

Infinium™ Global Diversity Array with Enhanced PGx-8 v1.0

Versatile genotyping solution
for pharmacogenomics,
disease, and diversity studies

- Comprehensive coverage of over 6,000 annotated variants from public PGx databases, including key genes like *CYP2D6*
- Genome-wide scaffold to detect common and low-frequency variants across a range of phenotypes
- Robust CNV detection and targeted amplification to allow PGx pseudogene disambiguation

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Introduction

The Infinium Global Diversity Array with Enhanced PGx-8 v1.0 BeadChip is the most comprehensive genotyping microarray on the market for supporting pharmacogenomic (PGx) research along with polygenic risk score development, ancestry determination, and genetic disease research. The array is built on an eight-sample BeadChip that contains more than 1.9 million markers on a genome-wide backbone (Figure 1, Table 1).

Other noteworthy attributes are the inclusion of more than 44,000 absorption, distribution, metabolism, and excretion (ADME) markers spanning more than 2000 genes and exceptional coverage of priority level A and B Clinical Pharmacogenetics Implementation Consortium (CPIC) variants (Figure 2, Table 1).^{1,2} High-impact PGx genes like *CYP2D6*, *CYP2B6*, and *TPMT* that have historically been challenging to discern are now accessible due to significant workflow improvements that enable disambiguation of pseudogenes. In addition, optional interpretation software allows you to generate a report containing metabolizer status and star allele calls.

Table 1: Product information^a

| Feature | Description |
|--|--------------------|
| Species | Human |
| Total number of markers ^b | 1,933,117 |
| Capacity for custom bead types | 175,000 |
| Number of samples per BeadChip | 8 |
| DNA input requirement | 200 ng |
| Assay chemistry | Infinium LCG |
| Instrument support | iScan System |
| Maximum iScan System sample throughput | ~1728 samples/week |
| Scan time per sample | 4.4 minutes |

a. Approximate values, scan times, and maximum throughput will vary depending on laboratory and system configurations
 b. Variants found on commercial manifest

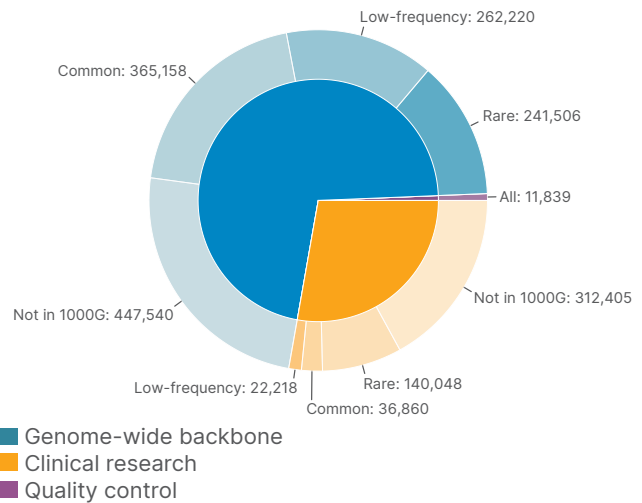


Figure 1: Summary of content—Plotted in the inner pie is the proportion of the array selected for genome-wide coverage, clinical research, and quality control (QC). The outer ring summarizes the weighted reference global allele frequency for unique variants present in the 1000 Genomes Project (1000G).³ Variants not in 1000G are labeled. Counts represent unique variants.

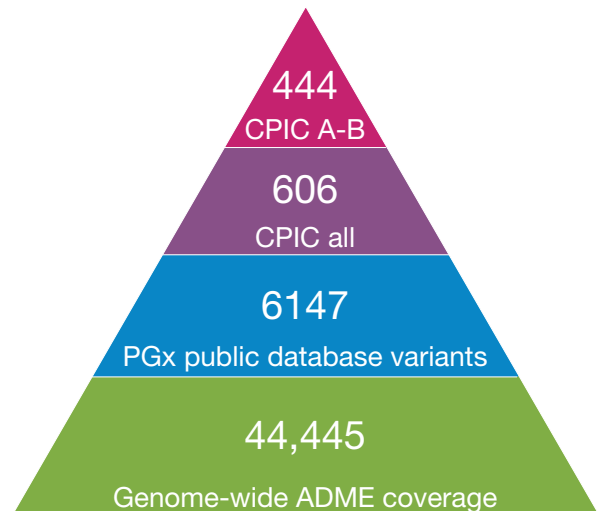


Figure 2: Broad spectrum of pharmacogenomics markers—Clinical research content developed from an extensive list of pharmacogenomics markers selected based on CPIC guidelines and the PharmGKB database.^{1,2} Content includes PGx public database variants, variants annotated in PharmGKB, PharmVar,⁴ CPIC, genome-wide PGx coverage, extended ADME genes, CPIC level A genes, including targeted imputation tag SNPs, and CPIC level A CNV tags.

