HHS Public Access

Author manuscript

Ann Neurol. Author manuscript; available in PMC 2016 February 01.

Published in final edited form as:

Ann Neurol. 2015 February ; 77(2): 215–227. doi:10.1002/ana.24305.

Coding mutations in *SORL1* and Alzheimer's disease

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Abstract

Importance—Common single nucleotide polymorphisms in the *SORL1* gene have been associated with late onset Alzheimer's disease (LOAD) but causal variants have not been fully characterized nor has the mechanism been established.

Objective—To identify functional *SORL1* mutations in patients with LOAD.

Design and Participants—This was a family- and cohort-based genetic association study. Caribbean Hispanics with familial and sporadic LOAD and similarly aged controls recruited from the United States and the Dominican Republic, and patients with sporadic disease of Northern European origin recruited from Canada.

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Main Outcome Measure(s)—Prioritized coding variants in *SORL1* detected by targeted re-sequencing and validated by genotyping in additional family members and unrelated healthy controls. Variants transfected into human embryonic kidney 293 (HEK) cell lines were tested for Aβ40 and Aβ42 secretion and the amount of the amyloid precursor protein (APP) secreted at the cell surface was determined.

Results—17 coding exonic variants were significantly associated with disease. Two rare variants (rs117260922-E270K and rs143571823-T947M) with MAF<1% and one common variant (rs2298813-A528T) with MAF=14.9% segregated within families and were deemed deleterious to the coding protein. Transfected cell lines showed increased Aβ40 and Aβ42 secretion for the rare variants (E270K and T947M) and increased Aβ42 secretion for the common variant (A528T). All mutants increased the amount of APP at the cell surface, though in slightly different ways, thereby failing to direct full-length APP into the retromer-recycling endosome pathway.

Conclusions and Relevance—Common and rare variants in *SORL1* elevate the risk of LOAD by directly affecting APP processing which, in turn can result in increased Aβ40 and Aβ42 secretion.

Keywords

SORL1; common and rare variants; amyloid β; Alzheimer's disease

INTRODUCTION

The sortilin-related receptor, L(DLR class) A-type repeats containing (*SORL1*) is a member of the vacuolar protein sorting-10 domain-containing receptor family, and participates in the intracellular vesicular sorting of APP after re-internalization from the cell surface[1, 2]. *SORL1* determines whether APP is sorted in the retromer recycling-endosome pathway or allowed to drift into the endosome-lysosome pathway where it is cleaved to generate Aβ. Variants in the *SORL1* gene might alter this activity, leading to an increase in Aβ that, in turn, contributes to the pathogenesis of late onset Alzheimer's disease (LOAD)[3]. To date, despite compelling evidence from case-control, family-based and genome-wide association studies (GWAS)[3–11], clearly pathogenic variants have not been identified making it difficult to investigate the functional consequences of specific *SORL1* mutations.

METHODS

Targeted re-sequencing and analysis methods

Sample Selection and Preparation. We sequenced one affected individual with LOAD, usually the proband, from 151 families with multiple affected family members. The mean age at onset for affecteds was 77.03 years (SD=8.93), ranging from 45 to 98 years. 69.5% of the family members were women and the mean years of education was 4.3 years (SD=4.61). We extracted genomic DNA from whole blood with 0.16% samples from saliva. Blood samples were extracted using the Qiagen method and saliva samples were extracted using the Oragene method. The DNA was then quantified using the PicoGreen detection method, following the manufacturer specifications (InVitrogen, Carlsbad CA).

We validated the prioritized variants by genotyping the sequenced probands and their 464 relatives, of whom 350 were affected and 114 were unaffected. For the sequencing experiment we pooled DNA samples using 235 samples across 24 pools with each pool comprising 10 unrelated samples (5 samples failed sequencing).

Targeted Re-sequencing. We performed the RainDance (http://raindancetech.com/targeted-dna-sequencing) for capture and then followed with pooled sequencing using the Illumina GAII platform (http://www.illumina.com). In total, we sequenced 201,510 bp including both exons and introns of the *SORL1* gene as well as the flanking region, covering from 121,312,961bp to 121,514,471bp.

Variant Calling and post-processing. We aligned the reads obtained from the pooled sequencing to the human reference genome build 37 using the Burrows Wheeler Aligner[12] (http://bio-bwa.sourceforge.net/). Quality control of the sequencing data was done using established methods, including base alignment quality calibration and refinement of local alignment around putative indels using the Genome Analysis Toolkit (GATK)[13]. We used SAMTOOLS[14] mpileup to call variants in the pooled dataset and validated calls by an independent calling algorithm called CRISP (Comprehensive Read analysis for Identification of Single Nucleotide Polymorphisms (SNPs) from Pooled sequencing)[15]. Variant calls were filtered using mpileup filters for base quality (baseQ bias), mapping quality (mapQ bias), strand bias, tail distance bias and number of non-reference reads to obtain high quality variants. Reliably called variants were annotated by ANNOVAR[16] including in-silico functional prediction using POLYPHEN[17] software extent of cross-species conservation using PHYLOP[18].

Genotyping. To validate novel variants discovered in probands, we genotyped the probands, and their family members. To investigate whether the allele frequencies for novel variants differed from unaffected persons in the general Caribbean Hispanic population, we genotyped 498 unaffected persons who were unrelated to any of the family members. These 498 individuals underwent the same phenotypic and diagnostic protocols. Genotyping was conducted on the Sequenom platform. When the Sequenom platform failed to generate genotype due to difficulties with primers, we performed Sanger sequencing.

Statistical Analysis. To assess whether a set of rare and common variants in *SORL1* increases the risk of LOAD, we performed a gene-wise analysis using in the SNP-set Kernel Association test (SKAT)[19] for heterozygous variants in exons and introns with and without adjustments for covariates such as age, sex and *APOE* genotype. We also used statically estimated haplotypes coupled with generalized estimating equations (GEE) to establish joint burden of 17 SNVs by accurately adjusting for the correlation between samples. To assess the individual effects of SNPs, we performed joint linkage and association analysis with PSEUDOMARKER[20] using all family members and unrelated controls. This analytical method allows us to analyze family data, unrelated subjects, or both to determine whether a variant is associated with disease. For constructing haplotypes, we used the R based haplo.stats package[21] (http://mayoresearch.mayo.edu/mayo/research/schaid_lab/software.cfm).

Functional studies

Site directed mutagenesis. *SORL1* E270K, A528T and T947M mutations were generated by site directed mutagenesis using human SORL1-MYC pcDNA3.1 as a backbone according to manufacturer's instructions[1, 2]. All mutant constructs were verified by sequencing.

