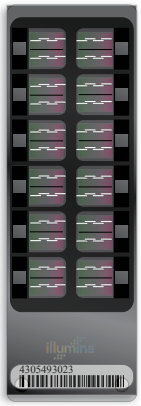
HumanOmniExpress BeadChip

Discover novel trait and disease associations with common tag SNPs at an attractive price.

Figure 1: HumanOmniExpress BeadChip



The HumanOmniExpress BeadChip is the industry's highest throughput array providing excellent coverage of common SNP variation as assessed by the International HapMap Project.

Overview

The HumanOmniExpress BeadChip delivers superior power for genome-wide association studies (GWAS), providing high sample throughput and comprehensive genomic content at the industry's best price. Using the proven iScan or HiScan™SQ System, this twelve-sample BeadChip offers unrivaled throughput of thousands of samples per week—the ideal solution for processing the greatest number of samples within a given budget. Optimized tag SNP content from all three HapMap phases has been strategically selected to capture the greatest amount of common SNP variation and drive the discovery of novel associations with traits and diseases. This product is customizable with up to 200,000 attempted beadtypes with the OmniExpress+ version of the BeadChip.

Ordering Information

HumanOmniExpress BeadChip Kit	Catalog No.
48 sample, single-use kit	WG-311-1120
288 sample, single-use kit	WG-311-1121
1152 sample, single-use kit	WG-311-1122

HumanOmniExpress Product Information

Feature	Description
Number of Markers	730,525
Number of Samples	12
DNA Requirement	200 ng
Assay	Infinium® HD
Instrument Support	HiScanSQ or iScan
Sample Throughput*	> 1,400 samples / week
Scan Time / Sample	5 minutes

% Variation Captured (r^2 > 0.8)	1kGP† MAF > 5%	1kGP† MAF > 1%
CEU	0.73	0.58
CHB + JPT	0.74	0.62
YRI	0.40	0.25

Data Performance	Value** / Product Specification
Call Frequency	99.84% / > 99% avg.
Reproducibility	99.99% / > 99.9%
Log R Deviation	0.15 / < 0.30‡

Spacing	Mean / Median / 90th%
Spacing (kb)	4.0 / 2.1 / 9.3

Marker Categories	Number of Markers
Number of SNPs with 10kb of RefSeq genes	392,197
Nonsynonymous SNPs (NCBI annotated)	15,062
MHC / ADME	7,459 / 16,649
Sex Chromosome (X / Y / PAR Loci)	18,055 / 1,409 / 471

* 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 reference samples.

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

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

© 2010, 2011 Illumina, Inc. All rights reserved.
© 2011 Illumina, Inc. All rights reserved.
Illumina, illuminaDx, BeadArray, BeadXpress, cBot, CSPro, DASL, Eco, Genetic Energy, GAIIx, 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. 370-2009-019 Current as of 07 October 2011

AGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAAC
TCAACGTACCGTAACGAACGTATCATTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGACGAAAAGAATGATAACAGTAACACACTTCTGTTAACCTT
CGACGAAAAGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACC
AACGTACCATTAAGAGCTACCGTGCAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGACGAAAAGAATGATAA
AGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAAC
GATTACTTGATCCACTGATTCAACGTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAGCAACGAGC
CGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGAAAAGAATGATAACAGTA