TWIST BIOSCIENCE

#WEMAKEDNA
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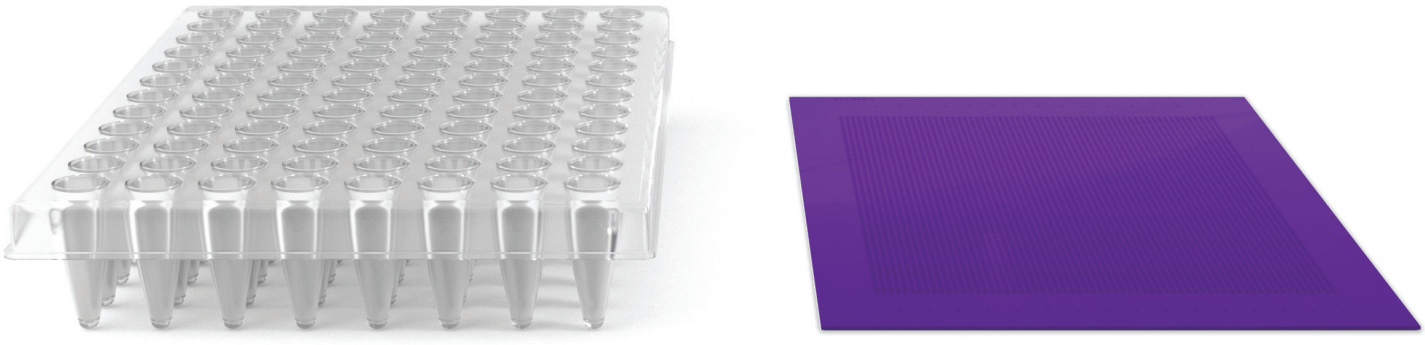
Writing the Future

GENES OLIGO POOLS LIBRARIES NGS



96 WELL PLATE
Makes 1 gene

TWIST SILICON PLATFORM
Makes 9,600 genes

#WeMakeDNA

At Twist Bioscience, we work in the service of customers who are changing the world for the better. In fields such as health care, agriculture, industrial chemicals, academic research and data storage, by using our synthetic DNA tools, our customers are developing ways to better lives and improve the sustainability of the planet. We believe that the faster our customers succeed, the better for all of us, and we believe Twist Bioscience is uniquely positioned to help accelerate their efforts.

HIGHLY SCALABLE DNA SYNTHESIS

Our technology is the first silicon-based DNA writing platform, enabling massively parallel synthesis of hundreds of thousands of unique oligo sequences per run. This technology accelerates the production of high quality synthetic biology and genomics tools at lower costs, speeding up discovery.

DESIGN ON A GRANDER SCALE

With more high performance tools at your fingertips, experimental designs can be expanded. Reexamine the intricacies of genetic pathways, genome editing, protein engineering and precision medicine with a new lens. With this new DNA synthesis platform, the full potential of synthetic biology and genomics is finally unleashed.

Twist Comprehensive Exome Panel

Great performance combined with the most comprehensive content

KEY BENEFITS

More Complete Coverage
- Covers 36.8 Mb of human protein coding regions
- Based on recent database releases

Retain Flexibility
- Easily spike-in content into comprehensive exome panel
- Effective across multiplex target enrichment workflows

Design Efficiency
- The panel targets 36.8 Mb with a design size of only 41.2 Mb
- Smaller design size reduces sequencing costs

Exome sequencing has become a widely used practice in clinics and diagnostics. The superior performance of the Twist Human Core Exome provides the optimal solution for sequencing of protein coding genes, while focusing on the most accurate curated subset—CCDS database. Twist now offers the Twist Comprehensive Exome Panel, expanding the content of the Twist Human Core Exome to offer coverage of greater than 99% of protein coding genes.

Increase Confidence in Your Variant Detection Experiments

Gene definitions are constantly being updated by dedicated consortia such as GENCODE, based on new information from large scale experiments. Thus, panels based on definitions from even several years ago may be missing a considerable portion of genes, and conversely may include some outdated sequences.

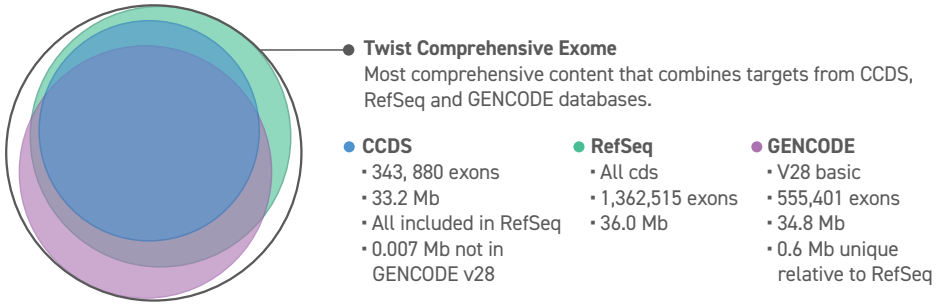


Figure 1. The composition of the Twist Comprehensive Exome panel shows best-in-class coverage at >99% of RefSeq, CCDS, and GENCODE databases.

The Comprehensive Exome Panel targets 36.8 Mb of human protein coding genes, (Figure 1) covering >99% of RefSeq, CCDS, and GENCODE databases. This is best in class coverage of the most up-to-date content, when compared to competitive products (Table 1).

Twist Custom Blended Panels

Custom blended panels with NGS QC for reliable performance

KEY BENEFITS

Exceptional, Consistent Performance

- Effective design, accurate synthesis, and detailed quality control maximize both capture uniformity and reproducibility
- High-fidelity double-stranded DNA probes offer high-quality, consistent performance

Tunable Coverage

- Adjustable coverage of ingredient panels without sacrificing performance
- Fast turnaround time to final panel

Blended Panels with NGS QC

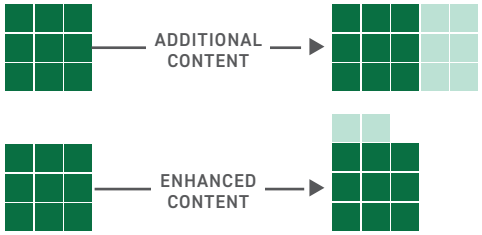
- In-house blending of the panel before shipment, thus preventing blending overburden
- NGS-based quality control of all probes ensures balanced probe representation and minimizes dropout

Twist Custom Blended Panels can be designed to cover a wide range of panel sizes, ratios, target regions, and multiplexing requirements — all with exceptional and consistent performance following our NGS quality control. Whether you design your own panel from scratch or add targets to enhance the content of existing panels, you can use your Custom Blended Panels with Twist's modular library preparation kits or seamlessly integrate them into an existing workflow.

CUSTOM PANELS	TWIST	COMPETITOR 1	COMPETITOR 2
Custom probes optimized for any size	X	X	X
Cater to custom production scales	X	X	X
NGS QC of panel	X	X	–
Pre-blend multiple panels	X	–	–

Table 1. Create custom panels with confidence by taking advantage of Twist's NGS quality control. We will also pre-blend multiple panels for you, saving you time and guaranteeing high-quality performance

Adding the additional content can be done in two ways:



Add or enhance Twist Custom Panel content. Adding content to the Twist Human Core Exome or Custom Panels increases the number of targets covered. Enhancing content augments the coverage of specific regions within your core panel.

Figure 1. Add additional content to existing panels to increase coverage or enhance existing content to boost coverage 0.1x–10x against the baseline.

By working with Twist Bioscience, not only will your panel contain scalable, optimized custom probes, but it will also pass our NGS quality control step. We can pre-blend multiple panels for you, saving you time while guaranteeing high-quality performance and analysis. We test for fidelity of the data as it comes out of the sequencers so you can rest assured that it is of high quality and aligns with what you expect.

EXOME (33.1 Mb) + CUSTOM PANEL (0.12 Mb)
2.8 Gb SEQUENCING/SAMPLE

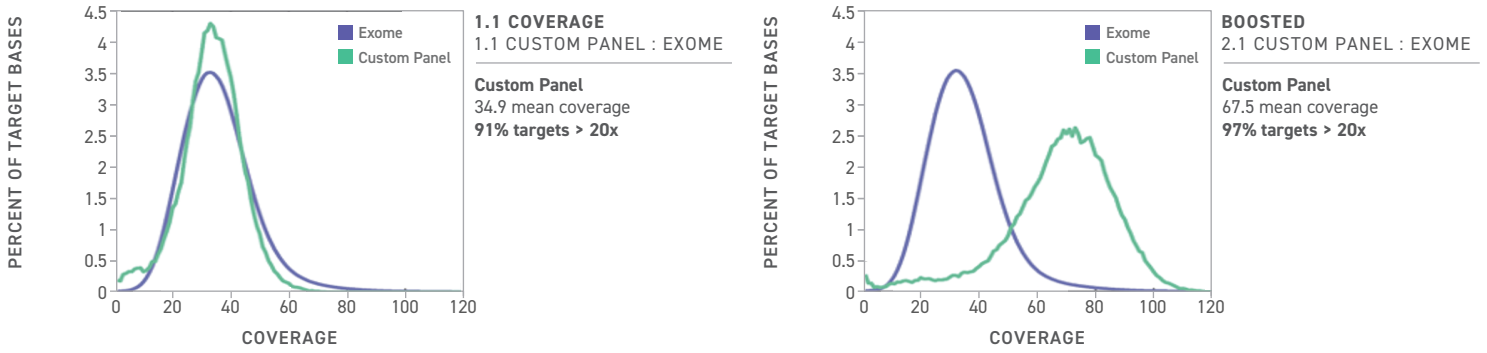


Figure 2. Blend multiple panels at the desired ratio to take advantage of tunable coverage. Boosted panels show performance of spike-ins and offer great performance for a wide range of coverage possibilities.

