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.

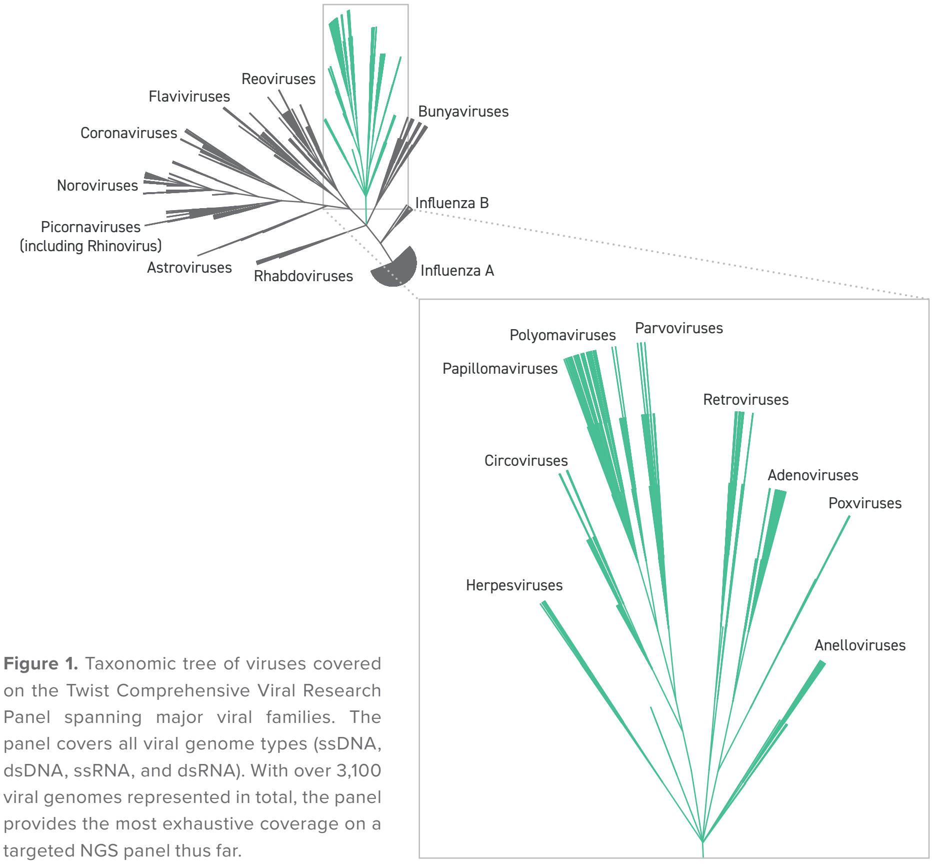

Figure 1. Taxonomic tree of viruses covered on the Twist Comprehensive Viral Research Panel spanning major viral families. The panel covers all viral genome types (ssDNA, dsDNA, ssRNA, and dsRNA). With over 3,100 viral genomes represented in total, the panel provides the most exhaustive coverage on a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

Comprehensive Detection of Viral Pathogens

The Twist Comprehensive Viral Research Panel targets viral sequences from 3,153 human and non-human viral species, including 15,488 different viral strains. Among the families of viruses targeted by the panel are coronaviruses, which were responsible for the COVID-19 pandemic, and influenza viruses, which rapidly evolve to impact flu season duration and related symptoms. All families that have at least one virus known to affect humans were included in the panel design (**Figure 1**). Viral sequencing data from the RefSeq, FluDB & VIPR databases were used in the design of this panel, generating over 1 million unique probes that tile the genome of each viral species. The panel also represents multiple viral genome types: single-stranded RNA, double-stranded RNA, single-stranded DNA, and double-stranded DNA. The Twist Library preparation kit is compatible with all nucleic acid types, thus enabling a wide variety of applications. These features will allow researchers to identify a large diversity of viruses in one reaction.

Identification of Novel & Highly Evolved Viral Pathogens

The Twist Comprehensive Viral Research Panel enables enrichment and identification of new and divergent viral species via hybrid capture and NGS. We determined the mismatch tolerance of the Twist Comprehensive Viral Research Panel using a series of synthetic influenza A hemagglutinin (HA) segments containing increasing levels of random single-base substitutions ranging from 5% to 30% from the wild-type sequence (derived from A/California/07/2009[H1N1]; GenBank accession number: NC_026433). We obtained full coverage at 1x with 1M total mapped reads for HA segments containing up to 10% variation from the reference sequence (**Figure 2**). Total capture decreased in samples with greater than 10% mismatches. The high mismatch tolerance of the Twist Comprehensive Viral Research Panel supports the discovery of novel and mutated viral species.

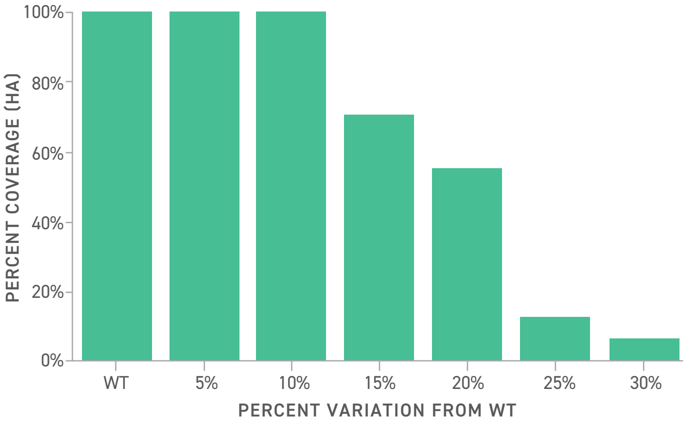

Figure 2: Capture of synthetic H1N1 influenza HA segments (Genbank accession number: MN416597) containing varying levels of random mismatches (0–30% from the wild-type sequence). Total reads (normalized to template length) for WT and variant HA segments (top), and percent coverage over the variant HA segment (bottom) are shown

