

Infinium™ Global Screening Array with Cytogenetics-24 v1.0 BeadChip

A powerful efficient assay for
genome-wide cytogenetic
analysis

- Updated, disease-focused content for discovery and validation studies
- 700K genome-wide probes with high marker-to-exon coverage for robust cytogenetic analysis
- 80K supplemental markers selected to enhance cytogenetic assay performance
- Compatible with powerful cytogenetic analysis software for data analysis and visualization



Introduction

Cytogenetic variation is associated with numerous disorders, including cancers, developmental conditions, and fetal anomalies. Properly designed single nucleotide polymorphism (SNP) arrays can be used to assess cytogenetic variations in chromosome structure, copy number, and segregation in a rapid and affordable assay. These microarrays offer researchers valuable insights into the genetic mechanisms of human health and disease.

The Infinium Global Screening Array with Cytogenetics-24 v1.0 (Figure 1) is an easy-to-use solution for investigating cytogenetic variability. To create this array, 80K cytogenetic-informative markers were added to 620K proven disease-targeted markers from the Infinium Global Screening Array-24 v3.0 (Table 1). Analysis for the Infinium Global Screening Array with Cytogenetics-24 v1.0 can be performed with various software packages, including NxClinical software (Bionano), a focused solution for investigating chromosomal aneuploidies.

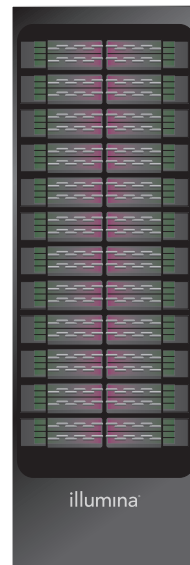


Figure 1: Infinium Global Screening Array with Cytogenetics-24 v1.0 BeadChip—The BeadChip is built on the trusted 24-sample Infinium HTS platform with ~700K markers to create a versatile cytogenetic screening tool.

Table 1: Infinium Global Screening Array with Cytogenetics-24 v1.0 information

Feature	Description
Species	Human
Total no. of markers ^a	~700K
No. of samples per BeadChip	24
DNA input requirement	200 ng
SNP replicates	15
No. of SNPs needed to call CNV	10
Assay chemistry	Infinium HTS
Instrument support	iScan System
Maximum iScan System sample throughput	~5760 samples/week
Scan time per sample ^b	~1.5 minutes

a. The total number of markers includes ~620K included in the Infinium Global Screening Array-24 plus ~80K cytogenetic-specific content.

b. Approximate values, scan times, and maximum throughput will vary depending on laboratory and system configurations.

Optimized global and high-value content

The Infinium Global Screening Array with Cytogenetics-24 v1.0 builds on the success of the consortium version of the Infinium Global Screening Array-24 v3.0 that has been widely adopted by a community of human disease researchers, health care networks, consumer genomics companies, and genomic service providers. The multiethnic, genome-wide backbone includes variants from key scientific databases (Figure 2).¹⁻⁵

Extensive coverage of disease-associated variants

The extensive backbone content on the Infinium Global Screening Array with Cytogenetics-24 v1.0 supports multiple applications, including validation of disease associations, risk profiling, preemptive screening research, and pharmacogenomics studies. Variant selection includes pathology classifications based on National Center for Biotechnology Information (NCBI), ClinVar, and American

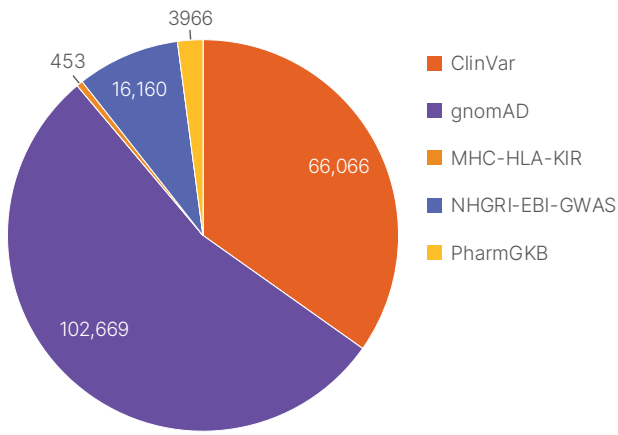


Figure 2: Clinical research content—BeadChip backbone content was expertly selected from reference scientific databases to create a highly informative assay for human health and disease research applications.

