DATA SHEET

Infinium™ Global Clinical Research Array-24 v1.0

Powerful, cost-effective genotyping solution for clinical research studies

- Comprehensive coverage of over 1.2M annotated variants from public research databases
- Genome-wide scaffold to detect common and low-frequency variants across a range of phenotypes
- Robust CNV detection and targeted amplification to allow pseudogene disambiguation
- Automated Infinium EX chemistry workflow supports a wide range of applications

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Introduction

The Infinium Global Clinical Research Array-24 v1.0 is a high-density BeadChip that enables customers to expand clinical research capabilities and achieve faster turnaround times (Figure 1, Table 1). The BeadChip is powered by the Infinium EX workflow for a scalable, cost-effective solution that supports automated and semiautomated workflows.

The Global Clinical Research Array-24 v1.0 BeadChip contains approximately ~1.2M carefully selected single nucleotide polymorphism (SNP) markers for research and discovery applications. The genome-wide content delivers high imputation accuracy at minor allele frequencies of > 1% across all 1000 Genomes Project (1KGP) populations.[1] The clinical research content includes variants with established disease associations and relevant pharmacogenomics (PGx) information. Content is derived from key clinical and research databases (Figure 2, Table 2).

Table 1: Product specifications

Feature	Description
Species	Human
Total number of markers[a]	1,157,992
Number of samples per BeadChip	24
DNA input requirement	100 ng
Capacity for custom bead types	50K
Assay chemistry	Infinium EX
Instrument support[a]	iScan System Infinium Automated Pipetting System 2.0 with ILASS Infinium Amplification System
Maximum iScan System sample throughput	~5760 samples/week
Scan time per sample[b]	~31 minutes

a. The Infinium EX chemistry workflow specifies the use of Infinium automation solutions.
b. Approximate values, scan times, and maximum throughput will vary depending on laboratory and system configurations.

ILASS, Illumina Lab Automation Software Solution

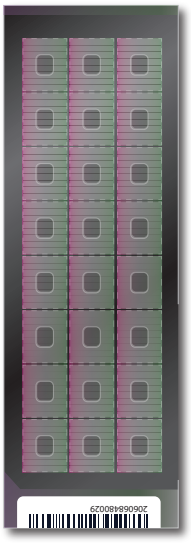

Figure 1: Infinium Global Clinical Research Array-24 v1.0— Features a multiethnic backbone with ~1.2M clinically relevant markers. The BeadChip uses Infinium EX chemistry for flexible and fast workflows.

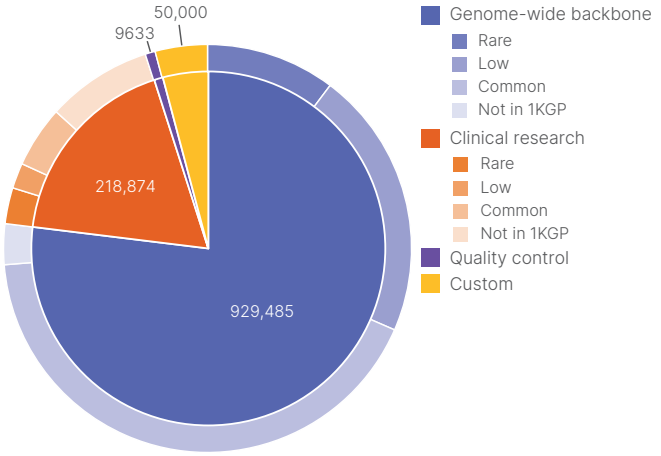

Figure 2: Summary of content—Plotted in the inner pie is the proportion of the array selected for genome-wide coverage, clinical research, and quality control (QC). The outer ring summarizes the weighted reference global allele frequency for unique variants present in 1KGP.[1] Variants not in 1KGP are labeled. Counts represent unique variants.

