

PRODUCT DATA SHEET

Human Genotyping Arrays

PRODUCT OVERVIEW

Human genotyping arrays are a robust and well-established tool for studies, such as validation, targeting common variants in large sample populations. Often used for genome-wide association studies (GWAS), arrays offer a high-throughput, cost-effective solution. Our arrays feature rapid data delivery with well-established analytical methods allowing for streamlined interpretation of results.

The **Human Omni Express + Exome Array** offers comprehensive coverage of the genome with 940,000 markers, 240,000 of which provide focused coverage of human exonic content, representing diverse populations and a range of common conditions.

Our **Methylation EPIC Array** interrogates over 850,000 methylation sites quantitatively across the genome at single-nucleotide resolution. Regions covered include: CpG sites outside of CpG islands, non-CpG methylated sites identified in human stem cells (CHH sites), differentially methylated sites identified in tumor versus normal, FANTOM5 enhancers, ENCODE open chromatin and enhancers, DNase hypersensitive sites and miRNA promoter regions.

The **Multi-Ethnic Genotyping Array (MEGA)**, offers >1.7 million markers with both genome-wide and exome-wide targets. It detects both common and rare variants across the most commonly studied five superpopulations and the imputation of variants in a vast number of subpopulations.

A genomic tool used for research applications is the **Global Screening Array (GSA)**. Applications includes disease risk pro-

High-throughput, cost-effective solutions for large-scale genomic studies

High call rates in all genotyping array offerings

Rapid and robust SNP calls

filings studies, pharmacogenomics research, wellness characterization, and complex disease discovery. It offers >640,000 markers including both genome-wide and exonic markers

Our genotyping array products feature Illumina BeadChip technology, offering industry-leading accuracy and reliability. Their highly optimized tag SNP content has been selected based on large-scale genomic data generated at the Broad Institute and other leading institutions. Included is analysis in our state of the art calling pipeline that delivers SNP calls shortly after processing in the laboratory and is compatible with other industry analysis tools.

PRODUCT REQUIREMENTS:

- 160ng of DNA (per sample) of input - Volume: 8ul, Concentration: 20ng/ul
- Fresh/frozen tissue and blood preferably yielding >500ng of DNA
- Minimum sample data including collaborator participant ID, collaborator ID, gender
- A HapMap control is required and included in the price for every set of samples

ARRAY OFFERINGS

Product	Utility	Total Markers	Typical Call Rate
Human Omni Express + Exome Array	Comprehensive coverage of common, rare, and exonic SNP content from the 1000 Genomes Project, enables the study of associations with traits and diseases.	960,000	>98%
MethylationEPIC Array	Methylation profiling microarray with extensive coverage of CpG islands, genes, and enhancers. Used for epigenome-wide association studies.	850,000	96% of CpGs
Multi-Ethnic Genotyping Array (MEGA)	Multi-purpose, multi-ethnic genotyping array. enabling genome-wide association studies for common and rare traits, across diverse populations.	1,780,000	>98%
Global Screening Array (GSA)	Combines multi-ethnic genome-wide content, curated clinical research variants, and quality control (QC) markers for precision medicine research.	640,000	>97%



FOR MORE INFORMATION

Web: genomics.broadinstitute.org

Email: genomics@broadinstitute.org