BROAD INSTITUTE

Human Genotyping Arrays

GENOMIC SERVICES

Product Data Sheet

Highlights

- High-throughput, cost-effective solutions for large-scale genomic studies
- High call rates in all genotyping array offerings
- Rapid and robust SNP calls

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 **Human Psych Array** offers >50,000 psychiatric disease-focused markers selected by a consortium of psychiatric genomics experts and is used by the Broad Institute Stanley Center for Psychiatric Research for a multitude of different studies investigating psychiatric diseases and disorders, including Schizophrenia* and Post Traumatic Stress Disorder (PTSD).

The **MEGA**, **Multi-Ethnic Genotyping Array**, 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 clinical research applications is the **Global Screening Array**. Applications include disease risk profiling 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.

Deliverable File Types

- IDAT
- GTC
- Ped/Map and/or Bed/Bim/Fam
- Bead Pool Manifest
- Summary Files

Input Requirements

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

* *'On risk' samples are billable even when quality deliverables are not met due to uncertainty in sample performance

Array Name	Total Number of Markers	Genome-Wide Markers	Exome-Specific Markers	Psychiatric Disease Markers	Typical Call Rate
Human Omni Express + Exome Array	940,000	700,000	240,000	-	>98%
Human Psych Array	589,000	271,000	277,000	50,000	>97%
MEGA (Multi-Ethnic Genotyping Array)	1,780,000	1,360,000	~420,000	-	>98%
Global Screening Array	640,000	574,000	66,000	-	>98%

* Sekar A, et al. Schizophrenia risk from complex variation of complement component 4. Nature. DOI: 10.1038/nature16549.