Table 2: High-value content from key research databases

Content	No. of markers[a]	Research application/note	Content	No. of markers	Research application/note
ACMG[2] 59 2016 gene coverage	31,382	Variants with known clinical significance identified from clinical WGS and WES samples	GO[7] CVS genes	191,340	Cardiovascular conditions
ACMG 59 all annotations	52,114		Database of Genomic Variants[8]	902,621	Genomic structural variation
ACMG 59 pathogenic	13,042		eQTLs[9]	4732	Genomic loci regulating mRNA expression levels
ACMG 59 likely pathogenic	5185		Fingerprint SNPs[10]	433	Human identification
ACMG 59 benign	3829		gnomAD exome[11]	427,536	WES and WGS results from unrelated individuals from various studies
ACMG 59 likely benign	10,812		HLA genes[12]	657	Disease defense, transplant rejection, and autoimmune disorders
ACMG 59 VUS	13,641		Extended MHC[12,c]	12,146	Disease defense, transplant rejection, and autoimmune disorders
AIMs[b]	2850	Ancestry-informative markers	KIR genes[3]	55	Autoimmune disorders and disease defense
			Neanderthal SNPs[13]	2731	Neanderthal ancestry and human population migration
APOE[3]	19	Cardiovascular disease, Alzheimer's disease, and cognition	Newborn/carrier screening gene coverage	46,152	Genes associated with childhood diseases included in the TruSight™ Inherited Disease Sequencing Panel[14]
			PharmGKB[15] all	4756	Human genetic variation associated with drug responses
ClinVar[4] variants	130,114	Relationships among variation, phenotypes, and human health	PharmGKB level 1A	210	
ClinVar pathogenic	37,292		PharmGKB level 1B	8	
ClinVar likely pathogenic	17,166		PharmGKB level 2A	32	
ClinVar benign	26,494		PharmGKB level 2B	43	
ClinVar likely benign	18,963		PharmGKB level 3	1743	
ClinVar VUS	22,932		PharmGKB level 4	413	
COSMIC[5] genes	533,547	Somatic mutations in cancer	RefSeq[16] 3' UTRs	23,070	3' untranslated regions[d]
CPIC[6] all	474	Variants with potential guidelines to optimize drug therapy	RefSeq 5' UTRs	11,199	5' untranslated regions[d]
CPIC-A	327		RefSeq All UTRs	33,296	Untranslated regions[d]
CPIC-A/B	3		RefSeq +/- 10 kb	690,988	Regulatory regions[d]
CPIC-B	18				
CPIC-C	43		RefSeq Promoters	46,363	2 kb upstream to include promoter regions[d]
CPIC-C/D	1		RefSeq Splice Regions	6941	Variants at splice sites[d]
CPIC-D	57				

a. The number of markers for each category may be subject to change.
b. Based on internal calculations.
c. Extended MHC is an 8 Mb region.
d. Of all known genes.

ACMG, American College of Medical Genetics; ADME, absorption, distribution, metabolism, and excretion; AIM, ancestry-informative marker; APOE, apolipoprotein E; COSMIC, catalog of somatic mutations in cancer; CPIC, Clinical Pharmacogenetics Implementation Consortium; EBI, European Bioinformatics Institute; eQTL, expression quantitative trait loci; gnomAD, Genome Aggregation Database; GO CVS, gene ontology annotation of the cardiovascular system; GWAS, genome-wide association study; HLA, human leukocyte antigen; KIR, killer cell immunoglobulin-like receptor; MHC, major histocompatibility complex; NHGRI, national human genome research institute; PharmGKB, Pharmacogenomics Knowledgebase; RefSeq, NCBI Reference Sequence Database; UTR, untranslated region; VUS, variant of unknown significance; WES, whole-exome sequencing; WGS, whole-genome sequencing.

