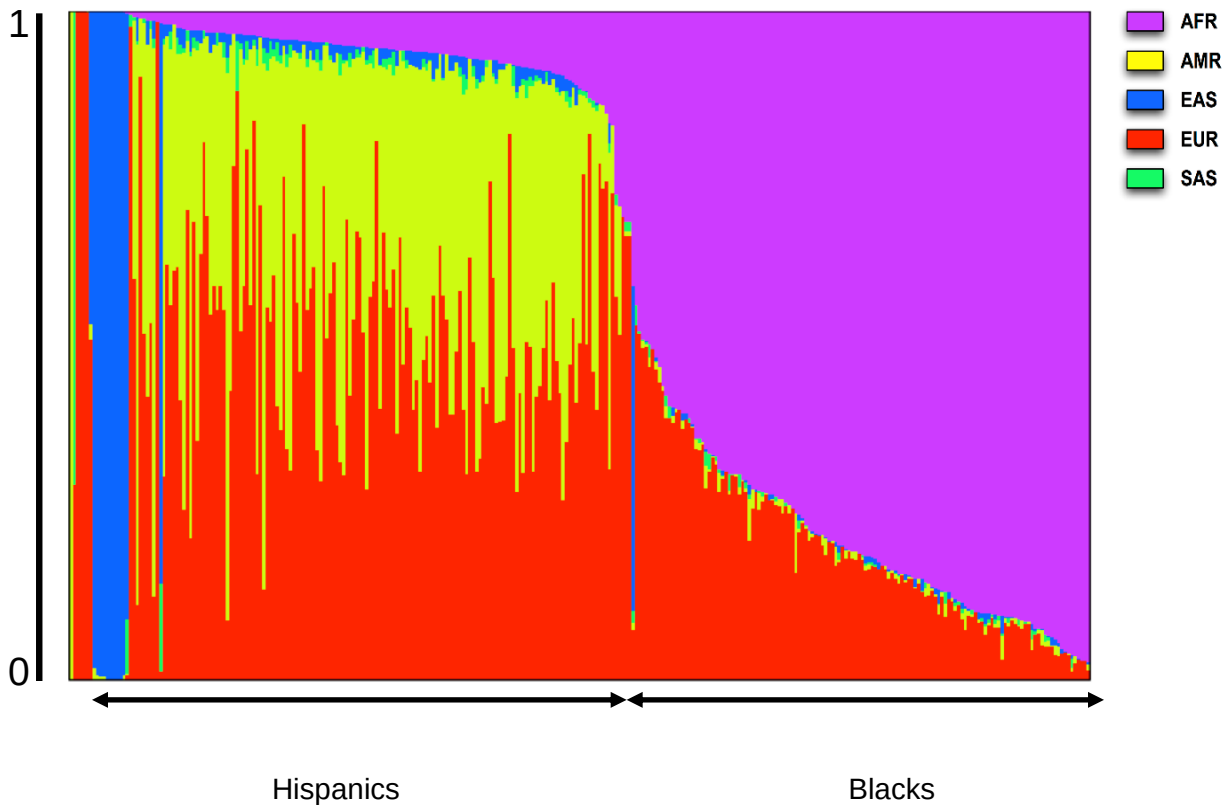
SUPPLEMENTAL MATERIALS

Study Population Genetic Admixture

These latter individuals were genotyped with Affymetrix UK Biobank Axiom single nucleotide polymorphism (SNP) arrays, which contain over 800,000 SNPs that have been selected to be informative over multiple racial/ethnic groups. Genetic datasets in these individuals were filtered to include only autosomal markers, markers with <5% missing genotypes, and markers with a minor allele frequency >1% using PLINK[1]. Additionally, datasets were pruned using LD-based Independent pair-wise pruning with a 50KB window, a step-size of 5, and r2 threshold of 0.2. Individual global ancestry estimations were computed with Admixture v1.3.0[2] in supervised mode. The supervised reference population was created by combining non-admixed individuals from the 1000Genomes[3] (1000G) and 88 individuals from an Indigenous American Population dataset provided by Esteban J. Parra(ENAM)[4]. Native American and African American Reference population individuals with admixture based upon the first 3 principal components using FlashPCA[5] were manually removed from the reference population dataset, so that reference 1000G + ENAM reference dataset used for ancestry estimation contained individuals without significant admixture. Admixture ancestry estimations were calculated using 200 bootstraps to obtain standard error estimations of the predictions. Estimations were performed on defined subsets and the complete Alzheimer's Cohort.



Supplemental Figure 1. UCD ADC Ancestry Estimates for Hispanics and Blacks. Each vertical spike corresponds to an individual and is colored by the proportion of each ancestry. The X-axis represents their self-reported ethnoracial group- either Hispanic or Black. The Y-axis represents the proportion (from 0-1). AFR=African; AMR=American Indian; EAS= East Asian; EUR=European; SAS=south Asian

Supplemental Table 1. ADC Longitudinal Cohort characteristics among individuals diagnosed as demented. All data are listed as frequencies (%) except for age and education which are listed as average +/- standard deviation

	Non-Hispanic White (n=860)	Black (n=121)	Hispanic (n=101)	Total (n=1082)
Age (yrs)	81 ± 9	81 ± 10	81 ± 10	81 ± 9
Gender (%F)*	53%	63%	64%	55%
Education yrs¶	14 ± 3	12 ± 4	9 ± 5	13 ± 4
APOE ε4 genotype***	60%	62%	32%	58%
Recruitment Source (% Clinic)***	79%	33%	20%	68%
Hypertension***	53%	79%	70%	57%
High Cholesterol	45%	52%	45%	46%
Diabetes***	12%	29%	25%	15%
Heart Disease	35%	33%	30%	35%
Stroke	16%	21%	18%	17%

P values for differences between Longitudinal cohort and Autopsied

*$p < 0.05$, ***0.0001 Fisher's exact between groups

¶ $p < 0.0001$ 1-way ANOVA, all groups differ significantly under Tukey-Kramer HSD

Supplemental References

[1] Chang CC, Chow CC, Tellier LC, Vattikuti S, Purcell SM, Lee JJ (2015) Second-generation PLINK: rising to the challenge of larger and richer datasets. *Gigascience* **4**, 7.

[2] Alexander DH, Novembre J, Lange K (2009) Fast model-based estimation of ancestry in unrelated individuals. *Genome Res* **19**, 1655-1664.

[3] Genomes Project C, Auton A, Brooks LD, Durbin RM, Garrison EP, Kang HM, Korbel JO, Marchini JL, McCarthy S, McVean GA, Abecasis GR (2015) A global reference for human genetic variation. *Nature* **526**, 68-74.

[4] Parra EJ (2007) Admixture in North America In *Pharmacogenomics in Admixed Populations,* Suarez-Kurtz G, ed. Landes Bioscience, Austin, TX, pp. 28-46.

[5] Abraham G, Inouye M (2014) Fast principal component analysis of large-scale genome-wide data. *PLoS One* **9**, e93766.