

# Infinium™ PsychArray-24 v1.3 BeadChip

Evaluate genetic variants associated with common psychiatric disorders using proven Infinium array technology.

## Overview

The Infinium PsychArray-24 v1.3 BeadChip (Figure 1) is a cost-effective, high-density array, developed in collaboration with the [Psychiatric Genomics Consortium](#) and several leading research institutions for large-scale genetic studies focused on psychiatric predisposition and risk. Content for the Infinium PsychArray-24 v1.3 BeadChip includes ~271,000 proven tag single nucleotide polymorphisms (SNPs) found on the Infinium Core-24 BeadChip, ~277,000 markers from the Infinium Exome-24 v1.1 BeadChip, and ~50,000 markers associated with common psychiatric disorders. These markers include genetic variants associated with the research of common psychiatric conditions such as:

- Schizophrenia
- Bipolar disorder
- Autism-spectrum disorders
- Attention deficit hyperactivity disorder
- Major depressive disorder
- Obsessive compulsive disorder
- Anorexia nervosa
- Tourette's syndrome

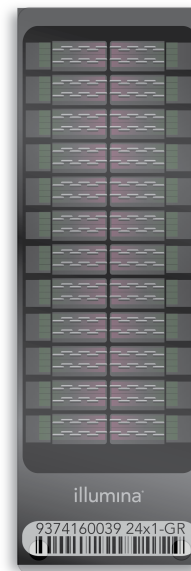
The Infinium PsychArray-24 v1.3 BeadChip is the ideal starting point for genomic studies focused on psychiatric disease.

## Robust and trusted, high-quality assay

The Infinium PsychArray-24 v1.3 BeadChip uses trusted Infinium assay chemistry to deliver the same high-quality, reproducible data (Table 1) that Illumina genotyping arrays have provided for over a decade. It is compatible with the Infinium FFPE QC and DNA Restoration Kits, enabling genotyping of formalin-fixed, paraffin-embedded (FFPE) samples. In addition, the high signal-to-noise ratio of the individual genotyping calls from the Infinium assay provides access to genome-wide copy CNV calling with a mean probe spacing of ~ 4.88 kb.

## High-throughput workflow

The Infinium PsychArray-24 v1.3 BeadChip uses the highly scalable 24-sample Infinium HTS format which enables laboratories to efficiently increase throughput as needed to support population-scale research and variant screening applications. The HTS format includes two different assay options, optimized based on processing throughput. For flexible throughput processing, the Infinium HTS assay provides the capability to run hundreds to thousands of samples per week. The Infinium HTS assay provides a rapid, three-day workflow that allows genotyping service providers and clinical researchers to gather data and advance studies quickly.



**Figure 1: The Infinium PsychArray-24 v1.3 BeadChip**—The Infinium PsychArray-24 v1.3 BeadChip is a comprehensive array that provides excellent coverage of relevant, consortium-selected markers associated with common psychiatric disorders.

**Table 1: Product information**

Feature	Description		
Species	Human		
Total number of markers	595,427		
Capacity for custom bead types	60,000		
Number of samples per BeadChip	24 Samples		
DNA input requirement	200 ng		
Assay chemistry	Infinium HTS		
Instrument support	iScan System		
Sample throughput <sup>a</sup>	~ 2304 samples/week		
Scan time per sample	iScan System 1.3 min		
Data performance	Value <sup>b</sup>	Product specification <sup>d</sup>	
Call rate	99.8%	> 99% avg.	
Reproducibility	99.99%	> 99.9%	
Log R deviation	0.09	< 0.30 <sup>c</sup>	
Spacing			
Spacing (kb)	Mean	Median	90th% <sup>c</sup>
	4.88	1.74	13.19

a. Estimate assumes 1 iScan System, 1 AutoLoader 2.x, 2 Tecan robots, and a 5-day work week.

b. Values are derived from genotyping 327 HapMap reference samples.

c. Value expected for typical projects using standard Illumina protocols. Tumor samples and samples prepared by methods other than standard Illumina protocols are excluded.

d. Excludes Y chromosome markers for female samples.

Optional integration of the Illumina Laboratory Information Management System (LIMS) into the workflow provides high laboratory efficiency with automation functionality, process tracking, and QC data tracking. The Illumina ArrayLab Consulting Service offers customized solutions to high-throughput genotyping labs that desire increased efficiency and overall operational excellence.

**Table 2: Marker Information**

Marker categories	No. of markers		
Nonsense markers <sup>b</sup>	25,880		
Missense markers <sup>b</sup>	221,268		
Synonymous markers <sup>b</sup>	14,994		
Mitochondrial markers <sup>c</sup>	350		
Indels <sup>c</sup>	12,458		
Sex chromosomes <sup>c</sup>	X 14,405	Y 2054	PAR/homologous 259

a. RefSeq - [NCBI Reference Sequence Database](#). Accessed October 2019.

b. Compared against the [University of California, Santa Cruz \(UCSC\) Genome Browser](#). Accessed October 2019.

c. [NCBI Genome Reference Consortium](#), Version GRCh37. Accessed October 2019.

Abbreviations: indel: insertion/deletion; PAR: pseudoautosomal region.

**Table 3: LD  $r^2 \geq 0.80$  from 1000G<sup>a</sup> at Various MAF Thresholds**

1000G Population <sup>b</sup>	LD Coverage ( $r^2 \geq 0.80$ )	
	MAF $\geq 5\%$	MAF $\geq 1\%$
AFR	0.47	0.31
AMR	0.71	0.53
EAS	0.77	0.64
EUR	0.75	0.60
SAS	0.72	0.56

a. Compared against Phase 3, version 5 of the [1000 Genomes Project](#) (1000G). Accessed July 2016.

b. See [www.1000genomes.org/category/frequently-asked-questions/population](http://www.1000genomes.org/category/frequently-asked-questions/population)  
Abbreviations: MAF, minor allele frequency; LD, linkage disequilibrium; AFR, African; AMR, Ad Mixed American; EAS, East Asian; EUR, European; SAS, South Asian.

## Ordering information

Infinium PsychArray-24 v1.3 Kit	Catalog No.
48 Samples	20024692
288 Samples	20024693
1152 Samples	20024694
Infinium PyschArray-24+ v1.3 Kit <sup>a</sup>	Catalog No.
48 Samples	20024695
288 Samples	20024696
1152 Samples	20024697

a. Enabled for custom content.

## Learn more

Learn more about the Infinium PsychArray-24 v1.3 BeadChip at [www.illumina.com/genotyping](http://www.illumina.com/genotyping)