department of Pathology, Northwestern University Feinberg School of Medicine, Chicago, Illinois, USA. [139]Cognitive Neurology and Alzheimer's Disease Center, Northwestern University Feinberg School of Medicine, Chicago, Illinois, USA. [140]VA Puget Sound Health Care System/GRECC, Seattle, Washington, USA. [141]Department of Neurology, Mayo Clinic, Rochester, Minnesota, USA. [142]Swedish Medical Center, Seattle, Washington, USA. [143]Department of Neurology, University of California, San Francisco, San Francisco, California, USA. [144]Department of Medicine, Duke University, Durham, North Carolina, USA. [145]University of Kansas Alzheimer's Disease Center, University of Kansas Medical Center, Kansas City, Kansas, USA. [146]Department of Genetics and Genomic Sciences, Mount Sinai School of Medicine, New York, New York, USA. [147]Department of Neuroscience, Mount Sinai School of Medicine, New York, New York, USA. [148]Department of Psychiatry, Mount Sinai School of Medicine, New York, New York, USA. [149]Department of Pathology and Immunology, Washington University, St. Louis, Missouri, USA. [150]USF Health Byrd Alzheimer's Institute, University of South Florida, Tampa, Florida, USA. [151]Fred Hutchinson Cancer Research Center, Seattle, Washington, USA. [152]Department of Psychiatry and Behavioral Sciences, Miller School of Medicine, University of Miami, Miami, Florida, USA. [153]Department of Pathology and Laboratory Medicine, Medical University of South Carolina, Charleston, South Carolina, USA. [154]Department of Neurology, University of Southern California, Los Angeles, California, USA. [155]Department of Neurology, Medical University of South Carolina, Charleston, South Carolina, USA. [156]Department of Neurology, Ralph H. Johnson VA Medical Center, Charleston, South Carolina, USA. [157]Department of Neurology, University of California, Irvine, Irvine, California, USA. [158]Department of Neurology, University of California, Davis, Sacramento, California, USA. [159]Institute for Memory Impairments and Neurological Disorders, University of California, Irvine, Irvine, California, USA. [160]Wien Center for Alzheimer's Disease and Memory Disorders, Mount Sinai Medical Center, Miami Beach, Florida, USA. [161]Rush Institute for Healthy Aging, Department of Internal Medicine, Rush University Medical Center, Chicago, Illinois, USA. [162]Department of Pathology, University of Alabama at Birmingham, Birmingham, Alabama, USA. [163]Sanders-Brown Center on Aging, Department of Biostatistics, University of Kentucky, Lexington, Kentucky, USA. [164]Department of Psychiatry, New York University, New York, New York, USA. [165]Department of Neurosciences, University of California, San Diego, La Jolla, California, USA. [166]Department of Pathology and Laboratory Medicine, Emory University, Atlanta, Georgia, USA. [167]Emory Alzheimer's Disease Center, Emory University, Atlanta, Georgia, USA. [168]Neurogenetics Program, University of California, Los Angeles, Los Angeles, California, USA. [169]Department of Neurology, Mayo Clinic, Jacksonville, Florida, USA. [170]Division of Genetics, Department of Medicine and Partners Center for Personalized Genetic Medicine, Brigham and Women's Hospital and Harvard Medical School, Boston, Massachusetts, USA. [171]Department of Neurology, Massachusetts General Hospital/Harvard Medical School, Boston, Massachusetts, USA. [172]Department of Pathology (Neuropathology), University of Pittsburgh, Pittsburgh, Pennsylvania, USA. [173]Department of Neurology, University of Alabama at Birmingham, Birmingham, Alabama, USA. [174]Neurogenomics Division, Translational Genomics Research Institute, Phoenix, Arizona, USA. [175]Department of Pathology, Duke University, Durham, North Carolina, USA. [176]Department of Genome Sciences, University of Washington, Seattle, Washington, USA. [177]Department of Medicine (Medical Genetics), University of Washington, Seattle, Washington, USA. [178]Sanders-Brown Center on Aging, College of Public Health, Department of Epidemiology, University of Kentucky, Lexington, Kentucky, USA. [179]Department of Pathology and Laboratory Medicine, University of California, Davis, Sacramento, California, USA. [180]Department of Biostatistics, Boston University, Boston, Massachusetts, USA.

[181]Department of Ophthalmology, Boston University, Boston, Massachusetts, USA. [182]Department of Neurology, Oregon Health & Science University, Portland, Oregon, USA. [183]Department of Neurology, Portland Veterans Affairs Medical Center, Portland, Oregon, USA. [184]Department of Pathology and Laboratory Medicine, University of California, Irvine, Irvine, California, USA. [185]Department of Neurology, Boston University, Boston, Massachusetts, USA. [186]Department of Pathology, Boston University, Boston, Massachusetts, USA. [187]Department of Neuropsychology, University of California, San Francisco, San Francisco, California, USA. [188]Department of Neurobiology and Behavior, University of California, Irvine, Irvine, California, USA. [189]Department of Neurology, Emory University, Atlanta, Georgia, USA. [190]Cleveland Clinic Lou Ruvo Center for Brain Health, Cleveland Clinic, Cleveland, Ohio, USA. [191]Department of Pathology, University of Michigan, Ann Arbor, Michigan, USA. [192]Department of Psychiatry, Johns Hopkins University, Baltimore, Maryland, USA. [193]Department of Medicine–Pulmonary, New York University, New York, New York, USA. [194]Department of Neurology, University of Miami, Miami, Florida, USA. [195]Department of Pathology, University of California, San Diego, La Jolla, California, USA. [196]School of Nursing Northwest Research Group on Aging, University of Washington, Seattle, Washington, USA. [197]Department of Neurology, Northwestern University Feinberg School of Medicine, Chicago, Illinois, USA. [198]Department of Pathology, University of Southern California, Los Angeles, California, USA. [199]Department of Neurology, Washington University, St. Louis, Missouri, USA. [200]Internal Medicine, Division of Geriatrics, University of North Texas Health Science Center, Fort Worth, Texas, USA. [201]Department of Internal Medicine, University of New Mexico Health Sciences Center, Albuquerque, New Mexico, USA. [202]Department of Laboratory Medicine and Pathology, Mayo Clinic, Rochester, Minnesota, USA. [203]Department of Neurology, University of Colorado School of Medicine, Aurora, Colorado, USA. [204]Alzheimer's Disease Center, New York University, New York, New York, USA. [205]Department of Epidemiology, Columbia University, New York, New York, USA. [206]Department of Neurology, University of California, Los Angeles, Los Angeles, California, USA. [207]Tanz Centre for Research in Neurodegenerative Disease, University of Toronto, Toronto, Ontario, Canada. [208]Department of Neurology, University of Texas Southwestern Medical Center, Dallas, Texas, USA. [209]Department of Pathology (Neuropathology), Rush University Medical Center, Chicago, Illinois, USA. [210]Department of Psychiatry, University of Southern California, Los Angeles, California, USA. [211]Department of Pathology, University of Washington, Seattle, Washington, USA. [212]Translational Medicine, Novartis Institutes for Biomedical Research, Cambridge, Massachusetts, USA. [213]Department of Pathology and Laboratory Medicine, University of Pennsylvania Perelman School of Medicine, Philadelphia, Pennsylvania, USA. [214]Department of Pathology, Johns Hopkins University, Baltimore, Maryland, USA. [215]Sanders-Brown Center on Aging, Department of Anatomy and Neurobiology, University of Kentucky, Lexington, Kentucky, USA. [216]Department of Pathology and Laboratory Medicine, University of California, Los Angeles, Los Angeles, California, USA. [217]Taub Institute on Alzheimer's Disease and the Aging Brain, Department of Pathology, Columbia University, New York, New York, USA. [218]Department of Psychiatry, Northwestern University Feinberg School of Medicine, Chicago, Illinois, USA. [219]Department of Psychiatry and Behavioral Sciences, Duke University, Durham, North Carolina, USA. [220]Department of Genetics, University of North Carolina at Chapel Hill, Chapel Hill, North Carolina, USA. [221]Department of Pathology, Oregon Health & Science University, Portland, Oregon, USA. [222]Evelyn F. McKnight Brain Institute, Department of Neurology, Miller School of Medicine, University of Miami, Miami, Florida, USA. [223]Department of Neurology and Memory Clinic, Hospital Network Antwerp, Antwerp, Belgium. [224]Laboratory for Cognitive Neurology, Department of Neurology, University of Leuven, Leuven, Belgium. [225]Department of Geriatric Medicine, Genetics Unit, Karolinska University Hospital Huddinge, Stockholm, Sweden. [226]Department of Neurobiology, Care Sciences and Society, KIADRC, Karolinska Institutet, Stockholm, Sweden. [227]Institute of Clinical Medicine/Neurology, University of Eastern Finland, Kuopio, Finland. [228]CHU Lille, Memory Center of Lille (Centre Mémoire de Ressources et de Recherche), Lille, France. [229]University Paris Descartes, EA 4468, AP–HP, Hôpital Broca, Geriatrics Department, Paris, France. [230]University of Bordeaux, Neuroepidemiology, Bordeaux, France. [231]INSERM, Neuroepidemiology, UMR 897, Bordeaux, France. [232]INSERM U1127, CNRS UMR 7225, Sorbonne Universités, UPMC Université Paris 06, UMRS 1127, Institut du Cerveau et de la Moelle