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Infinium® Omni2.5-8 v1.3 BeadChip

Next-generation GWAS content for genotyping and CNV analysis.

Overview

The Infinium Omni2.5-8 v1.3 BeadChip delivers comprehensive coverage of both common and rare SNP content from the 1000 Genomes Project (1kGP; MAF > 2.5%),[1] designed to be maximally informative for diverse world populations. Using the proven HiScan® or iScan® System, these 8-sample BeadChips offer high throughput and optimized tag SNP content, including full support of copy number variation (CNV) applications. The Infinium Omni2.5-8 v1.3 BeadChip is a powerful entry point into the Omni Roadmap, which provides researchers with step-wise, flexible access to 5 million variants per sample. Convenient kit packaging, a streamlined PCR-free protocol, and integrated analysis software are included to provide a comprehensive DNA analysis solution. This product is customizable with up to 200,000 attempted beadtypes with the Infinium Omni2.5-8+ v1.3 version of the BeadChip.

Figure 1: Infinium Omni2.5-8 v1.3 BeadChip—The 8-sample Infinium Omni2.5-8 v1.3 BeadChip supports rapid cost-effective studies with coverage of the latest common and rare variants from the 1000 Genomes Project, down to 2.5% minor allele frequency (MAF).

Table 1: Infinium Omni2.5-8 v1.3 BeadChip Product Information

Feature	Description	
Total Number of Markers	2,372,784	
Capacity for Custom Markers	200,000	
Number of Samples per BeadChip	8	
DNA Input Requirement	200 ng	
Assay	Infinium LCG	
Instrument Support	iScan or HiScan	
Sample Throughput[a]	~1067 samples / week	
Scan Time per Sample	iScan[a] 11.3 min	HiScan 6.5 min

	LD Coverage ($r^2 \geq 0.8$)		
Population[b]	1kGP[c] MAF > 1%	1kGP[c] MAF > 2.5%	1kGP[c] MAF > 5%
AFR	0.54	0.63	0.69
AMR	0.73	0.82	0.86
EAS	0.79	0.86	0.89
EUR	0.79	0.86	0.89
SAS	0.74	0.83	0.87

Data Performance	Value[d]	Product Specification	
Call Rate	99.8%	> 99% avg.	
Reproducibility	99.99%	> 99.9%	
Log R Deviation	0.11	< 0.30[d]	
Spacing	**Mean**	**Median**	**90th%[e]**
Spacing (kb)	1.23	0.65	2.83

a. Estimate assumes 2 iScan systems, one AutoLoader 2.x, 2 Tecan robots, and a 5-day work week.
b. See www.1000genomes.org/category/frequently-asked-questions/population
c. Compared against the Phase 3 1000 Genomes Project (1kGP) data release (2014).[1]
d. Values are derived from genotyping 455 HapMap reference samples.
e. Value expected for typical projects using standard Illumina protocols. Tumor samples and samples prepared by methods other than standard Illumina protocols are excluded.

Abbreviations: 1kGP, 1000 Genomes Project; MAF, minor allele frequency; LD, Linkage Disequilibrium.

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Table 2: Infinium Omni2.5-8 v1.3 BeadChip Marker Information

Marker Categories	Number of Markers[a]		
In RefSeq[b] Genes	1,064,781 (1,272,710[c])		
In RefSeq Exons	141,984		
In RefSeq Promoter Regions	50,214		
In ADME Genes	20,848 (26,663[c])		
In ADME Exons	2995		
MHC (Extended MHC[d])	11,116 (18,083)		
Overlap with Genes in COSMIC[e]	966,716		
Overlap with Genes in Gene Ontology[f]	251,141		
Nonsense Markers	375		
Missense Markers	31,986		
Synonymous Markers	32,421		
Silent Markers	77,193		
Mitochondrial Markers	180		
Indels	39		
Sex Chromosomes	X 53,258	Y 2091	Par Loci 2558

a. Compared against the June 2011 1kGP data release.
b. RefSeq - NCBI Reference Sequence Database.[2]
c. Within 10 kb.
d. MHC is a ~ 4 Mb region; extended MHC is a ~ 8 Mb region.
e. Catalog of somatic mutations in cancer.[3]
f. Gene Ontology Consortium.[4]
Abbreviations: ADME, absorption, distribution, metabolism, and excretion; MHC, Major Histocompatibility Complex.

Ordering Information

Infinium Omni2.5-8 v1.3 Kit	Catalog No.
16 samples	20001112
48 samples	20001113
96 samples	20001114
384 samples	20001115
Infinium Omni2.5-8+ v1.3 Kit*	**Catalog No.**
16 samples	20001116
48 samples	20001117
96 samples	20001118
384 samples	20001119

*Enabled for additional custom content

Learn More

To learn more about the Infinium Omni2.5-8 v1.3 BeadChip and other Illumina genotyping products and services, visit: www.illumina.com/applications/genotyping.html.

References

1. www.1000genomes.org Accessed 18 April 2014.
2. www.ncbi.nlm.nih.gov/refseq Accessed 6 July 2015.
3. http://cancer.sanger.ac.uk/cosmic Accessed 6 July 2015.
4. www.geneontology.org Accessed 6 July 2015.

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