



Cross-Cohort Collaboration Consortium  
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Portland, Oregon

Brief TOPMed Introduction

TOPMed Data Coordinating Center  
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# Trans-Omics for Precision Medicine (TOPMed)

- Part of the broader Precision Medicine Initiative
- Identify risk factors for heart, lung, blood and sleep disorders
  - Cross-study analyses to maximize power
  - Requires phenotype harmonization
- Develop targeted and personalized treatments
- Whole-genome sequencing – began Oct 2014, ~70k whole genomes at 30x completed, expect ~120k by end of year 3
- Additional ‘omics planned – RNAseq, metabolomics, Methylation, Proteomics

# Phase 1 and 2: 72K subjects

37 Different studies

Major Cohorts:

Framingham

Jackson

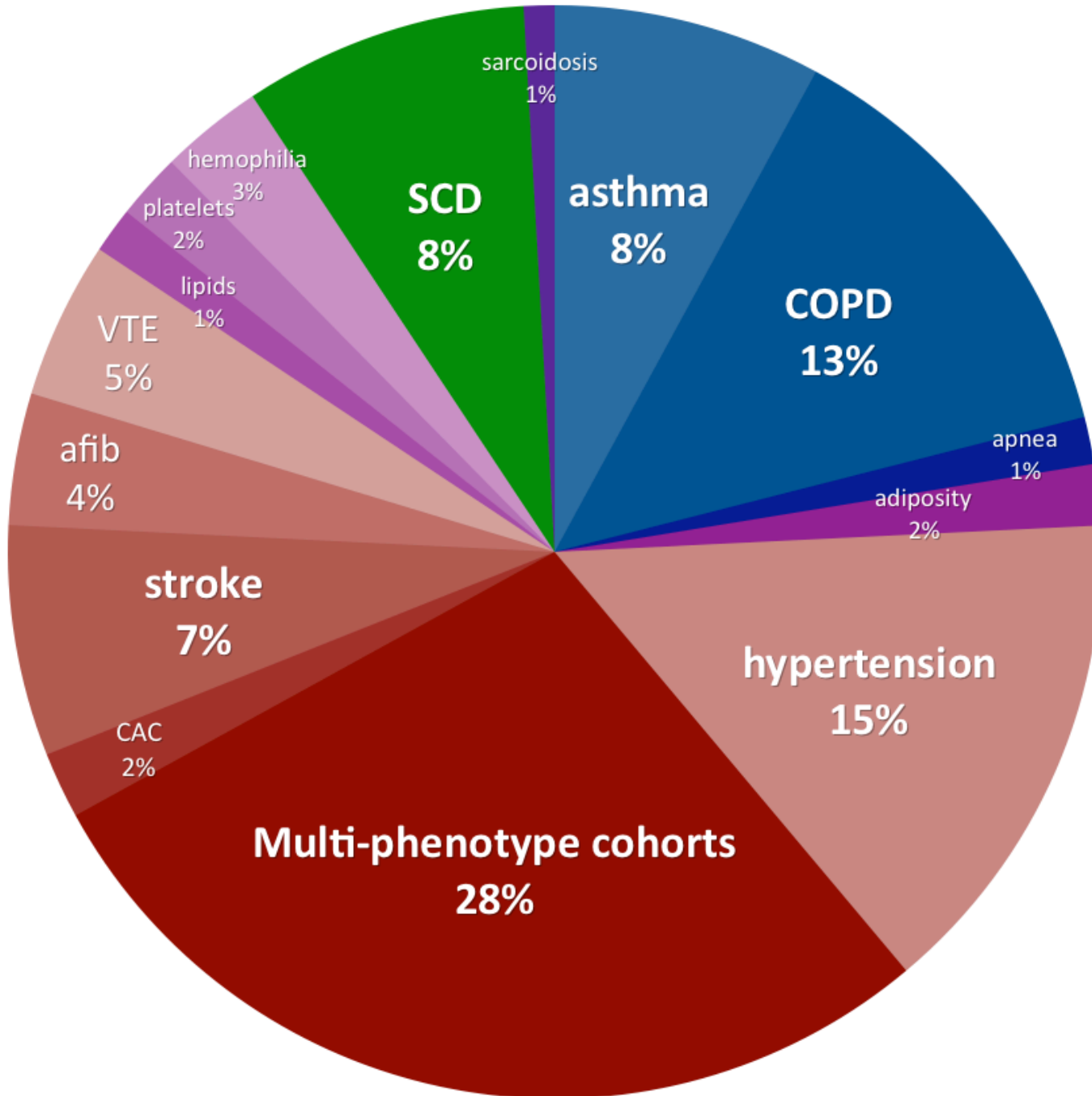
MESA

ARIC

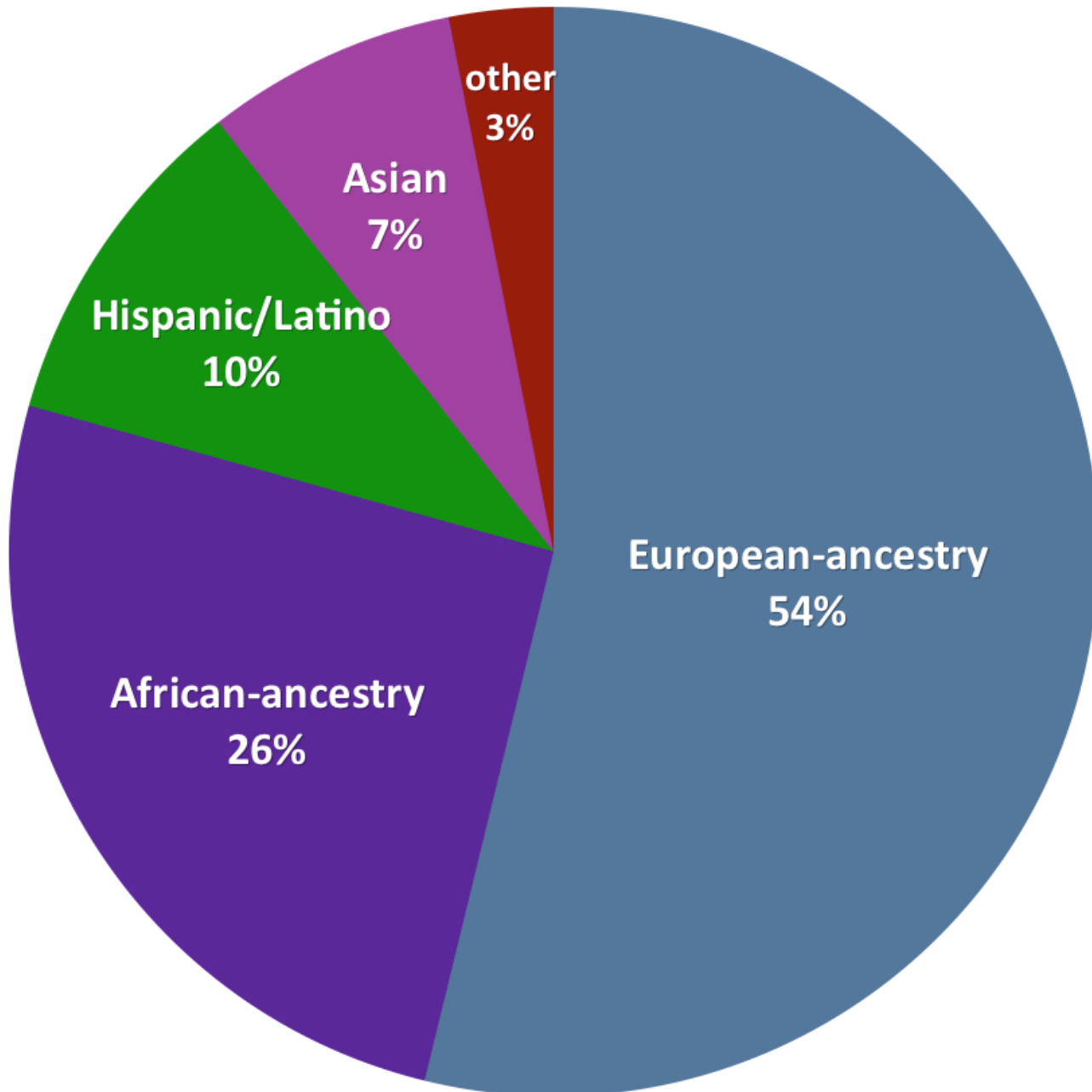
HCHS/SOL

CARDIA

WHI



**Phase 1 and 2: 72K individuals**





# Current Working Groups

Anthropometry – Adiposity

Asthma

Atherosclerosis

Blood Pressure

Bone Mineralization

COPD

Diabetes

EKG – Arrhythmia

Epigenetics

Family Studies

Heart Failure – Cardiac Function &  
Morphology

Hematology & Hemostasis

Inflammation Biomarkers

Kidney Function

Lipids

Lung Function

Metabolomics

Mitochondrial DNA

PFT

Population Genetics

Reproductive Health

Sarcoidosis

Sickle Cell Disease

Sleep

Smoking

Stroke

Structural Variation

