Microarray analysis

Axiom PangenomiX Array

Ethnic diversity at your fingertips—the Axiom PangenomiX Array hosts the largest population coverage on a high-throughput array.

The Applied Biosystems™ Axiom™ PangenomiX Array is a human genotyping research array designed for whole-genome imputation with globally diverse population coverage. It is an essential research tool in human genomics for applications such as genome-wide association studies (GWAS), population health initiatives, polygenic risk score development and implementation, and clinical research trials in drug discovery. The Axiom PangenomiX Array can scan the whole genome from as little as 100 ng of genomic DNA. This array enables identification of target single-nucleotide polymorphisms (SNPs), analysis of copy number variants (CNVs), human leukocyte antigen (HLA) typing, and more in a single, cost-effective assay with ready-to-use data analysis.

More than 800,000 markers were selected for high genomic coverage from phase 3 of the 1000 Genomes Project, yielding coverage for European, African, admixed American, East Asian, and South Asian populations. This means variants prevalent in different populations can be accurately represented and accounted for, leading to more inclusive research outcomes.

Contact us to learn more about discounts and offers available to you at **thermofisher.com/pangenomixcontact**.

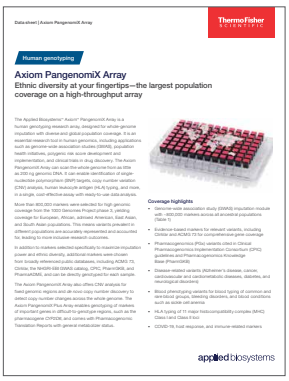
Features of the Axiom PangenomiX Array:

- **Global population coverage**—800,000+ markers across five ancestries: African, admixed American, East Asian, South Asian, and European, including coverage for Hispanic, non-Hispanic White, and non-Hispanic Black
- **Imputation-aware design**—enhanced imputation coverage and accuracy
- **Disease, pharmacogenomic, and pathogenic study**—from broadly referenced public databases, such as ACMG 73, ClinVar, CPIC, PharmGKB, NHGRI-EBI GWAS catalog, and Pharma ADME
- **Key variants of interest for disease-related variants**—Alzheimer's disease, cancer, cardiovascular and cardiometabolic diseases, diabetes, neurological disorders, SARS-CoV-2, host response, and immune-related markers
- **Blood-phenotyping variants**—blood typing of common and rare blood groups, bleeding disorders, and blood conditions, such as sickle cell anemia
- **HLA typing**—11 major histocompatibility complex (MHC) Class I and Class II loci
- **CNV analysis**—fixed regions and copy number discovery

Enhanced accuracy and coverage with imputation

The Axiom PangenomiX Array includes common variants that are intelligently selected by a proprietary, imputation-based marker selection strategy for genome-wide coverage in the five major ancestral populations. This process allows access to a vast number of low-frequency markers (minor allele frequency (MAF > 1%) and common markers (MAF > 5%) for any given population. The intelligent, imputation-aware design helps to ensure that the selection of markers offers the highest imputation accuracy across all ancestral populations. Combined with mitochondrial and Y-chromosome markers, the Axiom PangenomiX Array is a powerful tool to determine ancestry and migration patterns in genetic testing.

Broad-coverage, population-scale disease and PGx testing



Download the data sheet for the Axiom PangenomiX Array today

Axiom PangenomiX Array disease-specific risk variants.*

Category	Number of markers
Cancer	>13,000
Mental, behavioral, neurological, and neurodevelopmental	>4,300
Inherited eye disease	>3,700
Autoimmune and inflammatory disease	>1,150
Loss of function, autosomal inheritance	>3,600
Cardiovascular disease	>8,500
Respiratory disorder	>500
Diabetes	>1,500
Musculoskeletal disease	>5,900

* Disease categories as classified by NHGRI, OMIM®, and ClinVar databases.

Superior coverage and accuracy

How do we stack up against population-scale disease testing products on the market today? The Axiom PangenomiX Array was designed with your disease and PGx research studies in mind, based on years of expertise developing and testing arrays used in landmark population disease testing like the PMDA and UK Biobank arrays. Allow us to walk you through the Applied Biosystems™ Axiom™ array difference by contacting one of our knowledgeable predictive genomics professionals.

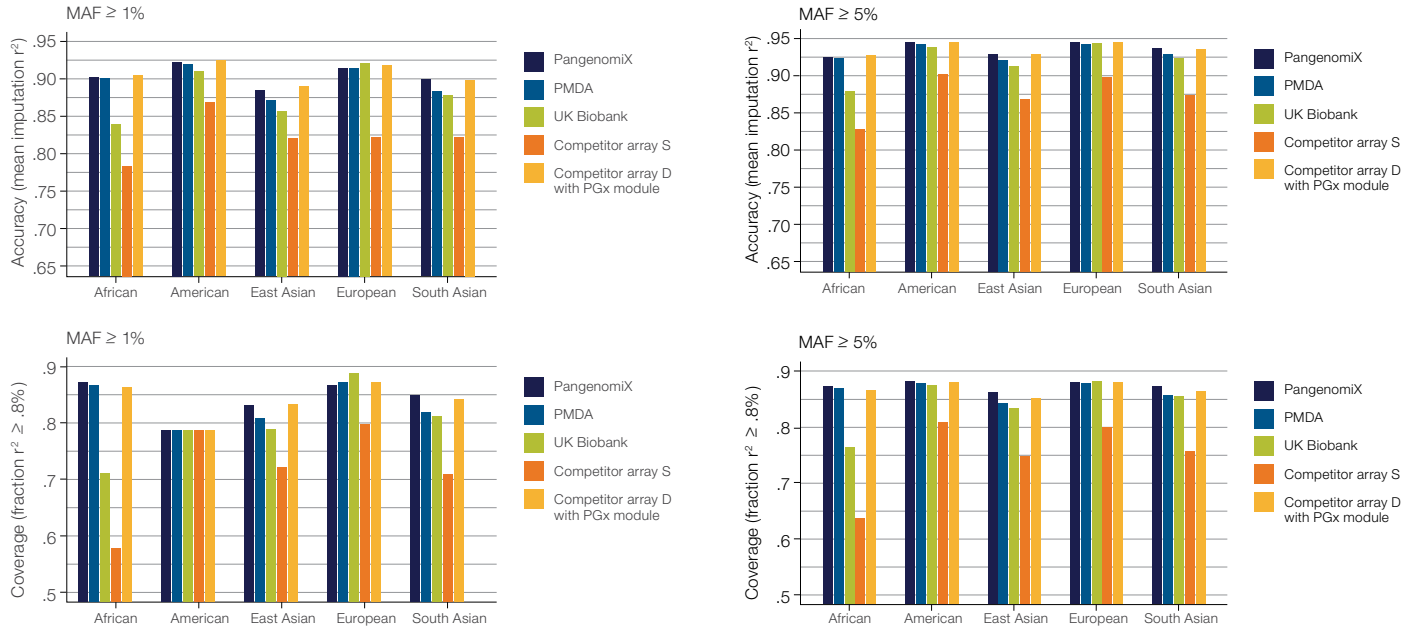


Figure 1. Comparison of coverage and accuracy by MAF and ancestral population. The Axiom PangenomiX Array uses imputation to deliver our highest level of accuracy and coverage in a human genotyping array for all main ancestral populations.

Experience the Axiom array difference at
thermofisher.com/pangenomix

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