Épinière, Paris, France. [233]AP–HP, Department of Genetics, Pitié-Salpêtrière Hospital, Paris, France. [234]INSERM U1061, La Colombière Hospital, Montpellier, France. [235]Institut de la Mémoire et de la Maladie d'Alzheimer (IM2A), Département de Neurologie, Hôpital de la Pitié-Salpêtrière, AP–HP, Paris, France. [236]Institut des Neurosciences Translationnelles de Paris (IHU-A-ICM), Institut du Cerveau et de la Moelle Épinière (ICM), Paris, France. [237]INSERM, CNRS, UMRS 975, Institut du Cerveau et de la Moelle Épinière (ICM), Paris, France. [238]Sorbonne Universités, Université Pierre et Marie Curie, Hôpital de la Pitié-Salpêtrière, AP–HP, Paris, France. [239]Department of Family Medicine, University of Washington, Seattle, Washington, USA. [240]Centre for Public Health, University of Iceland, Reykjavik, Iceland. [241]Group Health Research Institute, Group Health, Seattle, Washington, USA. [242]Institute for Translational Genomics and Population Sciences, Los Angeles BioMedical Research Institute at Harbor-UCLA Medical Center, Torrance, California, USA. [243]Centro de Biología Molecular Severo Ochoa (CSIC-UAM), Madrid, Spain. [244]Molecular Genetics Laboratory-Hospital, University of Central Asturias, Oviedo, Spain. [245]Human Genome Sequencing Center, Baylor College of Medicine, Houston, Texas, USA. [246]Department of Internal Medicine, Erasmus University Medical Center, Rotterdam, the Netherlands. [247]Netherlands Consortium on Health Aging and National Genomics Initiative, Leiden, the Netherlands. [248]Arizona Alzheimer's Consortium, Phoenix, Arizona, USA. [249]Banner Alzheimer's Institute, Phoenix, Arizona, USA. [250]Department of Psychiatry, University of Arizona, Phoenix, Arizona, USA. [251]Department of Clinical Sciences, University of Texas Southwestern Medical Center, Dallas, Texas, USA. [252]Departments of Psychiatry, Medicine, and Family and Community Medicine and South Texas Veterans Health Administration Geriatric Research Education and Clinical Center (GRECC), University of Texas Health Science Center at San Antonio, San Antonio, Texas, USA. [253]Institute for Stroke and Dementia Research, Klinikum der Universität München, Munich, Germany. [254]German Center for Neurodegenerative Diseases (DZNE), Munich, Germany. [255]Cambridge Institute for Medical Research, University of Cambridge, Cambridge, UK. [256]Department of Experimental and Clinical Medicine, Neurological Institute, University of Pisa, Pisa, Italy. [257]PharmaTherapeutics Clinical Research, Pfizer Worldwide Research and Development, Cambridge, Massachusetts, USA. [258]Institute of Neurology, Catholic University of Sacred Hearth, Rome, Italy. [259]Departments of Neurology, Pharmacology, and Neuroscience, Texas Tech University Health Science Center, Lubbock, Texas, USA. [260]Department of Psychiatry, Charité University Medicine, Berlin, Germany. [261]Institute of Public Health, University of Cambridge, Cambridge, UK. [262]Department of Medical Sciences, Institute of Biomedicine (iBiMED), University of Aveiro, Aveiro, Portugal. [263]Institute of Psychiatry, Psychology and Neuroscience, King's College London, London, UK. [264]Institute of Brain, Behaviour and Mental Health, Clinical and Cognitive Neuroscience Research Group, University of Manchester, Manchester, UK. [265]3rd Department of Neurology, Medical School, Aristotle University of Thessaloniki, Thessaloniki, Greece. [266]Division of Clinical Neurosciences, School of Medicine, University of Southampton, Southampton, UK. [267]Department of Psychiatry, University of Oxford, Oxford, UK. [268]Florida Alzheimer's Disease Research Center, Gainesville, Florida, USA. [269]Center for Translational and Systems Neuroimmunology, Department of Neurology, Columbia University Medical Center, New York, New York, USA. [270]Department of Health Services, University of Washington, Seattle, Washington, USA. [271]Memory Research and Resources Center, CMRR of Montpellier, Department of Neurology, Hospital Gui de Chauliac, Montpellier, France. [272]Department of Neurology, Montpellier University, Montpellier, France. [273]Memory Research and Resources Center, CMRR de Bordeaux, Bordeaux, France. [274]Neurogenetics Laboratory, Division of Neurosciences, Centre for Applied Medical Research, University of Navarra School of Medicine, Pamplona, Spain. [275]Department of Neurology, Complejo Asistencial Universitario de Palencia, Palencia, Spain. [276]Center for Applied Genomics, Children's Hospital of Philadelphia, Philadelphia, Pennsylvania, USA. [277]Departments of Biology and Neuroscience, Brigham Young University, Provo, Utah, USA. [278]Department of Neurology, Erasmus MC University Medical Center, Rotterdam, the Netherlands. [279]Department of Epidemiology and Biostatistics, Case Western Reserve University, Cleveland, Ohio, USA. [280]University of Bordeaux, Neuroepidemiology, UMR 897, Bordeaux, France. [281]These authors contributed equally to this work. [282]These authors jointly directed this work. Correspondence should be addressed to S.J.v.d.L. (s.vanderlee@erasmusmc.nl), J. Williams (williamsj@cardiff.ac.uk) or G.D.S. (gerardsc@mail.med.upenn.edu)