Twist Mitochondrial Panel

The mitochondrial genome encodes factors critical to energy production, which directly affects the energy state of the cell, tissue, and human individual. Pathogenic mutations of Mitochondrial DNA (mtDNA) are often implicated in a group of complex human diseases which can be difficult to diagnose such as metabolic & neurologic disorders as well as cancer. Interrogation of the human mitochondrial genome by targeted Next-Generation Sequencing (NGS) can help investigators shed light on the genetic mechanism behind mitochondrial disorders.

The Twist Mitochondrial Panel is a fixed content panel designed to cover all 16,659 base pairs (bp) and 37 genes of the mitochondrial genome (Table 1). This panel can be used as a standalone panel or as a spike-in with Twist's Human Core Exome, Comprehensive Exome as well as Twist's Custom Panels. Providing industry-leading coverage, uniformity, and flexibility, the Twist Mitochondrial Panel can help investigators enrich for, sequence, and analyze mtDNA variants contributing to disease including incidences of heteroplasmy.

Revolutionizing Target Enrichment

A critical component for successful targeted sequencing analysis is the quality of the capture reaction, which drives the uniformity of reads. A more uniform capture leads to more uniform sequencing, as indicated by lower fold80 base penalty scores. With higher uniformity, sequencing reads can effectively drive on target coverage, limiting wasted reads.

High uniformity is the combined result of the probe design algorithm, silicon-based synthesis of dsDNA probes, and calibration processes that ensure uniform amplification, GC content, and enrichment performance across all targets. NGS-based quality control of all Twist Panels ensures that all probes are present at the correct concentrations and that the reproducibility of results is independent of our production processes.

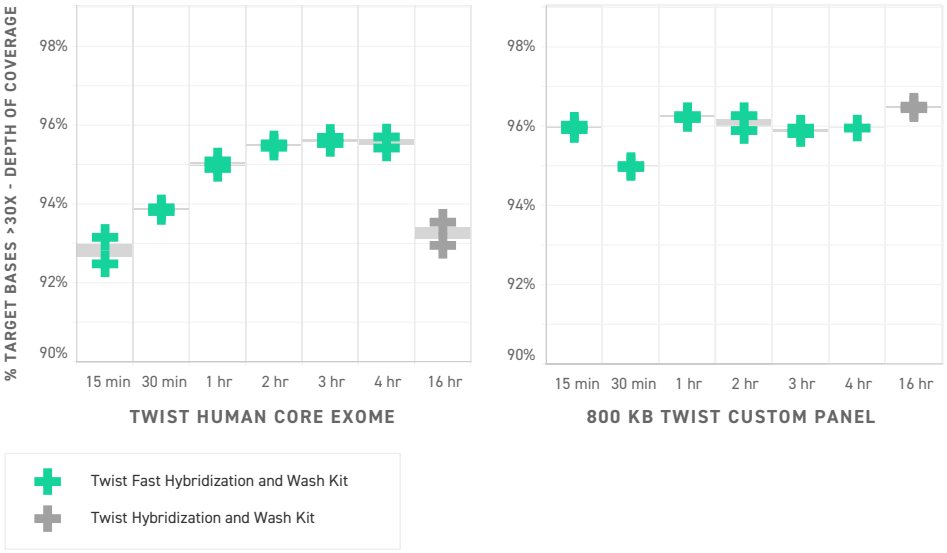
HUMAN MITOCHONDRIAL GENOME	
Bait Territory	16447
Design Efficiency	1.00
Mean Target Coverage	105
% Duplicates	0.01%
Uniformity (Fold-80 Base Penalty)	1.20
% TARGETED BASES AT	
10X	100%
20X	100%
30X	99.56%

Table 1. Twist Mitochondrial panel spiked into Twist Core Exome. Data obtained with 2.3 Mb (150X) sequencing. Complete coverage with excellent uniformity and sequencing efficiency is demonstrated.

Twist Fast Hybridization and Wash Kit

Choose to take your sample to the sequencer in a single day

NGS TARGET ENRICHMENT SOLUTIONS | TWIST BIOSCIENCE

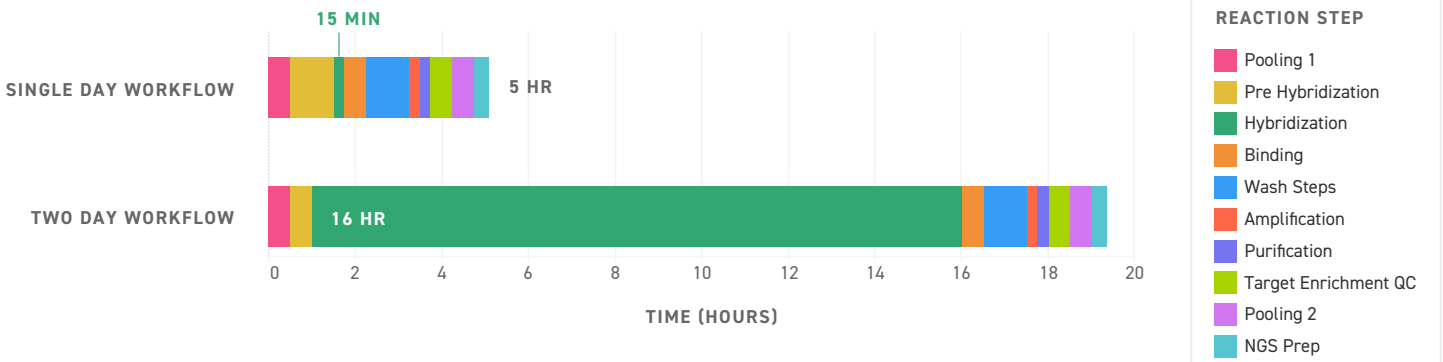


Depth of coverage achieved (% target bases at 30x) with various hybridization times. Genomic DNA (NA12878, Corriell) was hybridized and captured using either the Twist Human Core Exome (33.1 Mb) or an 800 kb Twist Custom Panel. Following sequencing, Picard HS_Metric tools (Pct_Target_Bases_30X) with default values were used for sequence analysis. Data were downsampled to 150x raw coverage of targeted bases for evaluation. Note that with both panels a 15-minute hybridization in Twist Fast Hybridization Solution produces an equivalent performance to the 16-hour hybridization using the standard Twist Hybridization and Wash Kit, and increasing hybridization times improves performance over the standard protocol.

Rapid, Streamlined, and Automatable Workflow

Twist has engineered the Fast Hybridization Solution to provide the excellent performance of its standard protocol in as little as 15 minutes. This quick hybridization is accompanied by a streamlined target enrichment workflow that can be completed in 5–8 hours (including time for library preparation), taking you from sample to sequencer within the same day.

The Fast Hybridization Solution workflow involves a single-tube dry-down and is fully automatable to accommodate high-throughput applications.



Twist Fast Hybridization Solution is a component of a streamlined target enrichment workflow that can be completed in as little as 5 hours.

NGS Methylation Detection System

Unparalleled efficiency in NGS methylation profiling

KEY HIGHLIGHTS

An end-to-end solution

- Convert unmethylated cytosines using a state-of-the-art, enzymatic process
- Capture with high-performance Twist probes and optimized reagents

Innovative library preparation

- Easily dropped into existing bisulfite sequencing analysis pipelines
- Superior mapping efficiency, GC uniformity, and sequencing metrics
- Detects 15% more CpGs than bisulfite method
- Less sample damage enables challenging sample inputs

Highly efficient Custom Panels*

- Sophisticated design, accurate synthesis, and detailed QC maximize capture uniformity and reproducibility
- Outstanding performance across panel sizes, target regions, and multiplexing requirements
- Easily add or enhance panel content

Optimized hybridization reagents

- Adjust hybridization timing without sacrificing performance
- Improved on-target rates with Methylation Enhancer

NEBNext® EM-seq™ Kit for Twist Targeted Methylation Sequencing

In partnership with New England Biolabs (NEB®), Twist Bioscience offers a new methylation sequencing workflow that improves the quality of libraries and removes the need for damaging bisulfite treatment during prep. The workflow features enzymatic conversion of unmethylated cytosines (Figure 1) to identify sites of 5-methyl-cytosine (5mC) and 5-hydroxymethyl-cytosine (5hmC).

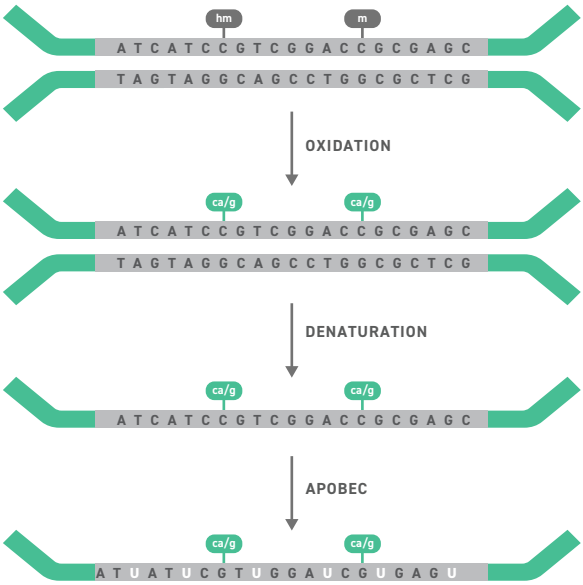
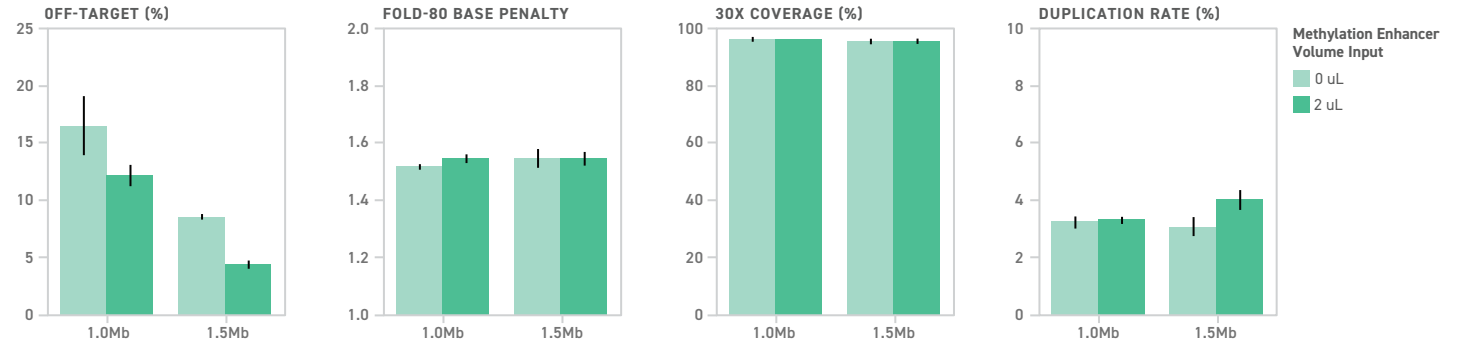


Figure 1. EM-seq conversion involves a series of enzymatic reactions to identify unmethylated cytosines. During the first reaction, ten-eleven translocation dioxygenase 2 (TET2) converts methylated cytosines (5mC and 5hmC) to 5-carboxycytosine (5caC) and the Oxidation Enhancer glucosylates 5hmC (5ghmC). These reactions protect 5mC and 5hmC from downstream deamination. The DNA is then denatured before APOBEC deaminates cytosines to uracils. Subsequent PCR amplification converts the modified 5mC or 5hmC into cytosines and uracils into thymines. After PCR, nucleotide representation is the same as observed for bisulfite converted DNA, making EM-seq compatible with existing analysis pipelines, for example Bismark and bwa-meth.



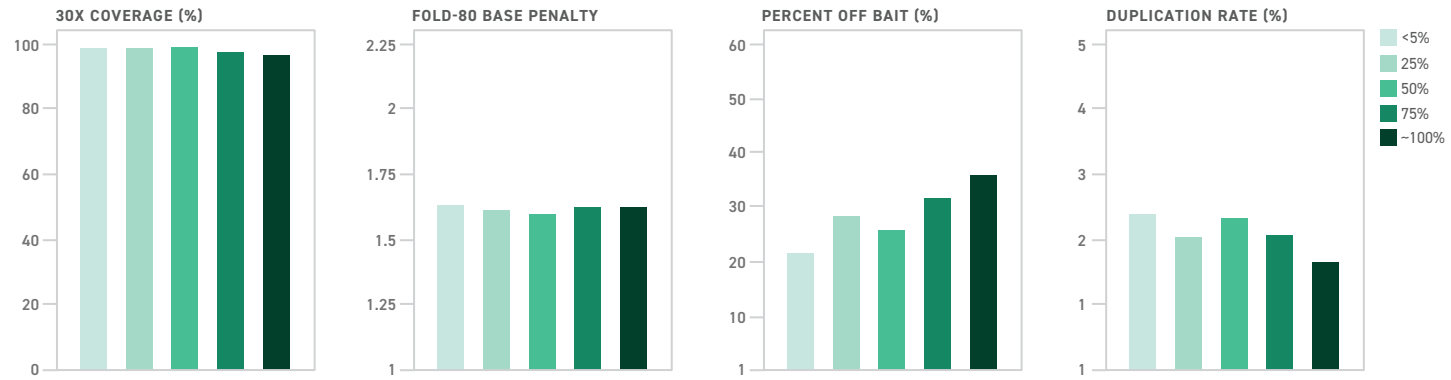


Figure 3. Detection of DMRs. The Twist Methylation Detection System efficiently captures differentially methylated regions of input DNA from 0 to 100% methylation, with minimal or no impact on sequencing metrics, including 30x coverage and uniformity (fold-80 base penalty).

Twist Comprehensive Viral Research Panel

Twist target enrichment solution for broad identification of novel & highly evolved viruses

KEY BENEFITS

Screen over 3,100 viral genomes in a single sample

- Contains over 1M unique probes to screen for 3,153 viral human and non-human pathogens
- Designed using sequences compiled from viral genomes across RefSeq, FluDB & VIPRdb databases
- Represents all viral families containing at least one virus known to infect humans

Detect & characterize novel viral species

- Enables surveillance of divergent viral species from environmental and human samples
- Differentiates between several viruses that may lead to similar symptoms

Co-infection detection of diverse viral species

- Designed to detect multiple viruses/ strains with a single capture

Complete end-to-end solution using One Codex software

- Publication-ready report generation containing viral species identification and percent of genetic makeup

The frequent emergence of novel viral pathogens with pandemic potential highlights the need for improved methods for detecting and surveilling novel pathogens. Unlike sequence-dependent approaches like qPCR, next-generation sequencing (NGS) can be used to identify viruses without existing sequence knowledge. Existing target enrichment panels substantially increase the analytical sensitivity of NGS for this purpose, but comprehensive panels for unbiased virus identification are lacking. Filling this unmet need, the Twist Comprehensive Viral Research Panel allows researchers to quickly capture and sequence unknown pathogens and highly divergent viral strains.

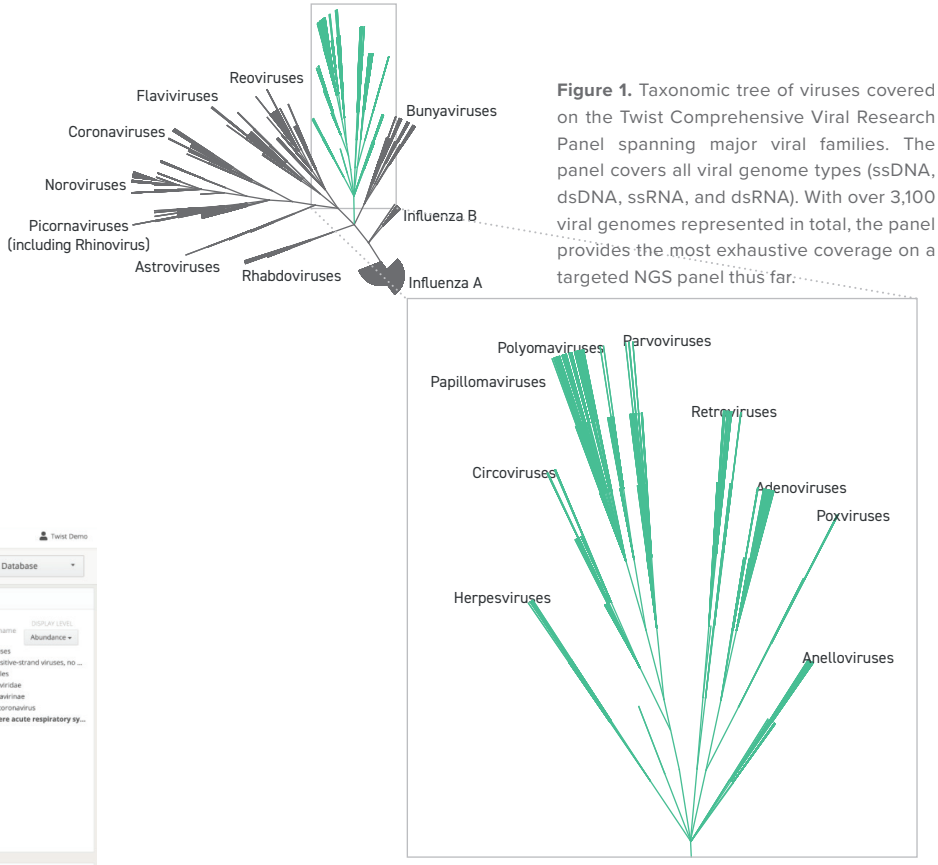
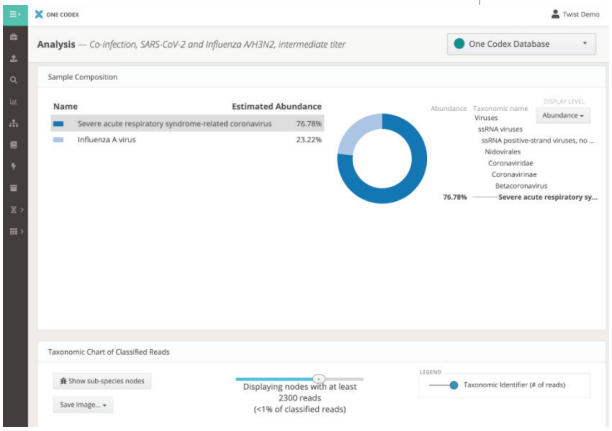


Figure 1. Taxonomic tree of viruses covered on the Twist Comprehensive Viral Research Panel spanning major viral families. The panel covers all viral genome types (ssDNA, dsDNA, ssRNA, and dsRNA). With over 3,100 viral genomes represented in total, the panel provides the most exhaustive coverage on a targeted NGS panel thus far.



One Codex user interface showing analysis results from the Twist Comprehensive Viral Research Panel

Twist Respiratory Virus Research Panel

Twist NGS target enrichment panel for accurate identification of respiratory viruses beyond SARS-CoV-2

KEY BENEFITS

Highly sensitive viral identification
- Detection of as little as 100 copies of viral material per virus

Detection of various respiratory pathogens in one sample
- Separate COVID-19 symptoms from those of other respiratory illnesses

Covers a comprehensive range of respiratory pathogens
- 41,047 probes covering viruses from six major viral clades
- At least 4x tiling in probe coverage for each species

Environmental surveillance
- Monitor viral transmission and evolution to enhance public health response

Analysis by One Codex
- Generate reports with viral species identification
- Get publication-ready visualizations

The COVID-19 pandemic has led to a rapid and collaborative response from the scientific community. Research teams are in need of reliable genomic tools to characterize samples including viral co-infections. SARS-CoV-2 infection leads to a range of symptoms that can vary drastically between subjects. This makes it hard to determine if those symptoms are strictly SARS-CoV-2-related, the result of a different respiratory pathogen(s), or a combination of the two. The Twist Respiratory Virus Research Panel makes detecting a comprehensive range of pathogens possible, allowing researchers to not only accurately detect the cause(s) of a subject's symptoms, but to also characterize the responsible viral pathogens.

Comprehensive Detection of Respiratory Pathogens

The Twist Respiratory Virus Research Panel was designed from the reference sequences for 29 common human respiratory viruses, including coronaviruses (CoV), influenza virus, adenoviruses, bocavirus (hBoV), enterovirus, metapneumovirus, parainfluenza viruses (hPIV), human rhinoviruses (HRV), measles morbillivirus (MeV), mumps virus (MuV), rubella virus, and respiratory syncytial virus (RSV) (Figure 1, Table 1), with at least 4x tiling in probe coverage for each viral species. Additional probes were designed to incorporate diversity from 77 additional rhinovirus strains, and to target diverse genomes representing each major influenza A and B outbreak since the year 2000 including the H1N1pdm09 virus which is the cause of 2009 H1N1 Pandemic.

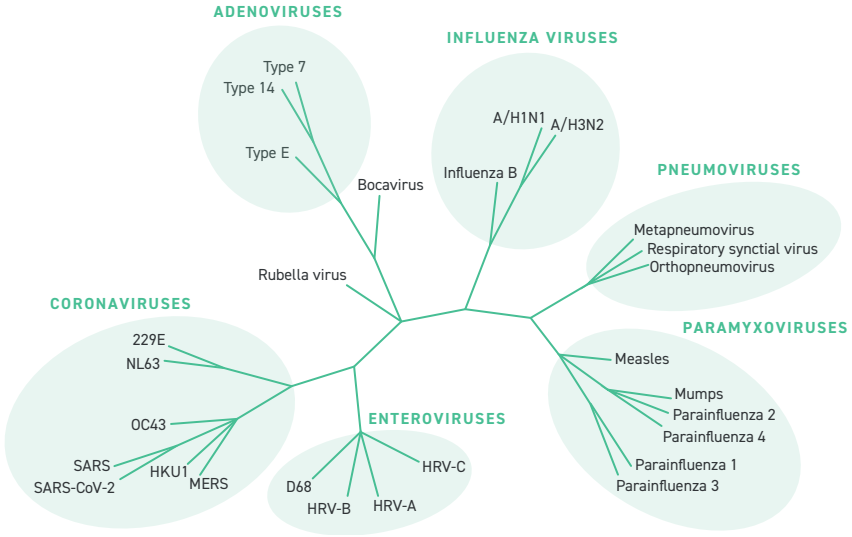


Figure 1. Taxonomic tree of viruses covered on the Twist Respiratory Virus Research Panel spanning the major respiratory viral clades.

Twist Pan-Viral Panel

Confident identification of over 1,000 viral human pathogens from a single sample

KEY BENEFITS

Screen for Over 1,000 Viral Genomes in a Single Sample

- Contains over 600,000 probes to screen for over 1,000 viral human pathogens
- Sequences compiled from RefSeq; known to affect humans

Increase Accuracy and Sensitivity of Detection

- NGS-based quality control of the probe library ensures high uniformity
- High capture efficiency for sensitive, specific NGS-based identification
- Circumvents the problem of low levels of virus within high levels of host genetic material

Save Time and Money

- Eliminates the need for costly, time-consuming PCR-based amplification or transcriptome-based sequencing approaches
- Expedites diagnosis and simplifies tracking of emerging viral infections

Next-generation sequencing (NGS) offers high-throughput, specific identification of infections in blood samples. In the case of viral infections, however, obtaining genetic material sufficient for sequencing can be a challenge due to the extremely low levels of virus often present. In these situations, target enrichment — which uses DNA-based hybridization probes to isolate specific sequences out of a mixed genomic sample — can increase the sensitivity and specificity of NGS-based efforts.

The Twist Pan-Viral Panel contains over 600,000 probes for the targeted enrichment of over 1,000 viral human pathogens from a single sample. It offers a simplified, efficient, and accurate method for screening patient samples to both improve diagnosis and track emerging viral infections.

Comprehensive, Curated Content

Compiled from the RefSeq database, the probe sequences in the Twist Pan-Viral Panel are complementary to viral sequences known to be associated with human infectious disease. The panel enables enrichment of these viral sequences for high-resolution NGS leading to high-sensitivity detection and confident identification of viral infections.

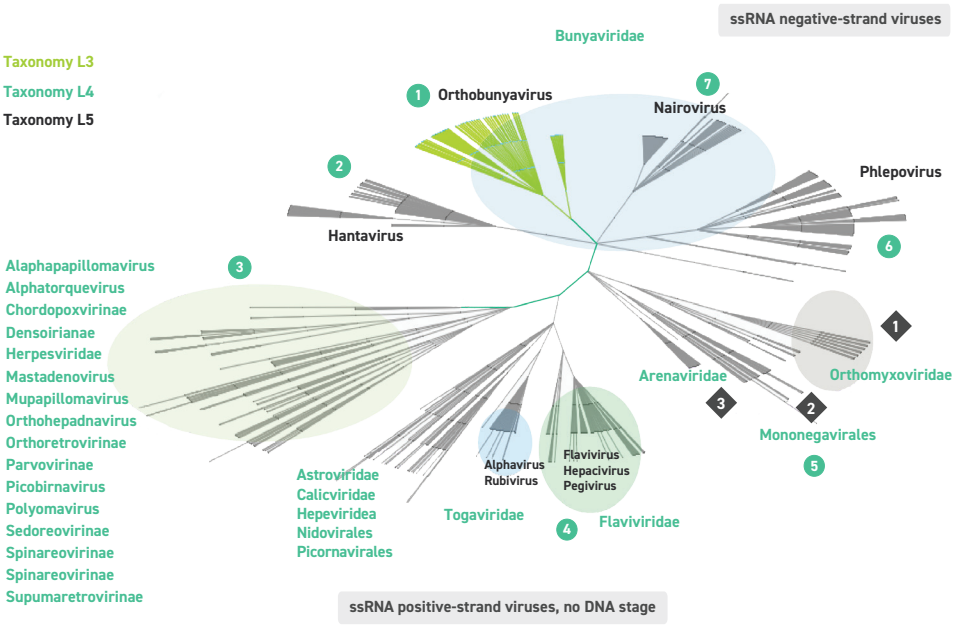


Figure 1. Phylogenetic tree depicting the Twist Pan-Viral Panel probe composition. The Pan-Viral Panel was developed in a joint effort between Twist Bioscience®, Illumina®, and U.S. Army Medical Research Institute of Infectious Diseases (USAMRIID). This map shows the general diversity of the over 1,000 genomes represented.

Twist Synthetic SARS-CoV-2 RNA Controls

The recent Coronavirus pandemic has led to the unprecedented need for diagnostic tests for detecting the presence of the SARS-CoV-2 virus in a variety of sample types. To address this need, laboratories around the world need high quality tools to enable them in catering to this rapidly expanding requirement for testing.

KEY HIGHLIGHTS

- Fully synthetic RNA generated from Twist Gene Fragments
- >99.9% viral genome coverage
- NGS sequence verified
- Positive control for both RT-PCR and NGS-based assays

SPECIFICATIONS

Standard Controls

- Biosafety: Level 1
- Storage Temperature: -70°C to -90°C
- Specification Range: Approximately $1x10^6$ copies/µL
- Physical State: Frozen liquid

