SUPPORTING INFECTIOUS DISEASE RESEARCH

SARS-Related Coronavirus 2, USA-WA1/2020 Recombinant Infectious Molecular Clone Plasmid Kit

Catalog No. NR-53762

Product Description:

Note: The vial labels for NR-53752 to NR-53758 indicate these products are a molecular clone in vector pU57. The correct vector is pUC57 and each plasmid produces a viral fragment that must be combined with additional fragments to produce the molecular clone. The NR-53755 label also lists this clone as wildtype (WT); however, NR-53755 is not WT and includes a T15102A silent mutation. The vectors for the recombinant infectious molecular clone from severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2), USA-WA1/2020 (GenBank: MT461669) was designed by RT-PCR amplification of SARS-CoV-2 virus (GenBank: MT020880) with restriction sites and four-nucleotide cohesive ends at the 5' and 3' insert termini and subcloned into the pUC57 expression vector.

The deposited plasmids were transformed into One Shot[™] TOP10 *E. coli* (Invitrogen[™] C404003), grown in Luria-Bertani or Terrific broth with ampicillin (100 µg per mL) for 1 day at 37°C in an aerobic atmosphere, extracted using a Plasmid *Plus* Maxi Kit (QIAGEN[®] 12963) and vialed in TE buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8.0).

Note: Infectious viral particles produced by use of this kit are a BSL3 organism. Virus production should be performed with appropriate biosafety controls.

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COMPONENT NUMBER	DESCRIPTION	LOT NUMBER	DATE OF MANUFACTURE
NR-53752	cDNA fragment A	70038955	16SEP2020
NR-53753	cDNA fragment B	70038946	16SEP2020
NR-53754	cDNA fragment C	70041812	19FEB2021
NR-53755	cDNA fragment D	70038948	16SEP2020
NR-53756	cDNA fragment E	70038949	16SEP2020
NR-53757	cDNA fragment F	70038950	16SEP2020
NR-53758	cDNA fragment G	70038951	16SEP2020
NR-53761	sgRNA-N	70038954	16SEP2020

Table 1: Molecular Clone Plasmid Kit Components

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Fable 2: Virus Fragment Plasmids (NR-53752 to NR-53758)					
TEST	SPECIFICATIONS	RESULTS			
Next-Generation DNA Sequencing	Report results	Consistent with depositor reported size ¹			
Genotypic Analysis Sequencing of insertion	≥ 99% sequence identity to depositor's sequence	100% sequence identity to depositor's sequence ^{2,3}			
Antibiotic Resistance					
Ampicillin (encoded by beta-lactamase gene <i>bla</i>) ⁴	<i>bla</i> sequence present	<i>bla</i> sequence present			
Agarose Gel Electrophoresis					
NR-53/52 Disposition with Soll (pro viol)	E E kh and a 2 kh	E E kh and a 2 kh (Figure 1)			
Digestion with Sall (pre-vial)	~ 5.5 KD and ~ 3 KD	\sim 5.5 kb and \sim 3 kb (Figure 1)			
NR-53753	~ 5.5 KD, ~ 1.3 KD and ~ 1.3 KD	\sim 5.5 kb, \sim 1.3 kb and \sim 1.3 kb (Figure 1)			
Digestion with Bsal (pre-vial)	~ 5 kb, ~ 1.5 kb and ~ 1.5 kb	~ 5 kb, ~ 1.5 kb and ~ 1.5 kb (Figure 2)			
Digestion with <i>Bam</i> HI + <i>Sal</i> Í (pre-vial)	~ 5 kb and ~ 3 kb	~ 5 kb and ~ 3 kb (Figure 2)			
Digostion with RsmBl (pro vial)	~ 4 kb ~ 2 kb and ~ 0.4 kb	≈ 4 kb ≈ 2 kb and ≈ 0.4 kb (Figure 3)			
NR-53758	~ 4 KD, ~ 2 KD and ~ 0.4 KD	~ 4 KD, ~ 2 KD and ~ 0.4 KD (Figure 5)			
Digestion with <i>Kpn</i> I and <i>SaI</i> I	~ 4.5 kb and ~ 2.5 kb	~ 4.5 kb and ~ 2.5 kb (Figure 4)			
Concentration by PicoGreen [®] Measurement					
NR-53752	≥ 2 µg/mL	0.8 μg in 30 μL per vial (27 μg/mL)			
NR-53753	≥ 2 µg/mL	0.4 μ g in 20 μ L per vial (20 μ g/mL)			
NR-53754	≥ 2 µg/mL	0.3 μ g in 20 μ L per vial (14 μ g/mL)			
NR-53755	≥ 2 µg/mL	1.7 μ g in 30 μ L per vial (56 μ g/mL)			
NR-53756	≥ 2 µg/mL	0.7 μg in 30 μL per vial (24 μg/mL)			
NR-53757	≥ 2 µg/mL	0.4 μg in 20 μL per vial (22 μg/mL)			
NR-53758	≥ 2 µg/mL	0.4 μg in 20 μL per vial (18 μg/mL)			
Amount per Vial					
NR-53752	Report results	0.8 µg			
NR-53753	Report results	0.4 µg			
NR-53754	Report results	0.3 µg			
NR-53755	Report results	1.7 µg			
NR-53756	Report results	0.7 µg			
NR-53757	Report results	0.4 µg			
NR-53758	Report results	0.4 µg			
OD ₂₆₀ /OD ₂₈₀ Ratio (pre-vial)	1.7 to 2.1	1.9 to 2.0			
Effective Bacterial Transformation					
Invitrogen [™] One Shot [™] TOP10 <i>E. coli</i> ≥ 50 colonies per ng ≥ 50 colonies per ng					

