

Infinium® HumanOmni5-4 v1.1 BeadChip

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



Figure 1: The Infinium HumanOmni5-4 v1.1 BeadChip—The 4-sample BeadChip is the ultimate array for whole-genome genotyping and CNV analysis. It provides base content of over 4.2 M markers with tag-SNP coverage down to 1% MAF and the flexibility to add up to 500,000 custom-designed markers.

Overview

The HumanOmni5-4 v1.1 and HumanOmni5-4+ v1.1 BeadChips (Figure 1) deliver comprehensive coverage of the genome, leveraging tag single-nucleotide polymorphisms (SNPs) selected from the International HapMap project and 1000 Genomes Project (1kGP).1 These powerful chips target genetic variation down to 1% minor allele frequency (MAF). The HumanOmni5-4+ v1.1 BeadChip provides the flexibility to add up to 500,000 custom markers, allowing researchers to tailor the BeadChip for targeted applications and populationcustomized studies. Using the proven iScan® or HiScan® systems, along with the Infinium LCG Assay, these 4-sample BeadChips offer high-throughput sample processing, and optimized content for wholegenome genotyping and copy-number variation (CNV) applications. This end-to-end DNA analysis solution includes convenient kit packaging, a streamlined PCR-free protocol, and integrated analysis software.

Table 1: Infinium HumanOmni5-4 v1.1 Product Information

Feature	Description		
Total Number of Markers	4,284,426		
Capacity for Custom Markers	Up to 500,0	00	
Number of Samples per BeadChip	4		
DNA Input Requirement	400 ng		
Assay	Infinium LCG Quad		
Instrument Support	iScan or HiScan		
Sample Throughput ^a	> 460 samples/week		
Scan Time per Sample	iScan 38 min	HiScan 15 min	
Variation Captured $(r^2 \ge 0.8)$	1kGP ^b MAF > 5%	1kGPb MAF > 1%	
CEU°	0.87	0.83	
CHB + JPT ^c	0.85	0.76	
YRI°	0.71	0.58	
Data Performance	Valued	Product Sp	ecification
Call Rate	99.9%	> 99% avg.	
Reproducibility	99.99%	> 99.9%	
Log R Deviation	0.095	< 0.30°	
Spacing	Mean	Median	90 th % ^d
Spacing (kb)	0.68	0.37	1.57
- E-tit 4 Hi0 4	A	4.7	

- a. Estimate assumes 1 HiScan system, 1 AutoLoader 2.x, 1 Tecan robot, and a 5-day work week.
- b. Compared against the June 2011 1kGP data release.
- $\textbf{c. See} \ www.1000 genomes.org/category/frequently-asked-questions/population. \\$
- d. Values are derived from genotyping 284 HapMap reference samples.
- e. Value expected for typical projects using standard Illumina protocols. Tumor samples and samples prepared by methods other than standard Illumina protocols are excluded. Abbreviations: 1kGP, 1000 Genomes project; MAF, minor allele frequency.

Table 2: Infinium HumanOmni5-4 v1.1 BeadChip Marker Information

Marker Illionnation			
Marker Categories	Number of Markers ^a		
In RefSeq Genes ²	2,010,538 (2,374,042b)		
In RefSeq Exons	306,047		
In RefSeq Promoter Regions	92,555		
In ADME Genes	33,371 (42,540b)		
In ADME Exons	5,767		
MHC (Extended MHC°)	24,482 (42,311)		
Overlap with Genes in COSMIC	1,830,712		
Overlap with Genes in Gene Ontology ³	474,003		
Nonsense Markers	933		
Missense Markers	69,667		
Synonymous Markers	62,308		
Silent Markers	172,934		
Mitochondrial Markers	195		
Indels	4,321		
Sex Chromosomes	X Y Par Loci 113,662 2,404 5,256		

a. Compared against the June 2011 1kGP data release.

Abbreviations: ADME, absorption, distribution, metabolism, and excretion; COSMIC, catalog of somatic mutations in cancer⁴; MHC, major histocompatibility complex.

Learn More

To learn more about the Infinium HumanOmni5-4 v1.1 BeadChips and other Illumina genotyping products and services, visit www.illumina. com/applications/genotyping.html.

References

- 1. www.1000genomes.org Accessed 18 April 2014.
- 2. www.ncbi.nlm.nih.gov/refseq Accessed 6 July 2015.
- 3. geneontology.org Accessed 6 July 2015.
- 4. cancer.sanger.ac.uk/cosmic Accessed 6 July 2015.

Ordering Information

Infinium HumanOmni5-4 v1.1 BeadChip Kit	Catalog No.
16 samples	WG-313-5001
48 samples	WG-313-5002
96 samples	WG-313-5003
384 samples	WG-313-5004
Infinium HumanOmni5-4+ v1.1 BeadChip Kit ^a	Catalog No.
16 samples	WG-313-5005
10 Samples	VVG-313-5005
48 samples	WG-313-5006
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48 samples	WG-313-5006

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b. Within 10 kb.

c. MHC is a ~4 Mb region; extended MHC is a ~8 Mb region.