ONLINE METHODS

Genotyping and quality control. *Stage 1. GERAD/PERADES.* Genotyping was performed at Life and Brain, Bonn, Germany, with Illumina HumanExome BeadChip v1.0 (n = 247,870 variants) or v1.1 (n = 242,901 variants). Illumina's GenTrain version 2.0 clustering algorithm in GenomeStudio or zCall[59] was used for genotype calling. Quality control filters were implemented for sample call rate excluding samples with >1% missingness, excess autosomal heterozygosity excluding outliers based on <1% and >1% MAF separately, sex discordance, relatedness excluding one of each pair related with identity by descent (IBD) ≥ 0.125 (the level expected for first cousins), and population outliers (non-European ancestry). Variants were filtered on the basis of call rate excluding variants with >1% missingness, genotype cluster separation excluding variants with a separation score <0.4, and Hardy–Weinberg equilibrium excluding variants with $P_{HWE} < 1 \times 10^{-4}$. Ten principal components were extracted using EIGENSTRAT, including the first three principal components as covariates had the maximum impact on the genomic control inflation factor, λ (ref. 60). After quality control, 6,000 LOAD cases and 2,974 elderly controls (version 1.0, 4,093 LOAD cases and 1,599 controls; version 1.1, 1,907 LOAD cases and 1,375 controls) remained. The version 1.0 array had 244,412 variants available for analysis and 239,814 remained for the version 1.1 array.

CHARGE. All four CHARGE cohorts were genotyped for the Illumina HumanExome BeadChip v1.0. To increase the quality of the rare variant genotype calls, the genotypes for all four studies were jointly called with 62,266 samples from 11 studies at the University of Texas HSC at Houston[61]. Quality control procedures for the genotype data were performed both centrally at UT Houston and at each study. The central quality control procedures have been described previously[61]. Minimum quality control included (i) concordance checking with GWAS data and removal of problematic samples; (ii) removal of individuals with low genotype completion rate (<90%); (iii) removal of variants with low genotype call rate (<95%); (iv) removal of individuals with sex mismatches; (v) removal of one individual from duplicate pairs; (vi) removal of first-degree relatives on the basis of genetically calculated relatedness (identity by state (IBS) > 0.45), with cases retained over controls; and (vii) removal of variants not called in over 5% of the individuals and those that deviated significantly form the expected Hardy–Weinberg equilibrium proportions ($P < 1 \times 10^{-6}$).

ADGC. Genotyping was performed in subsets at four centers: NorthShore, Miami, WashU, and CHOP (CHOP and ADC7 data sets) on the Illumina HumanExome BeadChip v1.0. One variant, rs75932628 (p.Arg47His) in *TREM2*, clustered poorly across all ADGC cohorts and was therefore regenotyped using a TaqMan assay. Data on all samples underwent standard quality control procedures applied to GWAS, including exclusion of variants with call rates <95% and filtering out of samples with call rate <95%. Variants with MAF >0.01 were evaluated for departure from Hardy–Weinberg equilibrium and any variants with $P_{HWE} < 10^{-6}$ were excluded. Population substructure within each of the five subsets (NorthShore, Miami, WashU, CHOP, and ADC7) was examined using principal-component analysis in EIGENSTRAT[62], and population outliers (>6 s.d. from the mean) were excluded from further analyses; the first three principal components were adjusted for as covariates in association testing. Prior to analysis, we harmonized the alternate and reference alleles over all data sets. See **Supplementary Table 3** for an overview of cohort genotype calling and quality control procedures. All sample genotyping and quality control were performed with blinding to participants' disease status.