College of Medical Genetics (ACMG) ClinVar annotations (Figure 3A).^{1,6} The BeadChip contains extensive coverage of phenotypes and disease classifications based on ClinVar, National Human Genome Research Institute, and European Bioinformatics Institute (NH GRI-EB I) genome wide association studies (GWAS) databases (Figure 3B).⁴

Focused content for cytogenetic research and discovery

To enable cytogenetic applications, the Infinium Global Screening Array with CytoGenetics-24 v1.0 includes 80K probes with a high marker-to-exon ratio categorized into four cytogenetic application tiers (Table 2). The content was carefully chosen through a cytogenetic consortium to produce an exceptional tool for genome-wide copy number variation (CNV) coverage for oncology, prenatal, postnatal, reproductive health, and genetic disease research.

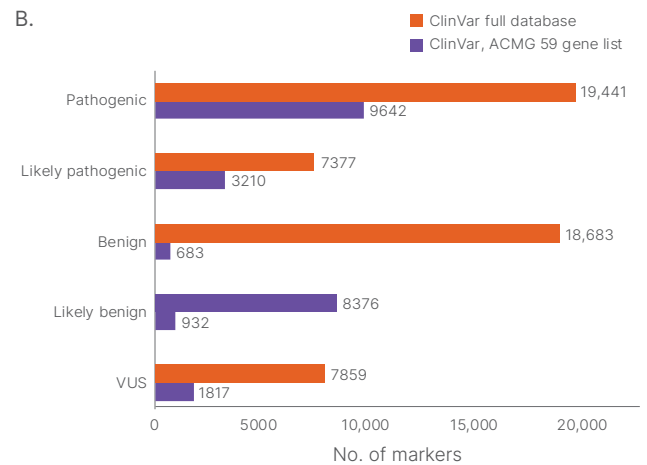
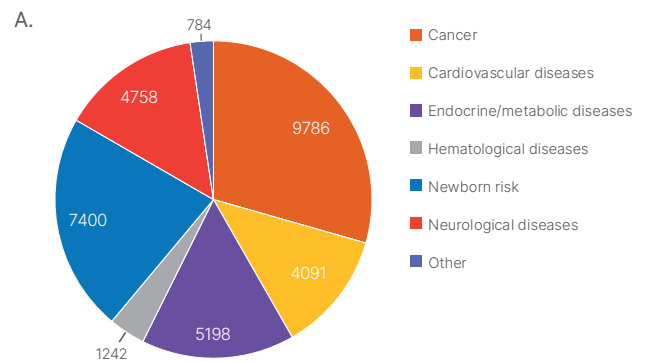


Figure 3: Broad coverage of disease categories—(A) Infinium Global Screening Array with CytoGenetics-24 v1.0 disease research content by category within the ClinVar database. Variant counts are subject to change. (B) Variants sorted by range of pathology classifications according to ACMG ClinVar annotations.

VUS, variant of unknown significance.

Optimized coverage and spacing for cytogenetic applications

Using SNP analysis to identify cytogenetic features requires careful selection of covered variants and sufficient spacing of markers across the target regions. The Infinium Global Screening Array with CytoGenetics-24 v1.0 was developed to ensure optimal coverage of key genes with spacing that supports improved CNV detection when compared to other commercially available arrays (Figure 4).

Table 2: Cytogenetic application tiers included on the Infinium Global Screening Array with Cyto genetics-24 v1.0

Application tier	Description	Genes in tier	Exons in tier	Average probe spacing	Median probes/exon	Exons with ≥ 1 probes	Exons with ≥ 3 probes
1	ClinGen pathogenic/likely pathogenic, haploinsufficient, and triploinsufficient ⁷	409	6214	1.25 kb	3	> 99%	> 99%
2	DDG2P Genes associated with cancer ⁸	1254	18,353	2.00 kb	2	> 99%	> 99%
3	Input from cytogenetics consortia mendeliome panel	2766	36,840	2.45 kb	1	> 99%	> 60%
4	OMIM Morbid Genes not otherwise tiered ⁹	456	5434	2.82 kb	1	> 80%	> 60%
Total		4885	66,841				

DDG2P, developmental disorders gene to phenotype.

