Supplementary Online Content


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eMethods

This supplementary material has been provided by the authors to give readers additional information about their work.
### eTable 1. Illumina Platforms Used for Genotyping and Quality Control Results in the Individual Datasets\(^{1-24}\)

<table>
<thead>
<tr>
<th>Genotyping platform</th>
<th>ACT</th>
<th>ADC1+2</th>
<th>ADC3</th>
<th>CHAP</th>
<th>Indianapolis</th>
<th>NIA-LOAD/NCRAD</th>
<th>ADGC*</th>
<th>MIRAGE 300k</th>
<th>MIRAGE 660k</th>
<th>GenerAAtions</th>
</tr>
</thead>
<tbody>
<tr>
<td>Genotyping platform</td>
<td>Illumina 660k</td>
<td>Illumina 660k</td>
<td>Illumina Omni Express</td>
<td>Illumina 1 M</td>
<td>Illumina 1 M</td>
<td>Illumina 610k and 370k</td>
<td>Illumina 1Mduo (v3)</td>
<td>Illumina 300k</td>
<td>Illumina 660k</td>
<td>Illumina 660k</td>
</tr>
<tr>
<td>Number of genotyped SNPs meeting QC thresholds</td>
<td>537,887</td>
<td>532,886</td>
<td>657,571</td>
<td>799,407</td>
<td>799,068</td>
<td>551,257</td>
<td>981,715</td>
<td>276,030</td>
<td>517,043</td>
<td>544,496</td>
</tr>
<tr>
<td>Number of samples meeting QC thresholds (cases/controls)</td>
<td>32/65</td>
<td>59/73</td>
<td>166/112</td>
<td>115/435</td>
<td>173/1,002</td>
<td>35/61</td>
<td>907/1,657</td>
<td>51/65</td>
<td>188/236</td>
<td>242/204</td>
</tr>
<tr>
<td>Number of principal components used</td>
<td>first 3</td>
<td>first 3</td>
<td>first 2</td>
<td>first 10</td>
<td>first 2</td>
<td>first 2</td>
<td>first 3</td>
<td>first 3</td>
<td>first 3</td>
<td>first 3</td>
</tr>
<tr>
<td>Number of genotyped and imputed SNPs in the final set</td>
<td>13,933,523</td>
<td>14,422,770</td>
<td>14,898,833</td>
<td>14,962,818</td>
<td>15,004,194</td>
<td>14,049,700</td>
<td>15,067,871</td>
<td>8,590,165</td>
<td>10,675,725</td>
<td>14,950,463</td>
</tr>
</tbody>
</table>

*Samples genotyped by the ADGC for this project were received from the AAG Study, ADCs, CHAP, Mayo Clinic, MSSM, NIA-LOAD/NCRAD, ROS/MAP/MARS/CORE, UM/VU, UP, WHICAP and WU*
**eTable 2.** Associations of rs115553053 in *HMHA1* and rs115882880 in *GRIN3B* in Analyses Conditioning on rs115550680 in *ABCA7*

<table>
<thead>
<tr>
<th>gene</th>
<th>SNP</th>
<th>chromosome</th>
<th>bp position</th>
<th>A1</th>
<th>A2</th>
<th>Freq1</th>
<th>OR</th>
<th>95% CI</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>HMHA1</td>
<td>rs115553053</td>
<td>19</td>
<td>1,082,844</td>
<td>t</td>
<td>c</td>
<td>0.05</td>
<td>1.70</td>
<td>1.43-1.97</td>
<td>0.0001</td>
</tr>
<tr>
<td>GRIN3B</td>
<td>rs115882880</td>
<td>19</td>
<td>1,001,777</td>
<td>a</td>
<td>c</td>
<td>0.10</td>
<td>1.39</td>
<td>1.22-1.56</td>
<td>0.0002</td>
</tr>
</tbody>
</table>

A1=minor allele; A2=wild type allele; Freq1=frequency of minor allele; OR=odds ratio; 95% CI=95% confidence interval