Stage 2. Twenty-two variants were successfully designed for replication genotyping on the Agena Bioscience MassARRAY platform. Genotyping was performed at Life and Brain, Bonn, Germany, and the Centre National de Génotypage (CNG), Paris, France. Twenty-one variants were successfully genotyped, with one variant (rs147163004 in *ASTN2*) failing visual cluster plot inspection. An additional nine variants were successfully genotyped using the Agena Bioscience MassARRAY platform or Thermo Fisher TaqMan assays at the CNG, Paris, France, in a subset of the replication samples, n = 16,850 (7,755 cases, 9,095 controls).

GERAD/PERADES and ACE quality control. Filters were implemented for sample call rate, excluding samples with >10% missingness and excess autosomal heterozygosity via visual inspection. Variants were filtered on the basis of call rate, excluding variants with >10% missingness, and Hardy–Weinberg equilibrium, excluding variants with $P_{HWE} < 1 \times 10^{-5}$ in either cases or controls.

IGAP and EADI QC. Variants were genotyped in three different panels, and quality control was performed in each panel separately. Samples with more than three missing genotypes were excluded, as were males heterozygous for X chromosome variants present within the genotyped panels. Variants were excluded on the basis of missingness >5%, Hardy–Weinberg equilibrium (in cases and controls separately) $< 1 \times 10^{-5}$, and differential missingness between cases and controls $< 1 \times 10^{-5}$, for each country cohort. All variants passed quality control. Principal components were determined using previously described methods.

Stage 3. Replication was performed using genotypes from 23 ADGC data sets as described above. The genotyping arrays used have been described in detail before for most data sets, except for the CHAP, NBB, TARCC, and WHICAP data sets. CHAP and WHICAP data sets were genotyped on the Illumina OmniExpress-24 array, while NBB was genotyped on the Illumina 1M platform. TARCC first-wave subjects were genotyped using the Affymetrix 6.0 microarray chip, while subjects in the second wave (172 cases and 74 controls) were genotyped using the Illumina HumanOmniExpress-24 BeadChip. Second-wave TARCC subjects (TARCC2) were genotyped together with 84 cases and 115 controls from second-wave samples ascertained at the University of Miami and Vanderbilt University. All samples used in stage 3 were imputed to the HRC haplotype reference panel[32,33], which includes 64,976 haplotypes with 39,235,157 SNPs that allows imputation down to an unprecedented MAF of 0.00008.

Prior to imputation, all genotype data underwent quality control procedures that have been described extensively elsewhere[2,7]. Imputation was performed on the Michigan Imputation Server (https://imputationserver.sph.umich.edu/) running Minimac3[63,64]. Genotypes from genome-wide, high-density SNP genotyping arrays for 16,175 Alzheimer's disease cases and 17,176 individuals with normal cognition were imputed. Across all samples, 39,235,157 SNPs were imputed, with the actual number of SNPs imputed for each individual varying based on the regional density of array genotypes available. As a subset of these samples had also been genotyped as part of stage 1, we examined the imputation quality for critical variants by comparing imputed genotypes to those directly genotyped by the exome array; overall concordance was >99%, while concordance among alternate allele genotypes (heterozygotes and alternate allele homozygotes) was >88.5% on average (n = 13,000 samples). Concordance between stage 3 imputed genotypes and exome chip genotypes for replicated SNPs is reported in **Supplementary Table 6**.

Analysis. *Stage 1.* We tested association with LOAD using logistic regression modeling for common and low-frequency variants (MAF > 1%) and implementing maximum-likelihood estimation using the score test and seqMeta package for rare variation (MAF ≤ 1%). Analyses were conducted globally in the GERAD/PERADES consortium and for each contributing center in the CHARGE and ADGC consortia under two models: (i) an 'unadjusted' model, which included minimal adjustment for possible population stratification, using country of origin and the first three principal components from principal-component analysis, and (ii) an 'adjusted' model, which included covariates for age and sex, as well as country of origin and the first three principal components. Age was defined as the age at onset of clinical symptoms for cases and the age at last interview for controls with normal cognition.

