

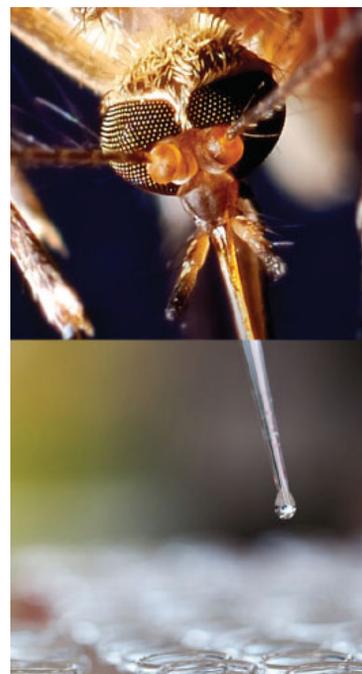
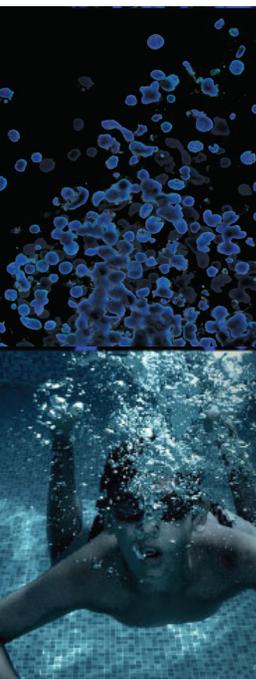


SARS-CoV-2 Reference Standards and Materials - Industry Perspectives from ATCC and BEI Resources

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Bioinformatician – ATCC
afrank@atcc.org

Marco Riojas, PhD
Scientist – BEI Resources
mriojas@atcc.org

Credible Leads to Incredible™



Agenda

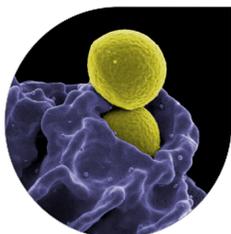
Industry Perspectives from ATCC and BEI Resources

- **History of ATCC, BEI Resources, and our respective missions**
- **Provide an overview of the available SARS-CoV-2 standards and reference materials in the ATCC and BEI catalogs**
- **Provide an overview of the NGS assembly pipeline and subsequent analysis**
- **Discuss the benefits of using NGS to authenticate our reference material**
 - Led to a discovery of a rare ORF6 deletion in the *passaged* Hong Kong isolate
- **Discuss our efforts to reduce genomic variability in cultured SARS-CoV-2**
 - Variability detected with multiplicity of infection (MOI), days post infection (dpi) and plaque picking techniques
- **The ATCC Genome Portal**
 - ATCC's enhanced authentication initiative

About ATCC

- Founded in 1925, ATCC is a not-for-profit organization with HQ in Manassas, VA, and an R&D and Services center in Gaithersburg, MD
- World's largest, most diverse biological materials and information resource for microbes – the “*gold standard*”
- Innovative R&D company featuring gene editing, microbiome, NGS, and advanced models
- cGMP biorepository
- Partner with government, industry, and academia
- Leading global supplier of authenticated cell lines, microorganisms, and molecular standards
- Sales and distribution in 150 countries, 19 international distributors
- Talented team of 450+ employees, over one-third with advanced degrees

ATCC Portfolio



Credible Collections

The ATCC collection of cell and microbial reference materials remain at the heart of incredible breakthroughs in scientific exploration. ATCC is dedicated to providing biological standards backed by cutting-edge authentication techniques and essential resources that accelerate innovative research and ensure scientific reproducibility within the life sciences.



Authentication Resources

Advanced techniques in authentication allow you to test for contamination and track phenotypic or genotypic changes before they become a problem. Researchers look to ATCC for a wide range of authentication resources to safeguard reproducibility and meet requirements for funding, publication, and quality control.

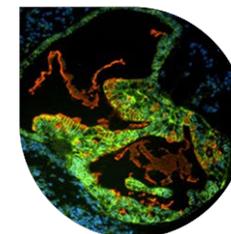


Custom Solutions

Each scientific project is unique, which is why ATCC tailors custom services to the individual needs of our partners. With an unmatched combination of extensive expertise, cutting edge technologies, best practices, and a world-renowned collection of cells and microbes, ATCC is your ideal solutions partner to guide you through your next project.

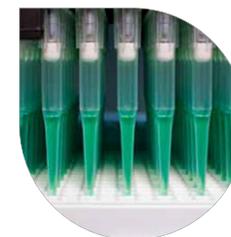
Better Models

Advanced biological models enable greater specificity and functionality to the researcher's toolkit. ATCC is committed to bringing cutting-edge biological models to researchers at the forefront of extraordinary innovation and scientific progress.



Quality Standards

Your research depends on protocols and tools you can trust. As part of our mission, ATCC is a leader in the creation and maintenance of biological and published laboratory standards that protect public interests and provide quality reference material, education, accreditation, and certification services to the industry.



Biorepository Services

With nearly a century of experience in biomaterial management, ATCC continues to support global health by offering biorepository services for worldwide storage and distribution of biological materials. Whether you need a cGMP-compliant facility, small- or large-scale storage, or flexible storage choices, we can manage biomaterials to your specifications.



BEI Resources

Biodefense and Emerging Infections Resources

History

The National Institute of Allergy and Infectious Diseases (NIAID) awarded the BEI Resources contract to ATCC in 2003.

Mission of BEI Resources

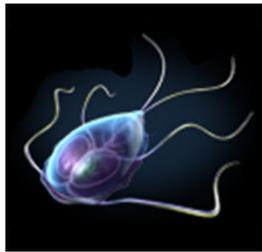
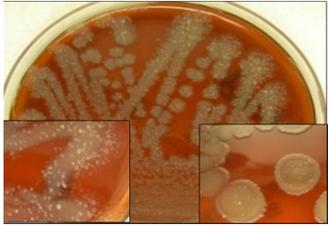
Provide NIAID with a central repository for the acquisition, authentication, production, preservation, storage, and distribution of a broad range of unique and quality assured research materials for the infectious disease research community that will aid in the development and evaluation of vaccines, therapeutics, and diagnostics.

Scope

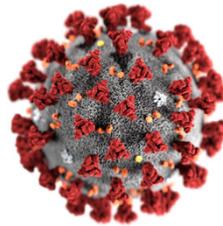
Reagents, tools and information covering NIAID's Category A, B, and C priority pathogens, emerging infectious disease agents, non-pathogenic microbes and other microbiological materials of relevance to the research community.



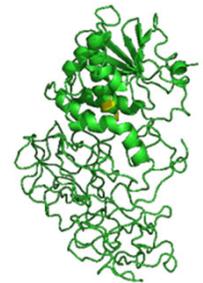
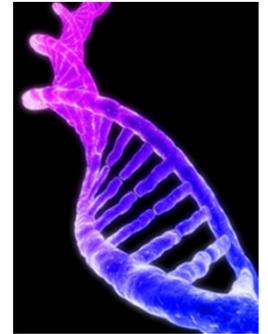
Biomaterials Available Through BEI Resources



- Bacteria
- Viruses
 - **SARS-CoV-2**
- Toxins
- Pathogenic fungi
- Parasitic protists
- Parasitic worms
- Host and vector cell lines
- Arthropod vectors



- Nucleic acids
 - Genomic DNA & RNA
 - Expression vectors
 - Sequenced clones
 - Libraries and arrays
- Monoclonal antibodies
- Polyclonal antisera
- Recombinant proteins
- Synthetic peptides and arrays
- Assays & panels





ATCC and BEI Resources SARS-CoV-2 Materials

Virus isolates, nucleic acids, synthetic molecular standards, and more

ATCC's SARS-CoV-2 Resources

- Available SARS-CoV-2 products include:
 - Genomic RNA
 - Heat inactivated virus
 - Synthetic molecular standards
 - Cell lines, etc.

- For a comprehensive list, please visit

www.atcc.org/coronavirus



Coronavirus Research Materials

When developing a new assay to detect SARS-CoV-2, having access to other coronavirus strains can be valuable for establishing inclusivity and specificity. To support this need, ATCC provides viral strains and nucleic acids representing alphacoronaviruses and betacoronaviruses known to cause disease in humans.

Strains

- Betacoronavirus 1, OC43
- Human coronavirus 229E

Nucleic acids:

- RNA from Betacoronavirus 1, OC43
- RNA from human coronavirus 229E
- Quantitative generic RNA from human coronavirus 229E
- Quantitative synthetic human coronavirus NL63 RNA
- Quantitative synthetic human coronavirus HKU1 RNA
- Quantitative synthetic MERS-CoV RNA
- Quantitative Synthetic SARS-CoV-2 (2019) RNA

We also offer a variety of coronavirus strains known to cause disease in feline, avian, and murine hosts, as well as the cell lines and media needed to cultivate them. These materials provide researchers with the tools needed to enhance the development of their assays.