**eTable 3.** Imputation Quality (R^2) Values for Significant SNPs Across all Datasets Included in the Analyses^1^-24

<table>
<thead>
<tr>
<th>GENE</th>
<th>SNP</th>
<th>CHR</th>
<th>BP location</th>
<th>ACT</th>
<th>ADC1/ADC2</th>
<th>ADC3</th>
<th>CHAP</th>
<th>Indiana-polis</th>
<th>NIA-LOAD/NCRAD</th>
<th>ADGC</th>
<th>Mirage 300k</th>
<th>Mirage 600k</th>
<th>GenerAAtions</th>
</tr>
</thead>
<tbody>
<tr>
<td>ABCA7</td>
<td>rs115550680</td>
<td>19</td>
<td>1,050,420</td>
<td>0.95</td>
<td>0.96</td>
<td>0.98</td>
<td>0.99</td>
<td>0.98</td>
<td>0.97</td>
<td>0.99</td>
<td>0.89</td>
<td>0.96</td>
<td>0.96</td>
</tr>
<tr>
<td>HMHA1</td>
<td>rs115553053</td>
<td>19</td>
<td>1,082,844</td>
<td>0.94</td>
<td>0.95</td>
<td>0.97</td>
<td>0.98</td>
<td>0.97</td>
<td>0.96</td>
<td>0.97</td>
<td>0.9</td>
<td>0.95</td>
<td>0.94</td>
</tr>
<tr>
<td>GRIN3B</td>
<td>rs115882880</td>
<td>19</td>
<td>1,001,777</td>
<td>0.92</td>
<td>0.92</td>
<td>0.97</td>
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<td>0.97</td>
<td>0.93</td>
<td>0.98</td>
<td>0.87</td>
<td>0.88</td>
<td>0.91</td>
</tr>
<tr>
<td>--</td>
<td>rs145848414</td>
<td>5</td>
<td>174,014,114</td>
<td>0.96</td>
<td>0.97</td>
<td>0.96</td>
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<td>0.97</td>
<td>0.97</td>
<td>0.97</td>
<td>0.96</td>
</tr>
</tbody>
</table>

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eFigure 1. Quantile-Quantile (Q-Q) Plots of Individual Datasets\textsuperscript{1-24} Based on the Fully Adjusted Model Showing the Deviation of the Observed $P$ Values From the Expected Values (ie, the Null Hypothesis)

Observed values corresponding to the expected values are plotted on or near the middle line between the $x$-axis and the $y$-axis (null hypothesis). Values moved towards the $y$-axis indicate observed $P$ values more significant than expected under the null hypothesis. An early separation of the expected from the observed indicates a large number of moderately significant $P$ values that are more significant than expected under the null hypothesis indicating cryptic population stratification, relatedness or genotyping errors. The genomic inflation factor ($\lambda$) expresses the departure of the median $p$-value from its expected position, $\lambda$ values >1 indicate inflation.

a) ACT
b) ADC1+ADC2
c) ADC3
d) CHAP

![Image of a scatter plot with a best fit line and lambda=1.031]
e) Indianapolis
f) NIA-LOAD/NCRAD

![Graph showing observed vs. expected -log(p-value)]

- Observed -log10[p-value]
- Expected -log10[p-value]

\[ \text{lambda} = 0.987 \]
g) ADGC
h) Mirage 300k
i) Mirage 660k
j) GenerAAtions

![Graph showing observed vs. expected -log_{10}(p-value)]

- **Observed** vs. **Expected -log_{10}(p-value)**
- **λ = 1.029**
**eFigure 2. Forest Plots of Odds Ratios (ORs) of SNPs Significant in the Main Analyses**

The ORs of the individual datasets\(^1\)\(^{24}\) are represented by squares (proportional to weights used in the meta-analysis) and associated confidence intervals (horizontal lines). The pooled meta-analysis OR is represented by the center line of the diamond, the associated confidence intervals are represented by the lateral tips of the diamond. The dashed vertical line represents no effect. Names of the individual studies with the corresponding ORs and p-values are shown on the left side of the graph. rs145848414 on chr 5q35.2 did not pass the MAF cut-off of the post-imputation quality control in the Mirage 300k and Mirage 660k datasets, therefore these datasets were excluded from the meta-analysis of this SNP. M-300=MIRAGE300k; M-660=Mirage660k, GenA=GenerAAtions; IA=Indianapolis

1) rs115550680 in *ABCA7*
2) rs115553053 in *HMHA1*
3) rs115882880 in \textit{GRIN3B}