Meta-analysis for common and low-frequency variants was undertaken in METAL using a fixed-effects inverse-variance-weighted meta-analysis. Rare variants were meta-analyzed in the SeqMeta R package. In the SeqMeta pipeline, cohort-level analyses generated score statistics through the function 'prepScores()', which were captured in *.Rdata objects. These *.Rdata objects contain the necessary information to meta-analyze SKAT analyses: the individual SNP scores, MAF, and a covariance matrix for each unit of aggregation. Using the 'singlesnpMeta()' and 'skatOmeta()' functions of SeqMeta, the *.Rdata objects for individual studies were meta-analyzed. The seqMeta coefficients and standard errors can be interpreted as a 'one-step' approximation to the maximum-likelihood estimates. Monomorphic variants in individual studies were not excluded as they contribute to the MAF information. Three independent analysts confirmed the meta-analysis results.

In the GERAD/PERADES consortium, 1,740 participants (888 LOAD cases and 852 controls) did not have age information available and were excluded from the adjusted analyses. Therefore, 16,160 cases and 17,967 controls were included in the unadjusted analyses, and 15,272 cases and 17,115 controls were included in the adjusted analyses. The primary analysis used the unadjusted model given the larger sample size this provided. See **Supplementary Figure 2** for quantile–quantile plots of unadjusted and adjusted analyses.

Stage 2. We tested association with LOAD using the score test and seqMeta package. Analyses were conducted under the two models described above, in the analysis groups indicated in **Supplementary Table 2**. Analyses were undertaken globally in the GERAD/PERADES cohort and by country in the IGAP cohorts, with the EADI1 cohort only including French participants and the ACE cohort including only Spanish participants. Following the format of the IGAP mega meta-analysis[2], four principal components were included for the EADI1 data set and one was included in the Italian and Swedish IGAP clusters. Meta-analysis was undertaken in the SeqMeta R package.

Stage 3. The association analyses performed followed stage 1 and stage 2 analytical procedures described below, and only variants in *ABI3*, *PLCG2*, and *TREM2* were examined. For gene-based testing, 10 variants in *ABI3*, 35 variants in *PLCG2*, and 13 variants in *TREM2* were examined.

Pathway and gene set enrichment analysis. The eight biological pathway clusters previously identified as enriched for association in the IGAP data set[37] were tested for enrichment in this rare variation study (**Supplementary Table 15**) to test whether the biological enrichments observed in common variants also apply to rare variants. Genes were defined without surrounding genomic sequence, as this yielded the most significant excess of enriched pathways in the common variation data set[37]. Gene-wide SKAT-O *P* values for the variants of interest were combined using Fisher's combined probability test. Given the low degree of LD[65] between rare variants, our primary analyses did not control for LD between pathway genes. However, as a secondary analysis, the *APOE* region was removed and, for each pair of pathway genes within 1 Mb of each other, the gene with the more significant SKAT-O *P* value was removed. This highly conservative procedure removes any potential bias in the enrichment test both from LD between the genes and dropping less significant genes from the analysis.

We also performed pathway analyses on the rare variant data presented using all 9,816 pathways used previously. The top pathways are related to lipoprotein particles, cholesterol efflux, B cell differentiation, and immune response, and they closely parallel the common variant results (**Supplementary Table 16**).

Protein interaction analysis. Previous analysis of normal brain co-expression networks identified four gene modules that were enriched for common variants associated with Alzheimer's disease risk in the IGAP GWAS. Each of these four modules was also found to be enriched for immune-related genes. The 151 genes present in two or more of these four modules were particularly strongly enriched for IGAP GWAS association. This set of 151 co-expressed genes thus contains genes of relevance to Alzheimer's disease etiology. To identify these genes and clarify biological relationships between them for future study, protein interaction analysis was performed. First, a list of high-confidence (confidence score > 0.7) human protein–protein interactions was downloaded from the latest version (v10) of the STRING database (http://string-db.org/). Then, protein interaction networks were generated as follows:

1. Choose a gene to start the network (the 'seed' gene).
2. For each remaining gene in the set of 151 genes, add it to the network if its corresponding protein shows a high-confidence protein interaction with a protein corresponding to any gene already in the network.
3. Repeat step 2 until no more genes can be added.
4. Note the number of genes in the network.
5. Repeat, choosing each of the 151 genes in turn as the seed gene.

The largest protein interaction network resulting from this procedure resulted in a network of 56 genes connected by high-confidence protein interactions. To test whether this network was larger than expected by chance, given the total number of protein–protein interactions for each gene, random sets of 151 genes were generated, with each gene chosen to have the same total number of protein–protein interactions as the corresponding gene in the actual data. Protein networks were generated for each gene as described above, and the size of the largest such network was compared to the observed 56-gene network. 1,000 random gene sets were generated, and none of them yielded a protein interaction network as large as 56 genes. Note that the procedure for generating the protein interaction network relies only on protein interaction data and is agnostic to the strength of GWAS or rare variant associations for each gene. Thus, the strength of genetic association in the set of 56 network genes can be tested relative to that in the original set of 151 genes without bias.

