Service Profile

SARS-CoV-2 Whole Genome Sequencing Services

Accelerating your SARS-CoV-2 research through the pandemic

To combat the COVID-19 pandemic, researchers require rapid solutions for SARS-CoV-2 viral surveillance. When studying emerging mutants, tracing existing outbreaks and advancing research into vaccines and drug development, every second counts. It may be difficult to keep pace with new developments when resources and time are limited.

QIAGEN® Genomic Services has risen to meet this need with our comprehensive SARS-CoV-2 Whole Genome Sequencing Services. Extend your in-house resources with the expertise and custom services that you expect from QIAGEN. This all-in-one genome sequencing solution delivers end-to-end support, from sample preparation to data analysis, to help accelerate your research. Our SARS-CoV-2 Whole Genome Sequencing Service offers the following benefits:

- **End-to-end service**: We take care of every step, from sample preparation to data analysis
- **Guidance and flexibility**: We aid in designing your project and help you make the right decisions
- **Expertise in SARS-CoV-2 genomics**: We leverage our optimized QIAseq® SARS-CoV-2 Primer Panel to efficiently sequence the entire viral genome
- **Ready-to-publish data**: We deliver comprehensive reports and data packages, allowing you to quickly pinpoint viral genome sequence variation across samples

Partner with us for expert guidance and dedicated service – from Sample to Insight® – for your SARS-CoV-2 research today.

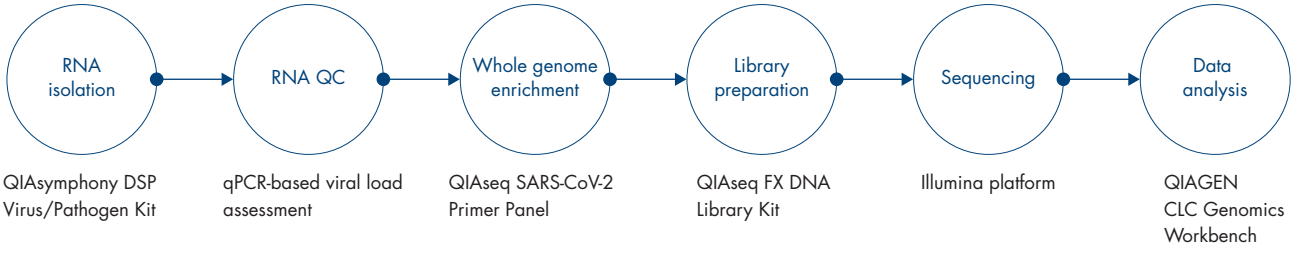


Figure 1. SARS-CoV-2 Whole Genome Sequencing workflow

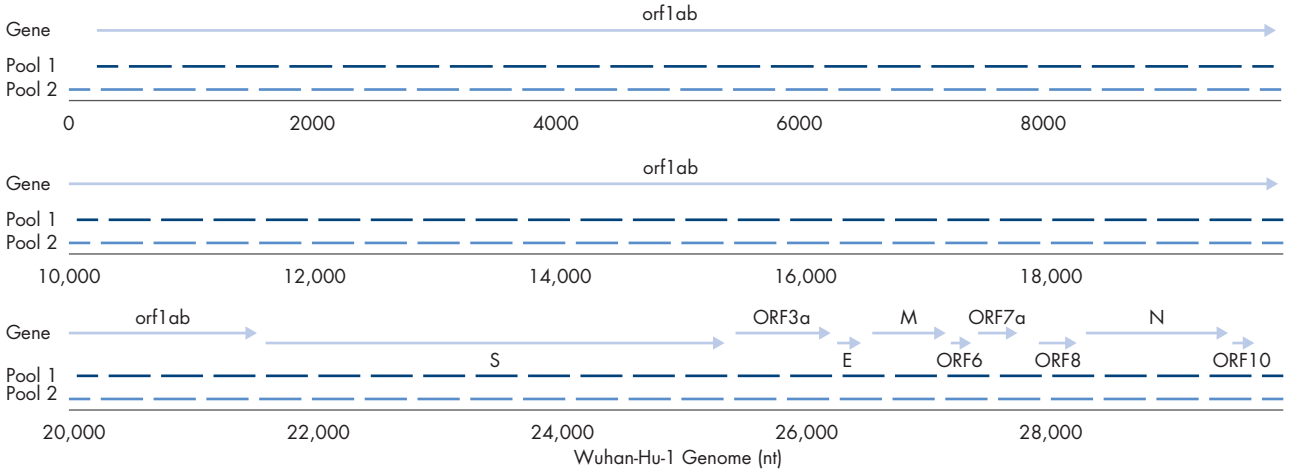


Figure 2. QIAseq SARS-CoV-2 Primer Panel amplicon scheme.

