HumanOmni1-Quad BeadChip

Discover new disease associations with the most advanced genomic content available.

FRESH WHOLE-GENOME CONTENT

The HumanOmni1-Quad BeadChip provides an unparalleled, extensive view of the genome, in a high-throughput format.

Intelligently selected SNPs from all three HapMap phases capture more genomic variation and provide the best combination of power, price and throughput available for genome wide association studies (GWAS) . Genome-wide coverage is combined with the most valuable, cutting-edge content, updated from the 1,000 Genomes Project and confirmed disease associations. High marker density and the fewest large gaps ensure precise CNV detection.

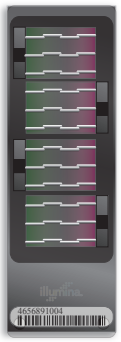
Efficient Infinium® marker design captures more genomic variation with fewer SNPs compared to arbitrary SNP selection. Convenient kit packaging, a streamlined PCR-free protocol, and integrated analysis software round out the comprehensive DNA analysis solution.

With the most up-to-date content and highest data quality, you can make more meaningful discoveries and take a faster path to publication.

Additional Information

Please visit www.illumina.com/dna or contact us at 1.800.809.4566 (1.858.202.4566 outside U.S.) or techsupport@illumina.com.

FIGURE 1: POPULAR MULTI-SAMPLE FORMAT



The HumanOmni1-Quad BeadChip's high-throughput format and low sample input requirements (200 ng) support rapid, cost-effective studies.

PRELIMINARY PRODUCT INFORMATION

PARAMETERS*	HUMANOMNI1-QUAD BEADCHIP
SNP Loci per Sample	1,140,419
Samples per BeadChip	4
DNA Input	200 ng per sample
Genomic Coverage	0.93 (CEU) / 0.92 (JPT+CHB) / 0.76 (YRI) at $r^2 > 0.8$
Content From the 1,000 Genomes Project	• Functional: 40,335 non-synonymous and splice site SNPs in Ensembl genes • Contiguous: 11,172 SNPs in four 1 Mb regions with GWAS signals for three or more disease traits (9p21, 8q24, 6q23.3, and 1p13.2) • GWAS regions: 40,343 SNPs in 100 smaller contiguous regions covering GWAS signals from NHGRI • Reported GWAS: 626 top associated SNPs from reported GWAS • Baylor Encode Regions: 2,598 SNPs in ten 100 kb regions resequenced in ~700 individuals
Additional High-Value Content	cSNPs, eSNPs, indels, and SNPs in mRNA splice sites, miRNA binding sites, introns, promoter regions, ADME genes, disease-associated SNPs, mitochondrial DNA, AIMs, ABO blood typing SNPs, PAR, Y-chromosome, MHC region, and HLA complex
CNV Content Available for Screening	More than 6,000 common and 5,000 rare CNV regions with 10–15 markers per region (defined by the Wellcome Trust Sanger Institute, Hospital for Sick Children in Toronto, and Harvard Medical School / Brigham and Women's Hospital), as well as regions defined and confirmed by deCode Genetics
Marker Spacing for CNV Discovery	1.2 kb median
Scan Times	12 minutes per sample on an iScan System, 1.25 hours per sample on a BeadArray™ Reader

*Estimated before final Gentrain; final statistics will vary

FOR RESEARCH USE ONLY

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