Infinium EX chemistry workflow

The Infinium Global Clinical Research Array-24 v1.0 BeadChip uses advanced Infinium EX chemistry for a rapid and accurate assay workflow. The Infinium EX chemistry workflow substantially reduces hands-on time and potential for human error, and results in data generation in as little as two days (Figure 3). Automated sample preparation and BeadChip handling are carried out using the Infinium Automated Pipetting System with ILASS and the Infinium Amplification System.

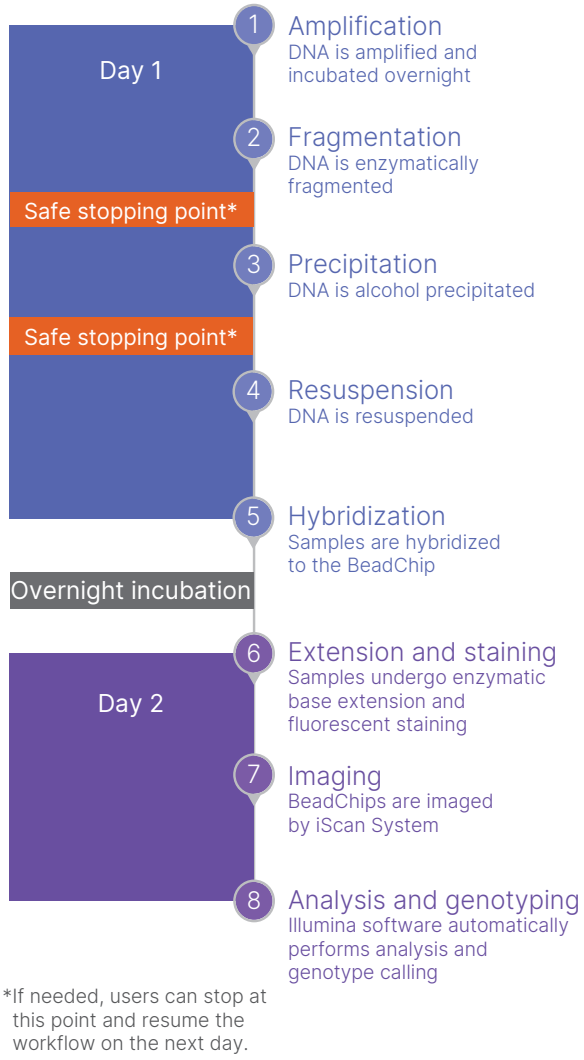

Figure 3: The Infinium EX 24-sample workflow provides a flexible two- or three-day workflow with minimal hands-on time

Diverse backbone with enhanced exonic coverage

The Infinium Global Clinical Research Array-24 v1.0 BeadChip is built on a global high-density SNP backbone that is optimized for cross-population imputation coverage. The genome-wide content includes enhanced tagging in exonic regions and enriched coverage of loci from genome-wide association studies (GWAS) with known disease or trait associations (Figure 2, Table 3).

Table 3: Marker information

Marker categories			No. of markers
Exonic markers[a]			157,821
Intronic markers[a]			474,445
Nonsense markers[b]			9986
Missense markers[b]			72,519
Synonymous markers[b]			18,196
Mitochondrial markers[b]			1032
Indels[c]			19,363
Sex chromosomes[c]	X	Y	PAR/homologous
	37,616	4427	822

a. RefSeq-NCBI Reference Sequence Database.[16]
b. Compared against the UCSC Genome Browser.[3]
c. NCBI Genome Reference Consortium, Version GRCh37.[17]

More than 132,135 exome markers were selected from individuals representing diverse ethnic backgrounds, including African Americans, Hispanics, Pacific Islanders, East Asians, Europeans, and individuals of mixed ancestry.[11] The array also features exonic content from populations in the ExAC database, including cross-population and population-specific markers with functionality annotations or strong evidence for association (Table 4).[18] The inclusive design allows for multiple applications, including polygenic risk scoring, nutrigenomics research, and clinical validation studies based on reported variants.