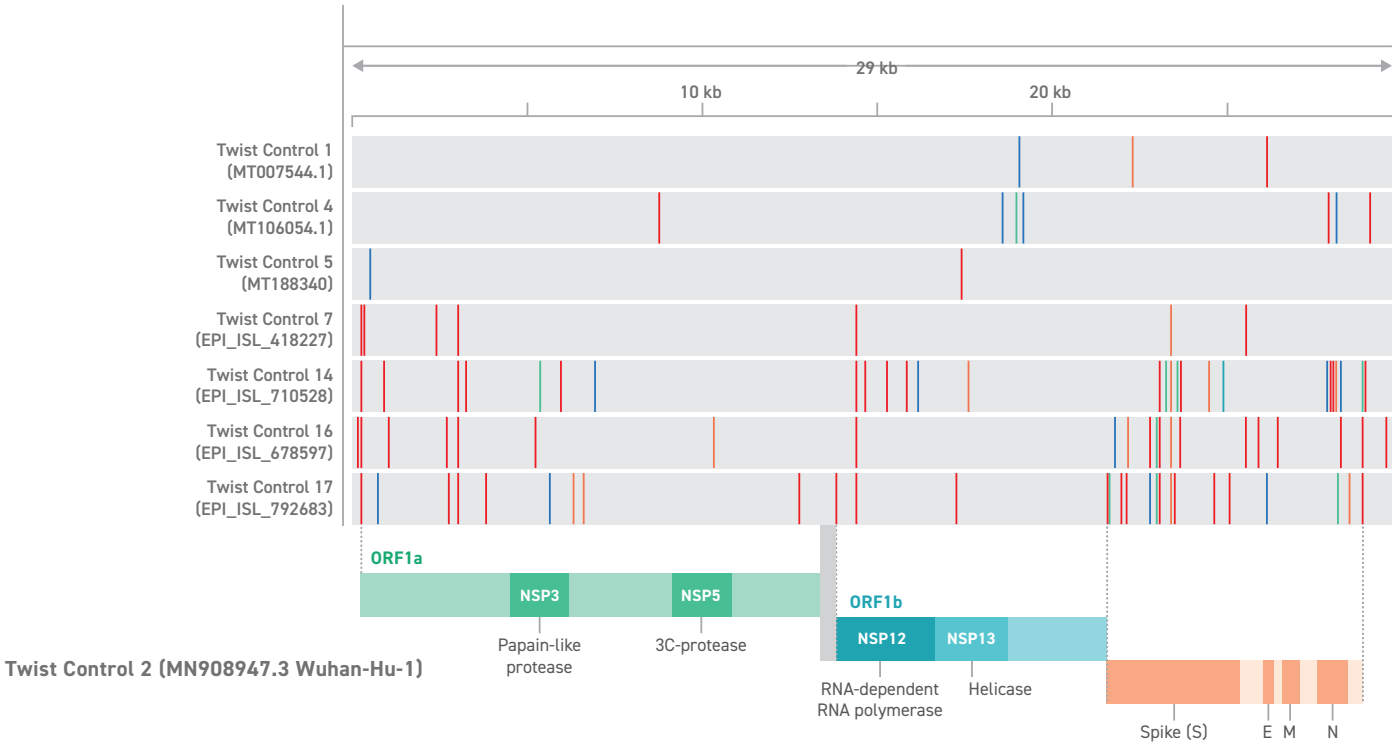
Assay Ready Controls

- Biosafety: Level 1
- Storage Temperature: -20°C
- Specification Range: Approximately $2x10^6$ copies/tube
- Physical State: Dried pellet

Positive controls provide quality control measures for a wide range of applications from diagnostic assay development to day-to-day testing including the verification and validation of diagnostic tests of both next-generation sequencing (NGS) and reverse transcription polymerase chain reaction (RT-PCR) assays. Synthetic viral controls are a powerful alternative to “live virus” controls which are viral nucleic acids extracted from either an infected patient or from live virus propagated in cell culture. Synthetic controls created through gene synthesis broaden access across diverse strains while mitigating safety and security concerns.

The Twist Synthetic SARS-CoV-2 RNA controls consist of six non-overlapping 5 kb fragments generated from Twist Gene Fragments then transcribed into ssRNA. These provide coverage of greater than 99.9% of the bases of the viral genome. Standard Controls are supplied in 100 µL at a concentration of approximately one million copies per microliter. Twist also offers certain controls in an Assay Ready Format that are supplied as a desiccated pellet. The Assay Ready Controls are supplied at approximately two million copies per tube.

For the most up to date listing see the Twist Synthetic RNA Controls Product Listing at twistbioscience.com.



Genome browser view showing the nucleotide variations among the select isolates (all isolates not shown). Seven of the strains were mapped to the reference isolate (MN908947.3). The colored lines indicate SNPs where Red is a “T”, Orange is a “G”, Green is an “A” and Blue is a “C”. The box diagram overlays the approximate location of the SNPs on top of the ORF/Gene structure of the virus. The Twist Controls 14, 16, and 17 represent the B.1.1.7, B.1.351 and P.1 variants respectively.

Twist Respiratory Virus Controls

Synthetic viral controls covering a broad range of human respiratory viruses

KEY HIGHLIGHTS

- Positive controls compatible for both qPCR and NGS-based assays, can be used as negative controls for routine SARS-CoV-2 assays.
- Can be useful in the identification of pathogens with similar symptoms, like SARS-CoV-2
- Cover a broad range of respiratory viruses, with similar content captured by the Twist Respiratory Virus Panel
- Fully synthetic RNA & DNA generated from Twist gene fragments
- >99.9% viral genome coverage
- NGS sequence verified

Research into human respiratory viruses has become a focal point with the advent of the SARS-CoV-2 pandemic. Respiratory viruses such as influenza viruses, rhinoviruses and coronaviruses often overlap symptomatically. It is therefore critical to distinguish between infectious agents driving a pandemic, such as SARS-CoV-2, and other viruses. It is also important to understand the source of the viral infection, and the subtleties of key variants that cause infectious diseases. The Twist Respiratory Virus Controls enable investigation into the biology of a broad range of viruses by NGS and qPCR. Included in the panel is a range of variants with comprehensive coverage of full length synthetic virus sequences, enabling distinction between key infectious agents.

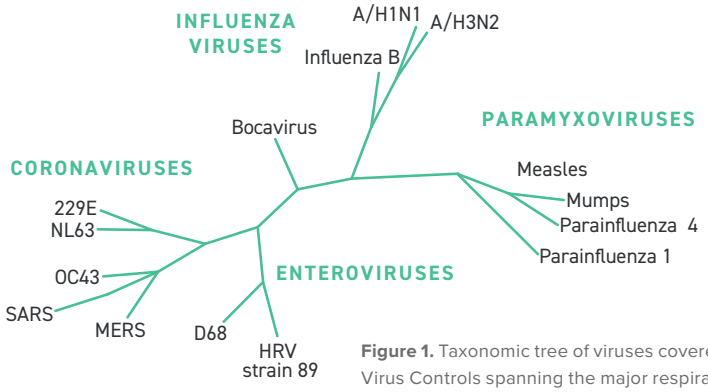


Figure 1. Taxonomic tree of viruses covered on the Twist Respiratory Virus Controls spanning the major respiratory viral clades.

PART NUMBER	NAME	ACCESSION	VIRUS TYPE	LENGTH (BASES)
103001	Twist Synthetic Influenza H1N1 (2009) RNA control	NC_026431, NC_026432, NC_026433, NC_026434, NC_026435, NC_026436, NC_026437, NC_026438	ssRNA (- sense)	13158
103002	Twist Synthetic Influenza H3N2 RNA control	NC_007366, NC_007367, NC_007368, NC_007369, NC_007370, NC_007371, NC_007372, NC_007373	ssRNA (- sense)	13627
103003	Twist Synthetic Influenza B RNA control	NC_002204, NC_002205, NC_002206, NC_002207, NC_002208, NC_002209, NC_002210, NC_002211	ssRNA (- sense)	14452
103004	Twist Synthetic Human bocavirus 1 DNA control	MG953830.1	ssDNA	5164
103005	Twist Synthetic Human enterovirus 68 RNA control	NC_038308.1	ssRNA (+ sense)	7367
103006	Twist Synthetic Human rhinovirus 89 RNA control	NC_001617.1	ssRNA (+ sense)	7152
103007	Twist Synthetic Mumps virus RNA control	NC_002200.1	ssRNA (- sense)	15384
103008	Twist Synthetic Human parainfluenza virus 1 RNA control	NC_003461.1	ssRNA (- sense)	15600
103009	Twist Synthetic Measles virus RNA control	NC_001498.1	ssRNA (- sense)	15894
103010	Twist Synthetic Human parainfluenza virus 4 RNA control	NC_021928.1	ssRNA (- sense)	17052
103011	Twist Synthetic Human coronavirus 229E RNA control	NC_002645.1	ssRNA (+ sense)	27317
103012	Twist Synthetic Human coronavirus NL63 RNA control	NC_005831.2	ssRNA (+ sense)	27553
103013	Twist Synthetic Human coronavirus OC43 RNA control	NC_006213.1	ssRNA (+ sense)	30741
103730	Twist Respiratory Virus Controls (13 Count)	N/A	N/A	N/A

Table 1. Virus name GenBank IDs, virus type, and length for each virus included in the Twist Respiratory Virus Controls.

Clonal Genes

Twist Bioscience is transforming gene synthesis, a process at the core of synthetic and molecular biology. Our silicon-based DNA writing platform significantly increases gene synthesis throughput and scalability, while also reducing turnaround time and price per base. Twist's Clonal Genes offering gives you the flexibility to get the DNA you want, the way you want it. Choose the amount of DNA, and the format you want it in to drive your research. Because every clonal gene is NGS-verified, you can be sure you're getting the perfect cloned gene every time.

Think on a new scale in your gene designs and accelerate your discoveries.

SPECIFICATIONS

- 0.3–5.0 kb cloned into a Twist Vector or your vector of choice
- 100% accurate NGS-verified gene sequences
- DNA mass options:
  - 50 ng–2 µg
  - 2–10 µg
  - 10–100 µg
  - 100 µg–1 mg

KEY BENEFITS

Your Sequence, Your Way

You choose:

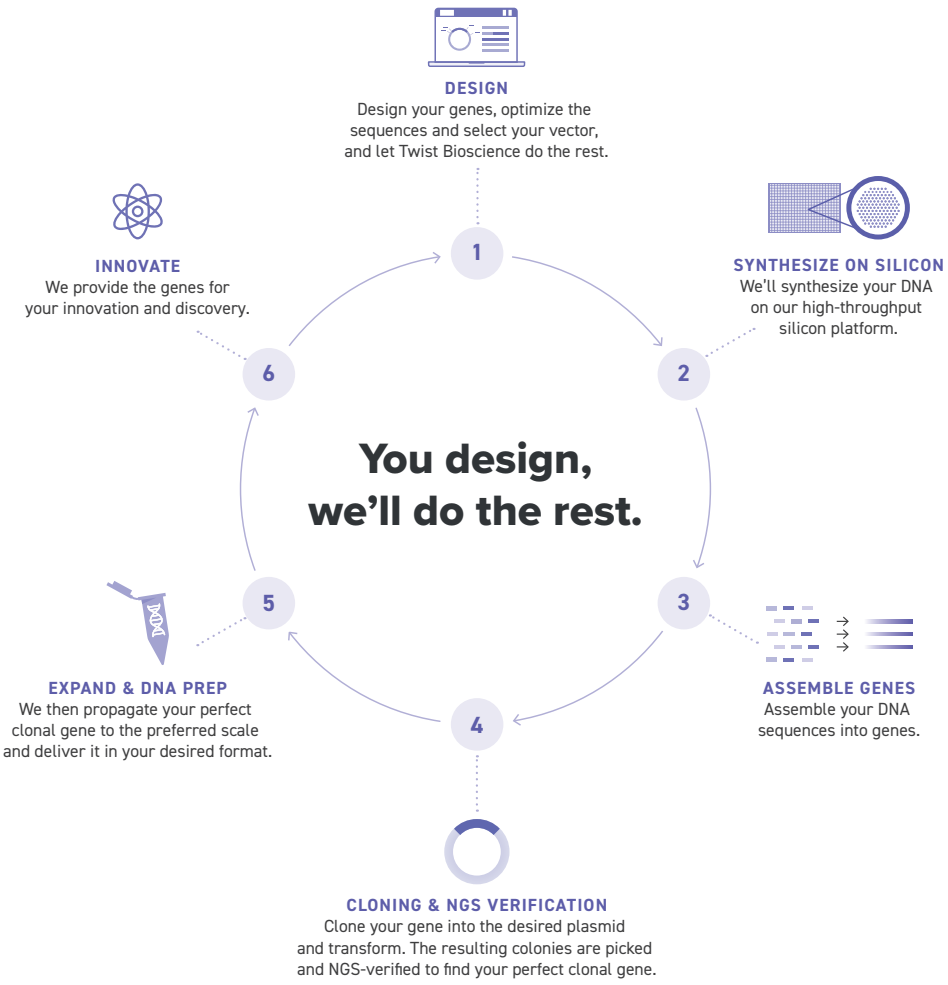
- Mass range
- Normalized concentration
- Suspension buffer
- Plasmid vector
- Insertion site
- Transfection grade or endotoxin free
- Shipping format (to add glycerol stocks or not)
- Add glycerol stocks

Rapid Turnaround Time

- From 11 business days

Scalable Synthesis

- No minimum order size
- Same turnaround regardless of order size



Twist Gene Fragments

Synthetic Gene Fragments are an inexpensive, rapid, and efficient way to build the genes you need for your research. Twist's silicon-based, high-precision DNA synthesis platform results in higher quality genes and significantly increased throughput and scalability.

Twist Gene Fragments improve your cloning process by minimizing colony screening. This allows you to save time and money by dramatically reducing cloning and sequencing costs. Think bigger, design on a grander scale, and accelerate your discoveries.

SPECIFICATIONS

- Double-stranded DNA
- Length: 0.3 – 1.8 kb
- Scale: 100 ng – 1 µg
- Ships in 6 to 9 business days
  - With adapters,
  - Without adapters,

KEY BENEFITS

Screen Less, Discover More

- Industry leading error rate
- Reduced cloning costs

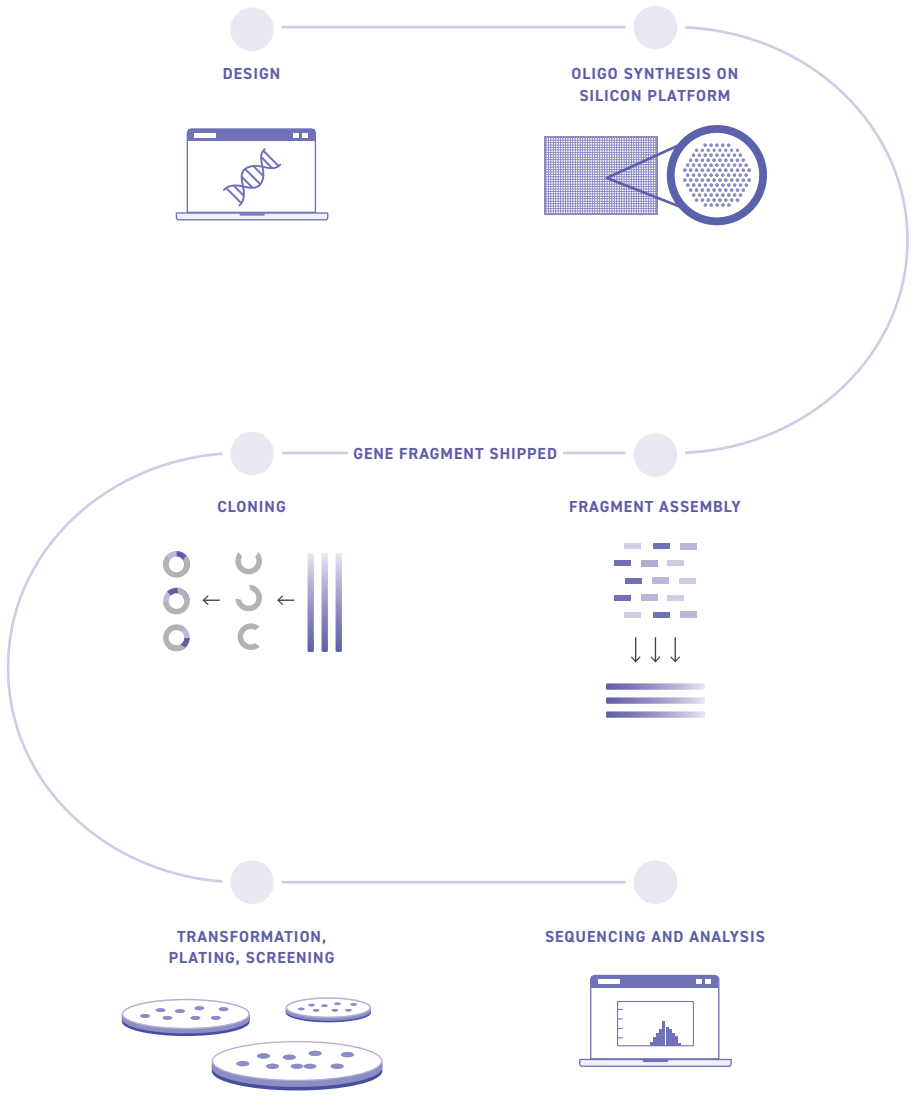
Think Bigger on a Budget

- No order limit
- Fixed price per base pair regardless of length

Your DNA, Your Way

- Easily assemble into larger genes or pathways
- Compatible with all downstream cloning methods
- Available with and without adapters

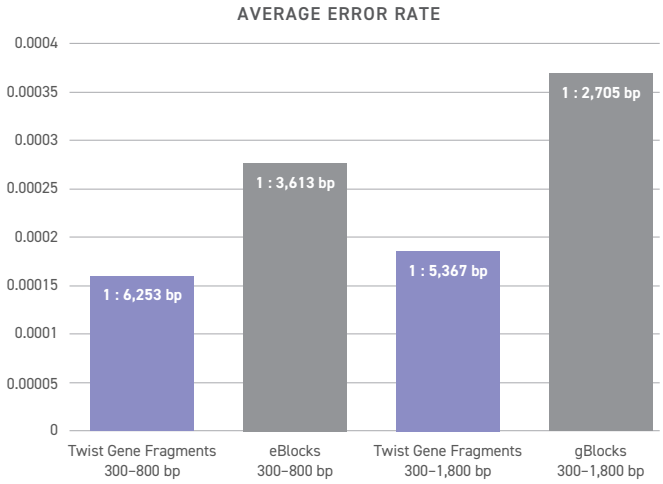
Design. Build. Test.



Industry Leading Error Rates

Twist Bioscience® utilizes its industry-leading production process to deliver quality Gene Fragments quickly, reliably, and affordably. Gene Fragments begin as oligonucleotides synthesized on Twist Bioscience's proven semiconductor-based silicon platform. The oligonucleotides are then annealed together, PCR amplified to produce a double-stranded DNA fragment and error-corrected through an enzymatic reaction. The resulting product is a ready-to-use Gene Fragment that is compatible with many applications.

To assess the quality of Twist Gene Fragments, identical dsDNA fragments from 300 bp to 1,800 bp in length were ordered from Twist and ordered from Integrated DNA Technologies, Inc. (IDT). Upon receipt of the fragments from each company, the DNA was cloned into pTwist Amp High Copy plasmid, transformed into DH10B-like cells, and plated onto LB Agar Plates with 100 µg/mL Carbenicillin. After overnight incubation at 37° C, 20 colonies were selected for each gene and sequence-verified using Next-Generation Sequencing.



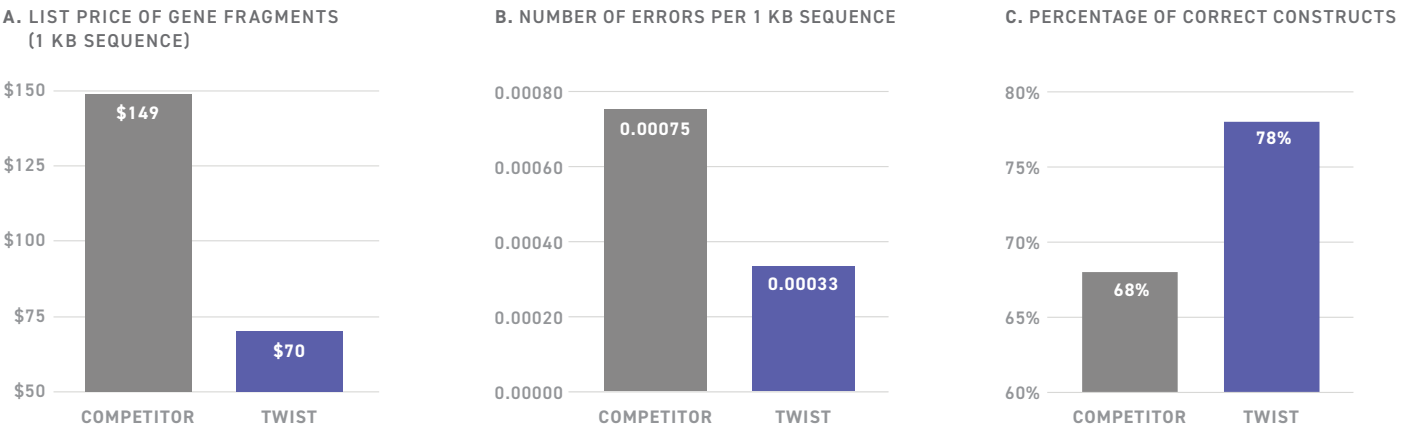
Sequences were ordered from Twist and IDT for genes ranging in length from 300 bp to 1,800 bp increasing by 100 bases between each gene. The graph represents the average error rate of all the sequences for a given product. Note: eBlocks have limited lengths, that dataset spans 300–800 bp. The error rate is derived from the total number of SNP's divided by the total number of base pairs sequenced adjusted and for sequencing parameters.

