

## Certificate of Analysis for NR-59606

# Middle East Respiratory Syndrome-Related Coronavirus, Isolate Hu/Riyadh-KSA-18013832/2018

### Catalog No. NR-59606

#### **Product Description:**

Middle East Respiratory Syndrome-Related coronavirus (MERS-CoV), isolate Hu/Riyadh-KSA-18013832/2018 was isolated from a nasopharyngeal swab from a patient with respiratory illness on August 30, 2018, in the Kingdom of Saudi Arabia (KSA). NR-59606 lot 70070749 was produced by infecting human colorectal adenocarcinoma cells (Caco-2; ATCC® HTB-37™) with the deposited material and incubating in Eagle's Minimum Essential Medium (ATCC® 30-2003™) supplemented with 2% fetal bovine serum (ATCC® 30-2020™) for 2 days at 37°C with 5% CO₂ to produce this lot. The cells and supernatant were spin-clarified at 1500 × g for 10 minutes at 4°C.

#### Passage History:

V(3)/C(1) (Centers for Disease Control and Prevention/BEI Resources); V = Vero cells, C = Caco-2

Lot: 70070749 Manufacturing Date: 16AUG2024

TEST	SPECIFICATIONS	RESULTS  Cell rounding and syncytia formation	
Identification by Infectivity in Caco-2 Cells	Cell rounding and syncytia formation		
Next-Generation Sequencing (NGS) of Complete Genome Using Illumina® iSeq™ 100 Platform (Refer to Appendix I for NGS information)	≥ 98% identity with MERS, Hu/Riyadh-KSA- 18013832/2018 (GenBank: MN723544)	99.98% identity with MERS, Hu/Riyadh-KSA- 18013832/2018 (GenBank: MN723544)	
Genome Copy (GC) Number by qPCR	Report results	9.4 × 10 <sup>9</sup> GC per mL	
Titer by TCID₅ Assay in Caco-2 Cells by Cytopathic Effect <sup>1,2</sup> (5 days at 37°C with 5% CO₂)	Report results	1.4 × 10 <sup>8</sup> TCID <sub>50</sub> /mL	
Sterility (21-day incubation) Harpo's HTYE broth, 37°C and 26°C, aerobic <sup>3</sup>	No growth	No growth	
Trypticase Soy broth, 37°C and 26°C, aerobic Sabouraud broth, 37°C and 26°C, aerobic	No growth No growth	No growth No growth	
Sheep blood agar, 37°C, aerobic Sheep blood agar, 37°C, anaerobic	No growth No growth	No growth	
Thioglycollate broth, 37°C, anaerobic DMEM with 10% FBS, 37°C, aerobic	No growth No growth	No growth No growth	
Mycoplasma Contamination			
Agar and broth culture (14-day incubation at 37°C)	None detected	None detected	
DNA detection by PCR of extracted Test Article nucleic acid	None detected	None detected	

<sup>&</sup>lt;sup>1</sup>The Tissue Culture Infectious Dose 50% (TCID<sub>50</sub>) endpoint is the 50% infectious endpoint in cell culture. The TCID<sub>50</sub> 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% (LD<sub>50</sub>) is expected to kill half of the animals exposed. A reciprocal of the dilution required to yield the TCID<sub>50</sub> provides a measure of the titer (or infectivity) of a virus preparation. <sup>2</sup>Titer was determined by cytopathic effect (CPE) and completed in triplicate (8.9 × 10<sup>7</sup> per mL, 1.6 × 10<sup>8</sup> per mL and 1.6 × 10<sup>8</sup> per mL). The average of the three values is reported.

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<sup>&</sup>lt;sup>3</sup>Atlas, Ronald M. Handbook of Microbiological Media. 3rd ed. Ed. Lawrence C. Parks. Boca Raton: CRC Press, 2004, p. 798.



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/Sonia Bjorum Brower/ Sonia Bjorum Brower

13 SEP 2024

Technical Manager or designee, ATCC Federal Solutions

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#### APPENDIX I: NGS Information for NR-59606 lot 70070749

Sequence analysis using fastp 0.23.4 and variant caller LoFreq resulted in the discovery of seven SNPs when compared to Middle East respiratory syndrome-related coronavirus strain Hu/Riyadh-KSA-18013832/2018, complete genome (GenBank: MK462253.1) (see Table I below).

Table I: Variants with different nucleotides between NR-59606 lot 70070749 and MK462253.1 (Middle East respiratory

syndrome-related coronavirus strain Hu/Riyadh-KSA-18013832/2018, complete genome)

Variant Type	Variant Position and Identified Alternative Base	Coverage	Length of Variant	Frequency of Variant	Gene (Region)	Amino Acid Mutation
SNP	C32T	491	1	100.0000%	3'UTR	Untranslated
SNP	A15629G	512	1	5.6641%	ORF1ab	K5118E
SNP	T19395A	662	1	8.1571%	ORF1ab	L6373Q
SNP	C21149A	423	1	100.0000%	ORF1ab	L6958I
SNP	C25009T	1236	1	100.0000%	S protein	S1185L
SNP	T26994A	707	1	5.9406%	ORF5	L52Q
SNP	T26994G	707	1	6.0820%	ORF5	L52Q

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