[Explore our full portfolio](#)

Microorganisms for Specificity Testing

Establishing analytical specificity is an essential part of assay validation, particularly when evaluating if whose results can affect public health. In many cases, the rapid and accurate identification of an infectious agent for administering timely treatment and preventing further transmission. To support researchers of COVID-19 detection assays, we have provided a list from the FDA of organisms that are recommended for testing. Explore our portfolio today!

Human coronavirus 229E	Enterobacteriaceae virus 1-4	Mycobacterium tuberculosis
Human coronavirus OC43	Influenza A & B	Streptococcus pyogenes
Human coronavirus HKU1	Enterovirus (e.g., EV68)	Bordetella pertussis
Human coronavirus NL63	Respiratory syncytial virus	Mycoplasma pneumoniae
SARS-CoV	Rhinovirus	Candida albicans
MERS-CoV	Chlamydia pneumoniae	Pseudomonas aeruginosa
Adenovirus (e.g., C1 Ad, 71)	Influenza B virus	Staphylococcus aureus
MPV	Legionella pneumophila	

Supporting Products

Cell Lines for SARS-CoV-2 Propagation

To develop new vaccines or test antiviral compounds, researchers need access to virus isolates. However, during the outbreak of a novel virus like SARS-CoV-2, it can be challenging to determine which propagation host is ideal for successful viral replication. In a recent study by [Liu et al.](#), it was discovered that SARS-CoV-2 can replicate to a high titer in Vero E6 and Vero E6 cells in the absence of trypan. These cell lines and the media needed to cultivate them are available at ATCC—explore our collection today.

[Explore Vero cell lines](#)

Supporting Products

Cell Lines for Enhanced Virus Production

The continued spread of deadly viruses necessitates the development of novel prevention and treatment options. However, the development of a new antiviral vaccine can be challenged by low-yielding manufacturing processes. To address this, ATCC used cutting-edge CRISPR/Cas9 gene-editing technology to develop STAT1 knockout cell lines capable of producing higher viral stocks. Discover how these advanced biological models can be used in your vaccine development research.

[Order STAT1-KO cell lines](#)

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Supporting Products

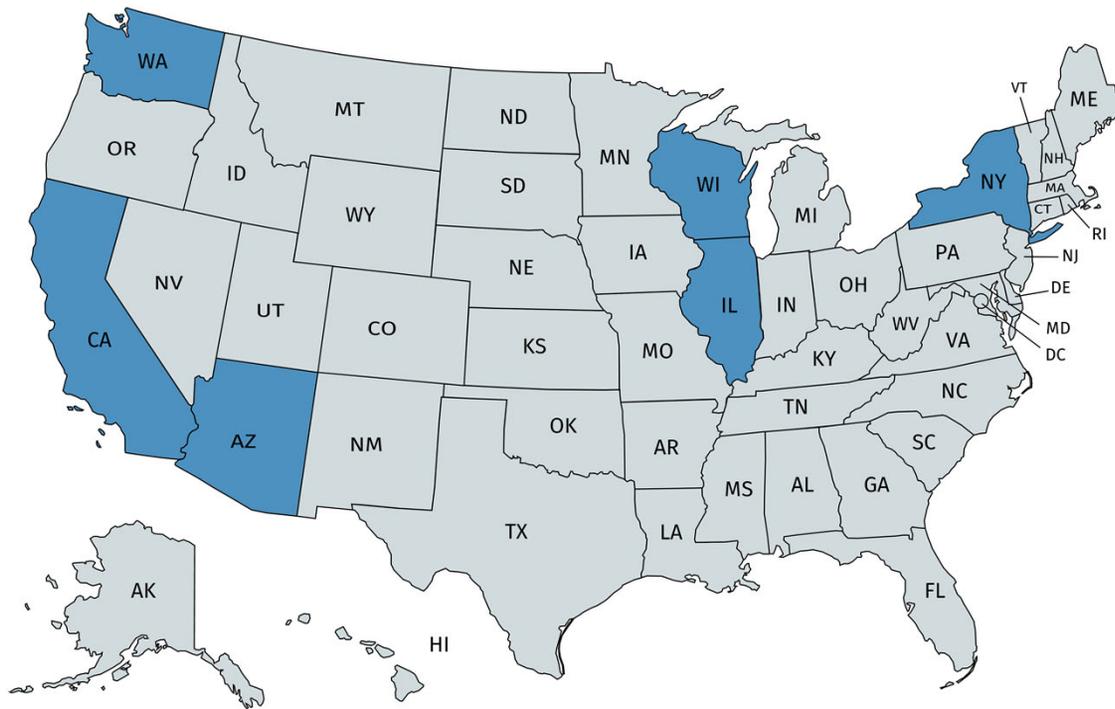
Cell Lines for Enhanced Virus Production

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[Order STAT1-KO cell lines](#)

Domestic SARS-CoV-2 Isolates Accessioned To-Date

Producing SARS-CoV-2 Isolates



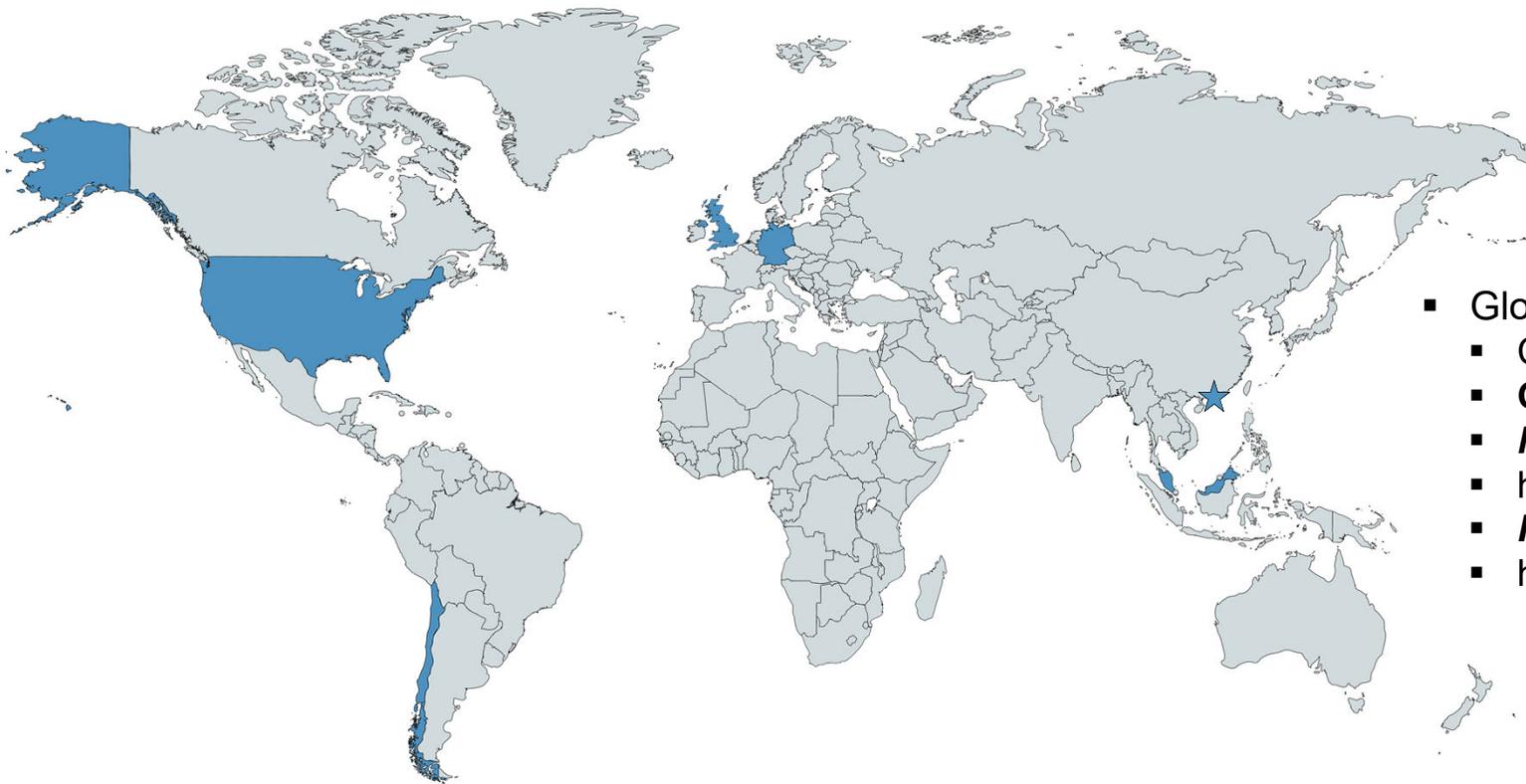
- United States isolates (12)
 - ***SARS-CoV-2/human/USA/USA-WA1/2020****
 - hCoV-19/USA/AZ1/2020
 - hCoV-19/USA/CA1/2020
 - hCoV-19/USA/CA2/2020
 - hCoV-19/USA/CA3/2020
 - hCoV-19/USA/CA4/2020
 - hCoV-19/USA/IL1/2020
 - hCoV-19/USA/NY-PV08410/2020
 - hCoV-19/USA/NY-PV08449/2020
 - hCoV-19/USA/NY-PV09158/2020
 - hCoV-19/USA/NY-PV09197/2020
 - hCoV-19/USA/WI1/2020