Table 2: Infinium Global Diversity Array with Enhanced PGx-8 v1.0 high-value content

| Content | No. of markers ^a | Research application/note | Content | No. of markers | Research application/note |
|--|-----------------------------|--|--|----------------|--|
| ACMG ⁵ 59 2016 gene coverage | 30,878 | | GO ¹¹ CVS genes | 331,520 | Cardiovascular conditions |
| ACMG 59 all annotations | 22,812 | | Database of Genomic Variants ¹² | 1,440,531 | Genomic structural variation |
| ACMG 59 pathogenic | 6753 | Variants with known clinical significance identified from clinical WGS and WES samples | eQTLs ¹³ | 6394 | Genomic loci regulating mRNA expression levels |
| ACMG 59 likely pathogenic | 2946 | | Fingerprint SNPs ¹⁴ | 481 | Human identification |
| ACMG 59 benign | 2051 | | gnomAD ¹⁵ exome | 502,547 | WES and WGS results from unrelated individuals from various studies |
| ACMG 59 likely benign | 3701 | | HLA genes ¹⁶ | 18,893 | Disease defense, transplant rejection, and autoimmune disorders |
| ACMG 59 VUS | 5330 | | Extended MHC ^{16,c} | 23,965 | Disease defense, transplant rejection, and autoimmune disorders |
| ADME ⁶ core and extended + CPIC genes | 49,705 | Drug absorption, distribution, metabolism, and excretion | KIR genes ⁷ | 154 | Autoimmune disorders and disease defense |
| ADME core and extended + CPIC genes +/- 10 kb | 57,588 | Includes regulatory regions | Neanderthal SNPs ¹⁷ | 2095 | Neanderthal ancestry and human population migration |
| AIMs ^b | 3047 | Ancestry-informative markers | Newborn/carrier screening gene coverage | 61,902 | Genes associated childhood diseases included in the TruSight™ Inherited Disease Sequencing Panel ¹⁸ |
| APOE ⁷ | 86 | Cardiovascular disease, Alzheimer's disease, and cognition | NHGRI-EBI GWAS catalog ¹⁹ | 32,585 | Markers from published GWAS |
| Blood phenotype genes ⁸ | 3036 | Blood phenotypes | PharmGKB ^{4,20} all | 5116 | Human genetic variation associated with drug responses |
| ClinVar ⁹ variants | 110,608 | Relationships among variation, phenotypes, and human health | PharmGKB level 1A | 297 | |
| ClinVar pathogenic | 20,719 | | PharmGKB level 1B | 8 | |
| ClinVar likely pathogenic | 8241 | | PharmGKB level 2A | 56 | |
| ClinVar benign | 29,366 | | PharmGKB level 2B | 49 | |
| ClinVar likely benign | 19,298 | | PharmGKB level 3 | 1911 | |
| ClinVar VUS | 24,342 | | PharmGKB level 4 | 446 | |
| COSMIC ¹⁰ genes | 1,043,886 | Somatic mutations in cancer | RefSeq ²¹ 3' UTRs | 46,399 | 3' untranslated regions ^d |
| CPIC ² all | 606 | Variants with potential guidelines to optimize drug therapy | RefSeq 5' UTRs | 30,386 | 5' untranslated regions ^d |
| CPIC-A | 413 | | RefSeq All UTRs | 74,608 | Untranslated regions ^d |
| CPIC-A/B | 3 | | RefSeq | 1,121,140 | All known genes |
| CPIC-B | 28 | | RefSeq +/- 10 kb | 1,262,045 | Regulatory regions ^d |
| CPIC-C | 43 | | RefSeq Promoters | 45,221 | 2 kb upstream to include promoter regions ^d |
| CPIC-C/D | 2 | | RefSeq splice regions | 12,106 | Variants at splice sites ^d |
| CPIC-D | 60 | | | | |