Cell culture and transfection. HEK293 cells stably expressing the Swedish APP mutant (APPsw)[22] were maintained in Dulbecco's modified Eagle's medium (DMEM, Gibco) with 10% fetal bovine serum and Geneticin (200 μg/ml). Wild-type SORL1-MYC pcDNA3.1 and three generated SORL1 mutant constructs (SORL1 E270K -MYC pcDNA3.1, SORL1 A528T -MYC pcDNA3.1, SORL1 T947M -MYC pcDNA3.1) were transfected transiently into HEK293 APPsw cells using Lipofectamine 2000 (Invitrogen). Stable clones were selected using Hygromycin (200 μg/ml) and Geneticin (400 μg/ml) to generate stable cell lines overexpressing either wild-type or mutant *SORL1*.

Aβ assays. Measurement of secreted Aβ40, Aβ42 and sAPPβ from culture medium in HEK293 APPsw cells[23], wild-type *SORL1* and mutant *SORL1* stable HEK293 APPsw cells by sandwich ELISA according to manufacturer's protocol.

Antibodies and Western Blot. Antibodies were used as follows: rabbit antibody to the C-terminus of SORL1 (S9200, Sigma); rabbit polyclonal antibody to PS1-NTF (A4, from our lab); mouse monoclonal anti-c-MYC (Invitrogen); rabbit polyclonal antibody to the C terminus of APP (Ab365, Sigma); mouse monoclonal anti-Aβ (6E10, Covance).

Culture medium from HEK293 APPsw cells, wild-type SORL1 and mutant SORL1 stable cell lines were harvested and subjected to immunoblotting. Secreted sAPPα levels were analyzed by western blot using anti-Aβ (6E10); samples were normalized to the protein concentration of the collected cell lysates, which were measured by BCA protein assay (Biorad). The cell lysates were analyzed in a Western blot with FL-APP (full-length APP), PS1-NTF (Presenilin 1), APP-CTFs (APP-β-CTF(C83) and APP-α-CTF(C99)). Band intensities were quantified using NIH Image J software and relative expression levels of FL-APP, total APP-CTFs, PS1 were normalized to β-actin. Bar graphs were normalized to wild-type SORL1 control.

Cell surface biotinylation: Cells were washed with Buffer A (PBS with 1 mM $MgCl_2$, pH 8.0) and incubated with 1 mg/ml Sulfo-NHS-LC-Biotin (Sigma) in buffer A for 20 min at 4°C to prevent internalization. Cells were then washed with ice-cold 20 mM glycine in Buffer A, lysed, and biotinylated proteins precipitated with Neutravidin beads (Thermo Sci).

Protein lysates were immunoblotted with Anti-C-terminal APP antibody (Ab365, Sigma) and Anti-C-terminal SORL1 antibody (S9200, Sigma). Immunoprecipitated cell surface APP (IP) was normalized to total APP (Input). Western blot bands intensities were measured with NIH Image J software. Bar graphs were normalized to wild-type control.

Co-Immunoprecipitation. Cells were lysed in 1% CHAPSO buffer[24], immunoprecipitated using G Plus beads with 2 μg mouse monoclonal anti-c-MYC antibody (for immunoprecipitation of SORL1-myc), immunoblotted with Anti-C-terminal APP antibody

(Ab365), and Anti-C-terminal SORL1 (S9200). Full-length APP co-precipitated with c-MYC antibody was quantified and normalized to the amount of immunoprecipated SORL1.

Statistical analysis. Graphpad Statistical software (GraphPad Prism 5) was used to generate Bar Charts and Anova with t-test was used to analyze statistical difference, followed by Bonferroni correction. One asterisk represents $p<0.05$; two asterisks represent $p<0.01$; and three asterisks represent $p<0.001$.

RESULTS

Genetic Analyses. Analysis of the sequence data allowed prioritization of 17 exonic coding variants including 13 non-synonymous mutations three frame-shift deletions and one synonymous mutation (Table 1). We validated variant calls by Sequenom genotyping in the sequenced probands, additional family members from 87 families that contained at least one heterozygous carrier (464 total familial subjects-350 affecteds and 114 unaffecteds) and 498 unrelated, age-matched Caribbean Hispanic controls. The combined gene burden SKAT[19] analysis confirmed that the joint burden of 17 heterozygous variants were significantly associated with LOAD ($p_{unadjusted} = 0.0009$; $p_{adjusted\ for\ age\ and\ gender\ covariates} = 0.0079$). The SKAT test assumes independence of observations but does not adjust for familial correlation. Thus, we conducted SKAT analysis on unrelateds creating a dataset by randomly selecting one member from each of the 87 families, and combined them with the 498 controls to create a “case-control” set. We repeated this process 1000 times to create 1000 case-control datasets and conducted SKAT analysis using unadjusted and age, sex and *APOE* adjusted models. 961 out of 1000 (96%) of the unadjusted model datasets and 909 out of 1000 (91%) adjusted model datasets produced significant p-values ($p<0.05$) for and respectively. We observed median p-values of $p=0.00067$ for the unadjusted model and $p=0.002$ for the adjusted model respectively (Fig. 5a and 5b). These observations are consistent with the SKAT analysis using all family members. In case of a null association we would have expected 5% of the datasets to produce nominally significant p-values. The significant deviation from the expectation provides further evidence of the joint burden of 17 SNVs in modifying LOAD risk.

Because of lack of appropriate methods for gene- or region-based burden methods for dichotomous traits that adjust for familial correlations, we performed additional haplotype analyses to assess the joint association of the 17 SNPs with LOAD and related traits. Defining the major allele as most frequent haplotype observed in 78% of the samples (Table 4a) and combining the remaining haplotypes into the minor allele, we computed association with LOAD using GEE. We included 933 (out of 962) subjects in the association analysis with haplotype pairs estimated at a posterior probability of $p=1$. The rare haplotypes increased disease risk and were strongly associated with LOAD (OR=1.9, p=6.9e-05) (Table 4b). This observation is consistent with the increased frequency of the minor alleles of several of the 17 SNPs in LOAD vs controls (Table 1).

To assess individual significance of the single nucleotide variants (SNVs), we conducted joint linkage and association of the 17 variants with LOAD in the subset of 87 families and the unrelated controls. The analysis revealed that all 17 SNVs were significantly associated

with disease at a Bonferroni corrected p-value p<0.0029. However, three of the variants showed significant segregation with disease under a dominant affecteds only model: rs2298813 (A528T; p=6.09E-7), rs117260922 (E270K; p=7.68E-7) and rs143571823 (T947M; p=7.0E-6). Variant rs2298813 was most frequent being present in 54 families, in contrast to variant rs117260922 detected in seven families, and variant rs143571823 detected in four families.

To assess whether these findings were applicable to ethnic groups other than Caribbean Hispanics, we also re-sequenced *SORL1* in 211 patients of Northern European ancestry (Table 2). We detected 13 rare missense variations and a 3 base-pair deletion eliminating a highly conserved residue p.N174 (Table 3). Seven of these variations are predicted to be damaging, including three novel variations. Of the 14 rare variations identified, seven overlapped with the mutations detected in the Caribbean Hispanic patients including two of the coding mutations rs2298813 and rs117260922. Their frequencies were higher than or comparable to Caucasian population in the 1000 genomes database, but much lower than observed in the Caribbean Hispanics.

We also compared the minor allele frequencies of the 17 coding-*SORL1* SNVs discovered in the Hispanics with those observed in the whole-genome sequencing (WGS) and the exome-chip data from the Alzheimer's Disease Neuroimaging Initiative (ADNI) dataset[25] (https://ida.loni.usc.edu/login.jsp?project=ADNI&page=HOME). We used baseline phenotypes from ADNI samples to compute frequencies of LOAD and mild cognitive impairment compared to controls. The frequency of the common SNP rs2298813 (A528T) (Table 1) was concordant with the observations in the Hispanic cohort, but the allele frequencies were much lower than in the Caribbean Hispanics. The rare SNP rs143571823 (T947M) was heterozygous in one ADNI control and was not found in any case. SNP rs117260922 (E270K) was not observed in the entire ADNI dataset. Differences in allele frequencies between Caribbean Hispanics and the Caucasians in the ADNI study could be conferred by differences in sequencing technologies, capture platforms, sequencing depth and variant calling algorithms in the two experiments. We evaluated the effects of the 45 rare *SORL1* missense mutations observed in the ADNI dataset at a sample MAF<0.01 using the SKAT test. The SKAT test of rare missense mutations in demented versus healthy controls in the ADNI samples was significant (p=0.037).

Caribbean Hispanics are known to be an admixed population, therefore we also investigated the association of the rs2298813 in a meta-analyses LOAD study African Americans[26]. The SNP was significant in African Americans at P=0.01 and is observed with a higher frequency in cases compared with controls.

Functional Analyses. We tested the impact of three most significant *SORL1* mutations on Aβ production. Clonal HEK293sw cell lines stably overexpressing similar quantities of wild-type and mutant *SORL1* were generated. Aβ40 and Aβ42 levels were then measured in conditioned media from the cells. Wild-type and mutant *SORL1* were expressed at the same levels, yet the E270K and T947M mutants both resulted in a significant increase in Aβ40 secretion (E270K, 171 ± 5.6% of control value, p <0.001; T947M, 202 ± 11.6% of control value, p <0.01; n=3 independent replications, Fig. 1a) and Aβ42 secretion (E270K, 214 ±

5.7% of control value, p <0.001; T947M, 221 ± 8.4% of control value, p <0.001; n=3 independent replications, Fig. 1b). The A528T mutant increased Aβ42 secretion moderately (158 ± 11.1% of control value, p <0.01; n=3 replications, Fig. 1b), but did not change the Aβ40 secretion (103 ± 3.3% of control value, p >0.05; n=3 independent replications, Fig. 1a).

All three mutations caused significant increases in sAPPα and sAPPβ secretion compared to wild-type *SORL1*. Thus, for sAPPα: (E270K, 266 ± 13.0% of control value, p <0.001; A528T, 246 ± 12.0% of control value, p <0.001; T947M, 259 ± 25.2% of control value, p <0.01; n=3 independent replications, Fig. 1d); and for sAPPβ: (E270K, 204 ± 7.2% of control value, p <0.001; A528T, 167 ± 3.5% of control value, p <0.01; T947M, 268 ± 10.3% of control value, p <0.001; n=3 independent replications, Fig. 1c). The *SORL1* mutants did not alter the levels of either total cellular APP holoprotein or PS1 (Fig. 1e). All the three mutants did increase the amounts of biotinylatable cell-surface APP (E270K, 286 ± 36.2% of control value, p <0.05; A528T, 365 ± 7.8% of control value, p <0.01, T947M, 294 ± 20.1% of control value, p <0.05; n=3 independent replications, Fig. 2a).

To understand how these mutants altered APP processing, we assessed the physical interaction of the mutants with APP. Co-immunoprecipitation experiments showed that all three mutations bound APP less well (E270K, ~41 ± 5.1% of control value, p <0.05; A528T, ~43 ± 5.9% of control value, p <0.05; T947M, ~34 ± 3.5% of control value, p <0.01; n=3 independent replications, Fig. 3). However, the mechanism by which this reduced APP:*SORL1* interaction occurred, differed significantly. The E270K and A528T mutants displayed normal levels of *SORL1* at the cell surface (E270K, 101 ± 7.0% of control value, p >0.05; A528T, 105 ± 10.1% of control value, n=3 replications, Fig. 2b), but failed to physically interact with APP on the cell surface, presumably due to the effect of the mutant on *SORL1* conformation. In sharp contrast, the T947M mutant showed decreased amounts of *SORL1* at the cell surface (~27 ± 4.5% of control value, *p <0.05; n=3 independent replications, Fig. 2b). The reduced abundance of this mutant at the cell surface clearly accounts for its failure to interact with APP at the cell surface.

DISCUSSION

Our results indicate that there may be both common and rare variants in *SORL1* in some population groups that increase the risk of LOAD. The association with *SORL1* has been confirmed in genetic studies of autopsy confirmed LOAD[6] and in two meta-analyses involving several thousand patients and controls[4, 9]. Although, three rare putative variants were identified in European patients with an early onset, autosomal dominant form of Alzheimer's disease, no confirmatory functional assessment was performed[27] and those variants were not detected in the present study. This suggests that the association between *SORL1* and LOAD may be related the presence of multiple rare coding mutations, some of which may be population specific.

We based our conclusions about the pathogenic nature of the mutations identified here on two levels of evidence as suggested here[28]. At the gene level, we demonstrated statistical evidence of an excess of multiple rare, damaging mutations that segregated significantly

among cases compared to controls. Previously, we found reduced expression of SORL1 increased the processing of APP into Aβ-generating compartments[3]. At the variant level, the evidence for pathogenesis of these variants was based on statistical association and segregation within affected families among Caribbean Hispanics, bioinformatics information indicating evolutionary conservation consistent with the deleterious mutations and functional studies in HEK293 cell lines indicating the effects of these mutations on APP processing.

The functional mutations investigated in the current study were either absent or much less frequent in patients of Northern European ancestry and in the ADNI dataset. While the frequency of rs2298813, the most common variant was still increased in cases compared with controls, the difference was not at the level observed in the Caribbean Hispanics and did not reach statistical significance. This may have resulted from the low frequency of this SNP or the small sample size. In contrast, among African Americans the allele frequency was similar to that among Caribbean Hispanics and the variant rs2298813 was found to be significantly associated with LOAD.

It is possible that within the Caribbean Hispanic population this mutation, rs2298812, and the other rare mutations increase risk of disease because they are more penetrant and because there is a strong pattern of inbreeding[29] compared to the other populations investigated. Similar observations have been made with in persons with *BRCA1* and *LRRK2* mutations. *BRCA1* mutations are more penetrant among large families of Ashkenazi ancestry with many cases, than in the general population[30], and the penetrance of the *LRRK2* G2019S mutation can vary by ethnic group among patients with Parkinson disease[31].