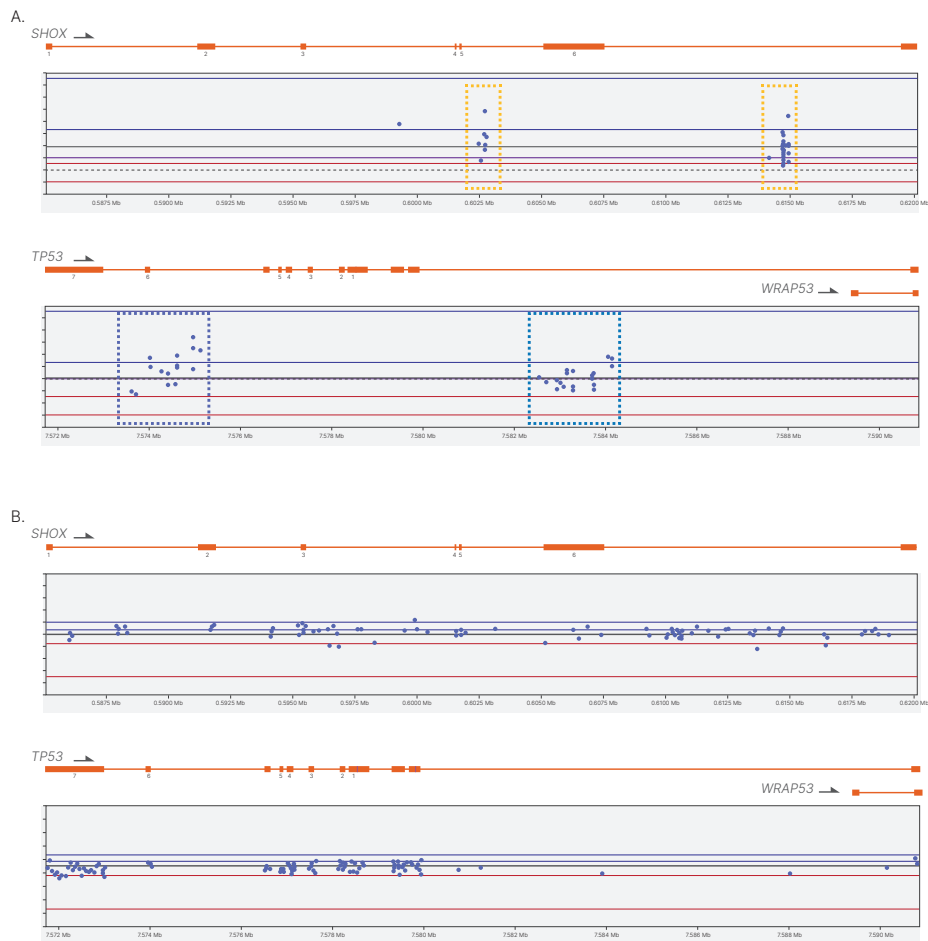


Figure 4: Cytogenetic variant coverage vs. similar cytogenetic array solution—(A) Commercially available cytogenetics array from other supplier with dense probe clusters (dashed gold boxes) and poor spacing and coverage in intronic and noncritical regions (dashed blue boxes), (B) supplemental content in Infinium Global Screening Array with Cyto genetics-24 v1.0 designed with improved spacing and focus on high-exonic, high-value coverage of key genes supporting gene structure and copy number analysis.

QC markers for sample tracking

The marker backbone on the Infinium Global Screening Array with Cytogenetics-24 v1.0 also includes ~10K quality control (QC) markers. The QC marker content enables important sample tracking functions, including ancestry determination and stratification, and facilitates higher throughput studies (Figure 5).

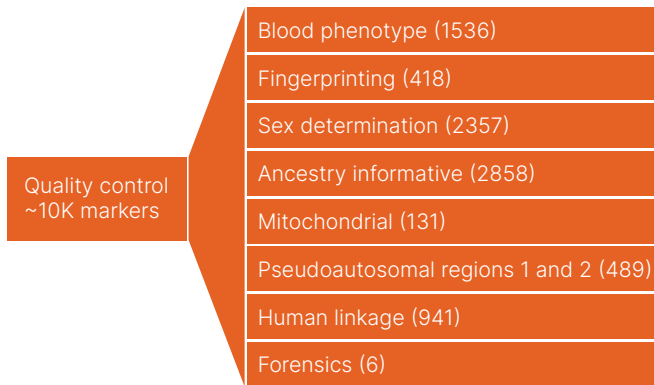


Figure 5: QC content by category—The BeadChip contains ~10K markers enabling various sample tracking functions such as sex determination, continental ancestry, human linkage, and more.

