# ACKNOWLEDGEMENTS

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Summary
This document includes recommended statements that acknowledge the ARIC study in general and its various components and ancillary studies. Authors should follow the guidelines of the journal to which they submit as to the format, location and sometimes necessity to abbreviate. That said, each component which funded data used in a paper should be acknowledged. Some data collection (e.g. laboratory data which was collected using reagents donated by companies, CMS or cancer registry data) have additional requirements. This document lists the biggest ancillary studies to ARIC but authors are responsible for knowing their own sources of support and acknowledge all sources relevant to the data included in their manuscript. For example, we haven't listed all lab ancillaries, CAC, accelerometry, and other ancillaries or donated reagents for visits 4 and 5 (e.g. troponin, NTproBNP, cysC, PI:Ballantyne) or FGF23 ancillary (PI:Matsushita).

General acknowledgements for ARIC and ARIC-NCS

ARIC
Include in the acknowledgement section of ALL PAPERS USING ARIC DATA:

The Atherosclerosis Risk in Communities study has been funded in whole or in part with Federal funds from the National Heart, Lung, and Blood Institute, National Institutes of Health, Department of Health and Human Services, under Contract nos. (HHSN268201700001I, HHSN268201700002I, HHSN268201700003I, HHSN268201700004I, HHSN268201700005I). The authors thank the staff and participants of the ARIC study for their important contributions.

ARIC Neurocognitive (ARIC-NCS)
The Atherosclerosis Risk in Communities Study is carried out as a collaborative study supported by National Heart, Lung, and Blood Institute contracts (HHSN268201700001I, HHSN268201700002I, HHSN268201700003I, HHSN268201700004I, HHSN268201700005I). Neurocognitive data is collected by U01 2U01HL096812, 2U01HL096814, 2U01HL096899, 2U01HL096902, 2U01HL096917 from the NIH (NHLBI, NINDS, NIA and NIDCD), and with previous brain MRI examinations funded by R01-HL70825 from the NHLBI. The authors thank the staff and participants of the ARIC study for their important contributions.
Ancillary study support of specific lab tests and donated reagents (Visits 6 and 7)

Visit 7 testing was covered by ARIC NCS but some reagents were donated. Visit 6 laboratory testing, phlebotomy, urine collection, and biospecimen processing was funded by ARIC Ancillary Study #2009.16 NIH/NIDDK grant, R01DK089174; PI: Selvin. The tests covered (and tests using donated reagents are listed below) are:

Minnesota laboratory:
- Serum: 1,5-anhydroglucitol, alanine aminotransferase, glycated albumin, serum albumin (for glycated albumin), aspartate aminotransferase, beta-2 microglobulin, serum creatinine, cystatin C, fructosamine, gamma-glutamyltransferase, glucose, magnesium, potassium
- Whole blood: glycated hemoglobin (hemoglobin A1c), hemoglobin
- Urine: urine creatine, urine albumin

Baylor laboratory:
- High-sensitivity cardiac Troponin T, N-terminal pro-Brain natriuretic peptide

Visit 6 and 7 laboratory tests funded by NIH/NHLBI grant R01 HL134320; multiPIs Ballantyne and Selvin.

Baylor laboratory:
- Total cholesterol, triglycerides, HDL-C and calculated LDL-C, high sensitivity CRP (visits 6 & 7)
- GDF15 (visits 6 & 7)
- High-sensitivity cardiac Troponin I, galectin 3 (visits 6 & 7; also relevant for visits 4 and 5)
- High-sensitivity cardiac Troponin T, N-terminal pro-Brain natriuretic peptide (visit 7; also relevant for visits 4, 5, and 6)

Visit 6 acknowledgement: Funding for laboratory testing and biospecimen collection at ARIC Visit 6 was supported by grant R01DK089174 from the National Institute of Diabetes and
Digestive and Kidney Diseases (NIDDK) of the National Institutes of Health (NIH). The authors thank the staff and participants of the ARIC study for their important contributions.