The three variants in *SORL1* identified in the present study show increased secretion of Aβ when transfected into HEK293 cell lines. Interestingly, the rs2298813 (A528T) variant was the most common among the Hispanics and present in 9% of unaffected healthy controls, but 15.6% in familial cases. Intriguingly, all three of these variants map onto or close to SNPs that were associated with LOAD in the original report by Rogaeva et al[3]. Thus, rs117260922 (E270K) is one nucleotide from SNP7 (rs12364988), rs2298813 (A528T) is SNP13, and rs143571823 (T947M) is located within 3KB region between SNP17 (rs55634) and SNP18 (rs11218340) and is in tight linkage disequilibrium with both SNPs (Fig. 4).

The molecular mechanisms underlying this apparently consistent effect of mutants on disease risk appears different between the three mutations. The E270K and the A528T mutants have similar levels of *SORL1* at the cell surface as wild-type SORL1-expressing cells. This result suggests that these two mutations do not affect the maturation and trafficking of *SORL1* to the cell surface. In contrast, the T947M mutant appears to reach the cell surface less well than wild-type *SORL1* or the other *SORL1* mutants. This suggests that the T947M mutant may act by causing misfolding of SORL1 in the endoplasmic reticulum and its destruction by quality control mechanisms before the SORL1 protein can reach the cell surface.

Taken together, these data indicate that inherited mutants impair interaction of *SORL1* with full-length APP, and thereby fail to direct full-length APP into the retromer-recycling

endosome pathway. As a result, in cells expressing mutant SORL1, more of the full-length APP is able to drift into the early and then late endosomes where it is sequentially cleaved by β-secretase and then by γ-secretase to generate increased amounts of Aβ as demonstrated here. Coding *SORL1* mutations associated with LOAD in this study likely account in part for the GWAS signals. We demonstrated that a common effect of such mutations is to alter Aβ production via changes in APP processing. However, it is conceivable that other rare mutations may alter different aspects of APP/Aβ metabolism. Indeed, a recently described[27] rare mutation (G511R) seemingly alters Aβ binding to SORL1 and may affect the ability of SORL1 to direct lysosomal targeting of nascent Aβ peptides[32]. When available, the first line of mechanism-based, disease-modifying therapies for carriers of *SORL1* mutations should likely be focused on modulating APP processing and Aβ production.

Acknowledgements

This work was supported by federal grants from the National Institutes of Health, specifically P50AG08702, R37AG15473, RO1AG037212 and the Marilyn and Henry Taub Foundation (to RM).

The Canadian Institutes of Health Research, National Institute of Health, Wellcome Trust, Medical Research Council, National Institute of Health Research, Ontario Research Fund and Alzheimer Society of Ontario (to PSG-H).

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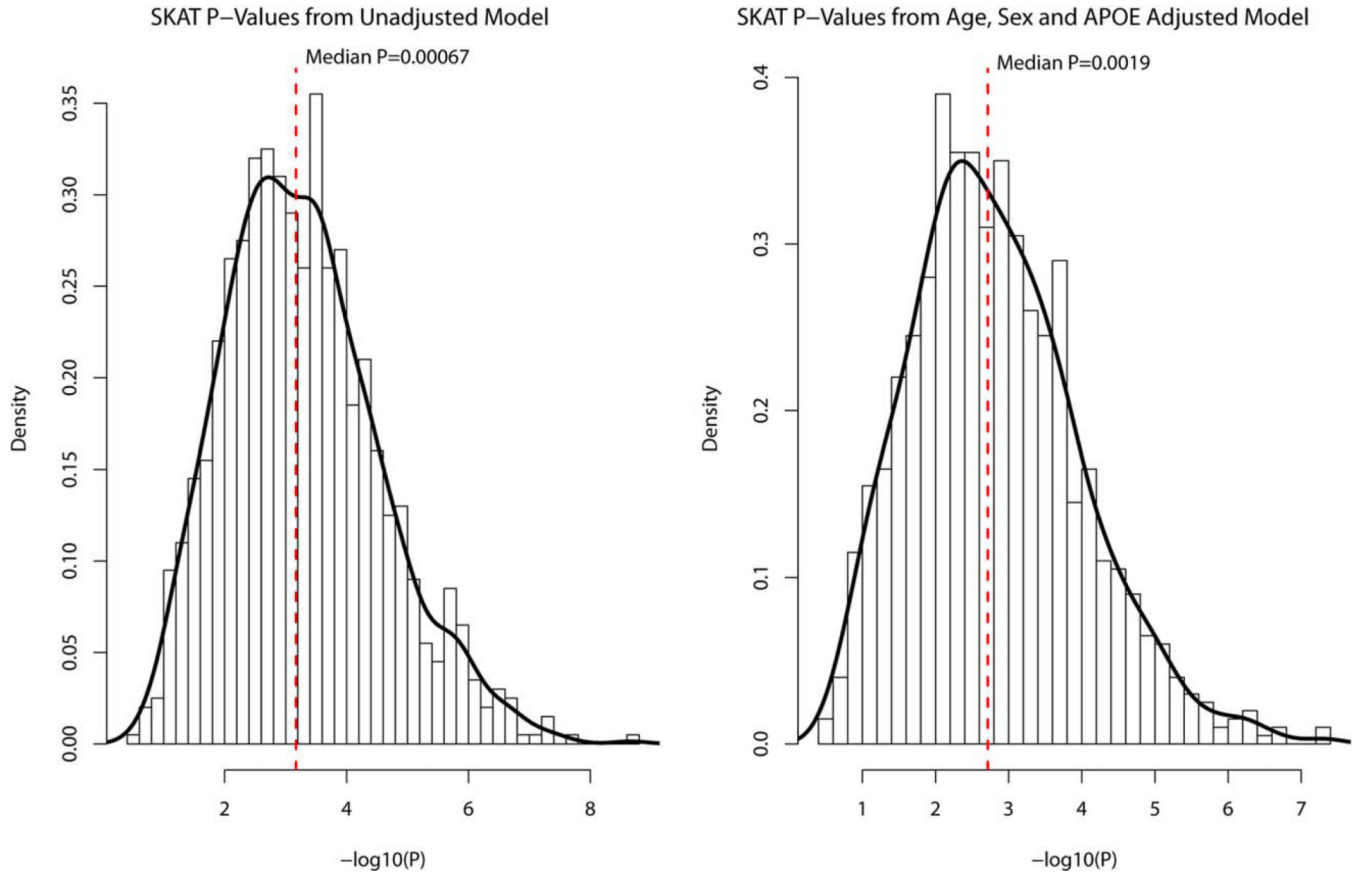

FIGURE 1.