All available as isolates from BEI Resources
* = cultured genome sequence publicly available

Italicized = available as gRNA from BEI Resources
Bold = also available as gRNA from ATCC

Global SARS-CoV-2 Isolates Accessioned To-Date

Producing SARS-CoV-2 Isolate



- Global isolates (6)
 - Chile/Santiago_op4d1/2020
 - **Germany/BavPat1/2020**
 - *hCoV-19/Italy/INMI1/2020*
 - hCoV-19/England/02/2020
 - **Hong Kong/VM20001061/2020***
 - hCoV-19/Singapore/2/2020

All available as isolates from BEI Resources
* = cultured genome sequence publicly available

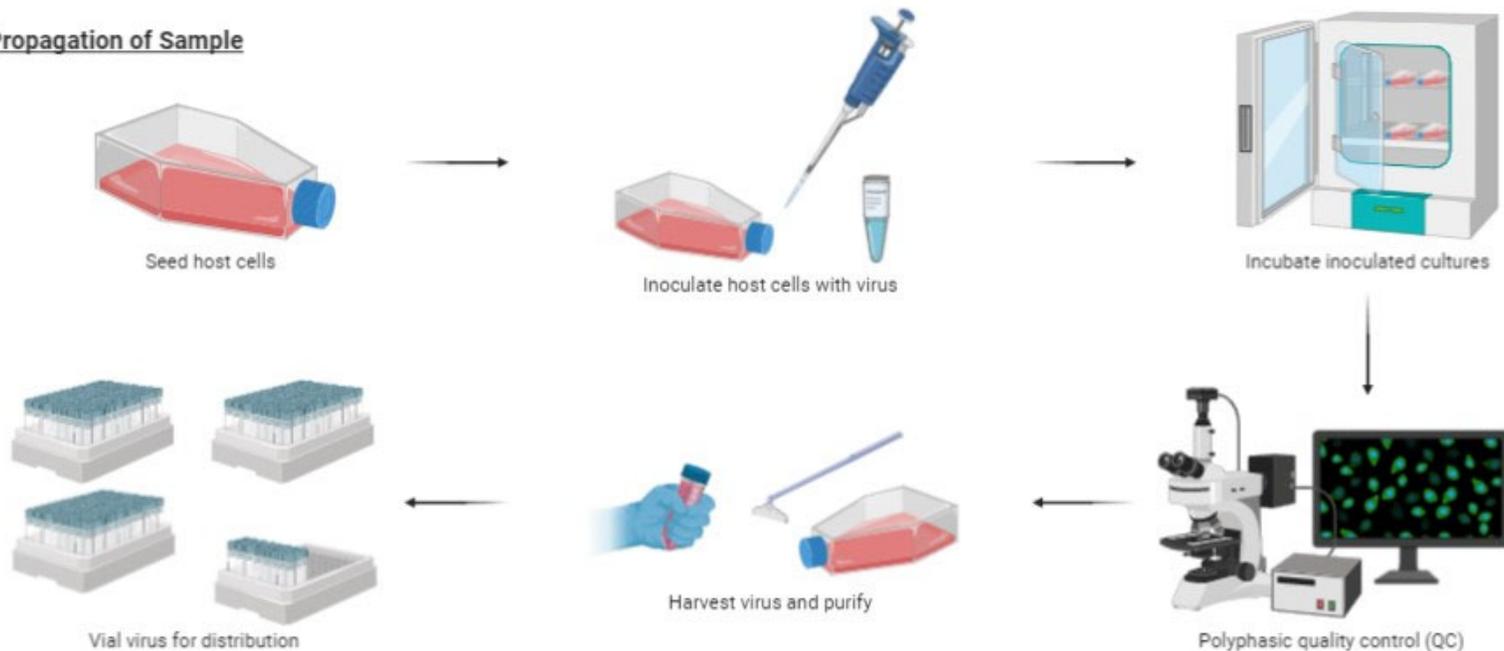
Italicized = available as gRNA from BEI Resources
Bold = also available as gRNA from ATCC

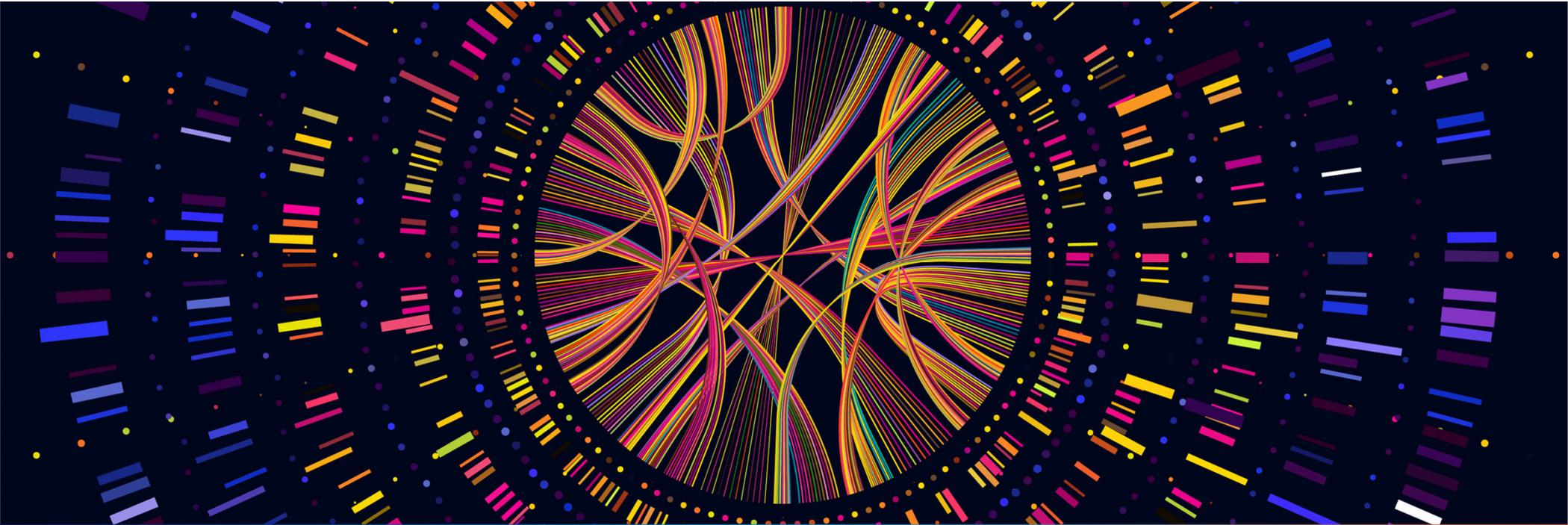
The SARS-CoV-2 Production Process Summarized

Submission of Sample



Propagation of Sample



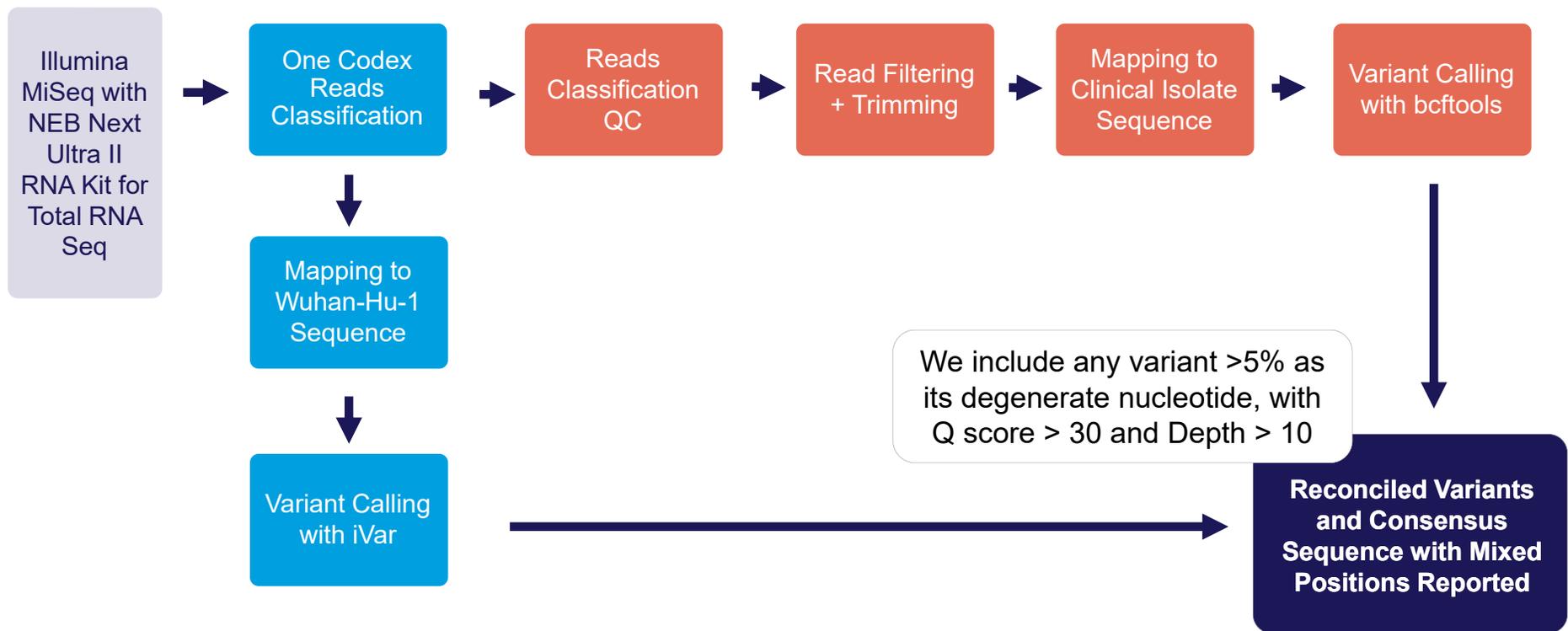


Sequencing SARS-CoV-2 Isolates

Insight from isolate sequencing, variant detection, and variant functional effects

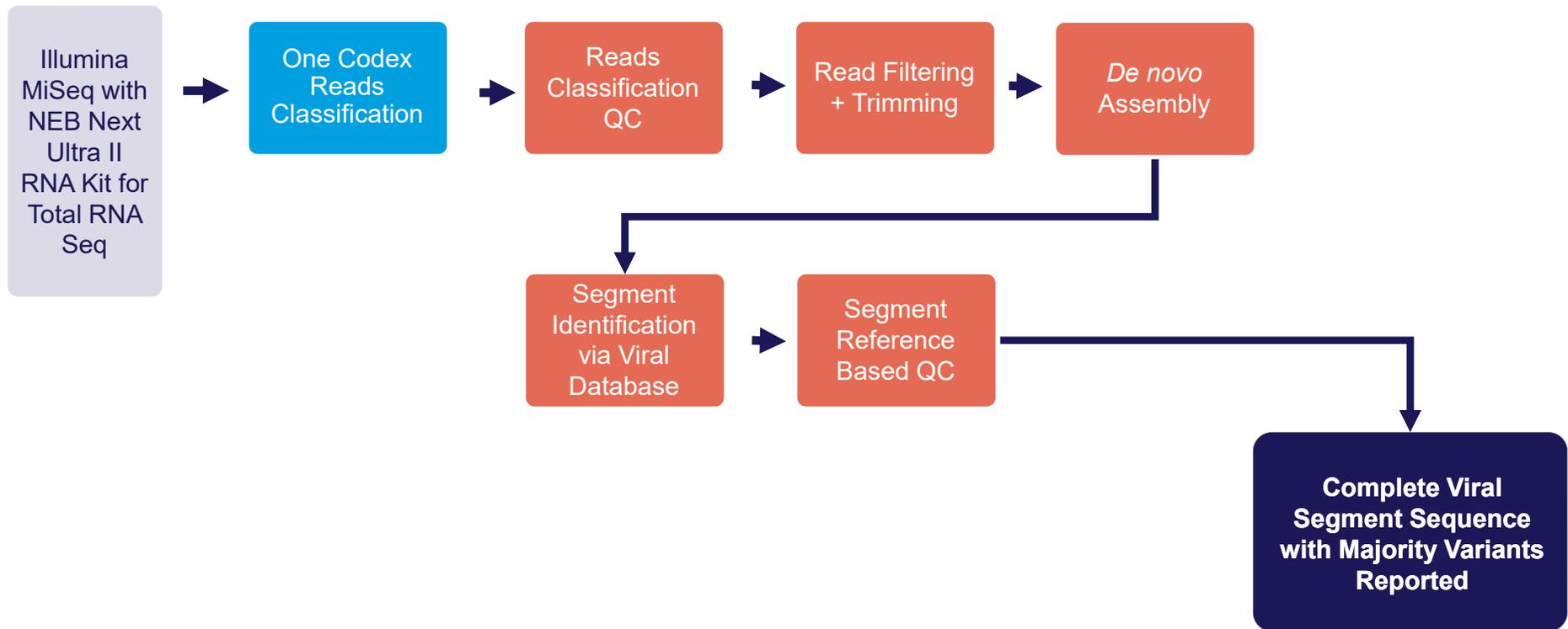
Reference-Based RNA Virus Pipeline

Sequencing SARS-CoV-2 Isolates



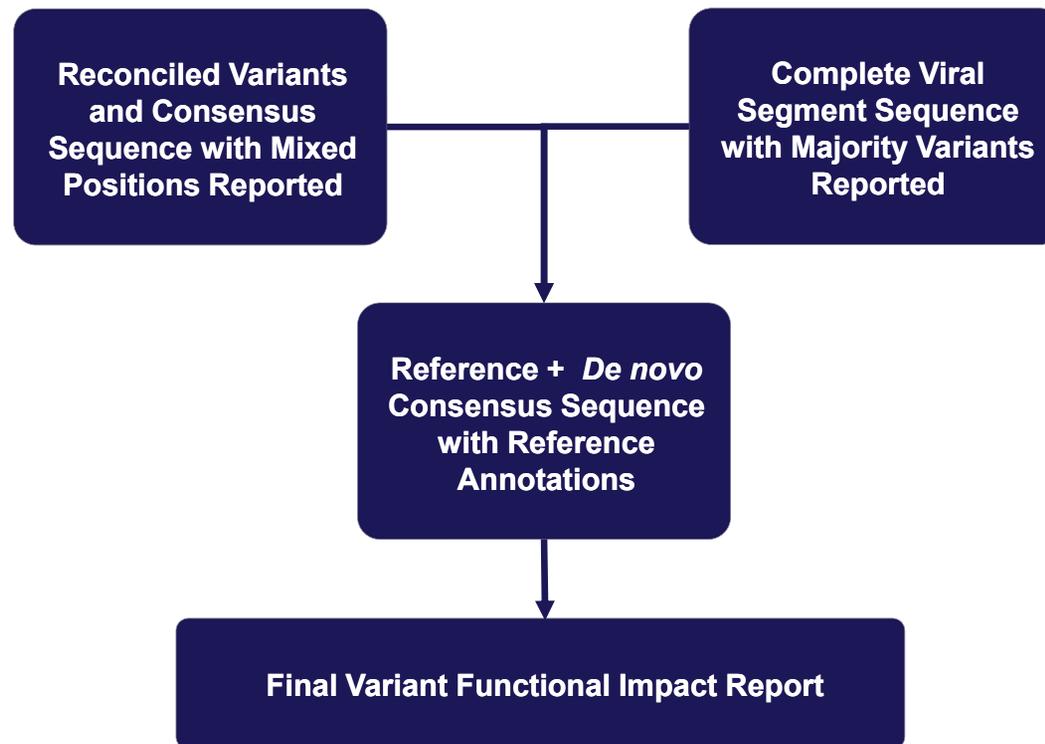
De novo-Based RNA Virus Pipeline

Sequencing SARS-CoV-2 Isolates



Cross Comparison, Annotation, and Functional Assessment

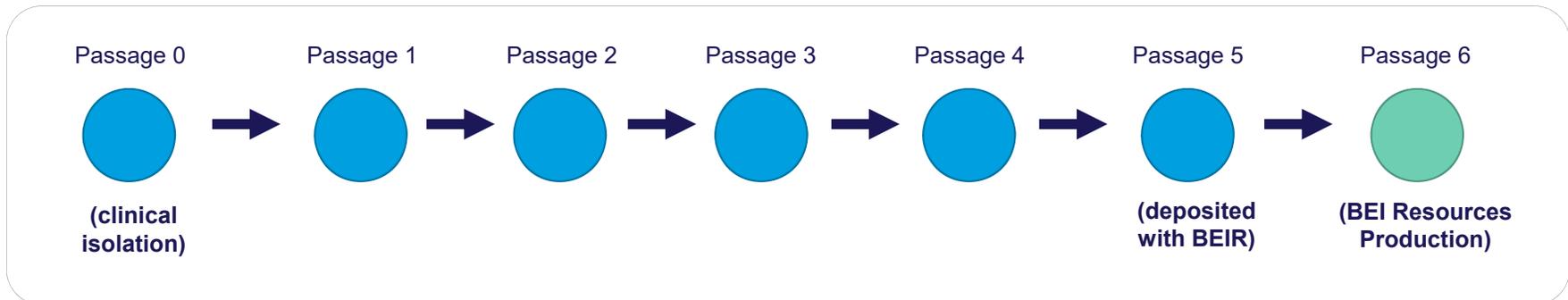
Sequencing SARS-CoV-2 Isolates



Hong Kong Isolate (BEI Resources NR-52282 + ATCC[®] VR-1991D[™])

Sequencing SARS-CoV-2 Isolates

- Originally isolated from a nasopharyngeal aspirate and throat swab from an adult male patient in Hong Kong on January 22, 2020
- Passaged 5 times at the Hong Kong University in Vero E6 cells prior to its deposit with BEI Resources
- Complete genome of the SARS-CoV-2 Hong Kong/VM20001061/2020 clinical isolate (Passage 0) was previously sequenced (GISAID: EPI_ISL_412028) and served as the reference genome



Hong Kong Isolate (BEI Resources NR-52282 + ATCC[®] VR-1991D[™])

Sequencing SARS-CoV-2 Isolates

- Passage 6 was produced by BEI Resources then sequenced by the ATCC Sequencing and Bioinformatics Center (SBC)
- We noted an unexpected 27 nucleotide deletion in the ORF6 region
 - Confirmed with Sanger sequencing
- Was this present before p6 production?
- How common is this mutation?
- What are the structural/functional implications?

