HCHS/SOL Consortia Involvement (Draft Incompelte Listing)

	Tracking Number	Acronym	HCHS/SOL Liaison	Genetic or Phenotypic	Details/Comments	Status
1	C-2024.01	CCC-Tobacco	Robert Kaplan / Carlos Rodriguez		Cross-Cohort Collaboration (CCC) is a harmonized dataset of twenty-three prospective cohort studies predominantly in the US.	SC approval May 2024
2	C-2023.06	Rosas – T2D	Gregory Talavera	Both	Classification of T2D and risk of comorbidities: the T2D Heterogeneity Consortium	SC approval September 2023
3	C-2023.05	Qi – T2D	Qibin Qi	Both	Classification of T2D	SC approval July 2023
4	C-2023.04	Bancks – T2D	Daniela Sotres	Both	T2D subtypes	SC approval August2023
5	C-2023.03	Wang - MicroCardio Co	Robert Kaplan		MicroCardio Consortium	SC approval June2023
6	C-2023.02	Terechenko - AI cardiac beat labeling	Robert Kaplan		AI cardiac beat labeling. Aims to develop and validate an accurate, reproducible, and replicable Deep Learning ECG model that labels each cardiac beat on a 12-lead ECG digital signal and classifies 13 unique types of cardiac beats	SC approval June2023
7	C-2023.01	Ballew - CKD Prognosis Consortium	Robert Kaplan		CKD-PC is tasked with compiling and meta-analyzing the best available data on kidney measures and clinical outcomes, and currently consists of over 100 cohorts, which arise from general, high-risk, or CKD populations. To date, the CKD-PC has published over 30 high impact papers with important implications for the definition, staging, and management of CKD.	SC approval June2023
8	C-2022.01	NCI	Gregory Talavera		NCI: National Cancer Institute Cancer Cohort Consoritum	SC approval September 2023
9	C-2021.01	gnomAD	Tamar Sofer	Genetic	gnomAD originally launched in 2014 as the Exome Aggregation Consortium (ExAC), is a coalition of investigators seeking to aggregate and harmonize exome and genome sequencing data from a variety of large-scale sequencing projects, and to make summary data available for the wider scientific community.	
1	C-2020.12	Gene-Lifestyle	Kari North	Gentic	A Multi-Ancestry Study of Gene-Lifestyle and Multi-Omics in Cardiometabolic Traits PI: Dabeeru C Rao	*Administrative insert 31Jan2024*
1	C-2020.11	PAGE	Kari North	Genetic	PAGE: Population Architecture Genomics and Epidemiology To gain better understanding of how genetic factors increase susceptibility to disease. PAGE has a successful long-running collaboration studying the genetics of understudied groups. With over 143 publications, past achievements include studies discovering and characterizing CVD and CVD risk factor loci, developing statistical tools and genotyping arrays that have enhanced genomic studies in multi-population	

	Tracking Number	Acronym	HCHS/SOL Liaison	Genetic or Phenotypic	Details/Comments	Status
					investigations, and investigating clinical applications of GWAS findings. PAGE Multi Ethnic Genotyping Array, is now the framework for the Global Diversity Array being used by the All of Us Research Program. Further, PAGE has developed an open and collaborative trainee-focused culture leading to hundreds of publications and dozens of PAGE trainees becoming faculty.	
1	C-2020.10	LAGENO-BC	Sylvia Smoller	Genetic	LAGENO-BC: Latin American Genetic/Genomics of Breast Cancer Consortium, subcohort of CONFLUENCE Discovery susceptibility loci and etiology of breast cancer by subtypes, develop PRS for personalized risk assessment, discover loci for breast cancer prognosis, long-term survival, response to treatment, and second breast cancer.	
1	C-2020.09	HISLA	Kari North	Genetic	Discovery and fine-mapping of genetic loci for anthropometric traits. The Hispanic/Latino Anthropometry (HISLA) Consortium began in 2012 for obesity-related traits, now includes 27 studies of HL adults (>70k), and 4 studies of children/adolescents (>2k) from the United States and Latin America. HISLA has analyzed densely imputed genetic data in a sample of HL adults to identify and fine-map genetic variants associated with BMI, height, and BMI-adjusted waist-to-hip ratio (WHRadjBMI) and discovered multiple new loci for these traits.	
1	C-2020.08	GUARDIAN	Robert Kaplan	Genetic	GUARDIAN: Genetics Underlying Disease in Hispanics Understanding the genetic basis and molecular mechanisms underlying rare genetic disorders.	
1	C-2020.07	GLIDE	John Shaffer, James Beck	Both	GLIDE: Gene-Lifestyle Interactions and Dental Endpoints International initiative to investigate the genetic factors and gene-environment interactions influence dental health outcomes. This work generated a GWAS publication (PMID: 31235808) that has been important in the field of dental caries and periodontitis genetics. Specifically, this work has (1) served as the largest GWAS to date for informing oral health polygenic risk scores, (2) showed important genetic correlations of dental diseases with systemic diseases, and (3) showcased the benefits and limitations of combining clinical and self-reported data on dental diseases.	
1	C-2020.06	GIANT	Kari North	Genetic	Genetic Investigation of Anthropometric Traits seeks to identify genetic loci that modulate human body size and shape, including height and measures of obesity. recently published results from the largest-known genome-wide association study (GWAS)—nearly 5.4 million people—and identified more than 12,000 genetic variants associated with variation in human height.	
1	C-2020.05	CHARGE	Robert Kaplan, Cathy Laurie	Genetic	Cohorts for Heart and Aging Research in Genomic Epidemiology Facilitate GWAS meta-analyses and replication opportunities among multiple large and well-phenotyped longitudinal cohort studies.	
1	C-2020.04	C4R	Robert Kaplan,	Both	CCC: Cross-Cohort-Collaboration	

	Tracking Number	Acronym	HCHS/SOL Liaison	Genetic or Phenotypic	Details/Comments	Status
			Greg Talavera (secondary)		Develop infrastructure, policies, and procedures to promote transparent and seamless scientific collaboration across multiple cohort studies.	
1	C-2020.03	ADSP	Hector Gonzalez	Genetic	Alzheimer's Disease Sequence Project Summary stats will be shared after main neurocognitive GWAS is published. The overarching goals of the Alzheimer's Disease Sequencing Project (ADSP) are to: 1) Identify new genes and genetic variations that contribute to increased risk for or protection against AD/ADRD, 2) Provide insight as to why these genes and variations impact AD/ADRD, 3)Identify potential avenues or approaches to transform genetic results into meaningful therapeutic targets for further development.	
2	C-2020.02	GCVRC	Larissa Aviles-Santa	Phenotypic	Global Cardiovascular Risk Consortium Incidence of CVD and attributable risk in relation to standard risk factors, by large geographic regions. GCVRC comprises harmonized data from nearly 1.7 Million individuals of 126 cohorts across 43 countries and aims to elucidate the distribution of five major cardiovascular risk factors (body mass index, systolic blood pressure, non-high-density lipoprotein cholesterol, current smoking, and diabetes) and their impact on cardiovascular disease (CVD) by geographical region and sex.The HCHS/SOL shared baseline data with the GCVRC. Although in the first analysis there was no allusion to race/ethnicity by world region, future analyses based on specific risk factors may do so.	
2	C-2020.01	PREPARED	Daniela Sotres-Alvarez	Phenotypic	Preconception Period Analysis of Risks and Exposures Influencing Health and Development Investigation of preconceptional exposures as determinants of long-term health outcomes for both mothers and their children.	
2	C-2011.01	NSRR	Susan Redline	Phenotypic	National Sleep Research Resource Repository for sharing large amounts of sleep data (polysomnography, actigraphy and questionnaire-based) from multiple cohorts, clinical trials, and other data sources with mission to advance sleep and circadian science by supporting secondary data analysis, algorithmic development, and signal processing through the sharing of high-quality data sets.	Underway https://sleepdata.org/
2		UNITED	Charles DeCarli	MRI	Global consortium on neuroimaging of neurodegenerative diseases The aim of the UNITED consortium is to improve diagnostics, treatment and eventually even prevention of neurodegenerative diseases worldwide.	Not yet formally approved
2		PRESTO/HCHS-SOL	Robert Kaplan / Jee-Young Moon		Ventura Prediction of Sudden Death in Multi-ethnic Communities (PRESTO) and HCHS/SOL Collaborative Study	

	Tracking Number	Acronym	HCHS/SOL Liaison	Genetic or Phenotypic	Details/Comments	Status
					SOL serves as population-based comparator for this community surveillance study in southern California on sudden cardiac arrest. Publication: "Risk Factors for Sudden Cardiac Arrest Among Hispanic/Latino Adults in Southern California: Ventura PRESTO and HCHS/SOL",	
2		PGC	Sylvia Smoller		Latinx Psychiatric Genetics Consortium The Psychiatric Genomics Consortium aims to enable rapid progress in elucidating the genetic basis of psychiatric disorders. It includes 800+ investigators from 36 countries and >400K subjects.	
2		C2P2	Ilir Agalliu / Robert Kaplan		Colorectal Pooling Project To understand the role of modifiable (BMI, waist circumference, physical inactivity, cigarette smoking, lack of NSAID/aspirin use, red/processed meat intake, Western diet pattern, low fiber/fruit/vegetable/calcium intake, alcohol use, sleep patterns, antibiotic use) and non-modifiable (height, diabetes, allergies, family history of CRC, and inflammatory bowel disease) risk factors for early-onset versus late-onset CRC and to create a resource for future studies of racial disparity research and blood-based biomarkers of CRC.	
2		COMPASS	Yasmin Mossavar-Rahmani, Robert Kaplan		Cardiometabolic Outcomes in Multiethnic Physical Activity and Sedentary Behavior Study The goal of this study is to collect repeat accelerometry data in order to refine understanding of the association between sedentary behavior/physical activities with CVD risk. The project features pooled analysis with the Framingham Heart Study, providing new opportunities for health disparities research by comparison across SOL Hispanics and non-Hispanics from Framingham.	
2		DBDC	Yasmin Mossavar-Rahmani, Qibin Qi, Robert Kaplan		Dietary Biomarkers Development Consortium The project will identify biomarkers for dietary intake using a randomized clinical trial design; data from HCHS/SOL alongside other population based cohorts, will be used to validate food biomarkers identified in the clinical trials.	
2		TOPMED	Robert Kaplan, Kari North		Trans-Omics for Precision Medicine TOPMed is part of a broader Precision Medicine Initiative, which aims to provide disease treatments tailored to an individual's unique genes and environment. TOPMed integrates whole-genome sequencing (WGS) and other omics (e.g., metabolic profiles, epigenomics, protein and RNA expression patterns) data with molecular, behavioral, imaging, environmental, and clinical data. HCHS-SOL constitutes one of the largest Hispanic groups in this multi-omics consortium.	