Infinium® OmniZhongHua-8 v1.3 BeadChip

Exceptional coverage of common, intermediate, and rare variation specific to Chinese populations.

Figure 1: Infinium OmniZhongHua-8 v1.3 BeadChip—The power and flexibility of the Infinium assay underlies the OmniZhongHua-8 v1.3 BeadChip. It offers exceptional coverage of common, intermediate, and rare SNP variation specific to Chinese populations as defined by the 1000 Genomes Project (1kGP).

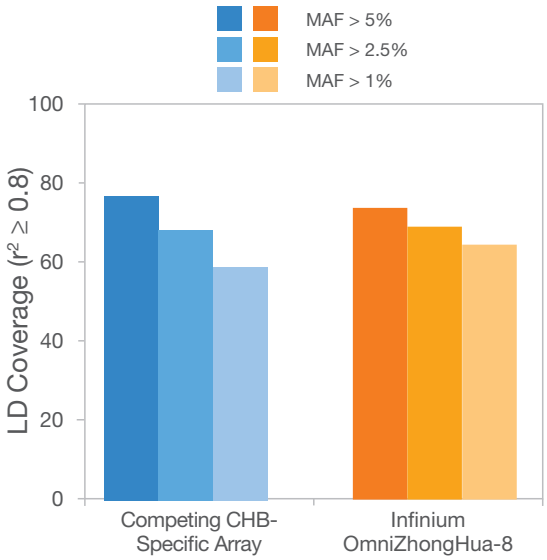

Figure 2: Array Coverage Comparison in Chinese Populations—Coverage calculations based on known common and rare Chinese population variants identified in the HapMap and 1kGP.

Overview

The first population-specific whole genome array from Illumina, the Infinium OmniZhongHua-8 v1.3 BeadChip delivers exceptional coverage of common, intermediate, and rare variation found within Chinese populations for genome-wide association studies (GWAS). Optimized tag single nucleotide polymorphism (SNP) content from all 3 HapMap phases and the 1kGP[1] has been strategically selected to create a population-focused array for the discovery of novel disease and trait associations in Chinese populations. Powered by the proven Infinium HD assay, the OmniZhongHua-8 v1.3 BeadChip combines industry-leading data quality with high sample throughput and comprehensive genomic content at an attractive price (Figure 1).

Comprehensive Coverage

The Infinium OmniZhongHua-8 v1.3 BeadChip provides coverage of 77% of common variation (minor allele frequency (MAF) > 5%), 73% of intermediate variation (MAF > 2.5%), and 65% of rare variation (MAF > 1%) in the Chinese population at $r^2 \geq 0.8$. This powerful chip provides greater coverage of intermediate and rare variation than the competing CHB array. It also offers equivalent coverage of common variation, making it the ideal starting point for Chinese population GWAS studies (Figure 2).

Proven Infinium Quality

The whole-genome Infinium HD assay underlies the power of the Omni family of microarrays. Genetic researchers worldwide use the Infinium HD assay for disease research, amassing a vast publication record. The Infinium OmniZhongHua-8 v1.3 BeadChip allows profiling of > 875,000 markers per sample. The assay is deployed with BeadArray technology from Illumina, delivering exceptionally high data quality for call rates (average > 99%), reproducibility (> 99.9%), and low sample repeat rates. High signal-to-noise ratios and low overall noise levels allow for precise, reliable calls and copy-number analyses.

Table 1: Infinium OmniZhongHua-8 v1.3 Product Information

Feature	Description		
Total Number of Markers	878,291		
Number of Samples per BeadChip	8		
DNA Input Requirement	200 ng		
Assay	Infinium HD Super		
Instrument Support	iScan® or HiScan®		
Sample Throughput[a]	960 samples/week		
Scan Time per Sample	~7.5 minutes		
LD Coverage ($r^2 \geq 0.8$)	**1kBP[b] MAF > 5%**	**1kBP[b] MAF > 2.5%**	**1kBP[b] MAF > 1%**
CHB	0.77	0.73	0.65
Data Performance	**Value[c]**	**Product Specification**	
Call Rate	99.8%	> 99% avg.	
Reproducibility	99.99%	> 99.9%	
Log R Deviation	0.14	< 0.30[d]	
Spacing	**Mean**	**Median**	**90th%[c]**
Spacing (kb)	3.30	1.69	7.77

a. Estimate assumes 1 HiScan system, 1 AutoLoader 2.x, 1 Tecan robot, and a 5-day work week.
b. Compared against the Phase 1 1000 Genomes Project (1kGP) data release (June 2011).[1]
c. Values are derived from genotyping 325 HapMap reference samples.
d. Value expected for typical projects using standard Illumina protocols. Tumor samples and samples prepared by methods other than standard Illumina protocols are excluded.

Abbreviations: LD, Linkage Disequilibrium; MAF, minor allele frequency.

Table 2: Infinium OmniZhongHua-8 v1.3 Marker Information

Marker Categories	Number of Markers[a]		
In RefSeq[b] Genes	387,986 (469,862[c])		
In RefSeq Exons	44,577		
In RefSeq Promoter Regions	20,420		
In ADME Genes	9883 (12,592[c])		
In ADME Exons	973		
MHC (Extended MHC)[d]	7770 (12,049)		
Overlap with Genes in COSMIC[e]	352,213		
Overlap with Genes in Gene Ontology[f]	93,823		
Nonsense Markers	88		
Missense Markers	10,485		
Synonymous Markers	11,512		
Silent Markers	22,489		
Mitochondrial Markers	107		
Indels	24		
Sex Chromosomes	X 20,464	Y 1772	Par Loci 1498

a. Compared against the June 2011 1kGP data release.
b. RefSeq - NCBI Reference Sequence Database, www.ncbi.nlm.nih.gov/refseq.
c. Within 10 kb.
d. MHC is a ~4 Mb region; extended MHC is a ~8 Mb region.
e. Catalog of somatic mutations in cancer, http://cancer.sanger.ac.uk/cosmic.
f. Gene Ontology Consortium, http://geneontology.org.

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

Learn More

To learn more about the Infinium OmniZhongHua-8 v1.3 BeadChip and other Illumina genotyping products and services, visit www.illumina.com/applications/genotyping.html.

References

1. www.1000genomes.org Accessed 18 April 2014.

Ordering Information

Infinium OmniZhongHua-8 v1.3 Kit	Catalog No.
16 samples	20004337
48 samples	20004338
96 samples	20004339
384 samples	20004340

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