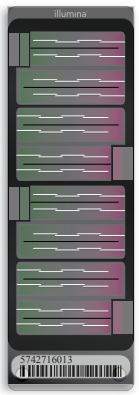
HumanOmni5-Quad BeadChip

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

Overview

The HumanOmni5-Quad (Omni5) BeadChip (Figure 1) delivers 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). 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, this four-sample BeadChip offers 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 flexibilty to add up to 500K custom-designed markers.

BeadChip Kit	Catalog No.
HumanOmni5-Quad DNA Analysis Kit (16)	WG-311-5001
HumanOmni5-Quad DNA Analysis Kit (48)	WG-311-5002
HumanOmni5-Quad DNA Analysis Kit (96)	WG-311-5003
HumanOmni5-Quad DNA Analysis Kit (384)	WG-311-5004
HumanOmni5-Quad+ Custom DNA Analysis BeadChip	Contact Illumina

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	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.

Illumina, Inc. • 9885 Towne Centre Drive, San Diego, CA 92121 USA • 1.800.809.4566 toll-free • 1.858.202.4566 tel • techsupport@illumina.com • illumina.com

FOR RESEARCH USE ONLY

© 2011 Illumina, Inc. All rights reserved.
Illumina, illumina*Dx*, BeadArray, BeadXpress, cBot, CSPro, DASL, DesignStudio, Eco, GAIIx, Genetic Energy, Genome Analyzer, GenomeStudio, GoldenGate, HiScan, HiSeq, Infinium, iSelect, MiSeq, Nextera, Sentrix, Solexa, TruSeq, VeraCode, the pumpkin orange color, and the Genetic Energy streaming bases design are trademarks or registered trademarks of Illumina, Inc.
All other brands and names contained herein are the property of their respective owners.
Pub. No. 370-2011-007 Current as of 08 October 2011

AGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAAC
TCAACGTACCGTAACGAACGTATCATTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGACGAAAAGAATGATAACAGTAACACACTTCTGTTAACCTT
CGACGAAAAGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACC
AACGTACCATTAAGAGCTACCGTGCAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGACGAAAAGAATGATAA
AGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAAC
GATTACTTGATCCACTGATTCAACGTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAGCAACGAGC
CGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGAAAAGAATGATAACAGTA