Service Profile

SARS-CoV-2 Whole Genome Sequencing Service

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 Service. 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® DIRECT SARS-CoV-2 Primer Kit 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.

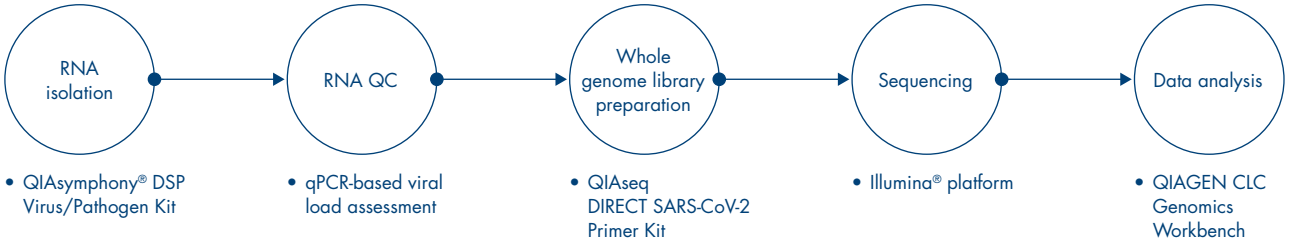

Figure 1. SARS-CoV-2 Whole Genome Sequencing workflow.

Efficient SARS-CoV-2 whole genome enrichment

QIAseq DIRECT SARS-CoV-2 Kits are specially designed to advance research into SARS-CoV-2 solutions for sequencing the entire viral genome. The SARS-CoV-2 single-stranded RNA can be mixed with host RNA during isolation from a sample. The kits enable reverse transcription of the RNA into cDNA with primers to specifically enrich for the viral genome and add Unique Dual Indices (UDIs) for sequencing. The panel consists of approximately 550 primers for creating 425 amplicons, covering the entire SARS-CoV-2 viral genome.

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 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.

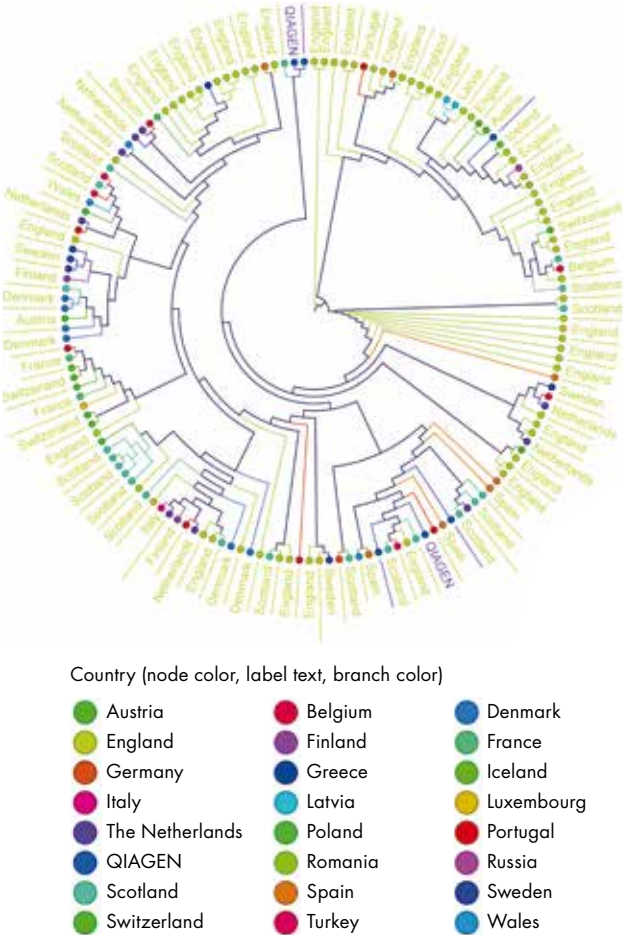

Figure 2. An example circular cladogram. In your report, it will show hypothetical phylogenetic relationships among the samples.

Service specifications

<table>
<tr><td>Consultation</td><td colspan="3">Free consultation with an expert to design an experimental setup that best meets your needs.</td></tr>
<tr><td rowspan="4">Sample requirements</td><td>Sample input</td><td>Isolation kit</td><td>Input requirements</td></tr>
<tr><td>Customer-isolated viral RNA</td><td>N/A</td><td>Minimum: 20 µl</td></tr>
<tr><td>Swab</td><td>QIAsymphony DSP Virus/ Pathogen Kit</td><td>1 swab or 150 µl of transportation media</td></tr>
<tr><td>Other</td><td colspan="2">Please inquire</td></tr>
<tr><td>Sample quality control</td><td colspan="3">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 or replace samples before proceeding.</td></tr>
<tr><td>Library preparation and quality control</td><td colspan="3">Library preparation using QIAseq DIRECT SARS-CoV-2 Kit.
Library quality control by gel electrophoresis to check for the right fragment size and concentration.
This is a STOP/GO point where it is possible to omit samples before proceeding.</td></tr>
<tr><td>Sequencing parameters</td><td colspan="3">Sequencing with Illumina NextSeq®, MiSeq or NovaSeq® systems
Paired-end reads
Read length of 149 bp
Read depth of 2 x 1 M reads on average
2 x 1 M reads per sample are recommended as a starting point</td></tr>
<tr><td rowspan="7">Complete data analysis</td><td colspan="3">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.</td></tr>
<tr><td>FASTQ quality control</td><td colspan="2">QC report and supplementary QC report (per sample)</td></tr>
<tr><td>FASTQ adapter and quality trimming</td><td colspan="2">Trimming report (per sample)</td></tr>
<tr><td>Mapping statistics and variants</td><td colspan="2">• 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)</td></tr>
<tr><td>Viral sequences</td><td colspan="2">• Consensus viral genome FASTQ file (per sample)
• Consensus sequence annotation (per sample)
• Circular cladogram</td></tr>
<tr><td>Merge data with data from previous projects</td><td colspan="2">Please inquire</td></tr>
<tr><td>Data delivery</td><td colspan="2">Encrypted USB/hard disk drive or cloud delivery</td></tr>
<tr><td>Final report and consultation</td><td colspan="3">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.</td></tr>
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Note: To maximize results and turnaround times service specifications are subject to change.

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

The QIAGEN Genomics Service is intended exclusively for research use only (RUO). This service is not intended for the diagnosis, prevention or treatment of a disease.

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