- a. The number of markers for each category are subject to change
- b. Based on internal calculations
- c. Extended MHC is a 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; NCBI: National Center for Biotechnology Information; UTR: untranslated region; VUS: variant of unknown significance; WES: whole-exome sequencing; WGS: whole-genome sequencing

The Global Diversity Array with Enhanced PGx-8 BeadChip is built on a high-density single nucleotide polymorphism (SNP) global backbone optimized for cross-population imputation genome coverage (Figure 1, Table 3). The combination of a high-density SNP backbone and clinical research variant coverage helps make the Infinium Global Diversity Array-8 v1.0 BeadChip the most cost-effective array within the Illumina portfolio. It is the array chosen by the [All of Us Research Program](#) that aims to sequence and genotype over 1 million individuals. The array is ideal for precision medicine programs interested in maximizing their return on genotyping investments.

Table 3: Marker information

| Marker categories | No. of markers | | |
|------------------------------------|----------------|------|----------------|
| Exonic markers ^a | 531,191 | | |
| Intronic markers ^a | 664,016 | | |
| Promoters ^a | 53,311 | | |
| Nonsense markers ^b | 28,224 | | |
| Missense markers ^b | 398,598 | | |
| Synonymous markers ^b | 34,000 | | |
| Mitochondrial markers ^b | 1318 | | |
| Indels ^c | 39,257 | | |
| Sex chromosomes ^c | X | Y | PAR/homologous |
| | 63,810 | 6215 | 5477 |

a. RefSeq, NCBI Reference Sequence Database.²¹

b. Compared against the UCSC Genome Browser.⁷

c. NCBI Genome Reference Consortium, Version GRCh37.²²

indel: insertion/deletion; PAR: pseudoautosomal region; UCSC: University of California Santa Cruz; NCBI: National Center for Biotechnology Information

Each Global Diversity Array with Enhanced PGx-8 v1.0 Kit includes BeadChips and reagents for amplifying, fragmenting, hybridizing, labeling, and detecting genetic variants using the high-throughput, streamlined Infinium workflow.

Exceptional exonic content

The Infinium Global Diversity Array with Enhanced PGx-8 v1.0 BeadChip includes enhanced tagging in exonic regions and enriched coverage to map loci from genome-wide association studies (GWAS) with previously identified disease or trait associations. More than 400,000

exome markers were gathered from 36,000 individuals from diverse ethnic groups, including African Americans, Hispanics, Pacific Islanders, East Asians, Europeans, and individuals of mixed ancestry. The array also features diverse exonic content from the ExAC database,²³ including cross-population and population-specific markers with either functionality or strong evidence for association (Table 4).

Table 4: Exonic coverage across populations

| Population(s) ^{a, b} | No. of markers |
|-------------------------------|----------------|
| NEF | 346,340 |
| EAS | 146,281 |
| AMR | 272,178 |
| AFR | 257,690 |
| SAS | 224,431 |
| NEF/EAS/AMR/AFR/SAS | 69,432 |

a. internationalgenome.org/category/population

b. Based on gnomAD, gnomad.broadinstitute.org/

NEF: non-Finish European; EAS: East Asian; AMR: ad mixed American; AFR: African; SAS: South Asian

Broad coverage of variants with known disease associations

The Infinium Global Diversity Array with Enhanced PGx-8 v1.0 BeadChip provides coverage of variants selected from the National Human Genome Research Institute genome-wide association studies (NHGRI-GWAS) catalog¹⁹ representing a broad range of phenotypes and disease classifications. This content provides powerful opportunities for researchers interested in studying diverse populations to test and validate associations previously found in European populations.

Clinical research content on the BeadChip enables validation of disease associations, risk profiling, preemptive screening research, and PGx studies. Variant selection includes a range of pathology classifications based on ClinVar and American College of Medical Genetics (ACMG) annotations.⁵ The BeadChip contains extensive coverage of phenotypes and disease classifications based on ClinVar and the NHGRI-GWAS catalog (Figure 3). Markers cover ACMG and ClinVar database variants with a range of phenotypes pathogenic, likely pathogenic, and

