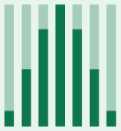
TWIST BIOSCIENCE

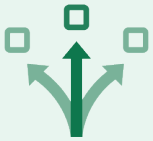
Twist NGS Target Enrichment Panels

Twist Bioscience provides a comprehensive selection of hybrid capture-based **targeted sequencing panels** designed for next-generation sequencing (NGS) platforms. Our portfolio includes **fixed panels**, predesigned for specific research areas, and **Alliance Panels**, developed in collaboration with industry leaders to address specialized applications. Twist also offers **custom target enrichment panels**, enabling you to design panels that target your specific genomic targets of interest.

ADVANTAGES



High performance
Double stranded probes offer exceptional on-target rates and uniform coverage.



Flexibility
Compatible with a wide range of sample inputs and sequencing platforms.

Customizability
Ability to modify or design bespoke panels.

DNA Sequencing Panels

Pairs with Twist's portfolio of DNA library preparation kits

GENOTYPING PANELS

Genotyping Panel – Human 600k

- Contains 594,275 probes targeted to 600,000 sites across the genome to key human variant locations
- Designed for human population genetics studies or pharmacogenomics research

VIRAL PANELS

Respiratory Virus Research Panel

- 41,047 probes covering viruses from six major viral clades
- Targeted against reference sequences for 29 common human respiratory viruses
- Able to detect viral loads as low as 100 viral genome copies

Comprehensive Viral Research Panel

- Over 1M unique probes target 3,153 viral genomes
- Capture ssDNA, dsDNA, dsRNA, and ssRNA viruses
- Long probes provide high mismatch tolerance for novel variant discovery

WHOLE EXOME PANELS

Exome 2.0

- Covers 36.5 Mb of human protein-coding and noncoding regions
- 99% of targets covered ≥20x

Exome 2.0 plus Comprehensive Exome Spike-in

- Combines full Exome 2.0 panel with an additional 1.14 Mb of content from ~20k probes spiked into Exome 2.0
- Improves coverage of key genes such as CFTR, TERT promoter, JAG1, and more

Human Comprehensive Exome

- Targets 36.8 Mb with a design size of only 41.2 Mb
- Covers greater than 99% coverage of protein-coding genes
- 99.3% of targeted regions covered at 20x with 5.3 Gb

Alliance CNTG Exome

- 41 Mb design provides highly uniform coverage of the entire exome as well as full coverage of the mitochondrial genome
- Demonstrated by Centogene to potentially increase diagnostic yield
- Covers a broad spectrum of disorders encompassing >7,000 rare diseases

Alliance VCGS v2 Exome

- 39.9 Mb exome panel with dedicated coverage boosting over clinically relevant genes that fall outside the gene coding regions traditionally targeted by exomes (i.e. known pathogenic loci in non-coding regions)
- Incorporates a backbone to the exome of probes covering SNPs in intergenic regions at approximately 25 kb intervals to improve copy number variation (CNV) calling

Alliance Clinical Research Exome

- Includes the content of Twist's original Core exome, adding coverage of the mitochondrial genome
- Contains additional validated coding and non-exonic regions of interest, such as the ACMG73 genes, supplemental coverage of regions from OMIM and COSMIC, and specific Broad Institute-defined targets

Alliance Canine Exome

- Contains more than 17k Genes/targets based on CanFam3.1, with additional coverage of genes/targets that are implicated in canine cancer
- Enables comparative genomic studies between canine and human genomes
- Covers coding exons of canine genes and includes regions of known importance in human cancers

EXOME SPIKE-IN PANELS

CNV Backbone Spike-in Panels (25 kb, 50 kb, or 100 kb)

- Improves read coverage with tiled probes to regions between genes (intergenic regions) at regular intervals across the genome, improving the signal for detecting CNV events
- Available in 100 kb (lower resolution), 50 kb (intermediate resolution), and 25 kb (higher resolution)
- Designed to pair with our best-in-class Exome 2.0 + Comprehensive Spike-in Panel

