HCHS/SOL Omics Data Inventory Summary from Visits 1, 2, and 3 Biospecimens
Updated May 2025

Omics Type	Visit 1 N=16415	Visit 2 N=11623	Visit 3 N=9864
Consented[1] at Time of Sample Selection	14840	10291	7895
Consented[1] at End of Visit Data Collection (Final Consent Status)	13206	10208	7895
WGS			
Sent to Lab	13871[2]	--	--
Data Available	13262	--	--
Data Availability Pending	306	--	--
GWAS			
Sent to Lab	12895[2]	--	--
Data Available	12737	--	--
Metabolomics			
Sent to Lab	14029[2]	5150[3]	0
Samples in Processing/Data Pending	7845	4331	0
Data Available	6180	817	0
Number of Available Samples Remaining[4]	794	5107	7811
RNA Sequencing			
Sent to Lab	7733[5]	0	0
Samples in Processing/Data Pending	0	0	0
Data Available	7000	0	0
Number of Available Samples Remaining[4]	5355	10138	7811
DNA Methylation			
Sent to Lab	13957[6]	7039[7]	0
Samples in Processing/Data Pending	9706	2660	0
Data Available	4247	3657	0
Selected in Funded Study	0	3007[8]	0
Number of Available Samples Remaining[4]	877	253	7811
Proteomics			
Sent to Lab	2000[9]	0	0
Samples in Processing/Data Pending	2000	0	0
Data Available	0	0	0
Number of Available Samples Remaining[4]	11085	10138	7811

Abbreviations: WGS, whole genome sequencing; GWAS, genome-wide association studies; RNA, ribonucleic acid; DNA, deoxyribonucleic acid.

1. Consent to use genetic samples in current and future research by investigators associated or not with HCHS/SOL
2. Eligibility criteria: participants with genotyping consent from 2nd version of ICT from (ICTB) and DNA sample available at time of sample selection
3. Visit 2 Metabolomics eligibility criteria (2 studies): (a) GOLD study participants whose stool sample collection were completed within 30 days, (b) participants with gut microbiome data or had obesity at either V1 or V2, and random sample of participants with non-missing V2 covariates
4. Number of participants with consent and available sample that have not been selected yet
5. Visit 1 RNA Sequencing eligibility criteria: participants with WGS data at time of sample selection

Run by nslye using data from the 2505 retrieval

HCHS/SOL Omics Data Inventory Summary from Visits 1, 2, and 3 Biospecimens
Updated May 2025

6. Visit 1 DNA Methylation eligibility criteria (5 studies): (a) SOL INCA MCI+ cases and controls, (b) Spirituality participants, (c) SOL FLOR mothers, (d) Sociocultural participants, (e) remaining participants with consent and DNA sample available at time of sample selection
7. Visit 2 DNA Methylation eligibility criteria (4 studies): (a) SOL INCA MCI+ cases and controls, (b) Sociocultural participants, (c) participants with gut microbiome data or obesity, and random sample of participants with non-missing V2 covariates, (d) CAC
8. AS#2016.12 DNA Methylation & Diabetes by Zhao; eligibility criteria: participants without history of cancer and non-missing V2 covariates
9. AS#2021.09 Biomarkers of CKD by Franceschini; eligibility criteria: participants with TOPMed WGS and RNASeq data, latest genetic consent, and self-reported background matches GWAS background

Ancillary Study Funding

Ancillary Study Number and PI Name	Title and Funding	Visit(s)
WGS		
2012.02 North, Kari	Population Architecture Using Genomics and Epidemiology (PAGE) CALiCo Phase II: Genetic Epidemiology of Causal Variants Across the Life Course (U01 HG007416)	1
2015.10 Boerwinkle, Eric	Whole Genome Sequence and Metabolomics for Gene Discovery in CVD (UM1 HG008898) Whole genome sequencing was performed at the Baylor College of Medicine Human Genome Sequencing Center.	1
2017.02 Kaplan, Robert	TOPMed: HCHS/SOL in the NHLBI Trans-Omics for Precision Medicine: HHSN268201600033I for genomic sequencing; and contract HHSN268201800002I for the TOPMed Informatics Research Center; R01HL-120393, U01HL-120393, and contract HHSN268201800001I for the TOPMed Data Coordinating Center.	1
2017.26 North, Kari	CALiCO/PAGE 3	1
GWAS		
North, Kari	The HCHS/SOL Genetic Analysis Center at the University of Washington was supported by NHLBI and NIDCR contracts (HHSN268201300005C AM03 and MOD03).	1
Metabolomics		
2013.08 Kaplan, Robert	GOLD 1 and GOLD 2: Gut Origins of Latino Diabetes Study (R01MD011389)	1 & 2
2015.10 Boerwinkle, Eric	Whole Genome Sequence and Metabolomics for Gene Discovery in CVD (UM1HG008898)	1
2017.02 Kaplan, Robert	TOPMed: HCHS/SOL in the NHLBI Trans-Omics for Precision Medicine See WGS above	1 & 2
2017.14 Bing, Yu	Metabolic signatures underlying cardiac structure for heart failure (R01HL168683)	1
RNA Sequencing		
2017.02 Kaplan, Robert	TOPMed: HCHS/SOL in the NHLBI Trans-Omics for Precision Medicine See WGS above	1
DNA Methylation		
2016.12 Zhao, Jinying	Methylomic signatures of socioenvironmental exposome on diabetes risk in Hispanics/Latinos (R01DK137254)	2
2017.02 Kaplan, Robert	TOPMed: HCHS/SOL in the NHLBI Trans-Omics for Precision Medicine See WGS above	1 & 2
2017.09	SOL INCA DNAm (RF1 AG061022)	1 & 2

HCHS/SOL Omics Data Inventory Summary from Visits 1, 2, and 3 Biospecimens
Updated May 2025

Ancillary Study Number and PI Name	Title and Funding	Visit(s)
Gonzalez, Hector Fornage, Myriam		
2017.19 Suglia, Shakira	Social Stress: Social stress, Epigenetics and Cardiometabolic Health among Latinos (R01MD013320)	1 & 2
2017.32 Daviglus, Martha Budoff, Matthew Gallo, Linda C Hou, Lifang	CAC: Presence and Extent of, and Factors Associated with Coronary Artery Calcium, Plaque Density, and Coronary Remodeling in Diverse US Hispanic/Latino Adults (R01HL152692)	2
2018.13 Shields, Alexandra	Assessing the Impact of Psychosocial Stress and Spirituality on Health	1 & 2
2019.05 Fernandez-Rhodes, Lindsay	Genetic, Psychosocial and Epigenetic Risk Factors for Preterm Birth and Low Birth Weight (internal funding)	1
Proteomics		
2021.09 Franceschini, Nora	Multi-omics biomarkers of chronic kidney disease in Hispanics/Latinos (R56HG013163, R01HG013163)	1