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Co-infection Viral Detection of Diverse Viruses in a Single Sample

The Twist Comprehensive Viral Research Panel can detect over 3,100 viral species simultaneously in a single sample. In a co-infection assay, we spiked four synthetic control viruses—one representing each viral genome type—into a single sample of human reference RNA to test the capture efficiency of the panel for each virus. Following target enrichment, we detected >99.8% of all four synthetic viruses at >=1X coverage with only 1.2M reads (**Figure 3**). The co-infection viral detection capability of this panel can be used for metagenomic surveillance applications in complex sample types (e.g., stool) or to improve diagnostic confidence in patient samples.

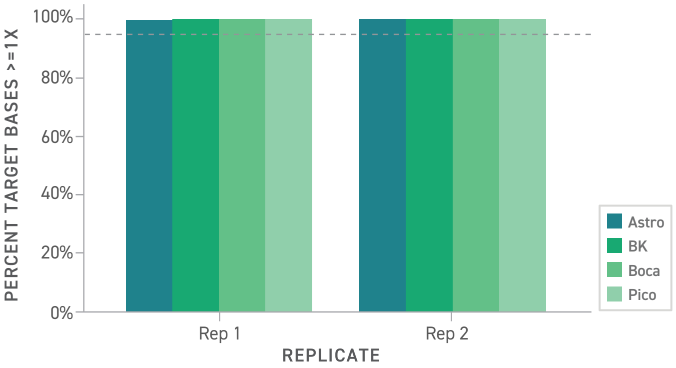


Figure 3: Co-infection with four different virus types (astrovirus: ssRNA, BK virus: dsDNA, bocavirus: ssDNA, and picobirnavirus: dsRNA) spiked into human RNA. The panel detected all four viruses with only 1.2M reads, demonstrating its ability to detect multiple viral species in a single sample with high fidelity.

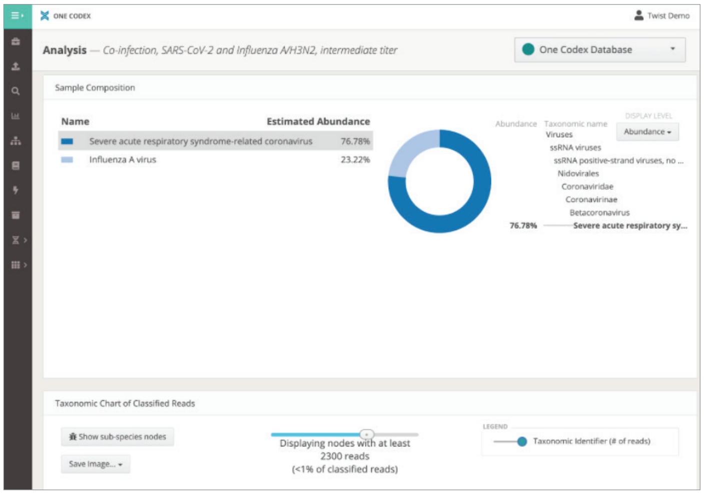
Straightforward Workflow

Paired with the Twist Total Nucleic Acids Library Preparation Kit and the Twist Target Enrichment workflow, the Twist Comprehensive Viral Research Panel provides an end-to-end path (**Figure 4**) for NGS-based multi viral identification that is both straightforward and cost-effective. Sequence data can be analyzed with the One Codex platform, which is included in the panel purchase.

1. Prepare libraries for hybridization
2. Hybridize capture probes with pools
3. Bind hybridized targets to streptavidin beads
4. Post-capture PCR amplify, purify, and perform QC
5. Sequencing
6. Analysis of sequencing reads on One Codex

One Codex Analysis

The Twist Comprehensive Viral Research Panel is bundled with One Codex, a cloud-based platform for metagenomic sequencing data analysis and visualization (**Figure 5**). Ideal for both research and clinical use cases, One Codex provides users with customizable workflows for interpreting and sharing viral-related NGS sequencing data. When purchasing the panel, customers are provided with detailed onboarding instructions and credits that grant access to the cloud platform.



Analysis — *Co-infection, SARS-CoV-2 and Influenza A/H3N2, intermediate titer*

Sample Composition

Name	Estimated Abundance
Severe acute respiratory syndrome-related coronavirus	76.78%
Influenza A virus	23.22%

Taxonomic Chart of Classified Reads

Displaying nodes with at least 2300 reads (<1% of classified reads)

Figure 5: One Codex user interface showing analysis results from the Twist Comprehensive Viral Research Panel

Twist Comprehensive Viral Research Panel is a component of the Twist Infectious Disease portfolio of products.

LEARN MORE

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ORDERING INFORMATION

103545: Twist Comprehensive Viral Research Panel with One Codex software, 2 Reactions, Kit

103547: Twist Comprehensive Viral Research Panel with One Codex software, 12 Reactions, Kit

103548: Twist Comprehensive Viral Research Panel with One Codex software, 96 Reactions, Kit

The Twist Comprehensive Viral Research Panel is for research use only, and subject to additional use restrictions as set forth in Twist's Supply Terms and Conditions: www.twistbioscience.com/supply-terms-and-conditions. The One Codex analysis platform is subject to user terms of use: app.onecodex.com/tos.