Trusted, high-quality assay

The Infinium Global Screening Array with Cytogenetics-24 v1.0 BeadChip uses trusted Infinium assay chemistry to deliver the same level of high-quality, reproducible results that Infinium genotyping arrays have provided for over a decade (Table 3). In addition, the high signal-to-noise ratio for individual genotyping calls, inherent in the Infinium assay, provides the data quality necessary for the genome-wide CNV analysis featured on the array. The BeadChip is also compatible with the [Infinium FFPE QC and DNA Restoration Kit](#), enabling genotyping of formalin-fixed, paraffin-embedded (FFPE) samples.

Table 3: 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	4.0 kb	2.0 kb	--
	Targeted	Backbone	
Resolution	~10 kb	~25 kb	

a. Values are derived from genotyping 2051 HapMap reference samples.
 b. Excludes Y chromosome markers for female samples.
 c. Based on results from the GenTrain sample set.
 d. Value expected for typical projects using standard Illumina protocols; tumor samples and samples prepared by nonstandard protocols are excluded.

Powerful analysis for cytogenetic research

Multiple array analysis software platforms can be used with the Infinium Global Screening Array with Cytogenetics-24 v1.0. For labs looking for a software solution, NxClinical software is available for fast, accurate, and comprehensive sample analysis. NxClinical software offers industry-standard algorithms, admin controls, and an integrated audit trail to ensure analysis accuracy and integrity. The easy-to-use software features information from current research databases to support variant annotations and provides phenotype-associated variant ranking. After data are analyzed, NxClinical software offers an array of data visualization tools to help organize and present results.

High-throughput workflow

The Infinium Global Screening Array with Cytogenetics-24 v1.0 uses the proven 24-sample Infinium HT BeadChip that enables laboratories to scale efficiently. The Infinium assay provides a three-day workflow that allows researchers to generate results quickly (Figure 6). For flexible throughput, the Infinium assay provides the capability to run up to 5760 samples per week using a single iScan™ System.

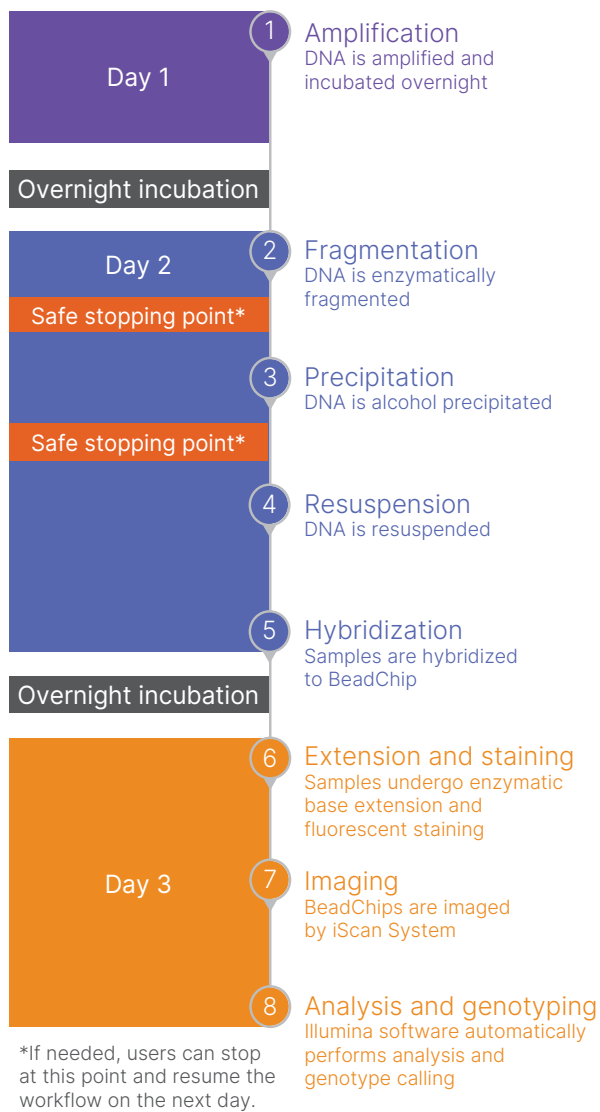


Figure 6: The Infinium HTS format provides a rapid three-day workflow with minimal hands-on time.