Gene set enrichment analysis of the protein network. The set of 56 network genes was tested for association enrichment in the IGAP GWAS using ALIGATOR[66], as was done in the original pathway analysis, using a range of *P*-value thresholds for defining significant SNPs (and thus the genes containing those SNPs). The same analysis was also performed on the 95 genes in the module overlap but not the protein interaction network (**Supplementary Table 17**). It can be seen that the 56 network genes account for most of the enrichment signal observed in the set of 151 module overlap genes.

The set of 56 network genes, the set of 151 module overlap genes, and the set of 95 genes in the module overlap but not the network were tested for enrichment of association signal in variants with MAF <1% using the gene set enrichment method described above. Both the set of 151 genes ($P = 1.17 \times 10^{-6}$) and the subset of 56 genes ($P = 1.08 \times 10^{-7}$) show highly significant enrichment for association in the rare variants with MAF <1%. It can be seen that the 56 network genes account for most of the enrichment signal observed in the set of 151 module overlap genes (**Supplementary Table 17**). Again, the subset of 56 genes accounts for most of the enrichment signal observed in the set of 151 genes, as the remaining 95 genes have only nominally significant enrichment ($P = 0.043$). Both the set of 151 genes ($P = 5.15 \times 10^{-5}$) and the subset of 56 genes ($P = 2.98 \times 10^{-7}$) show significant enrichment under a conservative analysis excluding the *APOE* region and correcting for possible LD between the genes (**Supplementary Table 17**). Thus, the rare variants show convincing replication of the biological signal observed in the common variant GWAS, and, furthermore, the protein network analysis has refined this signal to a set of 56 interacting genes. Given that *TREM2* has a highly significant gene-wide *P* value ($P = 1.01 \times 10^{-13}$) among variants with MAF <1%, enrichment analyses were run omitting it. Both the set of 151 genes ($P = 2.78 \times 10^{-3}$) and the subset of 56 genes ($P = 0.010$) (**Supplementary Table 18**) still showed significant enrichment of signal, suggesting that the contribution of rare variants to disease susceptibility in these networks is not restricted to *TREM2*. Biological follow-up of genetic results is labor intensive and expensive. It is therefore important to concentrate such work on the genes that are most important to Alzheimer's disease susceptibility. Thus, the rationale for reducing the gene set is that it defines a network of genes that are not only related through co-expression and protein interaction, but also show enrichment for genetic association signal. These genes are therefore strong candidates for future biological study.

Gene expression. We examined mRNA expression of the newly associated genes *PLCG2* and *ABI3* in post-mortem brain tissue from neuropathologically characterized individuals (508 persons): these genes are expressed at low levels in the dorsolateral prefrontal cortex of subjects from two studies of aging with prospective autopsy (ranked 12,965 out of 13,484 expressed genes)[67]. However, *ABI3* and *PLCG2* were more highly expressed in purified microglia/macrophages from the cortex of 11 subjects from these cohorts (ranked 1,740 and 2,600, respectively, out of the 11,500 expressed genes) (P.L.D.J., D.A.B. and C.C.W., unpublished data). These findings are consistent with the high levels of expression of both *PLCG2* and *ABI3* in peripheral monocytes, spleen, and whole blood reported by the ROADmap project and in microglia as reported by Zhang *et al.*[38]. From the same brain tissue, we examined methylation ($n = 714$)[68] and H3K9ac acetylation ($n = 676$) data and found differential methylation at four CpG sites and lower acetylation at two H3K9ac sites adjacent to *PLCG2* and *ABI3* in relation to increased global neuritic plaque and tangle burden (false discovery rate (FDR) < 0.05). Similarly, high *TREM2* expression has been shown to correlate with increasing neuritic plaque burden[69].