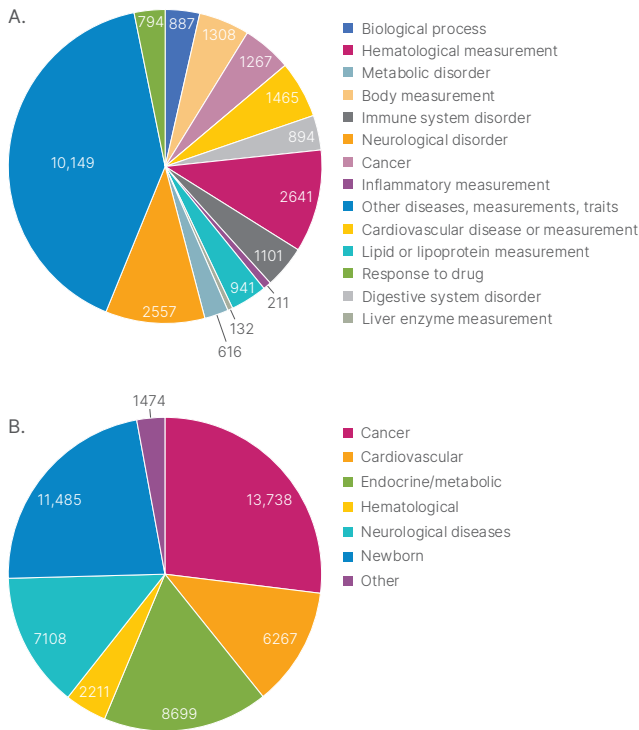


Figure 3: Disease research content covering diverse populations—The Global Diversity Array with Enhanced PGx-8 includes extensive coverage of numerous phenotypes and disease classifications based on (A) ClinVar categories and (B) NHGRI-GWAS categories.

variants of unknown significance (VUS), as well as benign variants (Figure 4).

Updated and relevant clinical research content

Clinical databases, such as ClinVar, are constantly evolving as new variants are added and variants change designation to “pathogenic” or “likely pathogenic.” The Infinium Global Diversity Array with Enhanced PGx-8 v1.0 BeadChip provides updated coverage of many of the high-value variants contained within these annotated databases. Variants included on the array consist of markers with known disease association based on ClinVar, the PharmGKB, and the National Human Genome Research Institute (NHGRI)-EBI database.¹⁹ The BeadChip also provides imputation-based tagSNPs for HLA alleles, extended MHC region, the KIR gene, and exonic content from the gnomAD¹⁵ database (Table 2, Figure 5).

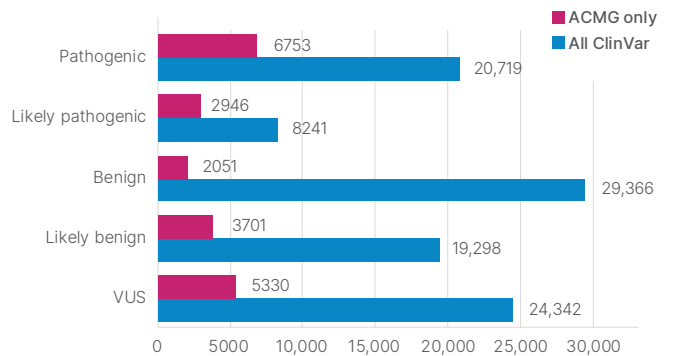


Figure 4: Distribution of variant pathology classifications according to ClinVar and ACMG annotations—Variants cover a range of pathogenic and nonpathogenic evidence.

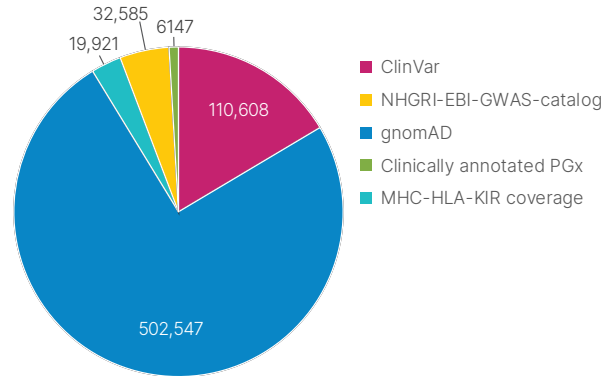


Figure 5: Clinical research content—The Infinium Global Diversity Array with Enhanced PGx-8 v1.0 BeadChip incorporates expertly selected clinical research content from key databases, supporting a broad range of applications.