I ne sequence was assembled pre-vial using the depositor's predicted sequence as the reference sequence. The complete plasmid sequence and map are provided on the BEI Resources webpage.

²The NR-53753 insert has two point mutations compared to the deposited GenBank sequence: T5409C (missense mutation resulting in ORF1ab mutation L1715S) and T8782C (silent mutation).

³The sequence MT461669 includes a silent mutation T15102A compared to the SARS-CoV-2, USA-WA1/2020 sequence (GenBank: MT020880).

⁴The antibiotic ampicillin degrades quickly during growth. Bacterial stationary phase should be minimized during plasmid replication to avoid plasmid loss and increased antibiotic concentrations may be necessary.

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TEST	SPECIFICATIONS	RESULTS
Next-Generation DNA Sequencing	~ 4490 base pairs	4490 base pairs ¹
Genotypic Analysis		
Sequencing of insert (~ 1730 base pairs)		
N gene and 3' UTR	≥ 99% sequence identity to SARS-CoV-2, USA-WA1/2020 (GenBank: MT020880.1)	100% sequence identity to SARS-CoV-2, USA-WA1/2020 (GenBank: MT020880.1)
T7 promoter sequence	T7 promoter sequence confirmed	T7 promoter sequence confirmed
Leader sequence (75 base pairs)	Leader sequence confirmed	Leader sequence confirmed
Poly-A tail sequence (25 base pairs)	Poly-A tail sequence confirmed	Poly-A tail sequence confirmed ²
Antibiotic Resistance		
Ampicillin (encoded by beta-lactamase gene bla) ³	bla sequence present	<i>bla</i> sequence present
Agarose Gel Electrophoresis		
Digestion with Sall (pre-vial)	~ 2.7 kb and ~ 1.8 kb	~ 2.7 kb and ~ 1.8 kb (Figure 5)
Concentration by PicoGreen [®] Measurement	≥ 2 µg/mL	0.1 μg in 20 μL per vial (5 μg/mL)
Amount per Vial	Report results	0.1 μg per vial
OD ₂₆₀ /OD ₂₈₀ Ratio (pre-vial)	1.7 to 2.1	1.9
Effective Bacterial Transformation		
Invitrogen™ One Shot™ TOP10 <i>E. coli</i>	≥ 50 colonies per ng	> 500 colonies per ng

The sequence was assembled pre-vial using the depositor's predicted sequence as the reference sequence. The complete plasmid sequence and map are provided on the BEI website.

²The NR-53761 poly-A tail sequence has an additional 8 nucleotides, resulting in a 33-base pair poly-A tail sequence. The longer poly-A tail is within normal poly-A variation for viral mRNA transcripts. For more information, please see Kim, D., et al. "The Architecture of SARS-CoV-2 Transcriptome." <u>Cell</u> 181 (2020): 914-921. PubMed: 32330414.

³The antibiotic ampicillin degrades quickly during growth. Bacterial stationary phase should be minimized during plasmid expansion to avoid plasmid loss and increased antibiotic concentrations may be necessary.



Figure 1: Agarose Gel of NR-53752

Lane 1: Invitrogen™ TrackIt™ 1 Kb Plus DNA Ladder Lane 2: NR-53752 Sall digested Lane 3: NR-53752 Bsal/Notl digested

Figure 2: Agarose Gel of NR-53753



Lane 1: Invitrogen™ TrackIt™ 1 Kb Plus DNA Ladder Lane 2: NR-53753 *Bsa*l digested Lane 3: NR-53753 *Bam*HI/*Sal*l digested

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Figure 3: Agarose Gel of NR-53756



Lane 1: Invitrogen™ TrackIt™ 1 Kb Plus DNA Ladder Lane 2: NR-53756 BsmBl digested



Lane 1: Invitrogen™ TrackIt™ 1 Kb Plus DNA Ladder Lane 2: NR-53758 undigested Lane 3: NR-53758 Kpnl/Sall digested





Lane 1: Invitrogen™ TrackIt™ 1 Kb Plus DNA Ladder Lane 2: NR-53761 *Sal*l digested

/Heather Couch/ Heather Couch

Program Manager or designee, ATCC Federal Solutions

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