

The suggested Acknowledgement Statement to accompany the dataset is:

The acknowledgment of the ARIC dataset(s) should always include acknowledgment of the ARIC contract (component I below) **AND** the genotypic/genomic dataset(s) (component II below) **AND** the dbGaP accession number (component III below).

Components of the ARIC dbGaP Acknowledgment Statements:

I. Atherosclerosis Risk in Communities (ARIC) Contract Acknowledgment (Use the following statement for **ALL** analyses resulting from ARIC dbGaP data).

“The Atherosclerosis Risk in Communities Study is carried out as a collaborative study supported by National Heart, Lung, and Blood Institute contracts (HHSN268201100005C, HHSN268201100006C, HHSN268201100007C, HHSN268201100008C, HHSN268201100009C, HHSN268201100010C, HHSN268201100011C, and HHSN268201100012C). The authors thank the staff and participants of the ARIC study for their important contributions.”

II. Genotypic/Genomic Dataset Acknowledgment (Use one or more of the following statements relevant to the specific datasets used in your analysis)

A. ARIC Candidate-gene Association Resource (CARE): “Funding for CARE genotyping was provided by NHLBI Contract N01-HC-65226.”

B. ARIC Gene Environment Association Studies (GENEVA): “Funding for GENEVA was provided by National Human Genome Research Institute grant U01HG004402 (E. Boerwinkle).”

C. CALiCo-ARIC Population Architecture of Genes and Environment (PAGE) Consortium

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D. NHLBI GO-ESP: Heart Cohorts Exome Sequencing Project (ARIC)

“This study is part of the NHLBI Grand Opportunity Exome Sequencing Project (GO-ESP). Funding for GO-ESP was provided by NHLBI grants RC2 HL103010 (HeartGO), RC2 HL102923 (LungGO) and RC2 HL102924 (WHISP). The exome sequencing was performed through NHLBI grants RC2 HL102925 (BroadGO) and RC2 HL102926 (SeattleGO).

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E. Michigan-CORnell-TEXas (MICORTEX)

The study that generated the genotype data was supported by the National Institute of General Medical Sciences (P50-GM65509). Findings based on these genotype data are reported in “Deep resequencing

reveals excess rare recent variants consistent with explosive population growth” Nat Commun. 2010 Nov30; 1:131. PMCID: PMC3060603.

F. Building on GWAS: the U.S. CHARGE consortium - Sequencing (CHARGE-S): ARIC

“This study is part of the Building on GWAS: the U.S. CHARGE consortium - Sequencing (CHARGE-S). Funding for CHARGE-S was provided by NHLBI grant 5RC2HL102419 through the American Recovery and Reinvestment Act of 2009 (ARRA). Additional funding was provided for this study as part of Disease 2020: Large-Scale Sequencing and Analysis Center Initiated Projects; sequencing was completed at the Human Genome Sequencing Center at Baylor College of Medicine under NHGRI grant U54HG003273. Data for the Building on GWAS: the U.S. CHARGE consortium - Sequencing was provided by Eric Boerwinkle on behalf of the Atherosclerosis Risk in Communities (ARIC) Study, L. Adrienne Cupples, principal investigator for the Framingham Heart Study, and Bruce Psaty, principal investigator for the Cardiovascular Health Study. A portion of this research was conducted using the Linux Cluster for Genetic Analysis (LinGA-II) funded by the Robert Dawson Evans Endowment of the Department of Medicine at Boston University School of Medicine and Boston Medical Center. The CHARGE-S investigators request that publications resulting from these data cite their original publication: Psaty BM, O’Donnell CJ, Gudnason V, Lunetta KL, Folsom AR, Rotter JJ, Uitterlinden AG, Harris TB, Witteman JC, Boerwinkle E; CHARGE Consortium. Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium: Design of prospective meta-analyses of genome-wide association studies from five cohorts. Circ Cardiovasc Genet 2:73-80, 2009.”

G. Trans-Omics for Precision Medicine (TOPMed) Whole Genome Sequencing (WGS) Project: ARIC

The TOPMed acknowledgement statement can be found at:
<https://www.nhlbiwgs.org/acknowledgements>

III. dbGaP Accession Number Acknowledgement (Use the following statement for **ALL** analyses resulting from ARIC dbGaP data).

The datasets used for the analyses in this manuscript were obtained from dbGaP through dbGaP accession study number (insert appropriate accession number).