QC markers for sample identification

The Infinium Global Diversity Array with Enhanced PGx-8 v1.0 BeadChip includes quality control (QC) markers for large-scale studies, enabling sample identification, tracking, ancestry determination, stratification, and more (Figure 6).

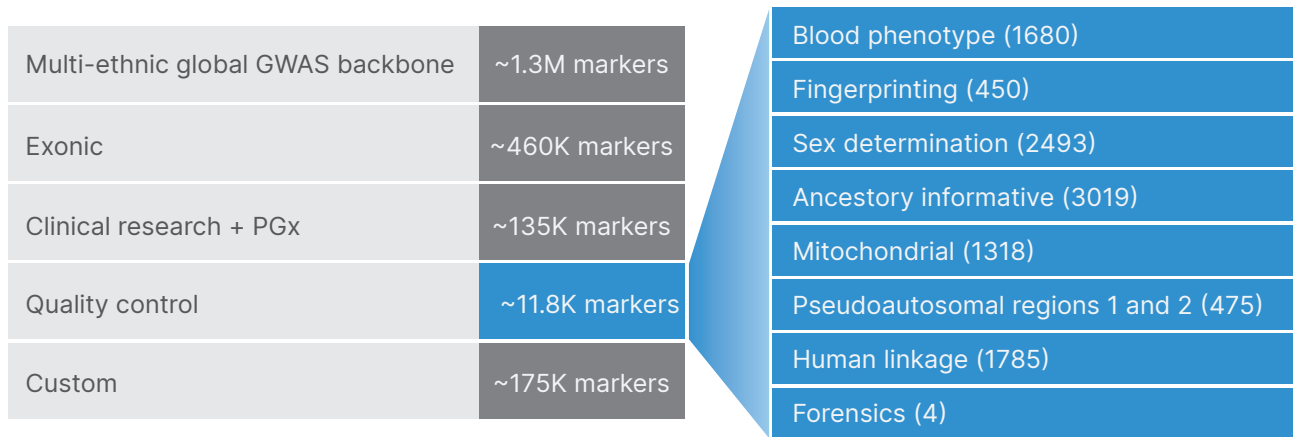


Figure 6: QC markers—QC variants on the array enable various capabilities for sample tracking such as sex determination, continental ancestry, human identification, and more.

Flexible content options

The Infinium Global Diversity Array with Enhanced PGx-8 v1.0 BeadChip can be customized to incorporate up to 175,000 custom bead types. The [DesignStudio™ Microarray Assay Designer](#) can be used to design targets such as SNPs, copy number variants (CNVs), and indels.

High-throughput workflow

The Infinium Global Diversity Array with Enhanced PGx-8 v1.0 BeadChip uses the proven Infinium 8-sample BeadChip format to enable laboratories to scale efficiently. For flexible throughput processing, the Infinium assay provides the capability to run up to 1728 samples per week using a single iScan® System. The Infinium assay provides a three-day workflow that allows users to gather and report data quickly (Figure 7).

Trusted high-quality assay

The Infinium Global Diversity Array with Enhanced PGx-8 v1.0 BeadChip uses trusted Infinium assay chemistry to deliver the same high-quality, reproducible data (Table 5) that Illumina genotyping arrays have provided for over a decade. In addition, the high signal-to-noise ratio of the individual genotyping calls from the Infinium assay provides access to genome-wide copy CNV calling.

Table 5: Data performance and spacing

| Data performance | Value ^a | Product specification ^b | |
|------------------|--------------------|------------------------------------|--------------------|
| Call rate | 99.7% | > 99.0% Avg | |
| Reproducibility | 99.99% | > 99.90% | |
| Spacing | | | |
| Spacing (kb) | Mean | Median | 90th% ^c |
| | 1.53 | 0.61 | 3.91 |

a. Values are derived from genotyping 2228 HapMap reference samples
 b. Excludes Y chromosome markers for female samples
 c. Based on results from GenTrain sample set

Summary

The high-density Infinium Global Diversity Array with Enhanced PGx-8 v1.0 BeadChip (Figure 8) provides a cost-effective solution for population-scale genetic studies, variant screening, and precision medicine research. The iScan System, Infinium assay technology, and integrated analysis software work together to create a versatile and comprehensive genotyping solution.