<table>
<thead>
<tr>
<th>Study Reference</th>
<th>OR</th>
<th>P-value</th>
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</thead>
<tbody>
<tr>
<td>ACT</td>
<td>4.65</td>
<td>1.1e-02</td>
</tr>
<tr>
<td>ADC1+2</td>
<td>1.14</td>
<td>8.4e-01</td>
</tr>
<tr>
<td>ADC3</td>
<td>1.59</td>
<td>1.2e-01</td>
</tr>
<tr>
<td>CHAP</td>
<td>1.51</td>
<td>1.5e-01</td>
</tr>
<tr>
<td>ADGC</td>
<td>1.53</td>
<td>5.0e-04</td>
</tr>
<tr>
<td>M-300</td>
<td>1.17</td>
<td>7.3e-01</td>
</tr>
<tr>
<td>M-660</td>
<td>1.33</td>
<td>2.3e-01</td>
</tr>
<tr>
<td>GenA</td>
<td>1.47</td>
<td>1.8e-01</td>
</tr>
<tr>
<td>IA</td>
<td>1.61</td>
<td>1.2e-02</td>
</tr>
<tr>
<td>LOAD</td>
<td>3.19</td>
<td>6.0e-02</td>
</tr>
</tbody>
</table>

Meta-\(P=6.3e-08\)
Heterogeneity-\(P=0.32\)

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4) rs145848414 on chr 5q35.2

<table>
<thead>
<tr>
<th>Gene</th>
<th>OR</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>ACT</td>
<td>22.61</td>
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</tr>
<tr>
<td>ADC1+2</td>
<td>1.99</td>
<td>1.8e-01</td>
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<tr>
<td>AIK3</td>
<td>2.51</td>
<td>2.5e-01</td>
</tr>
<tr>
<td>CHAP</td>
<td>7.67</td>
<td>4.4e-07</td>
</tr>
<tr>
<td>ADGC</td>
<td>2.31</td>
<td>3.4e-05</td>
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<tr>
<td>GainA</td>
<td>7.93</td>
<td>6.5e-07</td>
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<tr>
<td>IA</td>
<td>1.60</td>
<td>2.0e-01</td>
</tr>
<tr>
<td>LOAD</td>
<td>1.14</td>
<td>9.0e-01</td>
</tr>
</tbody>
</table>

Meta-P=6.9e-08
Heterogeneity-P=0.00
Methods

Description of cohorts

In the study included were subjects from the Adult Changes in Thought (ACT),\textsuperscript{15} the National Institute on Aging (NIA) Alzheimer’s Disease Centers (ADCs),\textsuperscript{13} the University of Miami/Vanderbilt University (UM/VU),\textsuperscript{2,9,22} the Mount Sinai School of Medicine (MSSM) Brain Bank,\textsuperscript{12} the Washington Heights Inwood Columbia Aging Project (WHICAP),\textsuperscript{24} The African American Alzheimer’s Disease Genetics (AAG) Study,\textsuperscript{16} the MIRAGE Study,\textsuperscript{11} NIA-LOAD/NCRAD,\textsuperscript{16} the Mayo Clinic,\textsuperscript{8} the Rush University Alzheimer’s disease Center (ROS/MAP, MARS/CORE),\textsuperscript{1,3-5} the Chicago Health and Aging Project (CHAP),\textsuperscript{7,10} the Indianapolis Ibadan Dementia Study (Indianapolis),\textsuperscript{21} the Genetic and Environmental Risk Factors for Alzheimer’s Disease Among African Americans (GenerAAtions) Study,\textsuperscript{17} the University of Pittsburgh (UP),\textsuperscript{14} and Washington University (WU).\textsuperscript{6,19,20,23} As described in the main text, the analyses were restricted to individuals of African American ancestry. All subjects were recruited under protocols approved by the appropriate Institutional Review Boards.

