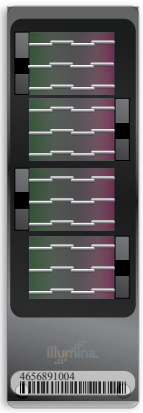
HumanOmni1-Quad BeadChip

Strategically selected SNPs and probes deliver powerful common variant GWAS and CNV discovery.

Figure 1: HumanOmni1-Quad BeadChip



The HumanOmni1-Quad BeadChip provides an extensive view of the genome in a high-throughput, cost-effective format.

Overview

The HumanOmni1-Quad BeadChip delivers powerful genome-wide association studies (GWAS) and copy number variation (CNV) discovery in diverse world populations through the integration of the latest high-value content from all three phases of the International HapMap Project and recently published disease association studies. Each Omni1-Quad BeadChip contains strategically selected markers that deliver dense, genome-wide coverage of functional variants, including non-synonymous and gene-centric single nucleotide polymorphisms (SNPs), while reducing tag SNP redundancy. Using the proven BeadArray™ Reader, or the iScan or HiScan™SQ systems, the high-throughput nature of this four-sample BeadChip allows researchers to complete studies quickly while capturing a large amount of variation, driving the discovery of novel associations with traits and diseases.

Ordering Information

HumanOmni1-Quad BeadChip Kit	Catalog No.
16 sample, single-use kit	WG-311-1110
48 sample, single-use kit	WG-311-1111
96 sample, single-use kit	WG-311-1112
384 sample, single-use kit	WG-311-1113

HumanOmni1-Quad Product Information

Feature	Description
Number of Markers	1,134,514
Number of Samples	4
DNA Requirement	200 ng
Assay	Infinium HD
Instrument Support	HiScanSQ, iScan, or BeadArray Reader
Sample Throughput*	576 samples / week
Scan Time / Sample**	13 minutes

% Variation Captured (r^2 > 0.8)	1kGP† MAF > 5%	1kGP† MAF > 1%
CEU	0.76	0.63
CHB + JPT	0.76	0.65
YRI	0.48	0.31

Data Performance	Value†† / Product Specification
Call Rate	99.87% / > 99% average
Reproducibility	100% / > 99.9%
Log R Deviation	0.13 / < 0.30§

Spacing	Mean / Median / 90th %
Spacing (kb)	2.63 / 1.25 / 6.39

Marker Categories	Number of Markers
Number of SNPs with 10kb of RefSeq genes	636,862
Nonsynonymous SNPs (NCBI annotated)	38,118
MHC / ADME	18,587 / 22,510
Sex Chromosome (X / Y / PAR Loci)	27,173 / 1,907 / 1,000

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

** Analysis performed using the iScan System.

† Compared against the June 2001 1kGP data release.

†† Values are derived from 282 reference samples.

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

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