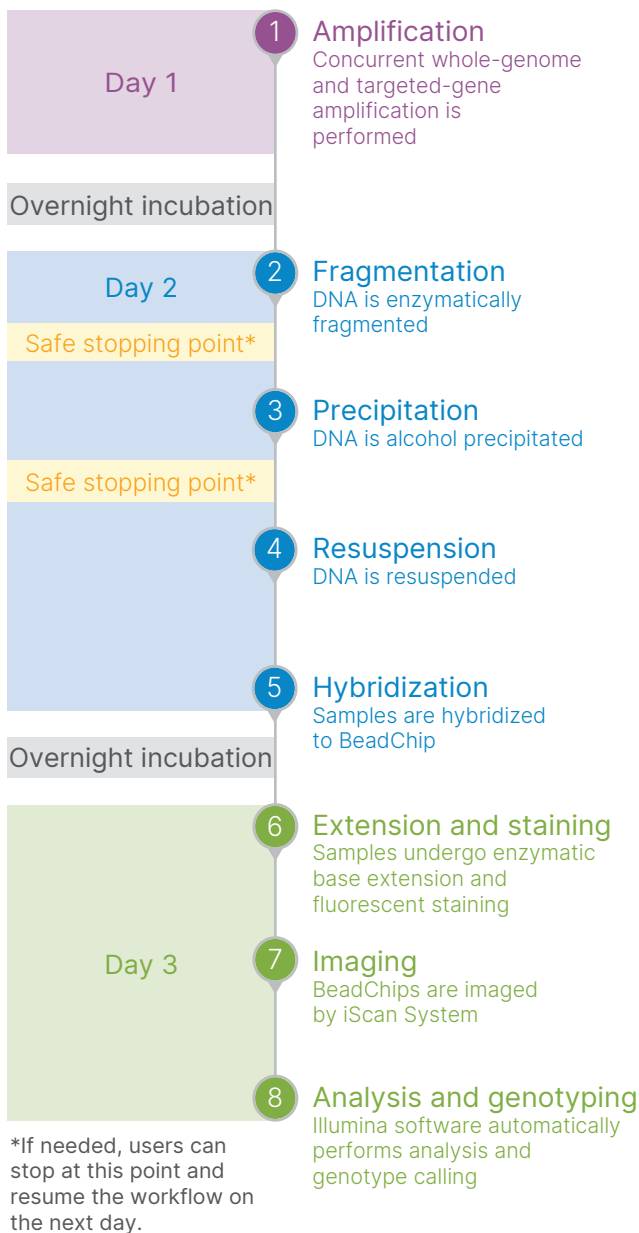


Figure 7: The Infinium eight-sample format workflow—The Infinium workflow provides a rapid three-day workflow with minimal hands-on time.

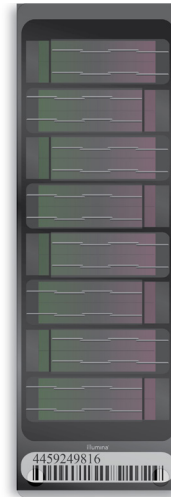


Figure 8: Infinium Global Diversity Array with Enhanced PGx-8 v1.0 BeadChip—Built on the trusted eight-sample Infinium platform.

Learn more

Pharmacogenomics. [Illumina.com/areas-of-interest/pharmacogenomics.html](https://www.illumina.com/areas-of-interest/pharmacogenomics.html)

Ordering information

Infinium Global Diversity Array with Enhanced PGx-8 v1.0 BeadChip, [Illumina.com/products/by-type/microarray-kits/infinium-global-diversity-pgx.html](https://www.illumina.com/products/by-type/microarray-kits/infinium-global-diversity-pgx.html)

| Infinium Global Diversity Array with Enhanced PGx-8 v1.0 | | |
|--|--|----------------|
| Catalog no. | Product | Add-on content |
| 20048873 | Infinium Global Diversity Array with Enhanced PGx + interpretation-8 v1.0 kit (48 samples) | No |
| 20048874 | Infinium Global Diversity Array with Enhanced PGx + interpretation-8 v1.0 Kit (384 samples) | No |
| 20048875 | Infinium Global Diversity Array with Enhanced PGx + interpretation-8 v1.0+ kit (48 samples) | Yes |
| 20048876 | Infinium Global Diversity Array with Enhanced PGx + interpretation 8 v1.0+ Kit (384 samples) | Yes |

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