The Adult Changes in Thought study (ACT): The ACT cohort\textsuperscript{15} is an urban and suburban elderly population from a stable HMO. The original cohort of 2,581 cognitively intact participants age ≥ 65 were enrolled between 1994 and 1998; of these 4% were African American.\textsuperscript{1}\textsuperscript{ENREF_1} An additional 811 participants were enrolled in 2000-2002 using the same methods except oversampling clinics with more minorities, resulting in an overall rate of 5% African Americans. More recently, a continuous enrollment strategy was initiated in which new participants are contacted, screened and enrolled to keep 2,000 active at-risk person-years accruing in each calendar year. This resulted in an overall enrollment of 4,729 participants as of June 2012, of whom 193 (4.1%) were African American. All clinical data are reviewed at a consensus conference. Dementia onset is assigned half way between the prior biennial and the exam that
diagnosed dementia. Enrollment for the eMERGE Study began in 2007. A waiver of consent was obtained from the IRB to enroll deceased ACT participants, and consent for data sharing was obtained from living participants. In total, ACT/eMERGE contributed data on 32 individuals with probable or possible AD and on 65 CNEs who were included in analyses.

**The African American Alzheimer’s Disease Genetics (AAG) Study.** Participants of the multisite AAG study\(^{18}\) that contributed to this study were recruited between 2008 and 2011 from communities surrounding four locations: Columbia University in New York City, North Carolina State A&T University in Greensboro, NC, University of Miami, Florida, and Vanderbilt University in Nashville, Tennessee. Participants were recruited from various sources, including naturally occurring retirement communities, churches, Black fraternal and other organizations, community centers, health fairs, physician’s offices, newspaper ads, and word-of-mouth. All participants were age 60 and older and described themselves as non-Hispanic and Black. A one-time in-person evaluation included a comprehensive neuropsychological test battery, a medical and neurological examination, and assessment of memory complaints, as well as an informant interview assessing functional status and possible change in cognitional and daily activities. These data were evaluated in a consensus conference and diagnoses were based on standard research criteria (e.g. NINCDS-ADRDA criteria for AD, Petersen (2001) criteria for MCI) and categorized according to NACC criteria. Blood was drawn and sent to the National Cell Repository for Alzheimer’s Disease (NCRAD). The current study included 624 people with AD and 161 controls from the AAG cohort. DNA was prepared by NCRAD for genotyping and sent to the genotyping site at Children’s Hospital of Philadelphia.

**The NIA ADC Samples (ADC):** The NIA ADC cohort\(^{13}\) included subjects ascertained and evaluated by the clinical and neuropathology cores of the 29 NIA-funded ADCs. Data collection
is coordinated by the National Alzheimer’s Coordinating Center (NACC). NACC coordinates collection of phenotype data from the 29 ADCs, cleans all data, coordinates implementation of definitions of AD cases and controls, and coordinates collection of samples. The ADC cohort consists of 228 autopsy-confirmed or clinically-confirmed African American AD cases, and 189 autopsy-confirmed or clinically-confirmed cognitively normal elders (CNEs) who were older than 60 years at death or at assessment. Based on the data collected by NACC, the ADGC Neuropathology Core Leaders Subcommittee derived inclusion and exclusion criteria for AD and control samples. The clinical evaluation was made using the Uniform dataset (UDS) protocol. AD cases were demented according to DSM-IV criteria or Clinical Dementia Rating (CDR) ≥ 1. Neuropathologic stratification of cases followed NIA/Reagan criteria explicitly, or used a similar approach when NIA/Reagan criteria were coded as not done, missing, or unknown. Cases were intermediate or high likelihood by NIA/Reagan criteria with moderate to frequent amyloid plaques and neurofibrillary tangle (NFT) Braak stage of III-VI. Persons with Down’s syndrome, non-AD tauopathies and synucleinopathies were excluded. All autopsied controls had a clinical evaluation within two years of death. Controls did not meet DSM-IV criteria for dementia, did not have a diagnosis of mild cognitive impairment (MCI), and had a CDR of 0, if performed. Controls who did not meet or were low-likelihood AD by NIA/Reagan criteria, had sparse or no amyloid plaques, and a Braak NFT stage of 0 – II. ADCs sent frozen tissue from autopsied subjects and DNA samples from some autopsied subjects and from living subjects to the ADCs to the National Cell Repository for Alzheimer’s Disease (NCRAD). DNA was prepared by NCRAD for genotyping and sent to the genotyping site at Children’s Hospital of Philadelphia. ADC samples were genotyped and analyzed in separate batches. The subjects included in this study were genotyped in three waves. While most neuropathologically- and clinically-characterized cases and CNEs were part of the first two waves (ADC1 and ADC2, n=62 cases and 77 CNEs), the
third wave consisted of clinically-identified living cases and CNEs (ADC3, n=166 cases and 112 CNEs).