Variants to p0	Frequency	Gene	Mutation
c12919t	0.62	ORF1ab (nsp9)	Silent
c21636t	0.87	S	P25L
g23607a	0.96	S	R682Q
y24034t	1.00	S	--
c24566g	0.73	S	Q1002E (Conservative)
Δ27264-27290	0.71	ORF6	Δ22-30 (ΔFKVSIWNLD)
t29862g	1.00	3' UTR	Untranslated

Hong Kong Isolate (BEI Resources NR-52282 + ATCC[®] VR-1991D[™])

Sequencing SARS-CoV-2 Isolates

- Was this present before p6 production? **Yes, the deposited material possessed the deletion**

Variant	p5 Frequency	p6 Frequency	Δ Frequency
c12919t	0.27	0.62	▲ 0.35
c21636t	0.79	0.87	▲ 0.08
g23607a	0.81	0.96	▲ 0.15
y24034t	1.00	1.00	0
c24566g	0.28	0.73	▲ 0.45
Δ27264-27290	0.51	0.71	▲ 0.20
t29862g	1.00	1.00	0

- How common is this mutation? **Rare in GISAID + NCBI**
- Of 24,456 strains in GISAID + NCBI (at time of access: May 13, 2020) only **two** strains contained this mutation
 - hCoV-19/England/CAMB-722A9/2020 (EPI_ISL_439593)
 - hCoV-19/England/CAMB-77F07/2020 (EPI_ISL_441819)

Hong Kong Isolate (BEI Resources NR-52282 + ATCC[®] VR-1991D[™])

Sequencing SARS-CoV-2 Isolates

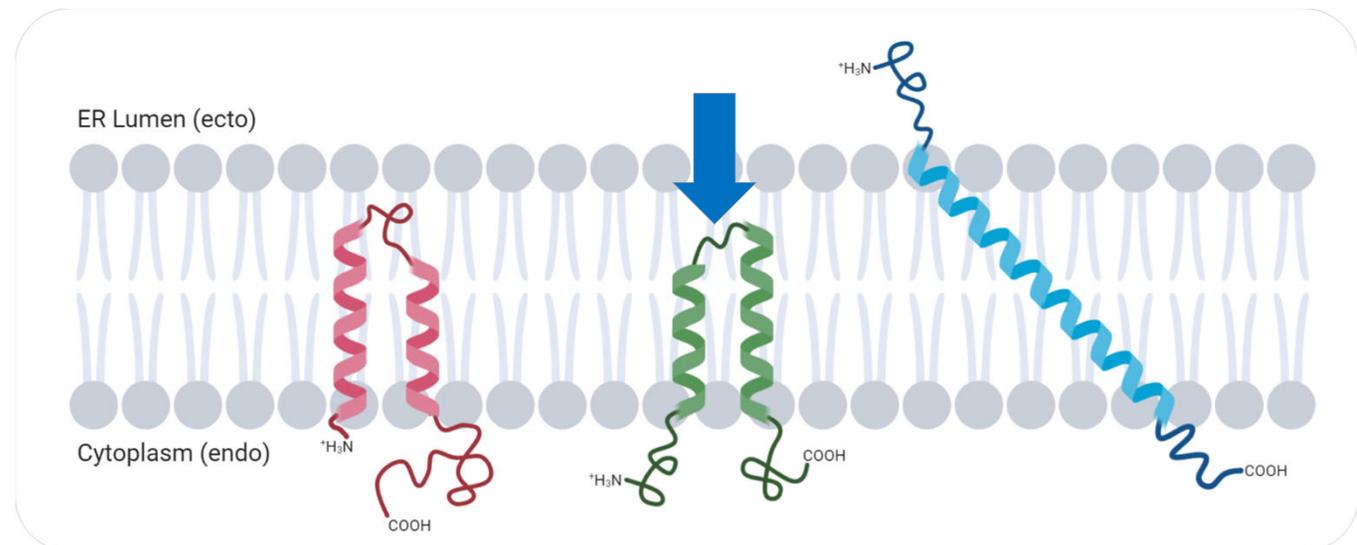
■ Structural implications

- Protein structure predicted with I-TASSER
 - 2 alpha helices → 1 alpha helix
- Transmembrane localization predicted with TMHMM2.0
 - N-endo C-endo (embed) → N-ecto C-ecto (trans)

■ Functional implications

- ORF6 plays a role in interferon (IFN) response in SARS-CoV
- C-terminus critical to interacting with IFN signaling pathway-mediating protein Nmi
- N-terminus has unknown function

Potential transmembrane localizations of the ORF6 protein from SARS-CoV Tor2 (left), SARS-CoV-2 Wuhan-Hu-1 (middle), and NR-52282 (right)



Riojas & Frank *et al.* 2020 ([bioRxiv](https://doi.org/10.1101/2020.06.09.134460)) 10.1101/2020.06.09.134460

Hong Kong Isolate (BEI Resources NR-52282 + ATCC[®] VR-1991D[™])

Sequencing SARS-CoV-2 Isolates

- Our hypothesis: Vero E6 cells are deficient in interferon response → **removal of selective pressure led to deletion?**

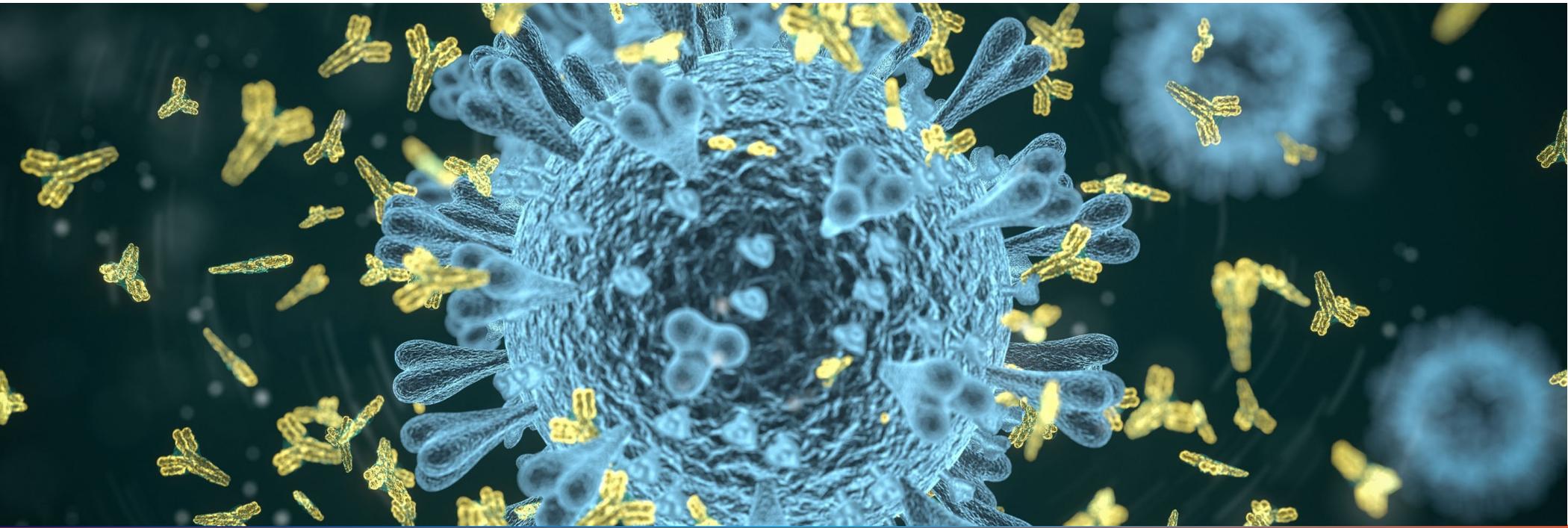


A Rare Deletion in SARS-CoV-2 ORF6 Dramatically Alters the Predicted Three-Dimensional Structure of the Resultant Protein