Histogram of −log10 of the probability values obtained from SNP-set Kernel Association Test (SKAT) analysis of 1,000 data sets created by randomly choosing 1 subject from each of the 87 families and 498 controls. The SKAT analysis was conducted assuming for the unadjusted model: Alzheimer disease (AD) ~ single nucleotide polymorphism (SNP) burden; and for the model with age, sex, and apolipoprotein E (APOE) ε4 status as covariates: AD ~ SNP burden + age + sex + APOE ε4 yes/no. [Color figure can be viewed in the online issue, which is available at www.annalsofneurology.org.]

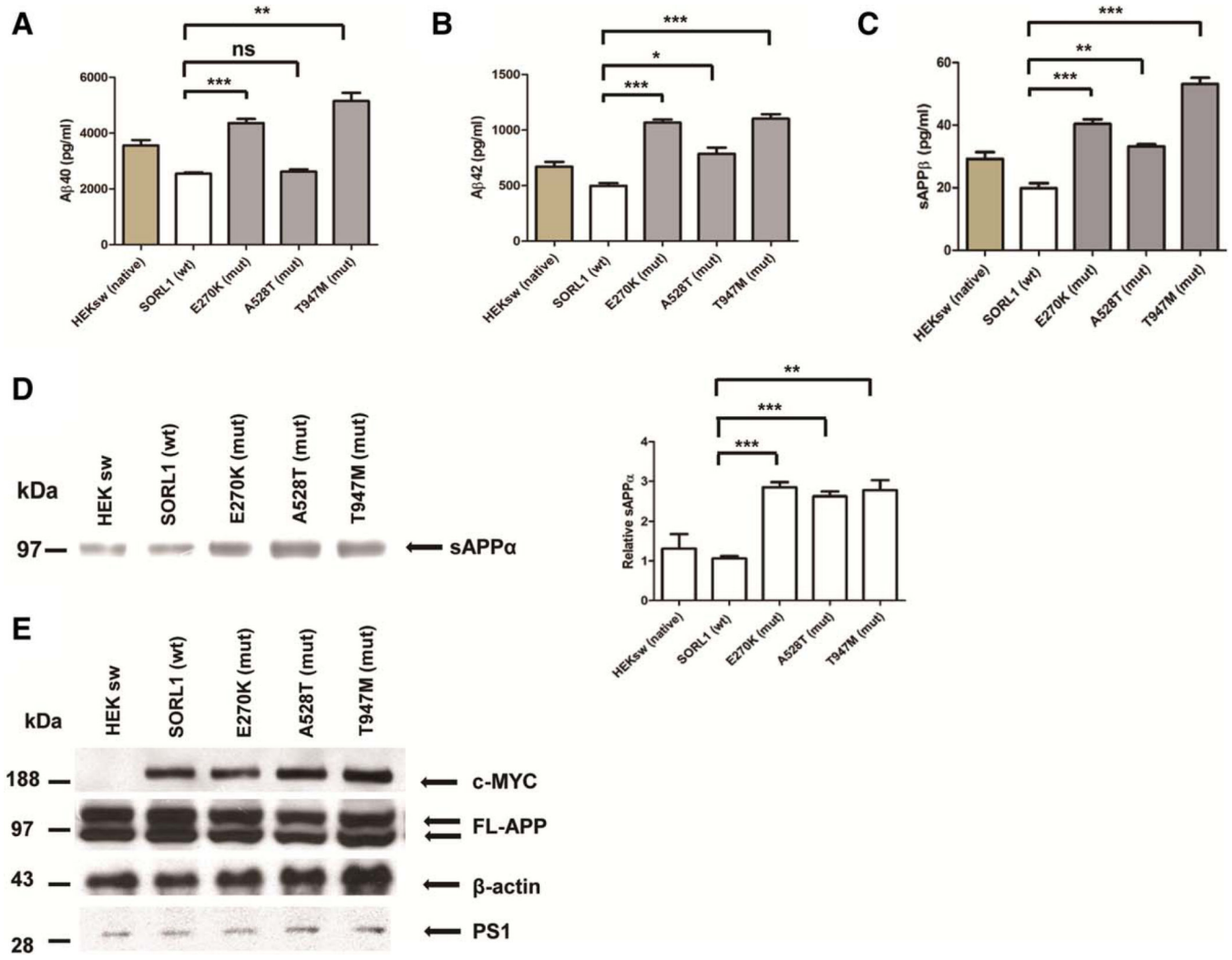

FIGURE 2.

Overexpression of SORL1 mutants leads to elevated Aβ secretion. (A–C) Measurement of secreted Aβ40, Aβ42 and sAPPβ from culture medium in stable HEK293 cells expressing the APP Swedish mutant (HEKsw) together with either wild-type (wt) SORL1 or mutant (mut) SORL1. Aβ levels were normalized to the protein levels of the cell lysates. Error bars = standard error of the mean. $*p < 0.05$, $**p < 0.01$, $***p < 0.001$, ns = not significant after Bonferroni correction; n = 3 independent replications. (D) Cultured media from cells were collected and subjected to Western blot and probed with 6E10 antibody to detect sAPPα. Bar graphs were normalized to control. $**p < 0.01$, $***p < 0.001$, after Bonferroni correction; n = 3 independent replications. (E) Cell lysates were harvested to perform Western blot of full-length amyloid precursor protein (FL-APP) and PS1. β-Actin was used as loading control; n = 3 independent replications.

