Infinium™ OmniExpress-24 v1.3 BeadChip

Customizable, high-density array for cost-effective, high-throughput genotyping and GWAS.

Overview

The customizable Infinium OmniExpress-24 v1.3 BeadChip offers an economical way to perform and support large genetic studies, especially large-scale genotyping studies. Developed in collaboration with several leading research institutions, the Infinium OmniExpress-24 v1.3 BeadChip includes all the tag single nucleotide polymorphisms (SNPs) found on the Infinium Core-24 BeadChip, plus over 240,000 markers from the Infinium HumanExome BeadChip (Table 1 and Table 3). The Infinium CoreExome-24+ v1.3 BeadChip has the added capacity to include up to 30,000 semicustom markers. In addition to performing cost-effective large-scale genotyping studies, the Infinium OmniExpress-24 v1.3 BeadChip can be used to obtain baseline sample data sets for various downstream applications quickly and easily. These applications include common variant, mitochondrial DNA (mtDNA), ancestry, sex confirmation, loss of-variant, and insertion/deletion (indel) detection studies. Infinium OmniExpress-24 v1.3 BeadChips use the trusted Infinium high-throughput screening (HTS) Assay. When combined with the proven iScan™ or HiScan™ System, this high-density, 24-sample BeadChip (Figure 1) delivers affordable, high-quality, genome-wide information across diverse world populations (Table 2).

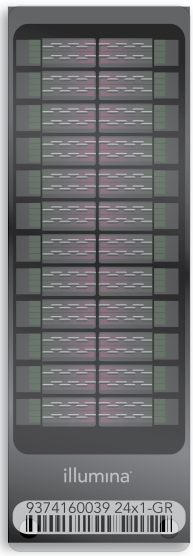

Figure 1: The Infinium OmniExpress-24 v1.3 BeadChip— The Infinium OmniExpress-24 v1.3 BeadChip provides excellent coverage of common SNP variation as assessed by the International HapMap Project.

Table 1: Product information

Feature	Description		
Species	Human		
Total number of markers	714,238		
Capacity for custom bead types	30,000		
Number of samples per BeadChip	24 Samples		
DNA input requirement	200 ng		
Assay chemistry	Infinium HTS		
Instrument support	iScan or HiScan System		
Sample throughput[a]	~ 2304 samples/week		
Scan time per sample	iScan System 2.5 min	HiScan System 3.5 min	
Data performance	**Value[b]**	**Product Specification[d]**	
Call rate	99.82%	> 99% avg.	
Reproducibility	99.99%	> 99.9%	
Log R deviation	0.10	< 0.30[c]	
Spacing			
Spacing (kb)	Mean 4.07	Median 2.23	90th%[c] 14.30

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 325 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.

Table 2: LD $r^2 \geq 0.80$ from 1000G[a] at various MAF thresholds

1000G population[b]	LD coverage ($r^2 \geq 0.80$)		
	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. Compared against Phase 3, version 5 of the 1000 Genomes Project (1000G). www.1000genomes.org. Accessed July 2016.
b. See www.1000genomes.org/category/frequently-asked-questions/population

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

Table 3: Marker information

Marker categories			No. of markers
RefSeq genes			328,685
RefSeq genes +/- 10 kb			395,677
RefSeq exons			47,277
RefSeq promoter regions			21,240
ADME genes			13,027
ADME genes +/- 10 kb			16,114
ADME exons			1593
MHC			4832
Extended MHC			7231
COSMIC genes			299,678
Genes in Gene Ontology			82,354
Nonsense markers[b]			127
Missense markers[b]			12,350
Synonymous markers[b]			10,889
Silent markers[c]			23,911
Sex chromosomes[c]	X 17,599	Y 1320	PAR/homologous 712

a. RefSeq - NCBI Reference Sequence Database. www.ncbi.nlm.nih.gov/refseq. Accessed September 2016.
b. Compared against the University of California, Santa Cruz (UCSC) Genome Browser. genome.ucsd.edu. Accessed August 2014.
c. NCBI Genome Reference Consortium, Version GRCh37. www.ncbi.nlm.nih.gov/grc/human. Accessed July 2016.

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

Ordering information

Infinium OmniExpress-24 v1.3 Kit	Catalog no.
48 samples	20024631
288 samples	20024632
1152 samples	20024633
Infinium OmniExpress-24+ v1.3 Kit[a]	**Catalog no.**
48 samples	20024634
288 samples	20024635
1152 samples	20024636

a. Enabled for additional custom content.

Learn more

To learn more about the Infinium OmniExpress-24 v1.3 BeadChip and other Illumina genotyping products and services, visit www.illumina.com/genotyping

References

1. PharmaADME Gene List. www.pharmaadme.org. Accessed August 2014.
2. Catalog of somatic mutations in cancer. cancer.sanger.uk/cosmic. Accessed July 2016.
3. Gene Ontology Consortium. www.geneontology.org. Accessed July 2016.
4. de Bakker PIW, McVean G, Sabeti PC, et al. A high-resolution HLA and SNP haplotype map for disease association studies in the extended human MHC. *Nat Genet*. 2006;38:1166–1172.

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