

HumanOmni2.5-8 BeadChip

Next-Generation GWAS Content for Genotyping and CNV Analysis

Figure 1: HumanOmni2.5-8 BeadChip



The eight-sample HumanOmni2.5 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).

Overview

The HumanOmni2.5-8 BeadChip delivers comprehensive coverage of both common and rare SNP content from the 1000 Genomes Project (1kGP; MAF > 2.5%), designed to be maximally informative for diverse world populations. Using the proven HiScan™ or iScan System, this eight-sample BeadChip offers high throughput and optimized tag SNP content, including full support of copy number variation (CNV) applications. The Omni2.5-8 BeadChip is a powerful entry point into the Omni Roadmap, which provides researchers with step-wise, flexible access to five million variants per sample. A convenient kit packaging, streamlined PCR-free protocol, and integrated analysis software are included to provide a comprehensive DNA analysis solution.

HumanOmni2.5-8 BeadChip Kit	Catalog No.
16 samples, single-use kit	WG-311-2511
48 samples, single-use kit	WG-311-2512
96 samples, single-use kit	WG-311-2513
384 samples, single-use kit	WG-311-2514

HumanOmni2.5-8 Product Information

Feature	Description
Number of Markers	2,379,855
Number of Samples	8
DNA Requirement	200 ng
Assay	Infinium® LCG
Instrument Support	HiScanSQ or iScan
Sample Throughput*	~1,067 samples / week
Scan Time / Sample	6.5 min (HiScan) 11.4 min (iScan)

% Variation Captured (r ² > 0.8)	1kGP* MAF > 5%	1kGP* MAF > 1%
CEU	0.83	0.73
CHB + JPT	0.83	0.73
YRI	0.65	0.51

Data Performance	Value** / Product Specification*
Call Rate	99.65% / > 99% avg
Reproducibility	99.99% / > 99.9%
Log R Dev	0.12 / < 0.30 [‡]

Spacing	Mean / Median / 90th%*
Spacing (kb)	1.19 / 0.64 / 2.76

Marker Categories	Number of Markers*
Number of SNPs with 10kb of RefSeq genes	1,231,382
MHC / ADME	19,238 / 27,335
Non synonymous SNPs	41,900
Sex Chromosome (X / Y / PAR Loci)	55,208 / 2,561 / 418
Mitochondrial	256

* Estimate assumes one HiScan system, one AutoLoader2, one Tecan Robot, and a five-day work week.

** Compared against June 2011 1kGP data release.

** Values are derived from genotyping 470 reference samples

‡ Value expected for typical projects, excluding tumor samples or any samples prepared not following standard Illumina protocols.

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