The Chicago Health and Aging Project (CHAP) is a longitudinal cohort study\textsuperscript{7,10} of all participating residents 65-years-of-age-and older of a geographically defined biracial community located on the southwest side of Chicago. At each of six data collection cycles (every three years), all subjects have undergone brief cognitive testing and a stratified random sample of about 500-600 subjects (aggregate 2844) has undergone detailed clinical evaluation. The subjects provided for analysis were diagnosed with prevalent or incident Alzheimer’s disease at these clinical evaluations.

The Genetic and Environmental Risk Factors for Alzheimer’s Disease Among African Americans (GenerAAtions) Study: Participants of the GenerAAtions Study\textsuperscript{17} were identified through the electronic claims database of the Henry Ford Health System. Community-dwelling African Americans aged 65 and older who had at least one encounter with the Henry Ford Health System in the three years prior to their recruitment and who had an available proxy informant were eligible for this study. Cases met NINCDS-ADRDA criteria for possible or probable AD, determined in a consensus conference which included a behavioral neurologist, psychiatrist, neuropsychologist, and a behavioral neurology nurse practitioner. Phenotypic and GWAS data were available for 242 AD cases and 204 cognitively normal controls. GWAS genotyping of this sample was performed using the Illumina 660 chip as previously described.

Indianapolis Cohort of the Indianapolis Ibadan Dementia Study, Indiana University (IU): The African American participants that were included in this study (173 cases, 1002 controls)\textsuperscript{21} were part of the community-based longitudinal comparative epidemiological study of African
Americans in Indianapolis, and Yoruba Nigerians living in the city of Ibadan. In 1992 enrollment staff employed home visits to randomly sampled residential addresses in 29 contiguous U.S. Census tracts. Entry criteria were: age ≥ 65, self-identified African American, and living at sampled address. At that time 2,212 participants were enrolled. In 2001 new participants were enrolled using random sampling from Medicare rolls, with entry criteria: age ≥ 70, and self identified African American. At that time 1,892 participants were enrolled. Participants were evaluated every two to three years with the Community Screening Interview for Dementia (CSI-D). Based on CSI-D scores individuals were selected for a full diagnostic clinical assessment including: CERAD neuropsychological battery, physical and neurological exam, and informant interview. Diagnoses were made by a panel of clinicians using standard criteria.25

**Mayo Clinic:** Included from the Mayo Clinic were 64 cases and 195 CNEs.8 All subjects were diagnosed by a neurologist at the Mayo Clinic in Jacksonville, Florida or Rochester, Minnesota. The neurologist confirmed a Clinical Dementia Rating score of 0 for all controls; cases had diagnoses of possible or probable AD made according to NINCDS-ADRDA criteria.25

**The MIRAGE Study (MIRAGE):** The MIRAGE study11 is a family-based genetic epidemiological study of AD that enrolled AD cases and unaffected sibling controls at 17 clinical centers in the United States, Canada, Germany, and Greece, and contributed 51 African American cases and 65 CNEs that were genotyped on the Illumina 300k chip and 188 African American cases and 236 CNEs that were genotyped on the Illumina 660k chip. In brief, families were ascertained through a proband meeting the NINCDS-ADRDA criteria for definite or probable AD. Unaffected sibling controls were verified as cognitively healthy based on a Modified Telephone Interview of Cognitive Status score ≥ 86.
Mount Sinai School of Medicine (MSSM): The MSSM dataset\textsuperscript{12} contains 29 African American AD cases (all neuropathologically confirmed) and 14 CNEs (all neuropathologically confirmed), recruited to the Mount Sinai Brain Bank. Subjects had been residents of the Jewish Home and Hospital in Manhattan and The Bronx, NY and were participants in a longitudinal study of aging and dementia.\textsuperscript{12} Brains were donated by the next of kin of deceased residents. AD diagnoses were based on clinical assessment including neuropathological assessments and subjects met CERAD criteria for definite AD or probable AD. CDR assessments, based on cognitive and functional status during the last 6 months of life, had been carried for every subject.

