

SARS-Related Coronavirus 2, Isolate hCoV-19/USA/MI-UM-10052670540/2023 (Lineage BA.2.86) in VTA Cells

Catalog No. NR-59638

For research use only. Not for use in humans.

Contributor:

Dr. Natalie Thornburg, Centers for Disease Control and Prevention, Atlanta, Georgia, USA

Manufacturer:

BEI Resources

Product Description:

Virus Classification: *Coronaviridae, Betacoronavirus*

Species: Severe acute respiratory syndrome-related coronavirus 2

Strain/Isolate: hCoV-19/USA/MI-UM-10052670540/2023

Original Source: Severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2), isolate hCoV-19/USA/MI-UM-10052670540/2023 was isolated from a human on August 3, 2023, in Michigan, USA.¹

Note: Genome sequence information is provided on the Certificate of Analysis and includes an analysis of all sequence variations observed for each lot.

Comments: Under the nomenclature system introduced by GISAID (Global Initiative on Sharing All Influenza Data), SARS-CoV-2, isolate hCoV-19/USA/MI-UM-10052670540/2023 is assigned lineage BA.2.86 (Pango v.4.3.1 PANGO-v1.22) and GISAID clade GRA using the Phylogenetic Assignment of Named Global Outbreak lineages (PANGO) tool.^{1,2,3} The complete genome of SARS-CoV-2, isolate hCoV-19/USA/MI-UM-10052670540/2023 has been sequenced (GISAID: EPI_ISL_18110065).^{1,2} The following mutations are present in the clinical isolate: Spike A27S, Spike A264D, Spike A570V, Spike D405N, Spike D614G, Spike D796Y, Spike E484K, Spike E554K, Spike F157S, Spike F486P, Spike G142D, Spike G339H, Spike G446S, Spike H69del, Spike H245N, Spike H655Y, Spike I332V, Spike I670V, Spike ins16MPLF, Spike K356T, Spike K417N, Spike L24del, Spike L212I, Spike L216F, Spike L452W, Spike N211del, Spike N440K, Spike N450D, Spike N460K, Spike N481K, Spike N501Y, Spike N679K, Spike N764K, Spike N969K, Spike P25del, Spike P26del, Spike P621S, Spike P681R, Spike P1143L, Spike Q498R, Spike Q954H, Spike R21T, Spike R158G, Spike R403K, Spike R408S, Spike S50L, Spike S371F, Spike S373P, Spike S375F, Spike S477N, Spike S939F, Spike T19I, Spike T376A, Spike T478K, Spike V70del, Spike V127F, Spike V213G, Spike V445H, Spike V483del, Spike Y144del, Spike Y505H, E (Envelope) T9I, M (Membrane) A63T, M A104V, M D3H, M Q19E, M T30A, N (Nucleocapsid) E31del, N G204R, N G243S, N P13L, N Q229K, N R32del, N R203K, N S33del, N S413R, NS3 T223I, NS8 T87I, NSP1

(Non-structural protein 1) S135R, NSP2 (Non-structural protein 2) A31D, NSP3 (Non-structural protein 3) A1892T, NSP3 G489S, NSP3 N1708S, NSP3 T24I, NSP3 V238L, NSP4 (Non-structural protein 4) L264F, NSP4 T327I, NSP4 T492I, NSP5 (Non-structural protein 5) P132H, NSP6 (Non-structural protein 6) F108del, NSP6 G107del, NSP6 S106del, NSP6 V24F, NSP9 (Non-structural protein 9) T35I, NSP12 (Non-structural protein 12) P323L, NSP13 (Non-structural protein 13) R392C, NSP14 (Non-structural protein 14) I42V, NSP15 (Non-structural protein 15) T112I.^{1,2} It was labeled as a variant under monitoring (VUM) GRA (BA.2.86+BA.2.86*), and first detected in Denmark/Israel/USA by the World Health Organization (WHO).^{1,4}

Note: One additional mutation, ORF6 D61L, is present in the GISAID reference sequence, but is not annotated on the GISAID website. Two additional mutations, Spike G35V and Envelope ΔV14, are present in NR-59639 and the reference sequence used for assembly (GenBank: [OR537351](#)) but are not present in the GISAID reference sequence.

