# Infinium<sup>™</sup> OmniExpress-24 v1.4 BeadChip

Customizable, high-density array for high-throughput genotyping studies

- Powerful array designed for genome-wide association studies (GWAS)
- Optimized tag SNP content from all three HapMap project phases to capture the greatest amount of common variation
- High-quality, reproducible data using trusted Infinium chemistry with a scalable workflow

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## Overview

The customizable Infinium OmniExpress-24 v1.4 BeadChip (Figure 1) offers an economical platform for performing large-scale genotyping studies. Developed in collaboration with several leading research institutions, the Infinium OmniExpress-24 v1.4 BeadChip includes all the tag single nucleotide polymorphisms (SNPs) found on the Infinium Core-24 BeadChip, plus over 240k markers from the Infinium HumanExome BeadChip (Table 1, Table 2). In addition, the Infinium OmniExpress-24+ v1.4 BeadChip has the capacity to add up to 30K custom markers.

In addition to large-scale genotyping studies, the Infinium OmniExpress-24 v1.4 BeadChip can be used to quickly and easily obtain baseline sample data for various downstream applications, including common variant, mitochondrial DNA (mtDNA), ancestry, sex determination, loss of variant, and insertion/deletion (indel) studies.

Feature	Description
Species	Human
Total number of markers	717,960
Capacity for custom bead types	30K
Number of samples per BeadChip	24
DNA input requirement	200 ng
Assay chemistry	Infinium HTS
Instrument support	iScan System
Sample throughput <sup>a</sup>	~ 2304 samples/week
Scan time per sampleª	2.5 min

Table 1: Product specifications

a. Approximate values, scan times, and maximum throughput will vary depending on laboratory and system configurations



Figure 1: Infinium OmniExpress-24 v1.4 BeadChip —Versatile BeadChip featuring coverage of common SNP variation as assessed by the International HapMap project.

### Table 2: Marker information

Category	Marker count
RefSeq genes <sup>1</sup>	330,672
RefSeq genes +/- 10 kb <sup>1</sup>	398,126
RefSeq exons <sup>1</sup>	49,434
RefSeq promoter regions <sup>1</sup>	21,411
ADME genes <sup>2</sup>	13,130
ADME genes +/- 10 kb <sup>2</sup>	16,238
ADME exons <sup>2</sup>	1631
MHC <sup>3</sup>	7306
HLA <sup>3</sup>	4927
COSMIC genes <sup>4</sup>	301,426
Genes in Gene Ontology <sup>5</sup>	82,830
Nonsense markers <sup>6</sup>	136
Missense markers <sup>6</sup>	12,564
Synonymous markers <sup>6</sup>	10,952
Silent markers <sup>6</sup>	25,782
Sex chromosomes <sup>6</sup> X	i i i i i i i i i i i i i i i i i i i

Abbreviations: ADME: absorption, distribution, metabolism, and excretion; HLA: human leukocyte antigen; MHC: major histocompatibility complex; PAR: pseudoautosomal region

# High-performance assay

The Infinium OmniExpress-24 v1.4 BeadChip uses the trusted Infinium high-throughput screening (HTS) assay chemistry to deliver a high-performance, accurate geno-typing solution. When combined with the iScan<sup>™</sup> System, this high-density, 24-sample BeadChip delivers affordable, high-quality, genome-wide information across diverse populations (Table 3, Table 4).

#### Table 3: Data performance and spacing

	Observedª	Product specification <sup>b</sup>	
Call rate	99.81%	> 99.0%	
Reproducibility	99.99%	> 99.9%	
Log R deviation	0.10	< 0.30°	
	Mean	Median	90th percentile°
Probe spacing	4.07 kb	2.23 kb	14.30
	Targeted	Backbone	
Resolution	~10 kb	~25 kb	

a. Values derived from genotyping 325 HapMap reference samples

 b. Value expected for typical projects using standard Illumina protocols—samples prepared by methods other than standard Illumina protocols are excluded
c. Excludes Y chromosome markers for female samples

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# Table 4: LD $r^2 \ge 0.80$ coverage at various MAF thresholds based on 1000 Genomes Project<sup>7</sup>

Demodetiens	LD coverage ( $r^2 \ge 0.80$ )			
Population <sup>a</sup>	MAF ≥ 1%	MAF ≥ 2.5%	MAF ≥ 5%	
AFR	0.26	0.34	0.42	
AMR	0.53	0.65	0.71	
EAS	0.66	0.73	0.78	
EUR	0.62	0.71	0.77	
SAS	0.57	0.67	0.72	

a. www.internationalgenome.org/category/population

Abbreviations: AFR: African; AMR: American, mixed ancestry; EAS: East Asian; EUR: European; LD: linkage disequilibrium; MAF: minor allele frequency; SAS: South Asian

### Learn more

Infinium OmniExpress-24 v1.4 BeadChip, illumina.com/ products/by-type/microarray-kits/infinium-omni-express. html

# Ordering information

Infinium OmniExpress-24 v1.4 Kit	Catalog no.
48 samples	20062061
288 samples	20062062
1152 samples	20062063
Infinium OmniExpress-24+ v1.4 Kit <sup>a</sup>	Catalog no.
48 samples	20062058
288 samples	20062059
1152 samples	20062060

## References

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