Table 4: Exonic coverage across populations

Population(s)[a,b]	No. of markers
NFE	101,035
EAS	51,542
AMR	77,131
AFR	71,027
SAS	69,412
NFE/EAS/AMR/AFR/SAS	35,547

a. www.internationalgenome.org/category/population
b. Based on gnomAD, gnomad.broadinstitute.org/

NFE, Non-Finnish European; EAS, East Asian; AMR, Ad Mixed American; AFR, African; SAS, South Asian

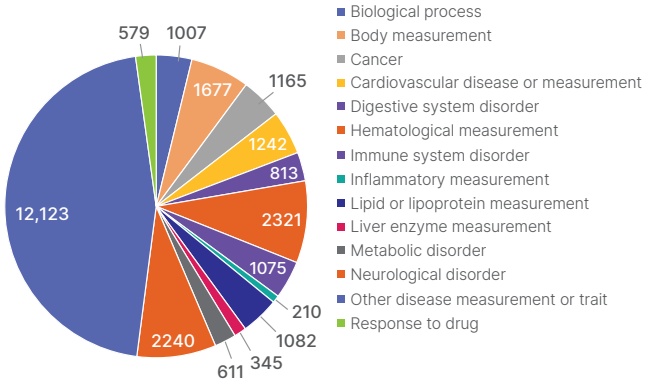

Figure 4: Disease research content covering diverse populations— The Infinium Global Clinical Research Array-24 v1.0 Includes extensive coverage of phenotypes and disease classifications based on NHGRI GWAS database categories.w

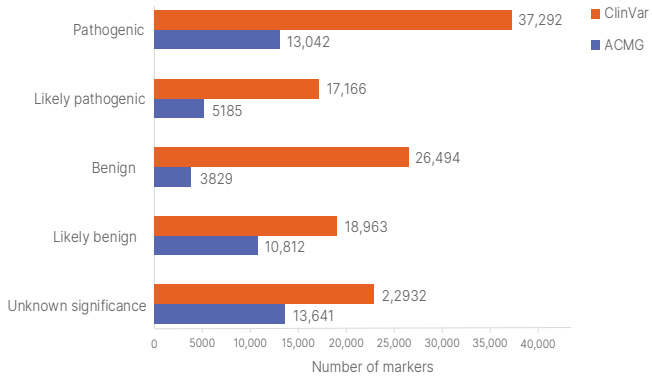

Figure 5: Distribution of variant pathology classifications according to ClinVar and ACMG annotations—Variants cover a range of pathogenic and nonpathogenic evidence.

Broad coverage of variants with known disease associations

The Infinium Global Clinical Research Array-24 v1.0 is designed for high-value clinical research applications. It provides coverage of variants selected from the National Human Genome Research Institute genome-wide association studies (NHGRI-GWAS) catalog[19] representing an extensive range of phenotypes and disease classifications. This content provides powerful opportunities for researchers interested in studying diverse populations.

Clinical research content on the BeadChip enables validation of previously identified disease associations, risk profiling, predictive screening research, and pharmacogenomic studies. Variant selection includes a range of pathology classifications based on ClinVar and American College of Medical Genetics (ACMG) annotations.[2,4] The content covers an extensive range of phenotypes and disease classifications based on ClinVar and the NHGRI-GWAS catalog (Figure 4).[19] Markers cover ACMG and ClinVar database variants with a range of phenotypes pathogenic, likely pathogenic, and variants of unknown significance (VUS), as well as benign variants (Figure 5).

Updated and research content

Databases, such as ClinVar, are constantly evolving with the addition of new variants and as variants change designation to “pathogenic” or “likely pathogenic” categories. Infinium Global Clinical Research Array-24 v1.0 provides updated coverage of many high-value variants contained within these annotated databases. Variants included on the array consist of markers with known disease associa-

tion selected from ClinVar, PharmGKB, and the NHGRI-EBI databases. The BeadChip also provides imputation-based tag SNPs for HLA alleles, extended MHC region, the KIR gene, and exonic content from the gnomAD database (Table 2, Figure 6).