Efficient SARS-CoV-2 whole genome enrichment

The QIAseq SARS-CoV-2 Primer Panel is a multiplex PCR primer set for whole genome amplification of SARS-CoV-2. Based on optimized primer sequences from the ARTIC Network (V3), the panel separates 400 bp amplicons into two PCR pools that together cover the entire SARS-CoV-2 genome. The primers have gone through an in silico check to reduce chances for dimerization during sample enrichment.

Comprehensive pathogen phylogenetic analysis – delivered

When paired with the QIAGEN CLC Genomics Workbench, your sequencing data will provide actionable insights into virus strain evolution and phylogenetics. High-quality trimmed reads are mapped to the Wuhan-Hu-1 (GenBank: MN908947.3) genome. Depending on the sample quality, variant detection down to 1% is then reported, and a consensus sequence computed, from the read alignments. CLC uses variants from each SARS-CoV-2 sample to measure the relatedness between the samples and generates a maximum likelihood phylogenetic tree. These results and more are provided in your comprehensive final report.

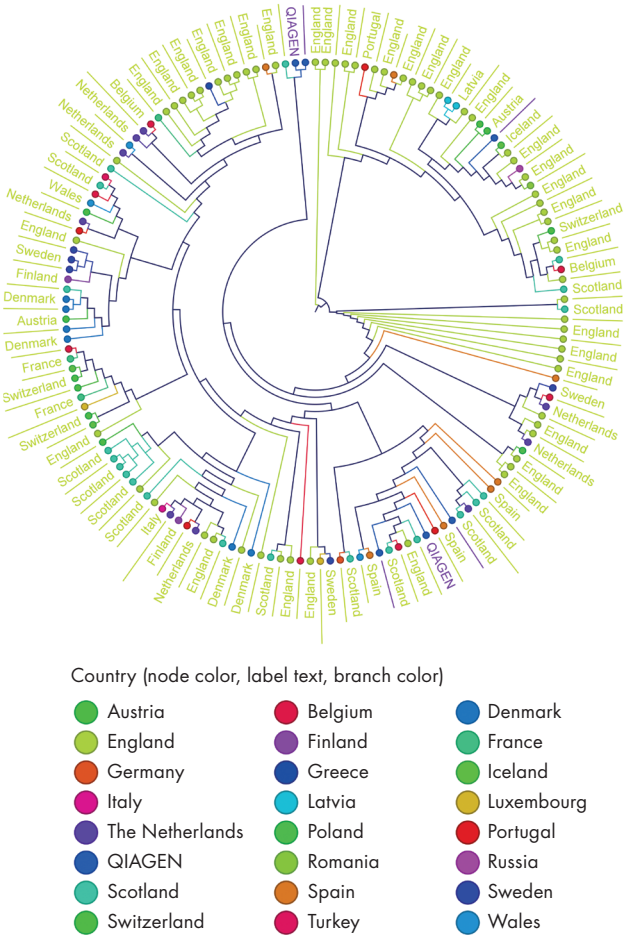


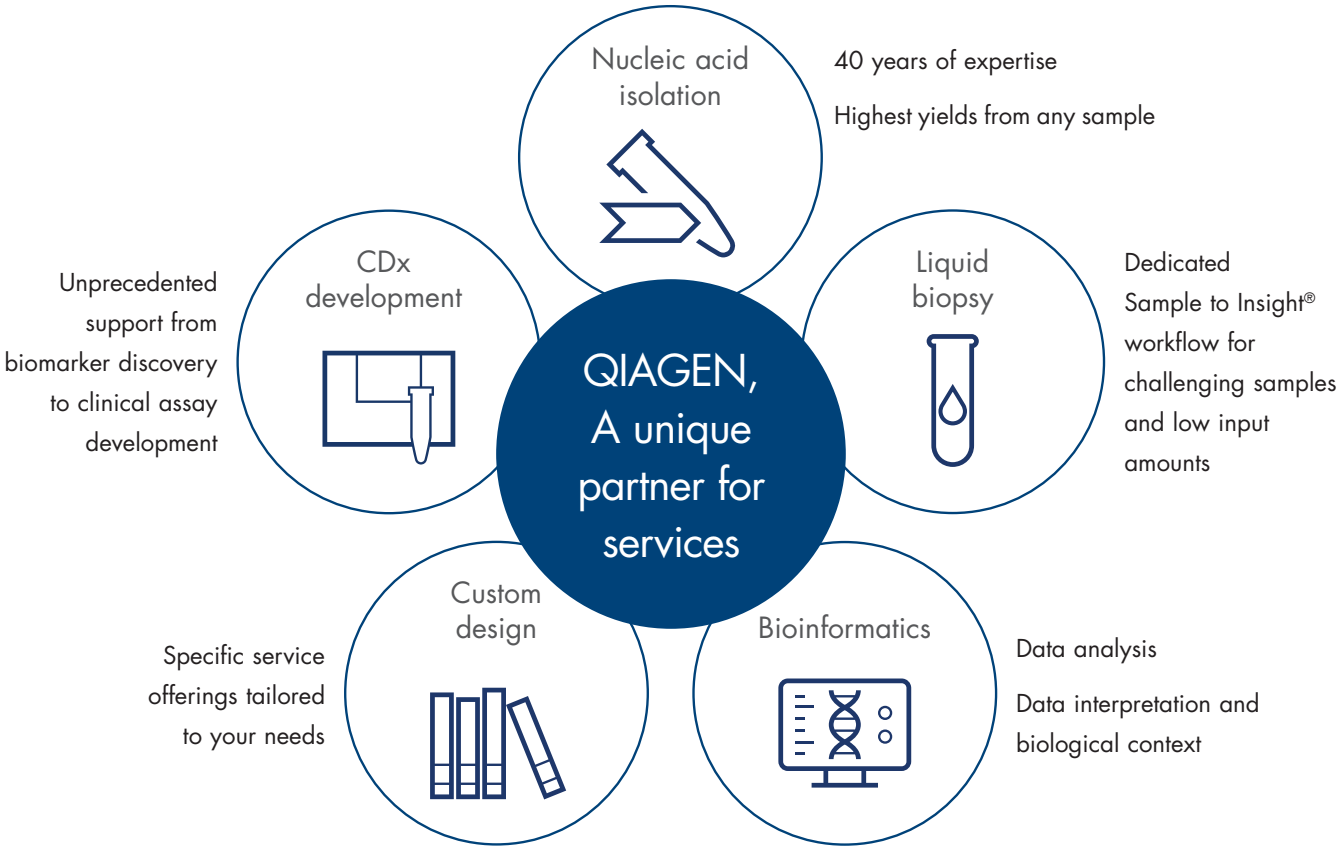
Figure 3. An example circular cladogram. In your report, it will show hypothetical phylogenetic relationships among the samples.