Riojas & Frank *et al.* 2020

doi: <https://doi.org/10.1101/2020.06.09.134460>

- Passage 6 genome available on GenBank as MT547814.1
- Further supporting evidence of this mutation arising independently was recently published in Addetia *et al.* ([bioRxiv](#))
 - 5 additional clinical isolates with the ORF6 Δ 22-30 deletion
 - Demonstrates SARS-CoV-2 ORF6 interactivity with specific host IFN factors, even with Δ 22-30 mutation
- Appears to disprove our hypothesis



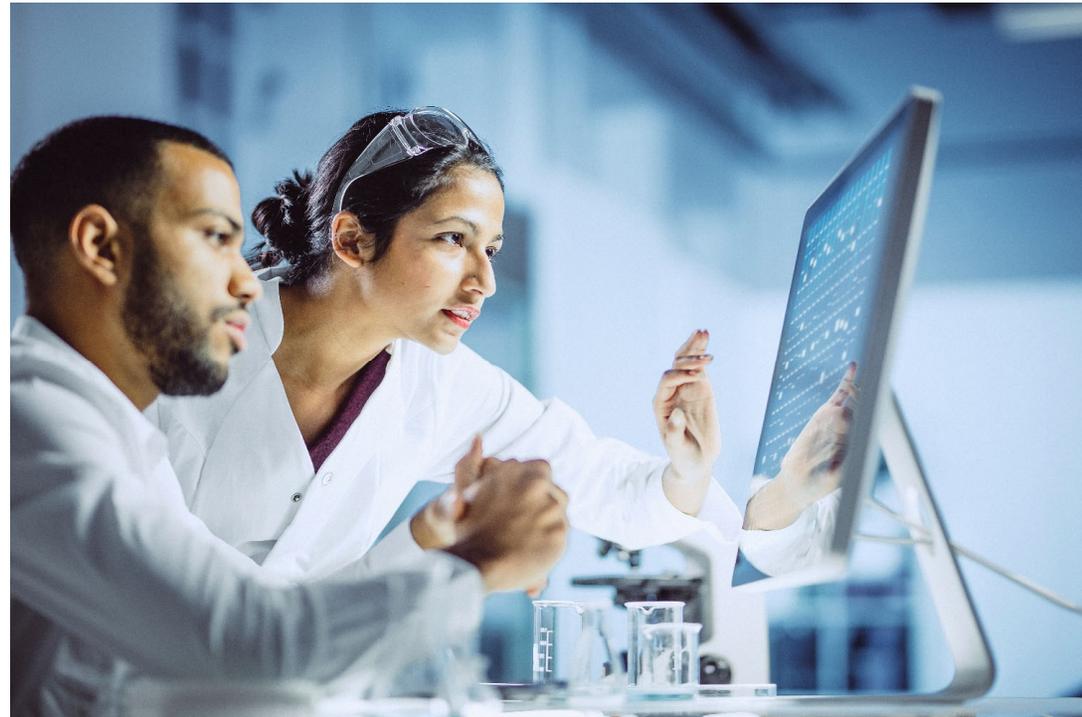
Toward Genomic Fidelity in Cultured SARS-CoV-2

Multiple approaches to reducing novel variants in culture

The Challenge of SARS-CoV-2 Genome Stability

Toward Genomic Fidelity in Cultured SARS-CoV-2

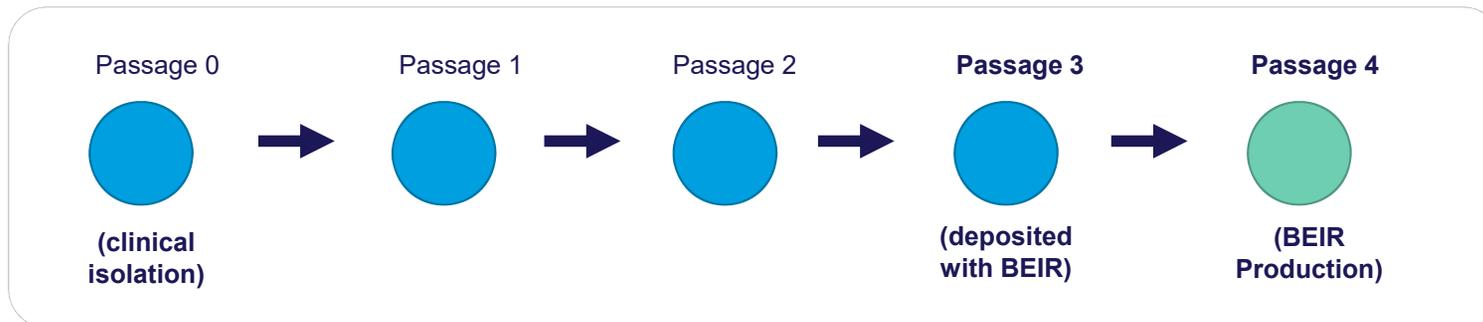
- Genomic stability of RNA viruses is a known challenge, but SARS-CoV-2 is less of a challenge than other RNA viruses
- However, a reasonably stable viral genome is critical for standardized material
- Variables we've investigated to reduce variants in SARS-CoV-2 isolates...
 - Varying MOI and DPI
 - Plaque picking



The WA1 Isolate (BEIR NR-52281 + ATCC® VR-1986D™)

Toward Genomic Fidelity in Cultured SARS-CoV-2

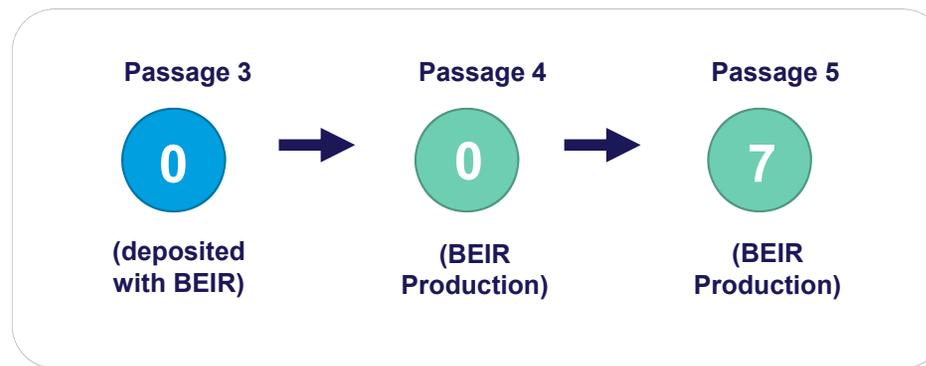
- Originally isolated from an oropharyngeal swab from a patient with a respiratory illness who had recently returned from travel to the affected region of China and developed clinical disease (COVID-19) in January 2020 in Washington, USA.
- Passaged 3 times at CDC in Vero (CCL-81) cells prior to deposit with BEI Resources
- Complete genome of the SARS-CoV-2 USA-WA1/2020 clinical isolate and initial passaging (Passages 0 + 1) were previously sequenced (GenBank: MN985325 + MT020880), and provided as reference genomes



The WA1 Isolate (BEIR NR-52281 + ATCC® VR-1986D™)

Toward Genomic Fidelity in Cultured SARS-CoV-2

Encircled numbers indicate # of variants detected at >5% frequency

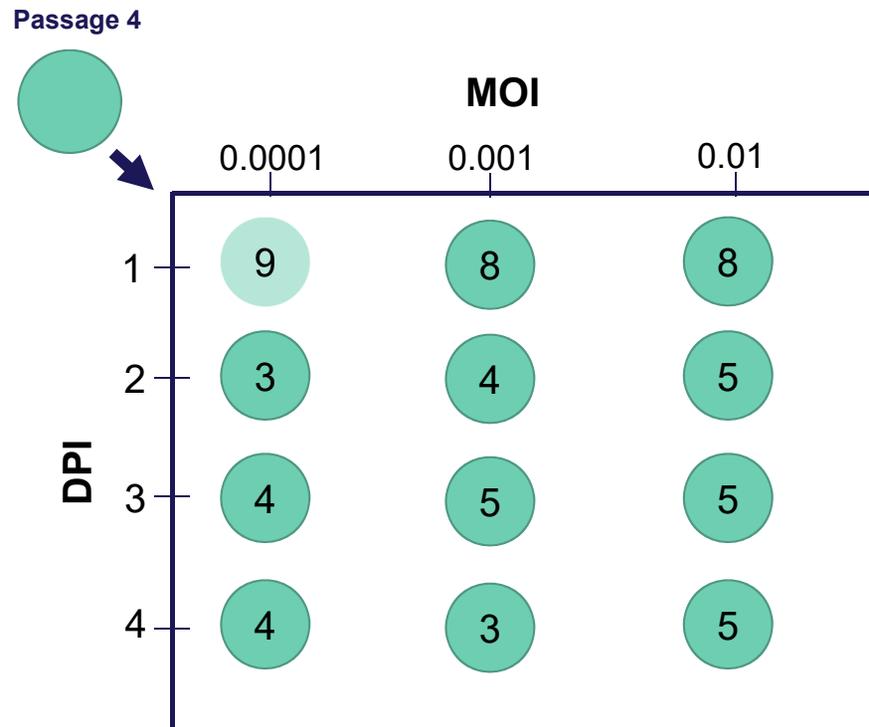


- Passages 4 and 5 were then sequenced for BEI Resources by ATCC SBC
- We saw no variants in passage 4, but 7 variants >5% in passage 5
- What factors can we adjust to increase fidelity to the genome of the deposited material in later passages and reduce the amount of variation?

