



# JAX COVID-19 WHOLE GENOME SEQUENCING

## WHY SEQUENCING?

Identifying variants and new viral strains is essential to understanding how SARS-CoV-2 is evolving in response to existing therapies, vaccines and tests. This information aids in the development of public health responses to limit the spread of the virus.

## TEST SPECIFICATIONS

Acceptable specimen types include nasopharyngeal swabs, oropharyngeal swabs, nasal mid-turbinate swabs, anterior nares specimens, sputum, saliva, and lower respiratory specimens.

Please visit <https://www.jax.org/coronavirus-information/provider-information> for comprehensive instructions for specimen storage, collection and transport.

- ✓ 98 amplicons designed to identify SARS-CoV-2-specific variants
- ✓ Sequenced using the Illumina NextSeq 500
- ✓ Classification of SARS-CoV-2 lineages from upper respiratory samples identified as Positive SARS-CoV-2 by Real Time Polymerase Chain Reaction (RT-PCR)
- ✓ Pangolin Lineage, NextStrain Clade assignment, CDC classification and detected amino acid deletions and substitutions of isolate included in the report

## GENE LIST

The SARS-CoV-2 virus has an RNA genome that is about 30,000 nucleotides long and encodes eleven genes:

ORF1ab	ORF7a
S	ORF7b
ORF3a	ORF8
E	N
M	ORF10
ORF6	



**Phone** (860) 837-2320

**Fax** (860) 837-2380

**Email** CGL\_CS@jax.org

**Shipping Address:**

The Jackson Laboratory  
Attn: Clinical Genomics Laboratory

10 Discovery Drive

Farmington, CT 06032