NIA-LOAD/NCRAD: The NIA LOAD Family Study\textsuperscript{16} recruited families with two or more affected siblings with LOAD and unrelated, CNEs similar in age and ethnic background. A total of 35 African American familial cases and 61 unaffected individuals were recruited through the NIA-LOAD study, NCRAD, and the University of Kentucky and included for analysis. One case per family was selected after determining the individual with the strictest diagnosis (definite > probable > possible LOAD). If there were multiple individuals with the strictest diagnosis, then the individual with the earliest age of onset was selected. The controls included only those samples that were neurologically evaluated to be normal and were not related to a study participant.

The Rush Studies (ROS/MAP/MARS/CORE): ROS/MAP are two community-based cohort studies.\textsuperscript{3-5} The ROS has been on-going since 1993, with a rolling admission. Through July of 2010, 1,147 older nuns, priests, and brothers from across the United States initially free of dementia who agreed to annual clinical evaluation and brain donation at the time of death completed their baseline evaluation. Of these, 89 self-reported African Americans were included in the current study. The MAP has been on-going since 1997, also with a rolling admission.
Through July of 2010, 1,392 older persons from across northeastern Illinois initially free of dementia who agreed to annual clinical evaluation and organ donation at the time of death completed their baseline evaluation and 97 self-reported African Americans were included in this meta-analysis. Details of the clinical and neuropathologic evaluations have been previously reported. A total of 130 persons passed genotyping QC. Of these, 30 met clinical criteria for AD at the time of their last clinical evaluation or time of death and met neuropathologic criteria for AD for those on whom neuropathologic data were available, and 100 were without dementia or MCI at the time of their last clinical evaluation or time of death and did not meet neuropathologic criteria for AD for those on whom neuropathologic data were available. MARS is a community-based cohort study of older African Americans with a rolling admission. Through July of 2010, 356 self-reported African Americans without known dementia who agreed to annual clinical evaluation completed their baseline evaluation. CORE is a community-based cohort study of older African Americans with and without dementia at baseline. Through July 2010, CORE has enrolled 218 older Africans without dementia at baseline.

**University of Miami/Vanderbilt University (UM/VU):** The UM/VU dataset contains 110 African American cases and 189 CNEs ascertained at the University of Miami and Vanderbilt University. Each affected individual met NINCDS-ADRDA criteria for probable or definite AD with age at onset greater than 60 years as determined from specific probe questions within the clinical history provided by a reliable family informant or from documentation of significant cognitive impairment in the medical record. Cognitively healthy controls were unrelated individuals from the same catchment areas and frequency matched by age and gender, and had a documented MMSE or 3MS score in the normal range.
**University of Pittsburgh (UP):** The University of Pittsburgh dataset\textsuperscript{14} contains 114 African American AD cases (of which 6 were autopsy-confirmed) recruited by the University of Pittsburgh Alzheimer’s Disease Research Center, and 79 African American CNEs ages 60 and older (2 were autopsy-confirmed). All AD cases met NINCDS/ADRDA criteria for probable or definite AD.

**The Washington Heights Inwood Aging Project (WHICAP).** The African American participants that were included in the present study (170 cases, 299 controls) were part of a longitudinal cohort study enrolled by a random sampling of Medicare recipients 65 years or older residing in northern Manhattan, New York.\textsuperscript{24} Each participant underwent an interview of general health and function, medical history, a neurological examination, and a neuropsychological battery. Baseline data were collected from 1999 through 2001. Follow-up data were collected at sequential intervals of 18 months. Diagnosis of dementia etiology was made based on standard criteria,\textsuperscript{25} and severity of dementia was assessed using the Clinical Dementia Rating scale.

**Washington University (WU):** An African American LOAD case-control dataset consisting of 87 cases and 30 healthy elderly controls was used in analyses for this study.\textsuperscript{6,19,20,23} Participants were recruited as part of a longitudinal study of healthy aging and dementia. Diagnosis of dementia etiology was made in accordance with standard criteria and methods.\textsuperscript{25} Severity of dementia was assessed using the Clinical Dementia Rating scale.
eREFERENCES


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