Determination of Residual DNA by qPCR in mRNA



1.0 PURPOSE

Drug Substance (DS) or mRNA Product intermediate (MPI) using a real time quantitative PCR (qPCR) assay designed to amplify the kanamycin resistance gene in the place.

2.0 SCOPE

This procedure applies to detection of the residual plasmid DNA in mRNA DS or MPI samples for validated constructs. ion and any

3.0 REFERENCED DOCUMENTS

Document #	Title
FRM-0736	Assay Performance Worksheet: SOP 1020 Determination of Residual DNA by qPCR
FRM-0795	SOP-1020 Residual DNA Calculation Sheet
SOP-0017	Maintaining a RNase Free Work Environment
SOP-0004	Operation and Maintenance of CCI Biological Safety Cabinets (BSC)
SOP-0033	Out of Specification (OOS)
SOP-0081	Preparation of Solutions and Samples in the GMP-Quality Control Laboratory
SOP-0082	Data Review and Reporting in the GMP Quality Control Laboratory
SOP-0210	Assignment of Assay Reference Numbers and use of QC Assay Performance Worksheets
SOP-0409	Quality Control Invalid Assay Procedure
SOP-0451	Operation and Maintenance of the CCI PCR System
SOP-0452	Personnel Flow and Gowning in the QC Bioassay Laboratories
SOP-0465	Use of the CCI Microcentrifuge and the CCI Centrifuge

Determination of Residual DNA by qPCR in mRNA

4.0 RESPONSIBILITIES

Department/ Functional Area	Responsibilities
Quality Control Laboratory Personnel	 Following all procedures outlined in this document, as applicable. Maintaining a RNase-Free work environment per SOP-0017. Following proper safety measures in the GMP laboratory. Documenting sample information and preparation in the appropriate laboratory notebook or QC controlled document
Quality Control Manager or Designee	 Ensuring that laboratory personnel are trained in this procedure. Ensuring that all procedures in this document are followed when applicable. Ensure that this procedure is revised as necessary Data Review

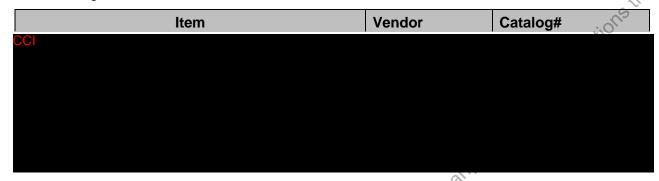
5.0 **DEFINITIONS**

Definition
Applied Biosystems Instruments
The PCR cycle at which an increase in reporter fluorescence above the baseline signal can first be detected
Degrees Celsius
Drug Substance
Deoxyribonucleic acid
Fluorescein
Good Manufacturing Practices
Isopropyl Alcohol
mRNA Product Intermediate
Molecular Weight
Milliliters
Millimolar
Nanograms
No Template Control
Personal Protective Equipment
Quantitative Polymerase Chain Reaction
Quality Control
Coefficient of Determination (square of correlation coefficient (R))
Second Derivative Maximum
Tetramethylrhodamine
Micrograms
Microliters

6.0 MATERIALS

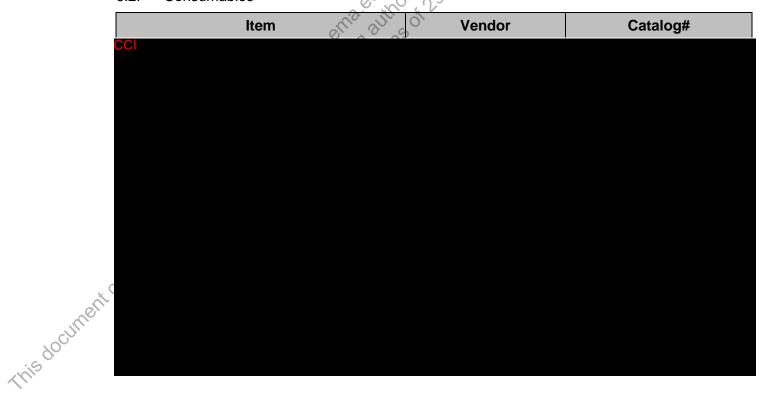
NOTE: Alternative vendors or part numbers may be used, provided the reagent grade or classification is maintained.

6.1. Reagents



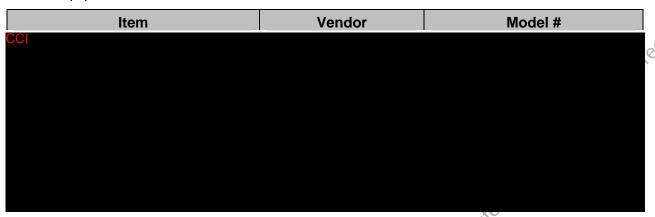
	Primer Name	Vendor	5'-Sequence-3'
CCI			

6.2. Consumables



Determination of Residual DNA by qPCR in mRNA

6.3. Equipment



7.0 SAFETY

7.1. Wear proper PPE (lab coat, gloves, safety glasses). Use Moderna Safety Manual as a reference. Follow all safety information provided on material SDSs.