In December 2019, an outbreak of a respiratory illness (COVID-19) began in Wuhan, Hubei Province, China. The outbreak is associated with a seafood market and although environmental samples from the market are positive for the novel coronavirus, an association with a particular animal has not been determined.⁵ SARS-CoV-2 has been isolated from patients from several countries and the sequences of some of these isolates have been deposited with GISAID.

Material Provided:

Each vial contains approximately 0.1 mL of cell lysate and supernatant from *Chlorocebus* (formerly *Cercopithecus*) *aethiops* kidney epithelial cells expressing transmembrane protease, serine 2 and human angiotensin-converting enzyme 2 (Vero E6-TMPRSS2-T2A-ACE2) infected with SARS-CoV-2, isolate hCoV-19/USA/MI-UM-10052670540/2023.

Note: If homogeneity is required for your intended use, please purify prior to initiating work.

Packaging/Storage:

NR-59638 was packaged aseptically in screw-capped plastic cryovials. The product is provided frozen and should be stored at -60°C or colder immediately upon arrival. For long-term storage, the vapor phase of a liquid nitrogen freezer is recommended. Freeze-thaw cycles should be avoided.

Growth Conditions:

Host: *Chlorocebus* (formerly *Cercopithecus*) *aethiops* kidney epithelial cells expressing transmembrane protease, serine 2 and human angiotensin-converting enzyme 2 (Vero E6-TMPRSS2-T2A-ACE2; VTA; BEI Resources NR-54970)

Growth Medium: Eagle's Minimum Essential Medium containing Earle's Balanced Salt Solution, non-essential amino acids, 2 mM L-glutamine, 1 mM sodium pyruvate and 1.5 g/L of sodium bicarbonate supplemented with 2% fetal bovine serum, or equivalent

Infection: Cells should be 60% to 70% confluent

Incubation: 3 to 5 days at 37°C and 5% CO₂

Cytopathic Effect: Cell rounding and sloughing

Citation:

Acknowledgment for publications should read “The following reagent was deposited by the Centers for Disease Control and Prevention and obtained through BEI Resources, NIAID, NIH: SARS-Related Coronavirus 2, Isolate hCoV-19/USA/MI-UM-10052670540/2023 (Lineage BA.2.86) in VTA Cells, NR-59638.”

Biosafety Level: 3

Appropriate safety procedures should always be used with this material. Laboratory safety is discussed in the following publication: U.S. Department of Health and Human Services, Public Health Service, Centers for Disease Control and Prevention, and National Institutes of Health. [Biosafety in Microbiological and Biomedical Laboratories \(BMBL\)](#). 6th ed. Washington, DC: U.S. Government Printing Office, 2020.

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Use Restrictions:

SARS-CoV-2 materials provided by BEI Resources under the EUSLA are made available for any legitimate purpose, including commercial purposes as long as they are to rapidly prevent, detect, prepare for, and respond to, the spread or transmission of the 2019 SARS-CoV-2. Any further transfer of the original material or any unmodified progeny must be done under the terms of the EUSLA, documented as described above and you must notify BEI Resources of each subsequent transfer. Any new materials made by you that are not the original material or unmodified progeny are excluded from this

requirement and you are free to share and commercialize those as your materials.

References:

1. [GISAID](#)
2. Rambaut, A., et al. “A Dynamic Nomenclature Proposal for SARS-CoV-2 Lineages to Assist Genomic Epidemiology.” *Nat. Microbiol.* 5 (2020): 1403-1407. PubMed: 32669681.
3. Mercatelli, D. and F. M. Giorgi. “Geographic and Genomic Distribution of SARS-CoV-2 Mutations.” *Front. Microbiol.* (2020): doi.org/10.3389/fmicb.2020.01800. PubMed: 32793182.
4. [WHO](#)
5. Gralinski, L. E. and V. D. Menachery. “Return of the Coronavirus: 2019-nCoV.” *Viruses* 12 (2020): 135. PubMed: 31991541.

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