Varying Multiplicity of Infection and Days Post Infection

Toward Genomic Fidelity in Cultured SARS-CoV-2

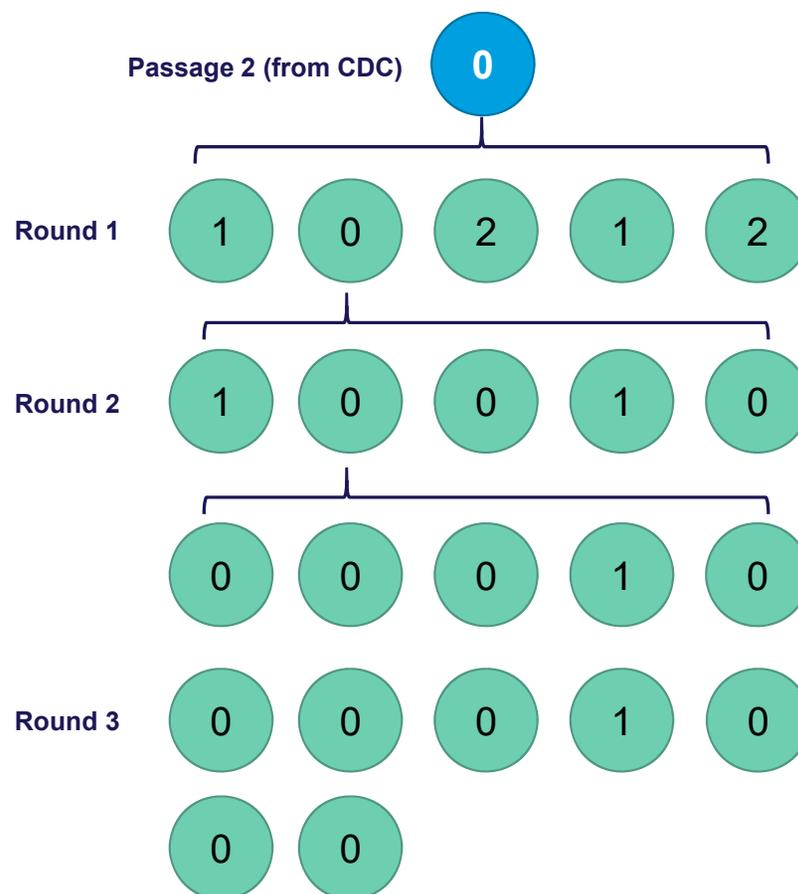
- We wanted to make an educated observation on the effect of **MOI** and **days post infection (DPI)** on number of variant nucleotides >5%
- Preliminary results
 - >1 DPI appears to be negatively correlated
 - MOI may be positively correlated
 - 1DPI + very low MOI suffered from poor sequencing coverage
- We continue to work on optimizing MOI and DPI to reduce variation



Plaque Picking for Purification

Toward Genomic Fidelity in Cultured SARS-CoV-2

- During production, can selection of viral plaques yield more homogenous SARS-CoV-2 populations?
 - Began with Passage 2 from the CDC, known to contain no variants
 - Performed 3 rounds of plaque picking, selecting the plaque with no variants per round
 - Saw progressively smaller portion of variants per plaque per round, suggests this is a viable approach for application requiring high genomic fidelity
- Selection of plaques without variants for continued propagation is being explored





The ATCC Genome Portal

Reference genomes for the ATCC bacteriology collection and beyond

ATCC's Enhanced Authentication Initiative

In 2019, ATCC made a pledge to raise credibility in science, starting with leveraging NGS to enhance our authentication processes

ATCC embarked on a project to...

1. Enrich the characterization of our biological collections
2. Provide whole-genome sequences paired with specific, authenticated materials researchers need to generate credible data



Bacteriology Bioinformatics Best Practices



Extract DNA with optimized, proprietary protocols to get the best quality input material
Avoid “garbage in, garbage out” data and results



Sequence on both Illumina® and Oxford Nanopore Technologies®
Impose strict quality control thresholds to save only highest quality reads per instrument



Combine data from both technologies to achieve high-quality, complete genomes
We perform hybrid genome assembly, leveraging the strengths of both platforms while avoiding biases and weaknesses of them individually



Annotate genomes to enable gene-level analyses
Provide users with a reliable annotation, so they can identify genes of interest rapidly to enable gene-specific research

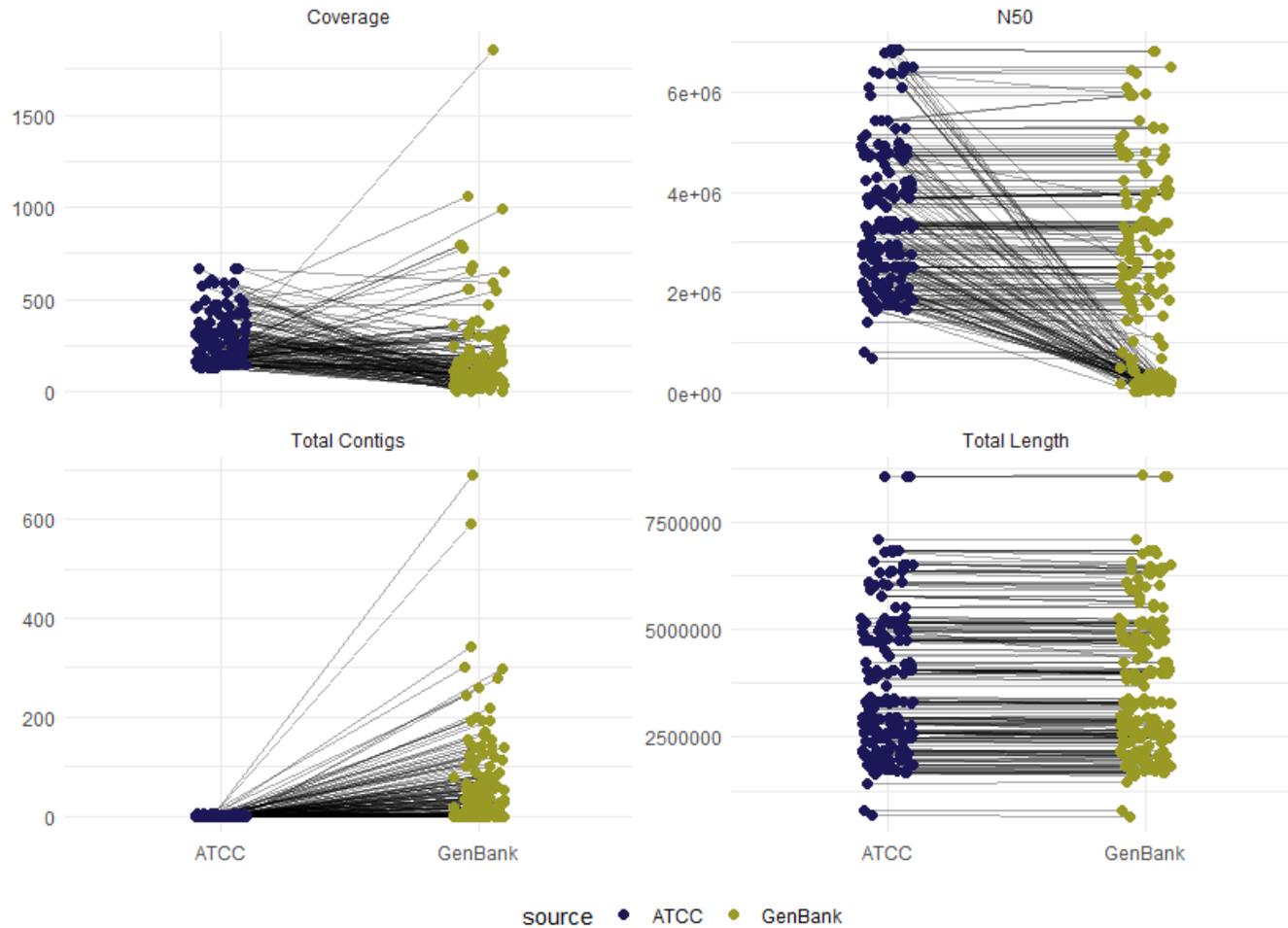


Confirm strain identity against highly curated databases
We’ve partnered with One Codex, an industry leader in bioinformatic bacterial identification, to verify our strain designations by using *k*-mer and genomic distance approaches