VTE



## NHLBI Trans-Omics for Precision Medicine Whole Genome Sequencing Program

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**Upcoming event of interest:** Analysis Commons Hands-On Workshop in Houston, January 24-25, 2017. This is a hands-on workshop to help facilitate genotype-phenotype analysis and discovery using WGS data.

### Agenda

**Register here:** <https://www.eventbrite.com/e/analysis-commons-hands-on-workshop-tickets-28585102812?utm-medium=discovery&utm-campaign=social&utm-content=attendeeshare&aff=escb&utm-source=cp&utm-term=listing>

## Whole Genome Sequencing in the NHLBI Trans-Omics for Precision Medicine

*Trans-Omics for Precision Medicine* (TOPMed), sponsored by the [National Institutes of Health's National Heart, Lung and Blood Institute](#) (NHLBI), is a program to generate scientific resources to enhance our understanding of fundamental biological processes that underlie heart, lung, blood and sleep disorders (HLBS). It is part of a broader *Precision Medicine Initiative*, which aims to provide disease treatments that are tailored to an individual's unique genes and environment. TOPMed will contribute to this initiative through the integration of whole-genome sequencing (WGS) and other -omics (e.g., metabolic profiles, protein and RNA expression patterns) data with molecular, behavioral, imaging, environmental, and clinical data. In doing so, this program seeks to uncover factors that increase or decrease the risk of disease, identify subtypes of disease, and develop more targeted and personalized treatments.

The *Whole Genome Sequencing* (WGS) project is part of NHLBI's TOPMed program and serves as an initial step for the larger initiative. In recent years, genetic research of complex disease using Genome-Wide Association Study (GWAS) and Exome-sequencing approaches has resulted in an unprecedented explosion of genetic discovery. However, a large portion of heritability in complex diseases remains elusive. Whole Genome Sequencing (WGS) will provide a comprehensive view of the genome, an opportunity to further understand the genetic architecture relevant to HLBS disorders, and an unprecedented resource to the scientific community.

The WGS project started in 2014 to generate deep WGS data for studies with diverse ancestries and extensive characterization of HLBS-related traits. The current TOPMed [project studies](#) have a variety of study designs including family, case-control, pharmacogenomic, cohort-based designs, founder populations and

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« **December** »

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[SICAL](#)

Note: All events are noted in Pacific time.

- [No Sample and Data Processing call](#)  
12/28/16
- [Lipids Working Group weekly call](#)  
12/28/16 -  
06:00 am to 07:00 am  
PST
- [Orientation for TOPMed](#)