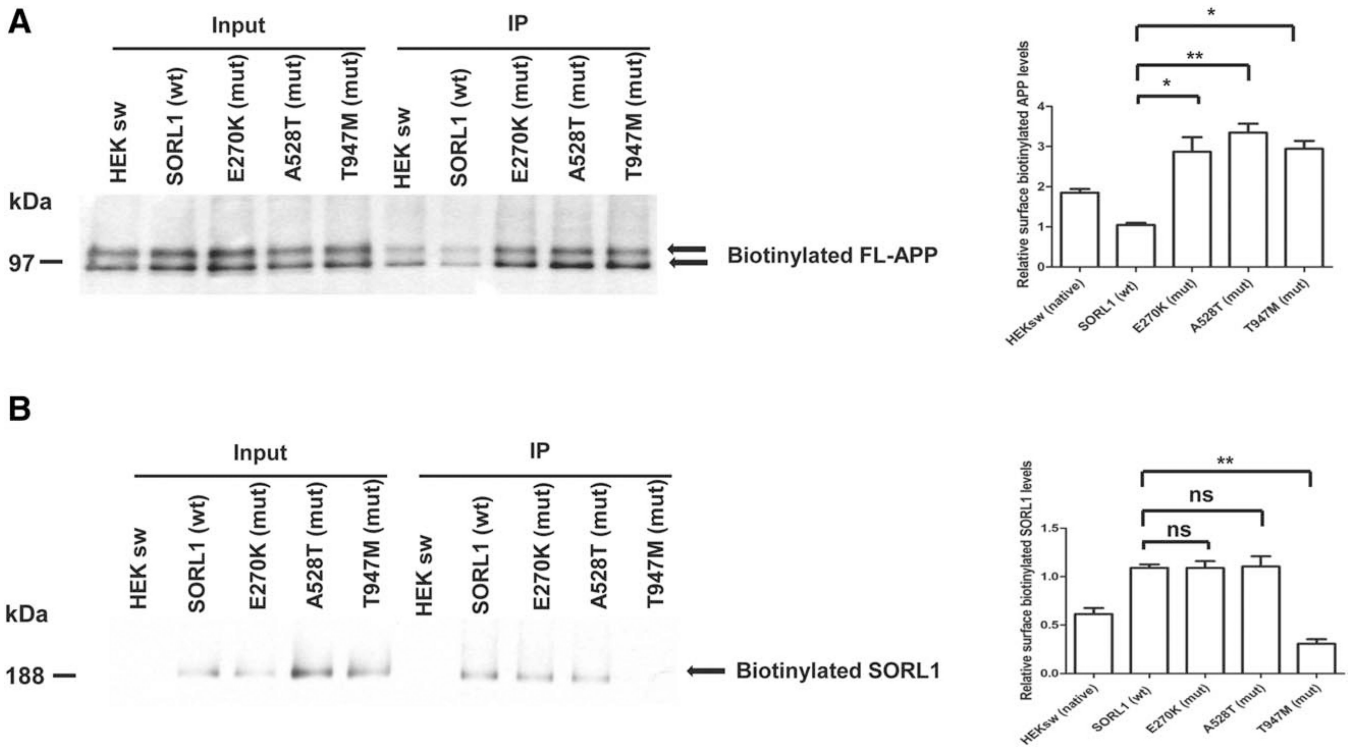

FIGURE 3.

The expression of SORL1 mutants (mut) leads to changes of cell surface amyloid precursor protein (APP) and SORL1 levels. Cell surface proteins were biotinylated and precipitated. Surface levels of APP and SORL1 were analyzed by Western blot. (A) APP levels at the cell surface are elevated in all 3 mutants. *$p < 0.05$, **$p < 0.01$, after Bonferroni correction, n = 3 replications. (B) SORL1 surface levels are decreased in the T947M mutant. **$p < 0.01$, ns = not significant, after Bonferroni correction, n = 3 replications. FL = full length; IP = immunoprecipitated; wt = wild type.

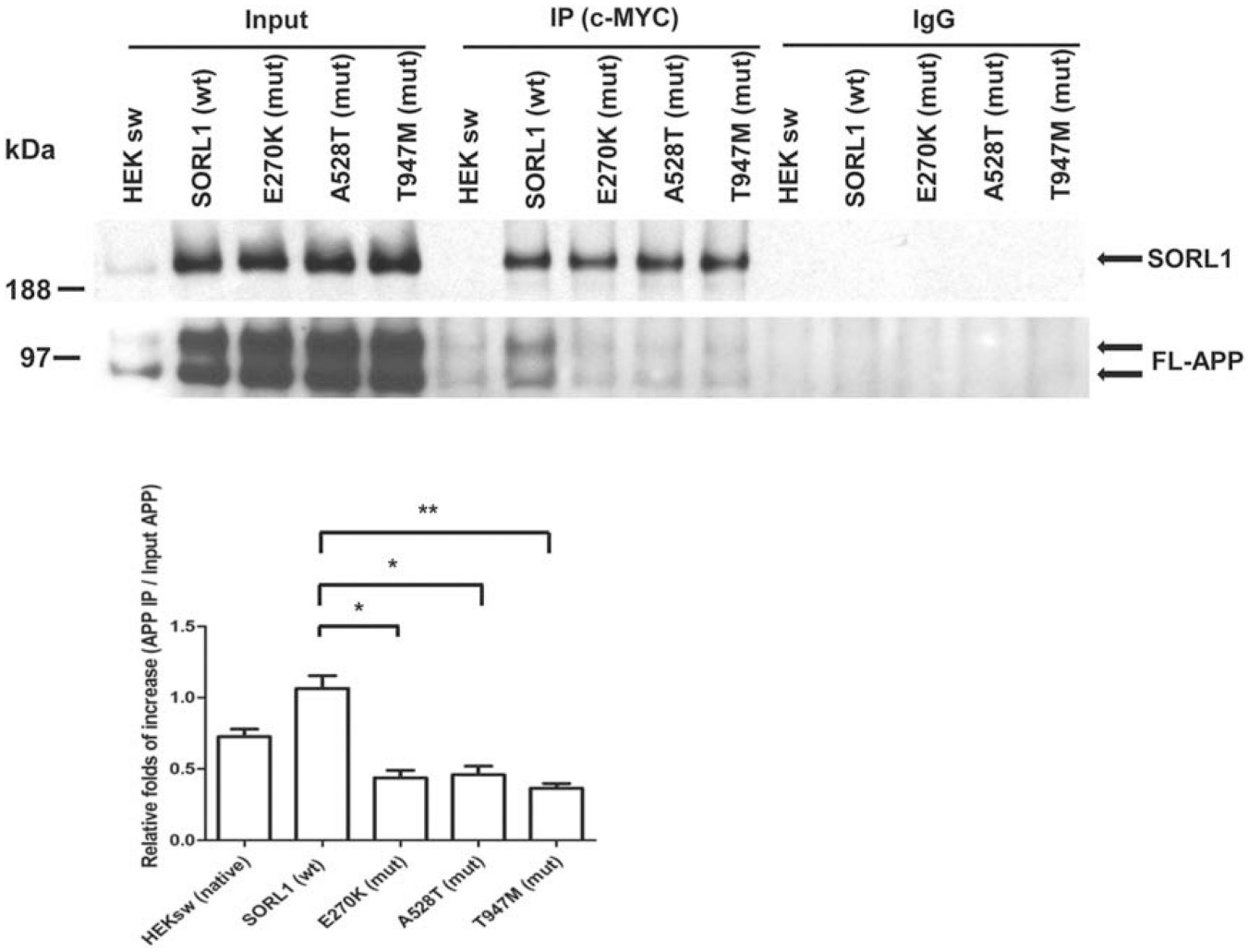

FIGURE 4.

All 3 SORL1 mutants (mut) have a reduced binding affinity to amyloid precursor protein (APP). SORL1 was pulled down from cell lysates with a c-MYC antibody and the amount of coprecipitated full-length APP (FL-APP) was measured. *$p < 0.05$, **$p < 0.01$, after Bonferroni correction, n = 3 replications. IgG = immunoglobulin G; IP = immunoprecipitated; wt = wild type.

