

SARS-Related Coronavirus 2, Isolate hCoV-19/Scotland/CVR837/2020

Catalog No. NR-53944

Product Description:

SARS-Related Coronavirus 2, Isolate hCoV-19/Scotland/CVR837/2020 was isolated from a throat swab from a human patient diagnosed with COVID-19, on July 17, 2020 in Scotland, United Kingdom. Deposited and labeled as SARS-CoV-2, isolate CVR-GLA-1 prior to the determination of the official name SARS-CoV-2, isolate hCoV-19/Scotland/CVR837/2020. NR-53944 lot 70041278 was produced by infecting *Cercopithecus aethiops* kidney epithelial cells with human signaling lymphocytic activation molecule (Vero-hSLAM) and incubating in Dulbecco's Minimum Essential Medium (ATCC® 30-2002™) supplemented with 2% fetal bovine serum (ATCC® 30-2020™) and 1% penicillin/streptomycin solution (ATCC® 30-2300™) for 5 days at 37°C with 5% CO₂.

Passage History:

VE(1)/VhSLAM(1) (University of Glasgow Centre for Virus Research/BEI Resources); VE = Vero E6 cells; VhSLAM = Vero-hSLAM cells

Lot: 70041278

Manufacturing Date: 29DEC2020

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| TEST | SPECIFICATIONS | RESULTS |
|---|---|--|
| Identification by Infectivity in Vero-hSLAM Cells | Cell rounding and detachment | Cell rounding and detachment |
| Next-Generation Sequencing (NGS) of Complete Genome Using Illumina® iSeq™ 100 Platform (Refer to Appendix I for NGS information) | ≥ 98% identity with SARS-CoV-2, isolate hCoV-19/Scotland/CVR837/2020 (GISAID: EPI_ISL_461705) | 99.99% identity with SARS-CoV-2, isolate hCoV-19/Scotland/CVR837/2020 (GISAID: EPI_ISL_461705) |
| Titer by TCID₅₀ Assay in Vero-hSLAM Cells by Cytopathic Effect¹ (7 days at 37°C and 5% CO ₂) | Report results | 2.8 × 10 ⁶ TCID ₅₀ per mL |
| Sterility (21-day incubation) Harpo's HTYE broth, 37°C and 26°C, aerobic ² Trypticase Soy broth, 37°C and 26°C, aerobic Sabouraud broth, 37°C and 26°C, aerobic Sheep blood agar, 37°C, aerobic Sheep blood agar, 37°C, anaerobic Thioglycollate broth, 37°C, anaerobic DMEM with 10% FBS, 37°C, aerobic | No growth No growth No growth No growth No growth No growth No growth | No growth No growth No growth No growth No growth No growth No growth |
| Mycoplasma Contamination Agar and broth culture (14-day incubation at 37°C) DNA detection by PCR of extracted Test Article nucleic acid | None detected None detected | None detected None detected |

¹The Tissue Culture Infectious Dose 50% (TCID₅₀) endpoint is the 50% infectious endpoint in cell culture. The TCID₅₀ is the dilution of virus that under the conditions of the assay can be expected to infect 50% of the culture vessels inoculated, just as a Lethal Dose 50% (LD₅₀) is expected to kill half of the animals exposed. A reciprocal of the dilution required to yield the TCID₅₀ provides a measure of the titer (or infectivity) of a virus preparation.

²Atlas, Ronald M. *Handbook of Microbiological Media*. 3rd ed. Ed. Lawrence C. Parks. Boca Raton: CRC Press, 2004, p. 798.

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27 APR 2021

Program Manager or designee, ATCC Federal Solutions

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APPENDIX I: NGS Information for NR-53944 lot 70041278

Sequence analysis using SBC v2.0 pipeline resulted in the discovery of two SNPs when compared to the reference sequence from EPI_ISL_461705 (see Table I below). Additionally, both the reference sequence EPI_ISL_461705 and NR-53944 lot 70041278 contained five SNPs when compared to GenBank MN908947 (SARS-CoV-2, isolate Wuhan-Hu-1, complete genome) (see Table II below). Quality scores over 60 indicate it is improbable that the variant call is incorrect.

Table I: Variants with different nucleotides between NR-53944 lot 70041278 and reference sequence EPI_ISL_461705

| Position in NR-53944_70041278 Sequence | Position in EPI_ISL_461705 Reference Sequence | Position in MN908947 Wuhan-Hu-1 Sequence | Reported MN908947 Wuhan-Hu-1 Sequence | Reported EPI_ISL_461705 Reference Sequence | Identified Alternative Base | Quality | Variant Type | Length of Variant | Frequency of Variant |
|--|---|--|---------------------------------------|--|-----------------------------|---------|--------------|-------------------|----------------------|
| 14625 | 14625 | 14679 | T | T | C | 274 | SNP | 1 | 0.058824 |
| 21498 | 21498 | 21552 | C | C | T | 9023 | SNP | 1 | 0.341141 |

Table II: Variants with different nucleotides between NR-53944 lot 70041278 and GenBank MN908947 (SARS-CoV-2, isolate Wuhan-Hu-1, complete genome)

| Position in NR-53944_70041278 Sequence | Position in EPI_ISL_461705 Reference Sequence | Position in MN908947 Wuhan-Hu-1 Sequence | Reported MN908947 Wuhan-Hu-1 Sequence | Reported EPI_ISL_461705 Reference Sequence | Identified Alternative Base | Quality | Variant Type | Length of Variant | Frequency of Variant |
|--|---|--|---------------------------------------|--|-----------------------------|---------|--------------|-------------------|----------------------|
| 187 | 187 | 241 | C | T | T | N/A | SNP | 1 | 1.000000 |
| 2983 | 2983 | 3037 | C | T | T | N/A | SNP | 1 | 1.000000 |
| 14354 | 14354 | 14408 | C | T | T | N/A | SNP | 1 | 1.000000 |
| 23349 | 23349 | 23403 | A | G | G | N/A | SNP | 1 | 1.000000 |
| 24334 | 24334 | 24388 | A | T | T | N/A | SNP | 1 | 1.000000 |