As seen in the figure above, Twist Gene Fragments had a nearly 2-fold improvement in average error rate over IDT gBlocks® across the entire size range and a 1.7-fold improvement over eBlocks across the range of 300–800 bp, with a 1:5,367 bp and 1:6,253 bp error rate respectively. Low error rates translate into fewer colonies that need to be picked and screened to find your perfect gene.

Accurate Gene Fragment Synthesis Accelerates Discovery

Twist Bioscience Gene Fragments enable researchers to build more constructs and minimize the time and cost of screening for perfect clones.

SPEND LESS MONEY AND LESS TIME FOR PERFECT CLONES



Gene Fragments data gathered comparing Competitor with Twist Bioscience, from publicly available information and a third party study. **A.** List price of 1 kb fragment shows Competitor pricing is $149 while Twist Bioscience pricing is $70. **B.** Error rate of 1 kb fragments show Competitor error rate is 1:1,319 bp while Twist Bioscience error rate is 1:3,000 bp. **C.** Total constructs used for Twist Bioscience was 50 and Competitor was 47. Data shows that % correct constructs for Competitor was 68% while Twist Bioscience was 78%.

Oligo Pools

SPECIFICATIONS

- ssDNA delivered in a pool
- Up to 300 nt sequences
- Pool sizes have a minimum of 2,000 sequences with no maximum
- >0.2 fmol per oligo
- Starting from 5 business day turnaround time

KEY BENEFITS

Precision Editing of Target Loci

- Accurate synthesis for specific targeting
- Industry-leading 1:2,000 nt error rate

Maximized Screening Efficiency

- Uniform synthesis ensures excellent oligo representation
- >90% of oligos represented within <2.5x of the mean

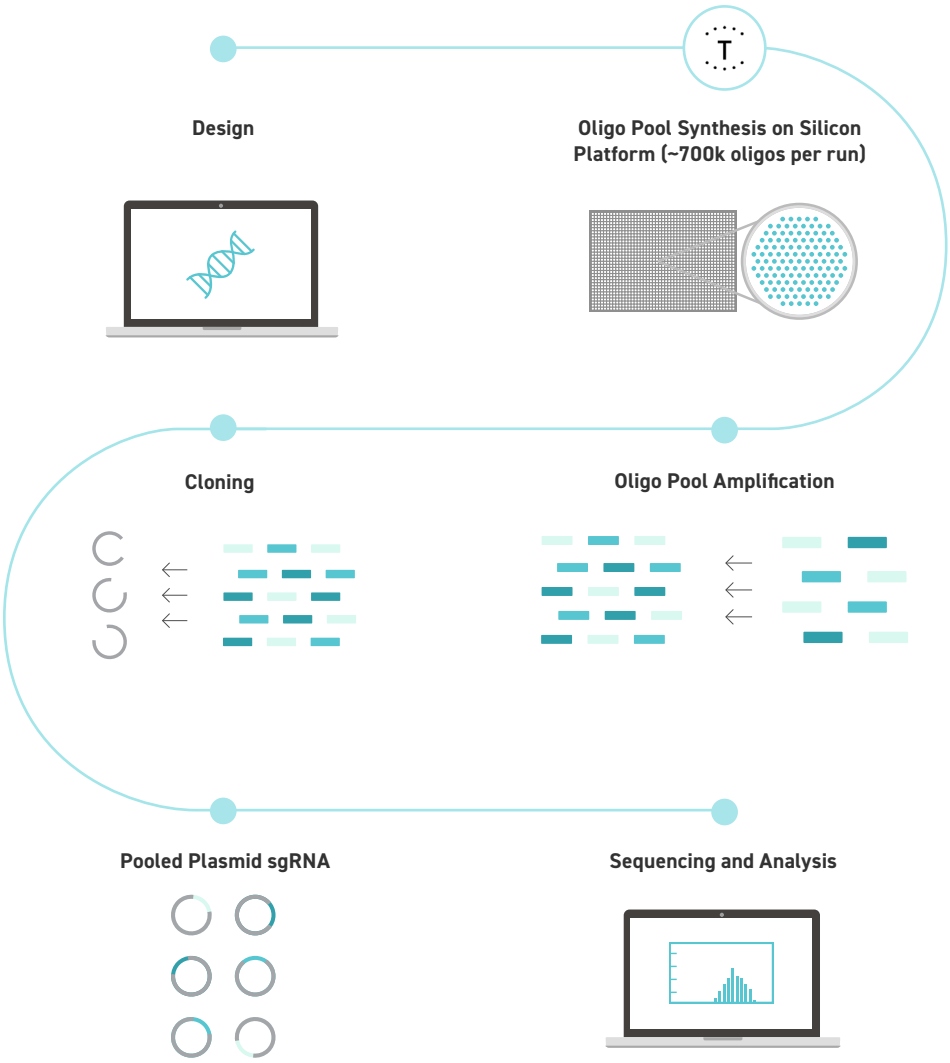
Flexible Pool Sizes to Fit Your Screen

- Design your pool for your assay
- Scalability to order the number of oligos you need

Twist Oligo Pools are highly diverse collections of single-stranded oligonucleotides synthesized using our silicon-based DNA writing technology. Our synthesis platform enables massively parallel production of hundreds of thousands of high-quality, accurate oligos per run.

Oligo pools are utilized in many applications including generation of CRISPR guide RNA (sgRNA) libraries, peptide and protein screens, and high-throughput reporter assays.

Design. Build. Test.



Highly Uniform and Accurate Synthesis for Specific and Efficient Targeting

Twist Bioscience's innovative silicon-based DNA writing technology is transforming DNA synthesis. Our proprietary oligonucleotide synthesis platform enables the massively parallel production of hundreds of thousands of high quality, highly accurate oligos per run, allowing the generation of complex and diverse CRISPR screening sgRNA libraries for precision gene editing and maximized screening efficiency.

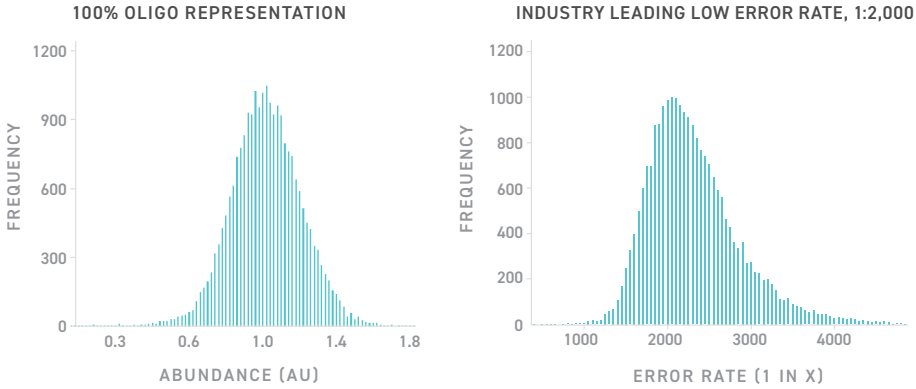


FIGURE A
Twist Oligo Pools are synthesized at high uniformity, 90% of sequences are present at signals within <2.5x of the mean, ensuring 100% representation [left]. Industry-leading error rate of 1:2,000 nt ensures high target specificity [right].

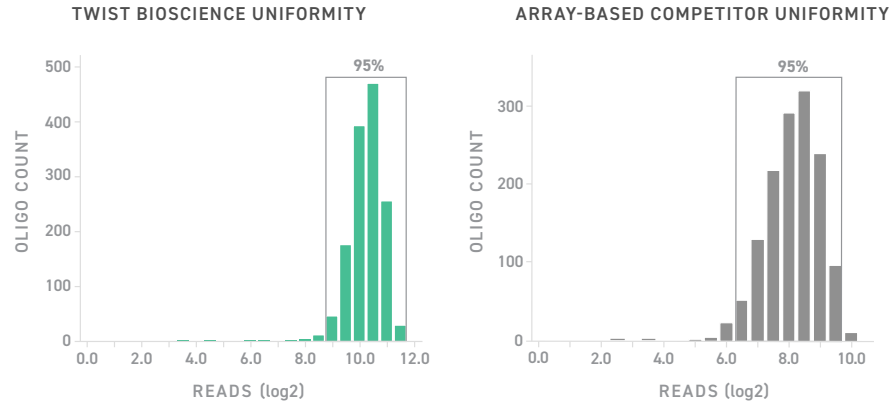


FIGURE B
Oligo pools synthesized by Twist Bioscience [left] and an array-based competitor [right] were amplified and cloned into a vector, and then sequenced to investigate oligo sequence representation. NGS-based validation of clones generated from each pool demonstrate that the sequences in the Twist Bioscience pool have more uniform sequence representation.

