

HumanOmni5-Quad BeadChips

Superior content. Unprecedented flexibility. The most powerful whole-genome array. Ever.

Overview

The HumanOmni5-Quad and HumanOmni5+ BeadChips (Figure 1) deliver the most comprehensive coverage of the genome, leveraging powerful tagSNPs selected from the International HapMap and 1000 Genomes Projects that target genetic variation down to 1% minor allele frequency (MAF). The Omni5+ provides the flexibility to add up to 500K custom markers, allowing researchers to tailor the BeadChip for targeted applications and population-customized studies. Using the proven HiScan® or iScan systems, along with the Infinium® LCG Assay, these four-sample BeadChips offer high-throughput sample processing, and optimized content for whole-genome genotyping and CNV applications. This end-to-end DNA analysis solution includes convenient kit packaging, a streamlined PCR-free protocol, and integrated analysis software.

Figure 1: HumanOmni5-Quad BeadChip



The four-sample Omni5 BeadChip is the ultimate array for whole-genome genotyping and CNV analysis, providing base content of over 4.3M markers with tag-SNP coverage down to 1% MAF and the flexibility to add up to 500K custom-designed markers.

HumanOmni5 v1.0 BeadChip

DNA Analysis Kits	Catalog No.
16 samples	WG-311-5001
48 samples	WG-311-5002
96 samples	WG-311-5003
384 samples	WG-311-5004

HumanOmni5+ v1.0 BeadChip

DNA Analysis Kits *	
16 samples	WG-311-5005
48 samples	WG-311-5006
96 samples	WG-311-5007
384 samples	WG-311-5008

* Enabled for custom content

HumanOmni5-Quad Product Information

BeadChip Content	Markers per Sample	
Total Fixed Markers	4,301,331	
Custom Markers	up to 500,000	
Feature	Description	
Number of Samples per BeadChip	4	
DNA Requirement	400 ng	
Assay	Infinium LCG	
Instrument Support	HiScanSQ or iScan	
Sample Throughput*	> 460 samples / week	
Scan Time / Sample	15 minutes (HiScan) 25 minutes (iScan)	
% Variation Captured (r ² > 0.8)	1kGP [†] MAF > 5%	1kGP [†] MAF > 1%
CEU	0.87	0.83
CHB + JPT	0.85	0.76
YRI	0.71	0.58
Data Performance	Value [§] / Product Specification	
Call Rate	99.9% / > 99% avg	
Reproducibility	99.99% / > 99.9%	
Log R Dev	0.12 / < 0.30**	
Spacing	Mean / Median / 90th%	
Spacing (kb)	0.68 / 0.36 / 1.57	
Marker Categories	Number of Markers	
Number of SNPs with 10kb of RefSeq genes	2,311,849	
Nonsynonymous SNPs (NCBI annotated)	84,004	
MHC / ADME	43,904 / 43,615	
Sex Chromosomes (X / Y / PAR Loci)	113,213 / 2,498 / 511	
Mitochondrial	267	
Indels / multi-base substitutions [‡]	4,722	

* 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 454 reference samples.

** Value expected for typical projects using standard Illumina protocols.

[‡] Provided by the 1kGP structural variation group.

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