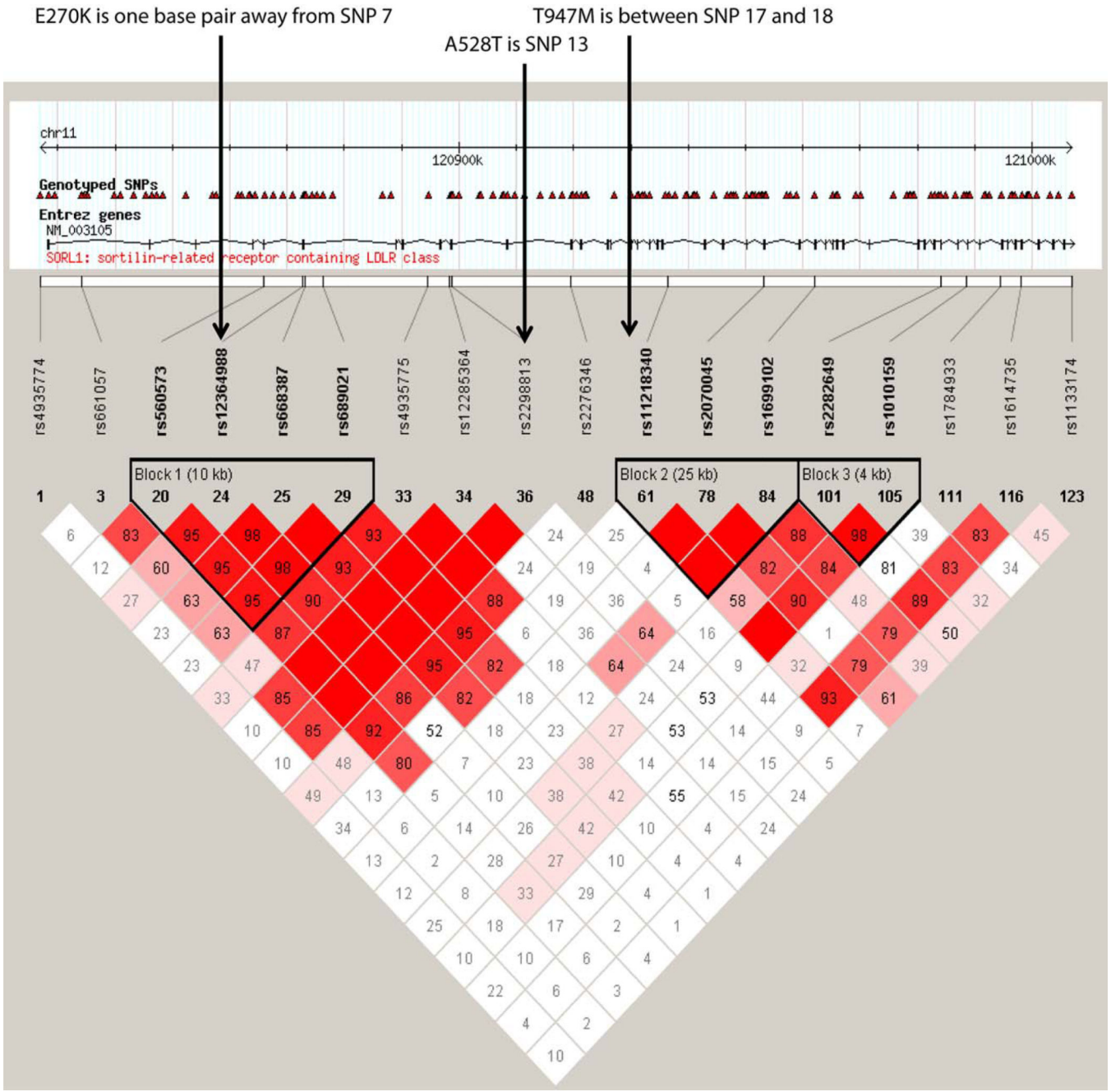

FIGURE 5.

Position of the coding mutations relative to the single nucleotide polymorphisms (SNPs) significantly associated with Alzheimer disease (Rogaeva et al[3]).

Table 1

List of variants prioritized for follow-up genotyping and p-values using linkage and association test implemented in Pseudomarker.

					CARIBBEAN HISPANIC FREQUENCY		ADNI OMNI CHIP FREQUENCY		ADNI WGS FREQUENCY						
SNP	BP (HG19)	P (LD+Link)	A1*	A2	Controls (n=498)	AFFECTED (n=87 fams, 462)	AD+MCI (n=531)	CONTROL (n=82)	AD+MCI (n=531)	CONTROL (n=281)	Function+	AA Change	ESP Frequency	Polyphen++	Conservation^
rs117260922	121367627	7.68E-07	1	3	0.010040	0.01166					NS	E270K	0.007529	D	C
rs2298813	121393684	6.09E-07	1	3	0.091370	0.15598	0.05849	0.047	0.05039	0.04029	NS	A528T	0.061536	P	C
11-121428111	121428111	1.49E-03	3	1	0.001004	0.00146					NS	E887G		B	C
rs143571823	121429476	7.00E-06	4	2	0.007028	0.00729			0.00000	0.00183	NS	T947M	0.004927	P	C
11-121437722	121437722	5.00E-05	2	3	0.002008	0.00583					NS	R1041S		B	C
rs1699107	121437819	1.41E-10	2	3	0.019080	0.02770			0.00194	0.00183	S	Q1074Q			
rs146903951	121440937	6.00E-06	2	4	0.007042	0.01020			0.01453	0.01648	NS	F1099L	0.007436	B	C
rs62617129	121444958	2.00E-03	3	1	0.003012	0.00583			0.00484	0.00366	NS	I1116V	0.006228	B	N
rs114830255	121454206	4.00E-06	1	3	0.001004	0.00875			0.00097	0.00183	NS	R1207Q	0.005298	B	N
11-121458818	121458818	1.16E-04	0**	4	0.000000	0.00292					FSD	C1302fs			
rs146353234	121461799	8.96E-07	4	1	0.002008	0.00583			0.00000	0.00366	NS	T1435S	0.000744	B	C
11-121474914	121474914	2.70E-03	4	2	0.002008	0.00292					NS	T1511I		B	C
11-121476260	121476260	8.86E-04	0	2	0.000000	0.00437					FSD	T1643fs			
rs62622819	121485599	1.50E-04	1	4	0.003012	0.00875			0.00969	0.00916	NS	H1813Q	0.006042	P	N
rs1792120	121491782	7.42E-10	3	1	0.013050	0.03353			0.00194	0.00183	NS	V1967I	0.0002	B	N
rs74811057	121495870	1.74E-03	3	1	0.014060	0.00583			0.00000	0.00183	NS	K2083R	0.013664	B	C
11-121498387	121498387	9.82E-04	0	3	0.000000	0.00437					FSD	R2163fs			

*Minor allele

**Homozygous wild type

+SNV Function: NS= Non-synonymous SNV, S= Synonymous SNV, FSD= Frame-shift Deletion

++Polyphen Prediction: D=Damaging, P=Possibly Damaging, B=Benign

^Phylop Conservation Prediction: C=Conserved, N=Not Conserved

Table 2

Demographic and clinical characteristics of sequenced individuals

Characteristics	Caribbean Hispanic Affecteds (n=154)	Caribbean Hispanic Unaffecteds (n=80)	N. European Caucasian Affecteds (n=211)
Mean Age at Onset or last examination: years ± SD	77.0 ± 8.9	83.9 ± 3.8	73.0 ± 7.8
Mean years of Education ± SD	4.3 ± 4.6	7.0 ± 4.0	not available
Women: n (%)	107 (69.5)	57 (71.3)	107 (50.7)
APOE ε4: %	22.8	11.9	38.0

Table 3

Coding *SORL1* variations detected in 211 cases of N. European ancestry

SNP	BP (HG19)	A1**	A2	# cases	MAF	1000g-CEU Frequency	ESP Frequency	Function+	AA Change	Polyphen++	Conservation^
11-121348942	del 121348942-121348944	del	ACA	2	0.005	NA	NA	deletion	173_174del	NA	C
rs117260922*	121367627	A	G	14	0.033	0.0059	0.007459	NS	E270K	D	C
rs150609294	121384931	C	A	1	0.002	0	0.001	NS	N371T	D	C
rs2298813*	121393684	A	G	18	0.045	0.0471	0.060366	NS	A528T	P	C
rs146903951*	121440937	C	T	3	0.007	0.0059	0.007921	NS	F1099L	B	C
rs62617129*	121444958	G	A	3	0.007	0.0059	0.006075	NS	I1116V	B	N
11-121458817	121458817	T	G	1	0.002	NA	NA	NS	Q1301H	B	C
11-121460792	121460792	G	T	1	0.002	NA	NA	NS	F1374L	D	C
rs199717181	121474988	A	G	1	0.002	0	0.000231	NS	G1536S	D	C
rs138580875	121475859	C	G	1	0.002	NA	0.000615	NS	W1563C	D	C
rs62622819*	121485599	A	T	5	0.012	0.0235	0.005999	NS	H1813Q	P	N
rs1792120*	121491782	G	A	1	0.002	0	0.01669	NS	V1967I	B	N
rs140327834	121495816	T	A	2	0.005	0	0.00423	NS	D2065V	D	C
rs74811057*	121495870	G	A	1	0.002	0	0.013229	NS	K2083R	B	C

*Found in Caribbean Hispanics

**Minor allele

+SNV Function: NS= Non-synonymous SNV

++Polyphen Prediction: D=Damaging, P=Possibly Damaging, B=Benign

^Phylop Conservation Prediction: C=Conserved, N=Not Conserved

Table 4

a): Haplotype Analysis SORL1 coding mutations: A) Frequency of haplotype combinations of the 17 SNPs (Haplo Stats)																		
Haplotype	**SNP1**	**SNP2**	**SNP3**	**SNP4**	**SNP5**	**SNP6**	**SNP7**	**SNP8**	**SNP9**	**SNP10**	**SNP11**	**SNP12**	**SNP13**	**SNP14**	**SNP15**	**SNP16**	**SNP17**	**hap.freq**
1	1	3	1	2	3	2	4	1	3	4	1	2	2	4	1	1	3	0.00028
2	1	3	1	2	3	3	4	1	3	4	1	2	2	4	1	1	3	0.01065
3	3	1	1	2	2	3	4	1	3	4	1	2	2	4	1	1	3	0
4	3	1	1	2	3	2	4	1	3	4	1	2	2	4	1	1	3	0.00161
5	3	1	1	2	3	3	4	1	3	4	1	2	2	4	1	1	1	0.00156
6	3	1	1	2	3	3	4	1	3	4	1	2	2	4	1	1	3	0.11336
7	3	1	1	2	3	3	4	1	3	4	1	2	2	4	3	1	3	0.00001
8	3	1	1	4	3	3	4	1	3	4	1	2	2	4	1	1	3	0.00156
9	3	3	1	2	2	3	4	1	3	4	1	2	2	4	1	1	3	0.00416
10	3	3	1	2	3	2	4	1	3	4	1	2	1	4	1	1	3	0.00156
11	3	3	1	2	3	2	4	1	3	4	1	2	2	1	1	1	3	0.00092
12	3	3	1	2	3	2	4	1	3	4	1	2	2	4	1	1	3	0.01759
13	3	3	1	2	3	2	4	1	3	4	1	2	2	4	1	3	3	0.00093
14	3	3	1	2	3	3	2	1	3	4	1	2	2	4	1	1	3	0.00938
15	3	3	1	2	3	3	4	1	1	4	1	2	2	4	1	1	3	0.00469
16	3	3	1	2	3	3	4	1	1	4	1	4	2	4	1	1	3	0.00103
17	3	3	1	2	3	3	4	1	3	2	1	2	2	4	1	1	3	0.00104
18	3	3	1	2	3	3	4	1	3	4	1	2	2	1	1	1	3	0.00533
19	3	3	1	2	3	3	4	1	3	4	1	2	2	4	1	1	3	0.78103
20	3	3	1	2	3	3	4	1	3	4	1	2	2	4	1	3	3	0.00481
21	3	3	1	2	3	3	4	1	3	4	1	2	2	4	3	1	3	0.02184
22	3	3	1	2	3	3	4	1	3	4	1	4	2	4	1	1	3	0.00157
23	3	3	1	2	3	3	4	1	3	4	4	2	2	4	1	1	3	0.00364
24	3	3	1	2	3	3	4	3	3	4	1	2	2	4	1	1	3	0.00468
25	3	3	1	4	3	2	4	1	3	4	1	2	2	4	1	1	3	0.00052
26	3	3	1	4	3	3	4	1	3	4	1	2	2	4	1	3	3	0.00416
27	3	3	1	4	3	3	4	1	3	4	1	2	2	4	3	1	3	0.00052

a): Haplotype Analysis SORL1 coding mutations: A) Frequency of haplotype combinations of the 17 SNPs (Haplo Stats)																	
Haplotype	**SNP1**	**SNP2**	**SNP3**	**SNP4**	**SNP5**	**SNP6**	**SNP7**	**SNP8**	**SNP9**	**SNP10**	**SNP11**	**SNP12**	**SNP13**	**SNP14**	**SNP15**	**SNP16**	**SNP17**	**hap.freq**
28	3	3	3	2	3	3	4	1	3	4	1	2	2	4	1	1	3	0.00105
29	3	3	3	2	3	3	4	1	3	4	1	2	2	4	1	3	3	0.00051

4b) Association test of Haplotype 19 using Generalized Estimation Equations (GEE)				
	BETA	**SE**	**Z**	**P**
h19haplotype	0.643541	0.16	15.83	6.91E-05

(subjects were coded based on haplotype copies of haplotype 19 (0=2 copies of 19, 1= 1copy of 19 and 2=0 copies of 19 Subjects with haplotype pairs estimated with posterior probability=1 used for the association analysis)