Slide 31

FA6 Briana: can this made into a viro focused pipeline?
Frank, Andrew, 10/19/2020

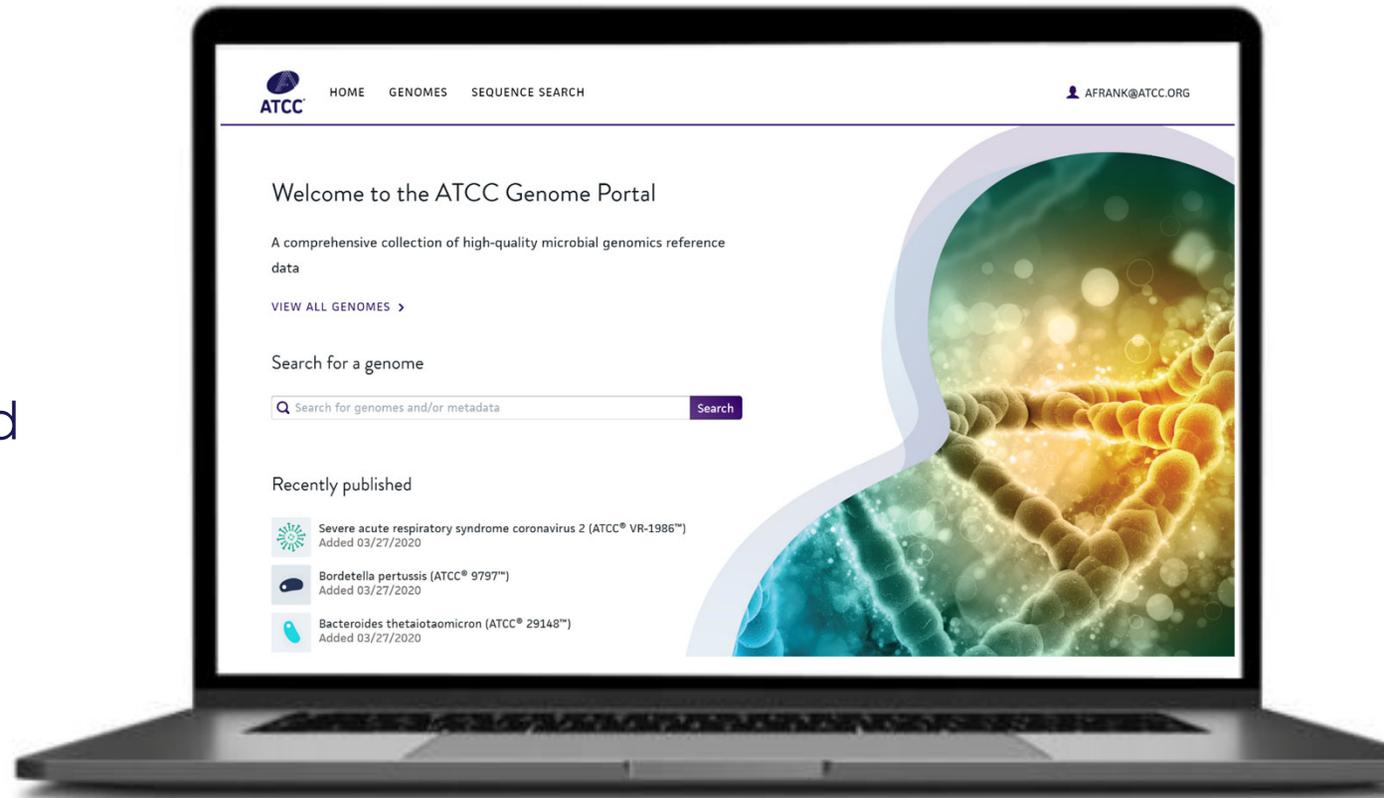
ATCC's Genomes Substantially Improve On Existing Assemblies



Genomes site

genomes.atcc.org

850+ genomes
tied to authenticated
ATCC material



Beyond Bacteriology

The ATCC Genome Portal – genomes.atcc.org

- The ATCC Genome Portal now hosts 6 coronavirus genomes + 36 additional virus genomes from the ATCC virology collection
 - VR-1986™ (2019-nCoV/USA-WA1/2020 RNA)
 - VR-1991™ (2019-nCoV/Hong Kong/VM20001061/2020 RNA)
 - VR-1992™ (2019-nCoV/Italy-INMI1 RNA)
 - VR-1994™ (2019-nCov/Germany/BavPat1/2020 RNA)
 - VR-740™ (Human coronavirus 229E)
 - VR-1558™ (Human coronavirus OC43)

- Coming soon for ATCC viruses...
 - 100 virus genomes from the ATCC virology collection
 - A dedicated tab for virus genomes listing variants + their frequencies to a reference virus genome

ATCC Genome Portal Viral Variant and Annotation View



HOME GENOMES SEQUENCE SEARCH DOCUMENTATION

LOG IN

> unclassified Betacoronavirus > **Severe acute respiratory syndrome coronavirus 2**

Severe acute respiratory syndrome coronavirus 2 (ATCC® VR-1986™)

Overview Genomic Variants Related Genomes Quality Control

Annotation Legend

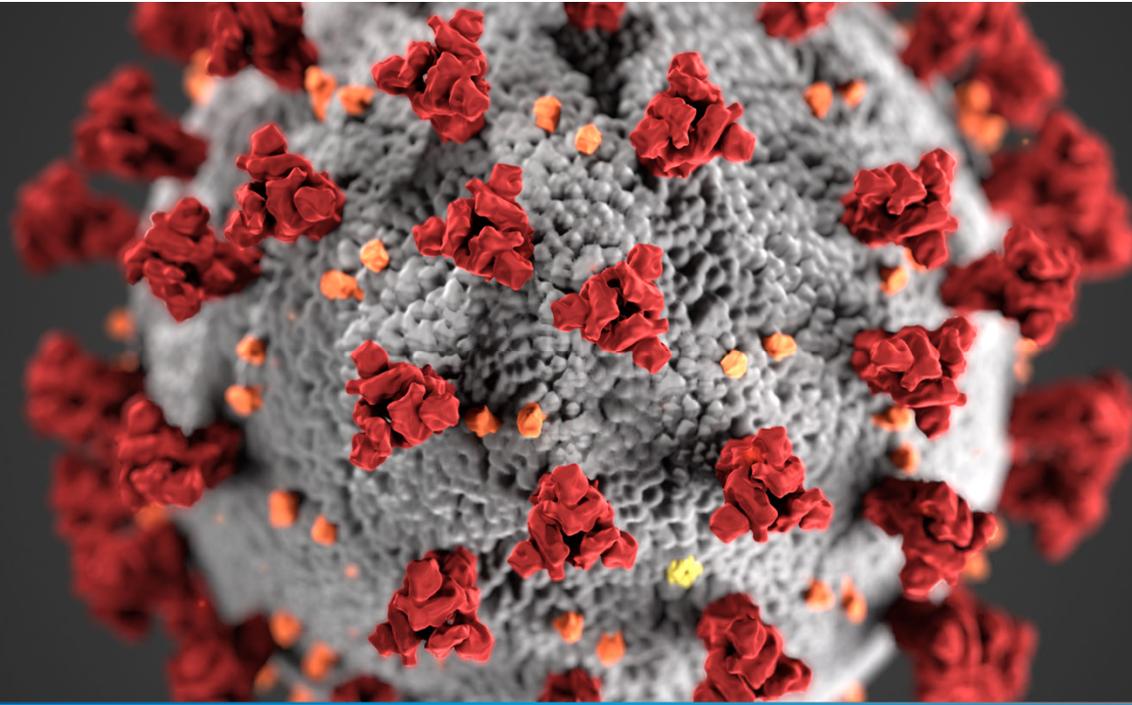


Filter annotations

Download Table CSV

ID	Position	Variant	Gene Name	Gene Product	Type	Jump
1	8782	C->T	ORF1ab	nsp4	mat_peptide	...
1	8782	C->T	ORF1ab	ORF1ab polyprotein	CDS	...
1	8782	C->T	ORF1ab	ORF1a polyprotein	CDS	...
2	18060	C->T	ORF1ab	ORF1a polyprotein	CDS	...
2	18060	C->T	ORF1ab	3'-to-5' exonuclease	mat_peptide	...
3	28144	C->T	ORF8	ORF8 Protein	CDS	...





Committed to Ending the COVID-19 Pandemic

ATCC and BEI Resources SARS-CoV-2 Work Continues

Committed to Ending the COVID-19 pandemic

- ATCC and BEI Resources remain committed to our public and private partners to continue the fight and ending the COVID-19 pandemic
- Both organizations continue to provide new SARS-CoV-2 standards materials on a regular basis, so check back often
- If you need help with ATCC SARS-CoV-2 materials, please contact tech@atcc.org. If you are unable to find material that fits your need, please contact sales@atcc.org.
- If you need help with BEI Resources SARS-CoV-2 materials, please contact contact@beiresources.org

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