Alliance Diversity SNP Panel

- 640,000 probes covering 1.4M SNPs for incorporation into exome workflows
- Allows for imputation of most variants down to MAF of 0.1% or less
- Variation in different populations can be examined across European, East Asian, South Asian, Admixed American, and African ancestries

Mitochondrial Panel

- Designed to cover all 16,659 base pairs (bp) and 37 genes of the human mitochondrial genome
- Can be used as a standalone panel or as a spike-in with any other panel, including exome panels

APPLICATION SPECIFIC HUMAN DNA PANELS

Alliance CNTG Rare Disease Panel

- 78,800 probe panel covering 7.6 Mb of content
- Includes more than 2,500 relevant rare disease-associated genes and covers ≥99.5% of targeted regions

Alliance CNTG Hereditary Oncology Panel

- Includes 72 selected cancer-associated genes and covers ≥99.5% of targeted regions
- Can be used to identify genetic predisposition to hereditary tumors, including breast cancer, gastrointestinal tumors, Li-Fraumeni syndrome, MEN1, MEN2, paragangliomas, and others

Human Ancient DNA Panel

- Targets 1.35 million SNPs, including all 1.23 million polymorphic sites from Fu et al. Nature 2015
- Designed for analyzing genetic variations in ancient DNA specimens, typically derived from bones and teeth
- Significantly reduces sequencing costs compared to shotgun sequencing by highly enriching human DNA fragments, enabling genome-scale data

RNA Sequencing Panels

Pairs with Twist's RNA Library Preparation Kit

RNA Exome

- Targets 35.8 Mb bases, covering 19,708 genes and 63,215 transcript isoforms
- Includes "Exon-aware" probe designs for protein coding regions, fusions and isoforms
- Substantial increase in the number of detected coding genes with both FFPE and Universal Human Reference (UHR) RNA

Alliance CeGaT RNA Fusion Panel

- Targets 3 Mb, panel contains 7,394 probes covering 160 fusion-associated genes with 66 genes in the breakpoint design
- Fusion genes selected are associated with approximately 30 cancer types
- Capable of detecting both known and novel gene fusions

DNA Methylation Sequencing Panels

Pairs with the Twist NGS Methylation Detection System

Human Methylome Panel

- Targets 3.98M CpG sites across 123 Mb of genomic content related to biologically relevant methylation markers
- Identifies 84% (17,915,988) of the CpG islands in the genome

Alliance Pan-Cancer Methylation Panel

- 13,090 probe design to cover 31 cancer types and 47 disease entities
- Probes cover 126,000 CpG sites and ~12,000 differentially methylated regions

Long Read Sequencing Panels

Pairs with the Twist long read library preparation and Standard Hyb v2 protocol

Alliance Long-Read PGx Panel

- 2 Mb panel targets 49 PGx-related genes, including key genes such as CYP2D6, HLA-A, and HLA-B
- Focus on important genes in pharmacogenomics that are critical to drug metabolism and patient therapeutic response

Alliance Dark Genes Panel

- 20 Mb panel targets 389 genes, including GBA and SMN1/2
- Enables sequencing of genes that are difficult or impossible to fully sequence with short-read technology

Custom Sequencing Panels

Pairs with Twist DNA, RNA, and DNA methylation library preparation kits

Custom Panels

- Design a panel targeting your unique regions of interest - with as few as 100 or as many as 1 million probes
- Proprietary design algorithms and dedicated bioinformatics support enable the rapid design, synthesis, and optimization of your panel
- NGS-based quality control ensures balanced probe representation and minimal dropout from lot to lot

Not finding what you're looking for or have questions? Interested in discussing custom panel options? Contact us at **sales@twistbioscience.com**. For more information visit our website at **twistbioscience.com/ngs**