Summary

The Infinium Global Screening Array with Cytogenetics-24 v1.0 is an easy-to-use, cost-effective option for accurate, and efficient screening of CNVs and disease-associated SNPs. The ~700K markers have been carefully selected for optimal cytogenetic analysis performance. Proven Infinium HT chemistry delivers high-accuracy detection of challenging targets and fast turnaround times for labs looking to efficiently process large numbers of samples.

Ordering information

Product	Catalog no.
Infinium Global Screening Array with Cytogenetics-24 v1.0 BeadChip (24 samples)	20122862
Infinium Global Screening Array with Cytogenetics-24 v1.0 BeadChip (48 samples)	20066469
Infinium Global Screening Array with Cytogenetics-24 v1.0 BeadChip (288 samples)	20066470
Infinium Global Screening Array with Cytogenetics-24 v1.0 BeadChip (1152 samples)	20066471

Learn more

[Infinium Global Screening Array with Cytogenetics-24 v1.0 BeadChip](#)

References

- Landrum MJ, Lee JM, Benson M, et al. [ClinVar: improving access to variant interpretations and supporting evidence.](#) *Nucleic Acids Res.* 2018;46(D1):D1062-D1067. doi:10.1093/nar/gkx1153
- Karczewski KJ, Francioli LC, Tiao G, et al. [The mutational constraint spectrum quantified from variation in 141,456 humans](#) [published correction appears in *Nature*. 2021 Feb;590(7846):E53]. *Nature.* 2020;581(7809):434-443. doi:10.1038/s41586-020-2308-7
- de Bakker PI, McVean G, Sabeti PC, et al. [A high-resolution HLA and SNP haplotype map for disease association studies in the extended human MHC.](#) *Nat Genet.* 2006;38(10):1166-1172. doi:10.1038/ng1885

4. Buniello A, MacArthur JAL, Cerezo M, et al. [The NHGRI-EBI GWAS Catalog of published genome-wide association studies, targeted arrays and summary statistics 2019](#). *Nucleic Acids Res.* 2019;47(D1):D1005-D1012. doi:10.1093/nar/gky1120
5. Whirl-Carrillo M, Huddart R, Gong L, et al. [An Evidence-Based Framework for Evaluating Pharmacogenomics Knowledge for Personalized Medicine](#). *Clin Pharmacol Ther.* 2021;110(3):563-572. doi:10.1002/cpt.2350
6. Miller DT, Lee K, Chung WK, et al. [ACMG SF v3.0 list for reporting of secondary findings in clinical exome and genome sequencing: a policy statement of the American College of Medical Genetics and Genomics \(ACMG\)](#) [published correction appears in *Genet Med.* 2021 Aug 3;:]. *Genet Med.* 2021;23(8):1381-1390. doi:10.1038/s41436-021-01172-3
7. Rehm HL, Berg JS, Brooks LD, et al. [ClinGen--the Clinical Genome Resource](#). *N Engl J Med.* 2015;372(23):2235-2242. doi:10.1056/NEJMSr1406261
8. Thormann A, Halachev M, McLaren W, et al. [Flexible and scalable diagnostic filtering of genomic variants using G2P with Ensembl VEP](#). *Nat Commun.* 2019;10(1):2373. Published 2019 May 30. doi:10.1038/s41467-019-10016-3
9. Amberger JS, Bocchini CA, Schiettecatte F, Scott AF, Hamosh A. [OMIM.org: Online Mendelian Inheritance in Man \(OMIM®\), an online catalog of human genes and genetic disorders](#). *Nucleic Acids Res.* 2015;43(Database issue):D789-D798. doi:10.1093/nar/gku1205



1.800.809.4566 toll-free (US) | +1.858.202.4566 tel
techsupport@illumina.com | www.illumina.com

© 2024 Illumina, Inc. All rights reserved. All trademarks are the property of Illumina, Inc. or their respective owners.
For specific trademark information, see www.illumina.com/company/legal.html.
M-GL-00726 v3.0