Service specifications

Consultation	Free consultation with an expert to design an experimental setup that best meets your needs and budget.		
Sample requirements	**Input sample**	**Isolation kit**	**Input requirements**
	Customer-isolated viral RNA	Not applicable	Minimum: 20 µl
	Swab	QIAsymphony® DSP Virus/Pathogen Kit	1 swab or 150 µl of transportation media
	Other	**Please inquire**	
RNA quality control	qPCR is used to assess the viral load For samples with a Ct value >30: a. The mapping rate will be lower b. There could be read coverage drop offs, which would give less confident variants This is a **STOP/GO** point where it is possible to omit samples, replace samples before proceeding or terminate the project.		
Reverse transcription and library preparation	• QIAseq SARS-CoV-2 Primer Panel The multiplexed PCR primer set is based on the ARTIC V3 primer set. • QIAseq FX DNA Library Kit Library quality control (QC) is assessed by gel electrophoresis to check for the right fragment size and concentration. This is a **STOP/GO** p oint where it is possible to terminate or adjust before proceeding.		
RNA sequencing parameters	• Sequencing with Illumina® NextSeq®500, NextSeq550, MiSeq® or NovaSeq™ systems • Paired-end reads • 149/151 bp read length • As indicated in the handbook, 2 x 1 M reads per sample are recommended as a starting point		
Complete data analysis	After analysis is complete, you will receive a comprehensive report with all the relevant data from your project. The table below lists some of the data that may be included in your report, depending on the services requested.		
	FASTQ quality control	QC report and supplementary QC report (per sample)	
	FASTQ adapter and quality trimming	Trimming report (per sample)	
	Mapping statistics and variants	• Mapping report (per sample) • Combined summary report (per sample) • Excel table and VCF file for unfiltered variants (per sample) • Excel table and VCF file for filtered variants (per sample)	
	Viral sequences	• Consensus viral genome FASTQ file (per sample) • Consensus sequence annotation (per sample) • Circular cladogram	
	Merge data with data from previous projects	**Please inquire**	
	Data delivery	Encrypted USB/hard disk drive or cloud delivery	
Final report and consultation	The final data analysis package contains an overview of data analysis and algorithms used, the files and tables listed above and publication-ready figures (PDFs provided as standard, please inquire for SVG or other formats). A teleconference is scheduled with QIAGEN scientists to discuss analysis and validation of results. Consultation and support will be provided for 90 days following delivery of data (for data delivery only projects), or delivery of data analysis (for data analysis inclusive projects). For extended support beyond 90 days, please inquire.		

How can we accelerate your research?

Our expert team is looking forward to learning about your research project and designing your customized service with QIAGEN.



Tell us about your project

For up-to-date licensing information and product-specific disclaimers, see the respective QIAGEN kit handbook or user manual. QIAGEN kit handbooks and user manuals are available at **www.qiagen.com** or can be requested from QIAGEN Technical Services or your local distributor.

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