AMP-AD gene expression data. RNA sequencing was used to measure gene expression levels in the temporal cortex of 80 subjects with pathologically

doi:10.1038/ng.3916

confirmed Alzheimer's disease and 76 controls without any neurodegenerative pathologies obtained from the Mayo Clinic Brain Bank and the Banner Sun Health Institute. The human RNA sequencing data are deposited in the Accelerating Medicines Partnership-AD (AMP-AD) knowledge portal housed in Synapse (https://www.synapse.org/#!Synapse:syn2580853/wiki/66722). After quality control, our post-mortem human cohort had 80 subjects with pathologically confirmed Alzheimer's disease and 76 controls without any neurodegenerative pathologies. Assuming two samples of 100 per group, two-sample *t* test, same s.d., we would have 80% power to detect effect sizes of 0.40, 0.49, and 0.59 at $P < 0.05$, 0.01, and 0.001, respectively, where effect size is the difference in means between two groups divided by the within-group s.d. The human RNA sequencing data overview, quality control, and analytic methods are available at the following Synapse pages, respectively: syn3163039, syn6126114, and syn6090802. Multivariable linear regression was used to test for association of gene expression levels with Alzheimer's disease diagnosis using two different models. In the simple model, we adjust for age at death, sex, RNA integrity number (RIN), tissue source, and RNA-seq flow cell. In the comprehensive model, we adjust for all these covariates, and brain cell type markers for five cell-type-specific genes (*CD68* (microglia), *CD34* (endothelial), *OLIG2* (oligodendroglia), *GFAP* (astrocyte), *ENO2* (neuron)) to account for cell number changes that occur with Alzheimer's disease neuropathology. *TREM2*, *PLCG2*, and *ABI3* expression is significantly higher in Alzheimer's disease temporal cortex before correcting for cell type (simple model), but this significance is abolished after adjusting for cell-type-specific gene counts (comprehensive model). This suggests that these elevations are likely a consequence of changes in cell types that occur with Alzheimer's disease, most likely microgliosis, given that *TREM2*, *PLCG2*, and *ABI3* are microglia-enriched genes[15] (**Supplementary Fig. 12 and Supplementary Table 19**).

Data availability. Summary statistics for the 43 genetic associations identified are provided in **Supplementary Table 6**.

Stage 1 data (individual level) for the GERAD exome chip cohort can be accessed by applying directly to Cardiff University. Stage 1 ADGC data are deposited in a NIAGADS- and NIA/NIH-sanctioned qualified-access data repository. Stage 1 CHARGE data are accessible by applying to dbGaP for all US cohorts and to Erasmus University for Rotterdam data. AGES primary data are not available owing to Icelandic laws. Stage 2 and stage 3 primary data are available upon request.

A detailed description of the Mayo Clinic RNA-seq data is available to all qualified investigators through the Accelerating Medicines Partnership in Alzheimer's Disease (AMP-AD) knowledge portal that is hosted in the Synapse software platform from Sage Bionetworks under Synapse IDs syn3157182 and syn3435792 (mouse data) and syn3163039 (human data).

59. Goldstein, J.I. *et al.* zCall: a rare variant caller for array-based genotyping: genetics and population analysis. *Bioinformatics* **28**, 2543–2545 (2012).
60. Devlin, B. & Roeder, K. Genomic control for association studies. *Biometrics* **55**, 997–1004 (1999).
61. Grove, M.L. *et al.* Best practices and joint calling of the HumanExome BeadChip: the CHARGE Consortium. *PLoS One* **8**, e68095 (2013).
62. Patterson, N., Price, A.L. & Reich, D. Population structure and eigenanalysis. *PLoS Genet.* **2**, e190 (2006).
63. Howie, B., Fuchsberger, C., Stephens, M., Marchini, J. & Abecasis, G.R. Fast and accurate genotype imputation in genome-wide association studies through pre-phasing. *Nat. Genet.* **44**, 955–959 (2012).
64. Fuchsberger, C., Abecasis, G.R. & Hinds, D.A. minimac2: faster genotype imputation. *Bioinformatics* **31**, 782–784 (2015).
65. Talluri, R. & Shete, S. A linkage disequilibrium–based approach to selecting disease-associated rare variants. *PLoS One* **8**, e69226 (2013).
66. Holmans, P. *et al.* Gene ontology analysis of GWA study data sets provides insights into the biology of bipolar disorder. *Am. J. Hum. Genet.* **85**, 13–24 (2009).
67. Lim, A.S.P. *et al.* 24-hour rhythms of DNA methylation and their relation with rhythms of RNA expression in the human dorsolateral prefrontal cortex. *PLoS Genet.* **10**, e1004792 (2014).
68. De Jager, P.L. *et al.* Alzheimer's disease: early alterations in brain DNA methylation at *ANK1*, *BIN1*, *RHBDF2* and other loci. *Nat. Neurosci.* **17**, 1156–1163 (2014).
69. Chan, G. *et al.* CD33 modulates TREM2: convergence of Alzheimer loci. *Nat. Neurosci.* **18**, 1556–1558 (2015).