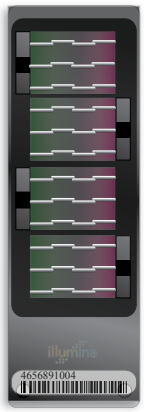
HumanOmni1S BeadChip

Step-wise coverage of SNPs down to 2.5% MAF.

Figure 1: HumanOmni1S BeadChip



The HumanOmni1S BeadChip provides a straightforward path for users of the Omni1-Quad or OmniExpress BeadChip to supplement their studies with the SNP content from the 1000 Genomes Project, down to 2.5% MAF.

Overview

The HumanOmni1S BeadChip delivers added power for genome-wide association studies (GWAS) through the integration of content from the 1000 Genomes Project (1kGP) data. Together with an Omni1-Quad or OmniExpress BeadChip, the Omni1S BeadChip provides access to both common and rare variants (targeting MAF>2.5%). Using the proven iScan or HiScan™SQ System, this eight-sample BeadChip offers high throughput for rapid integration of rarer SNP content into ongoing common-variant GWAS studies. With optimized tag SNP content, the Omni1S BeadChip drives the discovery of novel associations of rare variants with traits and diseases.

Ordering Information

HumanOmni1S BeadChip Kit	Catalog No.
16 sample, single-use kit	WG-311-1114
48 sample, single-use kit	WG-311-1115
96 sample, single-use kit	WG-311-1116
384 sample, single-use kit	WG-311-1117

HumanOmni1S Product Information

Feature	Description
Number of Markers	1,185,076
Number of Samples	8
DNA Requirement	200 ng
Assay	Infinium® HD
Instrument Support	HiScanSQ or iScan
Sample Throughput*	~960 samples / week
Scan Time / Sample	~7.5 minutes

% Variation Captured† (r^2 > 0.8)	1kGP† MAF > 5%	1kGP† MAF > 2.5%
CEU	0.65	0.58
CHB + JPT	0.65	0.57
YRI	0.37	0.30

Data Performance	Value** / Product Specification
Call Frequency	99.8% / > 99% avg.
Reproducibility	99.8% / > 99.9%
Log R Deviation	0.17 / < 0.30‡

Spacing	Mean / Median / 90%
Spacing (kb)	2.47 / 1.27 / 5.68

Marker Categories	Number of Markers
Number of SNPs with 10kb of RefSeq genes	586,877
Nonsynonymous SNPs (NCBI annotated)	5,641
MHC / ADME	1,716 / 7,429
Sex Chromosome (X / Y / PAR Loci)	26,451 / 319 / 0

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

† Compared against the June 2011 1kGP data release.

** Values are derived from genotyping 190 reference samples.

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

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AGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCATTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGACGAAAAGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGACGAAAAGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGACGAAAAGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAGCAACGACGCGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGAAAAGAATGATAACAGTA