HumanOmni2.5S-8 BeadChip

Stepwise Access to Variants down to 1% Minor Allele Frequency

Figure 1: HumanOmni2.5S BeadChip

The 8-sample Omni2.5S BeadCSip covers genetic variation down to 1% MAF and high-value regions of the genome, including targeted exonic content, MHC SNPs, and ADME genes.

Overview

The HumanOmni2.5S (Omni2.5S) BeadChip (Figure 1) provides over two million powerful markers selected from the 1000 Genomes Project (1kGP), targeting genetic variation down to 1% minor allele frequency (MAF). This content can be added to ongoing studies with Omni arrays for a total of up to 5 million markers per sample. The Omni2.5S can also be used as a standalone product to target the latest rare variants from the 1kGP. A semi-custom version of the BeadChip is also available, which can be tailored with up to 500K custom markers.

BeadChip Kit	Catalog No.
HumanOmni2.5S DNA Analysis Kit (16)	WG-311-2505
HumanOmni2.5S DNA Analysis Kit (48)	WG-311-2506
HumanOmni2.5S DNA Analysis Kit (96)	WG-311-2507
HumanOmni2.5S DNA Analysis Kit (384)	WG-311-2508

For researchers following the multi-use workflow, who initially amplified their samples with the OmniExpress, Omni1-Quad, or Omni2.5-Quad BeadChips, please contact Illumina customer support if you are interested in the multi-use Omni2.5S BeadChip. Customers who initially amplified their sample with the Omni2.5-8 BeadChip, should use the standard Omni2.5S-8 multi-use kit.

HumanOmni2.5S Product Information

Feature	Description	
Total Fixed Markers	2,015,318	
Number of Samples	8	
DNA Requirement	200 ng	
Assay	Infinium® LCG	
Instrument Support	HiScan™ or iScan	
Sample Throughput*	> 1067 samples / week	
Scan Time / Sample	6.5 minutes (HiScan) 11.4 minutes (iScan+)	
% Variation Captured (r^2 > 0.8)	**1kGP† MAF > 5%**	**1kGP† MAF > 1%**
CEU	0.61	0.61
CHB + JPT	0.63	0.56
YRI	0.36	0.29
Data Performance	**Value§ / Product Specification**	
Call Rate	99.95% / > 99% avg	
Reproducibility	100% / > 99.9%	
Log R Dev	0.095 / < 0.30**	
Spacing	**Mean / Median / 90th%**	
Spacing (kb)	1.45 / 0.79 / 3.43	
Marker Categories	**Number of Markers**	
Number of SNPs with 10kb of RefSeq Genes	1,160,001	
Nonsynonymous SNPs (NCBI Annotated)	57,360	
MHC / ADME	34,179 / 18,365	
Sex Chromosomes (X / Y / PAR Loci)	66,578 / 154 / 76	
Mitochondrial	31	
Indels / Multi-base Substitutions‡	2,781	

* Estimate assumes one HiScan system, one AutoLoader2, one Tecan robot, and a five-day work week.
† Compared against the June 2011 1kGP data release.
§ Values derived from 273 reference samples.
** Value expected for typical projects using standard Illumina protocols.
‡ Provided by the 1kGP structural variation group.

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AGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAAC
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