**Donated reagent acknowledgement:** Include the acknowledgement statement and check with the ancillary PI about providing a copy of the paper to the donor.

Reagents for the ALT, AST, GGT, beta-2 microglobulin, and fructosamine assays were donated by the Roche Diagnostics Corporation.

Reagents for the 1,5-anhydroglucitol assays were donated by GlycoMark, Inc.

Reagents for the glycated albumin assays were donated by the Asahi Kasei Pharma Corporation.

Reagents for the hs-cTnT, NT-proBNP and GDF15 assays were donated by the Roche Diagnostics Corporation.

Reagents for hs-cTnI and galectin 3 were donated by Abbott Diagnostics

**ARIC Carotid MRI Study**
The Atherosclerosis Risk in Communities Study is carried out as a collaborative study supported by National Heart, Lung, and Blood Institute contracts (HHSN268201700001I, HHSN268201700002I, HHSN268201700003I, HHSN268201700004I, HHSN268201700005I) with the ARIC carotid MRI examination funded by U01HL075572-01. The authors thank the staff and participants of the ARIC study for their important contributions.

**ARIC Cancer**
Studies on cancer in ARIC are also supported by the National Cancer Institute (U01 CA164975). and the National Heart, Lung, and Blood Institute, National Institutes of Health, Department of Health and Human Services, under Contract nos. (HHSN268201700001I, HHSN268201700002I, HHSN268201700003I, HHSN268201700004I, HHSN268201700005I). The authors thank the staff and participants of the ARIC study for their important contributions.
The content of this work is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

Cancer incidence data have been provided by the Maryland Cancer Registry, Center for Cancer Surveillance and Control, Department of Mental Health and Hygiene, 201 W. Preston Street, Room 400, Baltimore, MD 21201. We acknowledge the State of Maryland, the Maryland Cigarette Restitution Fund, and the National Program of Cancer Registries (NPCR) of the Centers for Disease Control and Prevention (CDC) for the funds that helped support the availability of the cancer registry data.

**ARIC Omics**

ARIC GWAS data (including HapMap and 1000G imputed data):
Include the following statement in addition to the general ARIC acknowledgement statement:

Funding was also supported by R01HL087641, R01HL059367 and R01HL086694; National Human Genome Research Institute contract U01HG004402; and National Institutes of Health contract HHSN268200625226C. Infrastructure was partly supported by Grant Number UL1RR025005, a component of the National Institutes of Health and NIH Roadmap for Medical Research.

**ARIC, CHS and FHS WES Freeze 3 and 4 data**
Include the general ARIC acknowledgement statement after the following statement:

Funding support for “Building on GWAS for NHLBI-diseases: the U.S. CHARGE consortium” was provided by the NIH through the American Recovery and Reinvestment Act of 2009 (ARRA) (5RC2HL102419). Data for “Building on GWAS for NHLBI-diseases: the U.S. CHARGE consortium” 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. Sequencing was carried out at the Baylor College of Medicine Human Genome Sequencing Center and supported by the National Human Genome Research Institute grants U54 HG003273 and UM1 HG008898.

The Framingham Heart Study is conducted and supported by the NHLBI in collaboration with Boston University (Contract No. N01-HC- 25195), and its contract with Affymetrix, Inc., for genome-wide genotyping services (Contract No. N02- HL-6-4278), for quality control by Framingham Heart Study investigators using genotypes in the SNP Health Association Resource (SHARe) project. A portion of this research was conducted using the Linux Cluster for Genetic Analysis (LinGA) computing resources at Boston University Medical Campus. This CHS research was supported by contracts HHSN268201200036C, HHSN268200800007C, N01 HC55222, N01HC85079, N01HC85080, N01HC85081, N01HC85082, N01HC85083, N01HC85086 and grants HL080295, HL087652, HL105756 from the National Heart, Lung, and Blood Institute (NHLBI) with additional contribution from National Institute of Neurological Disorders and Stroke (NINDS). Additional support was provided through AG023629 from the National Institutes on Aging (NIA). A full list of CHS principal investigators and institutions can be found at CHS-NHLBI.org.