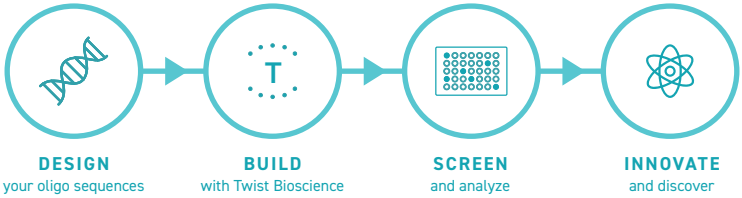
Sequencing Analysis of Oligo Pools

Twist Bioscience Oligo Pool	Array-Based Competitor Oligo Pool	
100%	>99.5%	sgRNA Recovered
~87%	>~74%	% correct sequence (MiSeq)
~100%	>~70%	% correct sequence (Sanger, 10 clones)

Sequencing analysis of oligo pools generated by Twist Bioscience and an array-based competitor demonstrate that the Twist Oligo Pools contain 100% of the expected sequences and a higher percentage of correct sequences than the competitor pool.

Libraries Made Easy from Design to Build

Think big, screen once. Let Twist build for you.



LIBRARIES THAT YIELD VIABLE VARIANTS

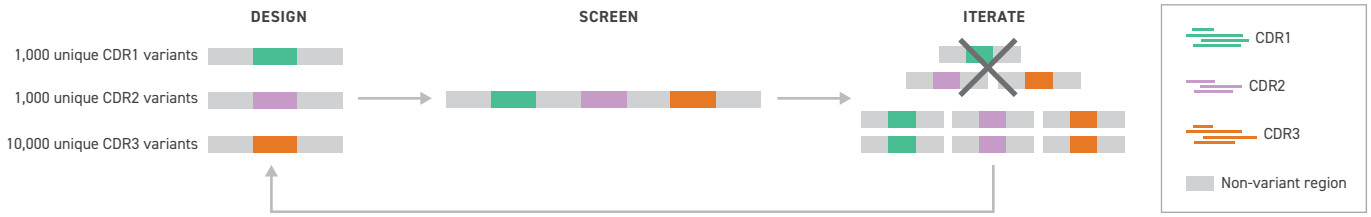
Combinatorial Variant Libraries

Our Combinatorial Variant Libraries are designed to create gene variants that express proteins with better stability, binding affinity, and enzymatic activity. Whether it be antibody humanization libraries or controlled complexity discovery libraries, our variant cassettes can be seamlessly incorporated into single or multiple scaffolds to yield >10^{10} variants.

	DEGENERATE (NNK/NNS)	TRIM/TRIMER CONTROLLED	TWIST COMBINATORIAL VARIANT LIBRARIES
Eliminates sequence bias	No	No	Yes
Number of codons available	32	20	All 64
Prevents undesirable motifs	No	No	Yes
Allows codon optimization	No	No	Yes
Avoids stop codons	No	Yes	Yes

User-Defined CDR Libraries

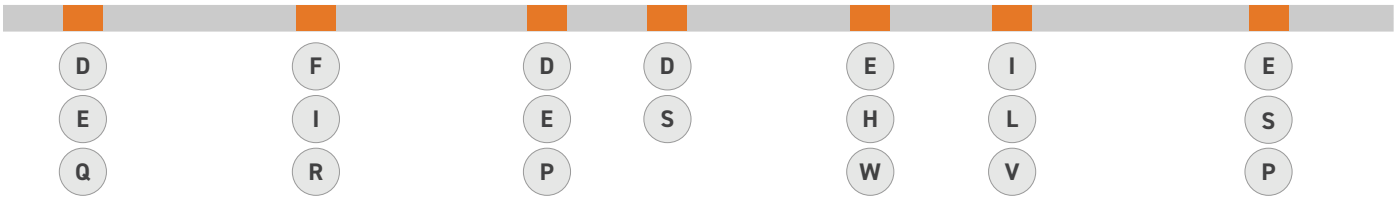
Our Precision Variant Library allows you to choose what unique CDR (complimentary defining regions) sequences you want to be incorporated into the choice of framework(s). Each CDR can be codon-optimized to avoid the creation of unwanted restriction sites. Machine learning has become an integral part of scientific research and has been used as a tool to analyze antibody libraries and identify unique CDR combinations that would yield, for example, higher affinity and specificity. Coupled with Twist's silicon-based synthesis platform, explicit library combinations generated from the analysis can be synthesized and seamlessly incorporated into a fully synthetic library to refine the exploration of the variant space. Since every library is NGS QC'd, negative data can be used to identify mutations that do not yield improved functions, and those can be removed in the next iteration of library design.



SOLD (Spread-Out Low Diversity) Libraries

Twist's SOLD Libraries are a time- and money-saving tool for mapping protein sequences, allowing you to explore the complex relationship between a protein and its environment. It enables targeted exploration of the sequence space encoded by mutating multiple positions simultaneously scattered across the parental sequence to generate a diverse library of proteins.

These high-fidelity libraries are a fast and cost-effective alternative to NNK, trinucleotide mutagenesis (TRIM) technology, error prone PCR, random mutagenesis and DNA Shuffling. Unlike the Combinatorial Variant Libraries (CVLs), SOLD Libraries offer precise incorporation of diversity across the parental sequence without the restriction of variant domains. In addition, SOLD Libraries allow you to explore multiple mutations simultaneously, unlike Site Variant Libraries (SVLs).



Site Saturation Variant Libraries

Twist's Site Saturation Variant Libraries allow you to investigate the relationship between sequence and protein structure and function. These libraries are capable of generating 99% of desired variants and come in pooled or pooled-per-position options. They enable screening of 1–20 different amino acids (and up to 64 codons) at each position and a comprehensive investigation of sequence variants.

	ERROR PRONE PCR	DEGENERATE (NNK/NNS)	TWIST SITE SATURATION VARIANT LIBRARIES
Eliminates sequence bias	No	No	Yes
Number of codons available	Unknown	32	All 64
Prevents undesirable motifs	No	No	Yes
Allows codon optimization	No	No	Yes
Avoids stop codons	No	Yes	Yes

Site Saturation Variant Libraries enable efficient sampling of a protein's sequence space in screening assays. The figure below is data from a Twist Site Saturation Variant Library with variants at 65 positions (19 variants per position). The bars represent a different amino acid position, with each color indicating the observed variant frequency. All variants are present in the expected ratios.

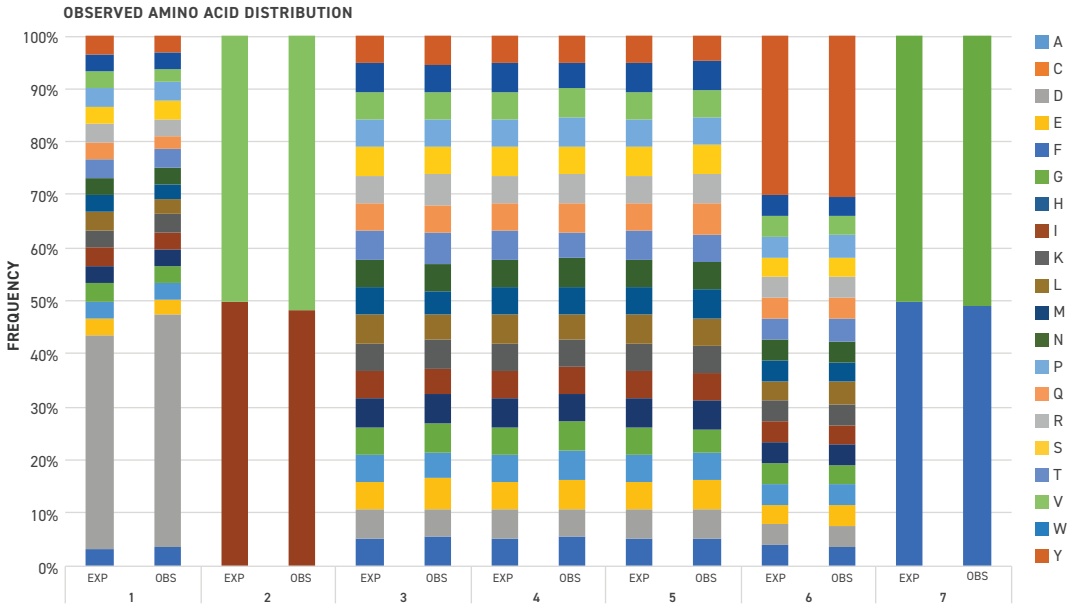
BUILT-IN QUALITY

At Twist, we use our molecular biology expertise to precisely and efficiently construct variant libraries. Our single-base control approach allows us to deliver high-diversity libraries without motifs that could confound your screening process. We deliver fully-customized libraries of unparalleled quality, with desired variants present at user-defined ratios.

Below you'll see a CVL example representative of that quality. Variants in seven sequential amino acid positions were generated, and all have expected variants at the positions shown, with nearly all at the desired ratio:

· At positions 1 and 6, the wild type amino acid was requested at 40% (position 1) and 30% (position 6). The remaining 18 amino acids were all requested to be as low as 3.3%.

· At position 3 to 5, all 19 amino acid residues were requested and observed at 5.3%.



Twist Bioscience's silicon-based platform enables the fabrication of customized libraries at the base-by-base level. The ability to precisely capture the variant diversity enables a comprehensive screen of the variant space while eliminating the risk of missing key variants.

"Working with Twist...was a great experience...[Twist's] support was amazing. We have performed the first validation selections which looks promising..."

DR. AHUVA NISSIM
PROFESSOR IN ANTIBODY AND THERAPEUTIC ENGINEERING,
QUEEN MARY UNIVERSITY OF LONDON