

SARS-Related Coronavirus 2, Isolate New York-PV08410/2020

Catalog No. NR-53514

Product Description:

Severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2), isolate New York-PV08410/2020 was isolated on March 16, 2020 from a nasal swab collected from a patient with a fatal respiratory illness in New York, USA. NR-53514 lot 70036345 was produced by infecting *Cercopithecus aethiops* kidney cells (Vero E6; ATCC® CRL-1586™) with the deposited material in Eagle's Minimum Essential Medium (ATCC® 30-2003) supplemented with 2% fetal bovine serum (ATCC® 30-2020) for 3 days at 37°C with 5% CO₂.

Passage History:

VE6(1)/VE6(2) (The Icahn School of Medicine at Mount Sinai Medical School/BEI Resources); VE6 = Vero E6 cells

Lot: 70036345

Manufacturing Date: 15JUN2020

TEST	SPECIFICATIONS	RESULTS
Identification by Infectivity in Vero E6 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 NY-PV08410 (GenBank: MT370900.1)	100% identity with SARS-CoV-2, isolate NY-PV08410 (GenBank: MT370900.1)
Titer by TCID₅₀ Assay in Vero E6 Cells by Cytopathic Effect¹ (6 days at 37°C and 5% CO ₂)	Report results	1.6 × 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.

/Heather Couch/

Heather Couch

20 AUG 2020

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APPENDIX I: NGS Information for NR-53514 lot 70036345

Reference sequence from GenBank MT370900.1 contained ambiguous bases (N; referred to as Amb Ref in the Table below) in nine regions. Sequence analysis of NR-53514_70036345 resulted in filling-in of these ambiguous regions of the reference sequence MT370900.1 and demonstrated that these nine ambiguous regions matched GenBank MN908947.3 (SARS-CoV-2, isolate Wuhan-Hu-1, complete genome) sequence. Two SNPs were discovered in NR-53514_70036345 when compared to the reference sequence MT370900.1. Additionally, both the reference sequence MT370900.1 and NR-53514_70036345 contained six SNPs when compared to GenBank MN908947.3 (see Table below). Quality scores over 60 indicate it is improbable that the variant call is incorrect.

Position in NR-53514_70036345 Sequence	Position in MT370900 Reference Sequence	Position in MN908947 Sequence	Reported MN908947 Sequence	Reported MT370900 Reference Sequence	Identified Alternative Base	Quality	Variant Type	Length of Variant	Frequency of Variant
186	186	241	C	T	T	n/a	SNP	1	1.0000000
1004	1004	1059	C	T	T	n/a	SNP	1	1.0000000
2982	2982	3037	C	T	T	n/a	SNP	1	1.0000000
6321	6321	6376	TAATCTTG CC	N (×10)	TAATCTTG CC	n/a	Amb Ref	10	1.0000000
6373	6373	6428	*	N (×698)	*	n/a	Amb Ref	698	1.0000000
14353	14353	14408	C	T	T	n/a	SNP	1	1.0000000
21157	21157	21212	*	N (×170)	*	n/a	Amb Ref	170	1.0000000
21355	21355	21410	*	N (×58)	*	n/a	Amb Ref	58	1.0000000
21417	21417	21472	*	N (×80)	*	n/a	Amb Ref	80	1.0000000
22157	22157	22212	CT	NN	CT	n/a	Amb Ref	2	1.0000000
22173	22173	22228	TTTAGAAC C	NNNNNNN NN	TTTAGAAC C	n/a	Amb Ref	9	1.0000000
22191	22191	22246	*	N (×20)	*	n/a	Amb Ref	20	1.0000000
22218	22218	22273	GTT	NNN	GTT	n/a	Amb Ref	3	1.0000000
23348	23348	23403	A	G	G	n/a	SNP	1	1.0000000
23551	23551	23606	C	C	T	222	SNP	1	0.4391635
25508	25508	25563	G	T	T	n/a	SNP	1	1.0000000
27506	27506	27561	G	G	T	220	SNP	1	0.8291815

* If N > 10, the sequence of the variant is not reported in the table above. For all nucleotides in these variants, the identified alternative base is the same as the reported MN908947.3 sequence.