For manuscripts with ARIC exome chip data only:
Include the following statement in addition to the general ARIC acknowledgement statement:

Funding support for “Building on GWAS for NHLBI-diseases: the U.S. CHARGe consortium” was provided by the NIH through the American Recovery and Reinvestment Act of 2009 (ARRA) (SRC2HL102419).

ARIC methylation (HM450) data (blacks and whites) with exome chip PCs
Include the following statement in addition to the general ARIC acknowledgement statement:

Funding was also supported by 5RC2HL102419 and R01NS087541.
ARIC WES Freeze 4 and exome chip data
Include the following statement in addition to the general ARIC acknowledgement statement:

Funding support for “Building on GWAS for NHLBI-diseases: the U.S. CHARGE consortium” was provided by the NIH through the American Recovery and Reinvestment Act of 2009 (ARRA) (5RC2HL102419). Sequencing was carried out at the Baylor College of Medicine Human Genome Sequencing Center (U54 HG003273 and R01HL086694).

ARIC GWAS and exome chip data
Include the following statement in addition to the general ARIC acknowledgement statement:

Funding was also supported by R01HL087641, R01HL059367 and R01HL086694; National Human Genome Research Institute contract U01HG004402; and National Institutes of Health contract HHSN268200625226C.

Infrastructure was partly supported by Grant Number UL1RR025005, a component of the National Institutes of Health and NIH Roadmap for Medical Research. Funding support for “Building on GWAS for NHLBI-diseases: the U.S. CHARGE consortium” was provided by the NIH through the American Recovery and Reinvestment Act of 2009 (ARRA) (5RC2HL102419).

Metabolomics and exome chip data
Include the following statement in addition to the general ARIC acknowledgement statement:

Funding support for “Building on GWAS for NHLBI-diseases: the U.S. CHARGE consortium” was provided by the NIH through the American Recovery and Reinvestment Act of 2009 (ARRA) (5RC2HL102419). Metabolomics measurements were sponsored by the National Human Genome Research Institute (3U01HG004402-02S1).

ARIC WGS Freeze 3 data (low pass) only
Include the following statement in addition to the general ARIC acknowledgement statement:
Funding support for “Building on GWAS for NHLBI-diseases: the U.S. CHARGE consortium” was provided by the NIH through the American Recovery and Reinvestment Act of 2009 (ARRA) (5RC2HL102419). Sequencing was carried out at the Baylor College of Medicine Human Genome Sequencing Center and supported by the National Human Genome Research Institute grants U54 HG003273 and UM1 HG008898.

ARIC WES Freeze 3 or 4 and ESP data only
Include the following statement in addition to the general ARIC acknowledgement statement:

Funding support for “Building on GWAS for NHLBI-diseases: the U.S. CHARGE consortium” was provided by the NIH through the American Recovery and Reinvestment Act of 2009 (ARRA) (5RC2HL102419). CHARGE sequencing was carried out at the Baylor College of Medicine Human Genome Sequencing Center (U54 HG003273 and R01HL086694). Funding for GO ESP was provided by NHLBI grants RC2 HL-103010 (HeartGO) and exome sequencing was performed through NHLBI grants RC2 HL-102925 (BroadGO) and RC2 HL-102926 (SeattleGO).

Metabolomics, ARIC WES Freeze 4 and ARIC WGS Freeze 3 (low pass) data
Include the following statement in addition to the general ARIC acknowledgement statement:

Funding support for “Building on GWAS for NHLBI-diseases: the U.S. CHARGE consortium” was provided by the NIH through the American Recovery and Reinvestment Act of 2009 (ARRA) (5RC2HL102419). Metabolomics measurements were sponsored by the National Human Genome Research Institute (3U01HG004402-02S1). Sequencing was carried out at the Baylor College of Medicine Human Genome Sequencing Center and supported by the National Human Genome Research Institute grants U54 HG003273 and UM1 HG008898.