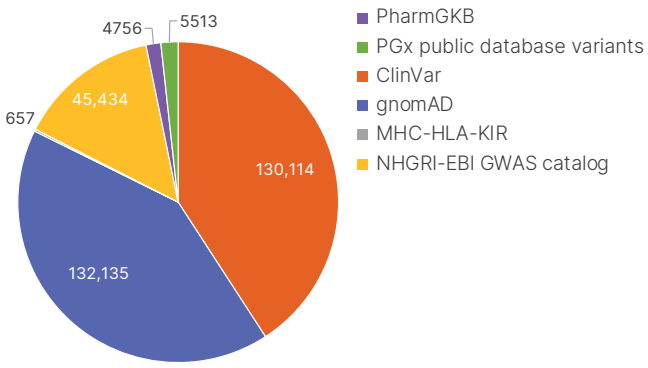

Figure 6: Clinical research content—Expertly selected clinical research content from key databases supports a broad range of applications.

QC markers for sample identification

The Infinium Global Clinical Research Array-24 v1.0 includes ~10K quality control (QC) markers. QC markers on the BeadChip are selected to facilitate high-throughput studies and enable important sample functions, including sample tracking, ancestry determination, and stratification (Figure 7).

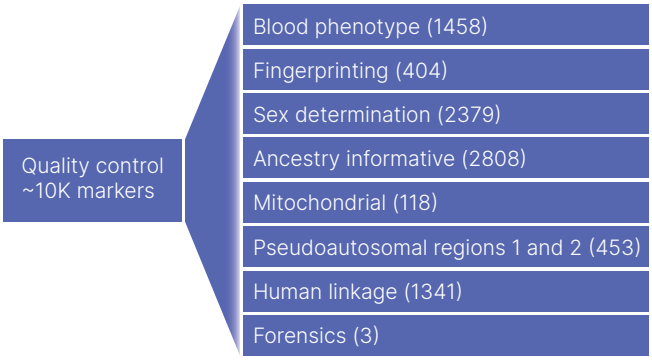

Figure 7: QC content by category—The BeadChip contains ~10K QC markers enabling various functions, such as sample tracking, sex determination, continental ancestry, human linkage, and more.

High-performance assay

The Infinium Global Clinical Research Array-24 v1.0 BeadChip uses trusted Infinium assay chemistry to deliver a high-performance, accurate genotyping solution. In addition, the high signal-to-noise ratio of the individual genotyping calls from the assay provides access to genome-wide copy CNV calling (Table 5).

Table 5: Data performance and spacing

Data performance	Observed[a]	Product specification[b]	
Call rate	99.7%	> 99.0 avg	
Reproducibility	99.99%	> 99.90	
Log R deviation	0.12[c]	< 0.30 avg[d]	
	Mean	Median	90th percentile[c]
Probe spacing	2.65 kb	1.30 kb	6.14

a. Excludes Y chromosome markers for female samples.
b. Based on results from GenTrain sample set.
c. Value expected for typical projects using standard Illumina protocols.

Summary

The Infinium Global Clinical Research Array-24 v1.0 provides a cost-effective, high-density genotyping assay for a range of research applications. When combined with the Infinium Automated Pipetting System with ILASS and the Infinium Amplification System, the BeadChip provides a high-throughput option for labs looking to analyze large numbers of samples with limited hands-on processing.

Learn more

Infinium Global Clinical Research Array-24 v1.0

Infinium Amplification System

Infinium Automated Pipetting System with ILASS

Ordering information

Infinium Global Clinical Research Array-24 v1.0 kit	Catalog no.
24 samples	20065215
96 samples	20068337
1152 samples	20068338
Infinium Global Clinical Research Array-24+ v1.0 kit[a]	
24 samples	20068351
96 samples	20068352
1152 samples	20068353

a. Customers should select BeadChips annotated with + symbol for adding customizable content.

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