HumanOmni2.5 BeadChip

Most powerful microarray for SNP and CNV analysis leveraging 1000 Genomes Pilot data

Figure 1: HumanOmni2.5 BeadChip

The four-sample HumanOmni2.5 BeadChip supports rapid cost-effective studies with unprecedented coverage of the latest common and rare variants from the 1000 Genomes Project

Overview

The HumanOmni2.5 BeadChip delivers the most comprehensive coverage of both common and rare SNP content from the 1000 Genomes Project (1kGP; MAF > 2.5%), designed to be maximally powerful for diverse world populations. Using the proven iScan or HiScan™SQ System, this four-sample BeadChip offers high throughput and optimized tag SNP content, including full support of copy number variation (CNV) applications. The Omni2.5 BeadChip is a powerful entry point into the 2010 GWAS Roadmap, which provides researchers with favorable pricing and step-wise, flexible access to five million variants per sample. It is supported by the Infinium® Multi-Use Workflow, which allows researchers to prepare their sample once and deploy it across multiple Roadmap arrays as they are released. A convenient kit packaging, streamlined PCR-free protocol, and integrated analysis software are included to provide a comprehensive DNA analysis solution.

HumanOmni2.5 BeadChip Kit	Catalog No.
16 sample, single-use kit	WG-311-2501
48 sample, single-use kit	WG-311-2502
96 sample, single-use kit	WG-311-2503
384 sample, single-use kit	WG-311-2504
16 sample, multi-use kit	WG-311-1127
96 sample, multi-use kit	WG-311-1128

HumanOmni2.5 Product Information

Feature	Description
Number of Markers	2.45 million
Number of Samples	4
DNA Requirement	200 ng
Assay	Infinium HD
Instrument Support	HiScanSQ or iScan
Sample Throughput*	~480 samples / week
Scan Time / Sample	~15 minutes

% Variation Captured (r^2 > 0.8)	1kGP MAF > 5%	1kGP MAF > 2.5%
CEU	0.89	0.86
CHB + JPT	0.89	0.87
YRI	0.72	0.71

Data Performance	Value† / Product Specification
Call Rate	99.78% / > 99% avg
Reproducibility	99.99% / > 99.9%
Log R Dev	0.13 / < 0.30‡

Spacing	Mean / Median / 90th%
Spacing (kb)	1.18 / 0.63 / 2.74

Marker Categories	Number of Markers
Number of SNPs with 10kb of RefSeq genes	1,233,932
Nonsynonymous SNPs (NCBI annotated)	49,564
MHC / ADME	11,149 / 27, 895
Sex Chromosome (X / Y / PAR Loci)	57,061 / 1,897 / 554
Mitochondrial	93

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

† Values are derived from genotyping 467 reference samples

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

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