ARIC RNAseq or miRNAseq data
Include the following statement in addition to the general ARIC acknowledgement statement:

RNA sequencing was carried out at the Baylor College of Medicine Human Genome Sequencing Center and supported by the National Human Genome Research Institute grants U54 HG003273 and UM1 HG008898.
Whole genome sequencing (WGS) for the Trans-Omics in Precision Medicine (TOPMed) program was supported by the National Heart, Lung and Blood Institute (NHLBI). WGS for “NHLBI TOPMed: Atherosclerosis Risk in Communities (ARIC)” (phs001211) was performed at the Baylor College of Medicine Human Genome Sequencing Center (HHSN268201500015C and 3U54HG003273-12S2) and the Broad Institute for MIT and Harvard (3R01HL092577-06S1). Centralized read mapping and genotype calling, along with variant quality metrics and filtering were provided by the TOPMed Informatics Research Center (3R01HL-117626-02S1). Phenotype harmonization, data management, sample-identity QC, and general study coordination, were provided by the TOPMed Data Coordinating Center (3R01HL-120393-02S1). We gratefully acknowledge the studies and participants who provided biological samples and data for TOPMed.

The Genome Sequencing Program (GSP) was funded by the National Human Genome Research Institute (NHGRI), the National Heart, Lung, and Blood Institute (NHLBI), and the National Eye Institute (NEI). The GSP Coordinating Center (U24 HG008956) contributed to crossprogram scientific initiatives and provided logistical and general study coordination. The Centers for Common Disease Genomics (CCDG) program was supported by NHGRI and NHLBI, and whole genome sequencing was performed at the Baylor College of Medicine Human Genome Sequencing Center (UM1 HG008898 and R01HL059367).

Funding was also supported by 5RC2HL102419 and R01HL131136.
ARIC WGS from CCDG
Include the following statement in addition to the general ARIC acknowledgement statement:
The Genome Sequencing Program (GSP) was funded by the National Human Genome Research Institute (NHGRI), the National Heart, Lung, and Blood Institute (NHLBI), and the National Eye Institute (NEI). The GSP Coordinating Center (U24 HG008956) contributed to crossprogram scientific initiatives and provided logistical and general study coordination. The Centers for Common Disease Genomics (CCDG) program was supported by NHGRI and NHLBI, and whole genome sequencing was performed at the Baylor College of Medicine Human Genome Sequencing Center (UM1 HG008898 and R01HL059367).

Analysis Commons – Resource for Data Analysis
Include the following statement in addition to the general ARIC acknowledgement statement:
The Analysis Commons was funded by R01HL131136.

Proteomic (SomaLogic) data
Special requirements: In addition to including the the general ARIC acknowledgement and the acknowledgement below, anyone using the data needs to be covered by the ARIC SomaLogic Data Use Agreement (master at JHU with joinder to their own university and individual agreement signed, copies kept on file by their site PI and JHU aricjhu@jhu.edu). As per the DUA, all papers, abstracts and presentations need to be reviewed by SomaLogic (the authors are responsible but aricjhu@jhu.edu shares papers automatically to help with uniform compliance).

Include the following statement in addition to the general ARIC acknowledgement statement:
SomaLogic Inc. conducted the SomaScan assays in exchange for use of ARIC data. This work was supported in part by NIH/NHLBI grant R01 HL134320.
**Data availability statement:** Pre-existing data access policies for each of the parent cohort studies specify that research data requests can be submitted to each steering committee; these will be promptly reviewed for confidentiality or intellectual property restrictions and will not unreasonably be refused. Please refer to the data sharing policies of these studies. Individual level patient or protein data may further be restricted by consent, confidentiality or privacy laws/considerations. These policies apply to both clinical and proteomic data.