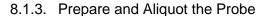
8.0 PROCEDURE

NOTE: Refer to Attachment 2 for BSC location map

- 8.1. Assay preparation: Perform the following preparation steps as needed.
 - 8.1.1. Preparation of Primers and Probes (In a Negative BSC)
 NOTE: Record preparation of stock primer tubes, probes and carrier RNA on FRM-0180 in the solution preparation logbook per SOP-0090.
 - 8.1.2. Prepare and Aliquot the Primers
 - 8.1.2.1. The standard desalting purified forward and reverse primers are ordered as CC
 - 8.1.2.2. Spin the primer tubes at **CCI** in the microcentrifuge before opening them to make sure all the lyophilized primer is at the bottom of the tubes.
 - 8.1.2.3. Check the amount of primer synthesized in the tube, in CCI of TE buffer (For Example: add CCI primer to obtain the CCI stock).
 - 8.1.2.4. Vortex for CC to dissolve the lyophilized primer.
 - 8.1.2.5. Spin the primer tubes at CCI in the microcentrifuge.
 - 8.1.2.6. Aliquot CCI of each primer into CCI tubes.

Determination of Residual DNA by qPCR in mRNA

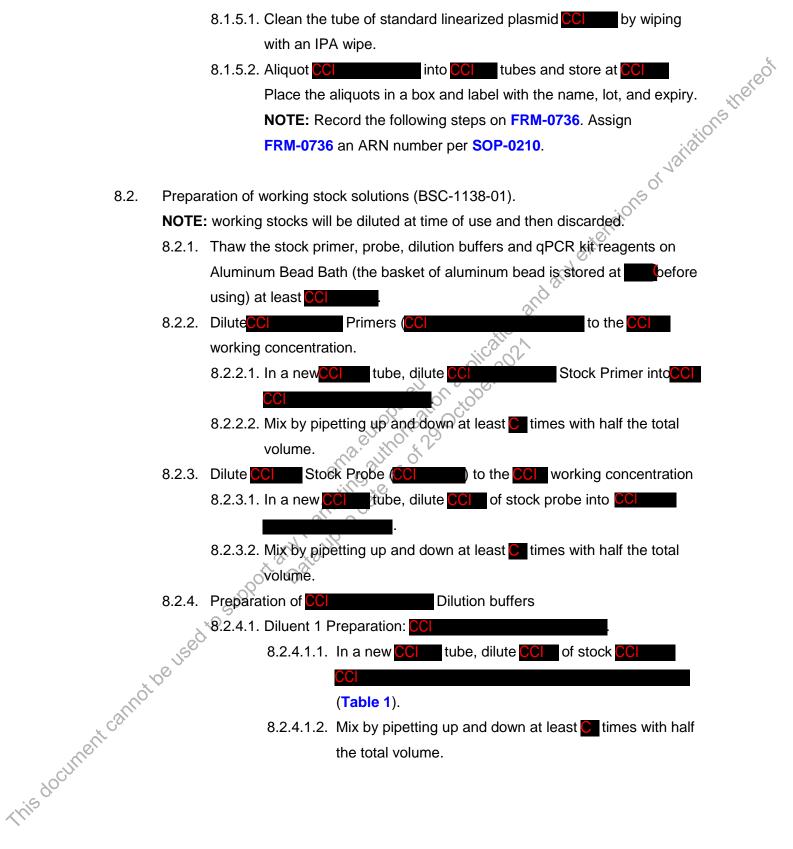
8.1.2.7. Store the aliquots at CCI Assign an expiry date of 1 year from the date of receipt of the lyophilized primers. Place the aliquots in a box and label with the primer name, lot, and expiry.



8.1.3.1.3. CCI

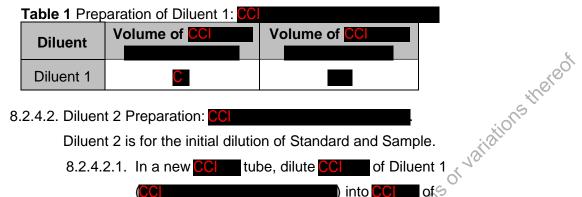
- sions of variations thereof 8.1.3.1. The HPLC purified probe is ordered as CC 8.1.3.1.1. **CC** 8.1.3.1.2. **CC**
- in the microcentrifuge 8.1.3.2. Spin the primer tubes at CC before opening it to make sure all the lyophilized probe is at the bottom of the tube.
- 8.1.3.3. Check the amount of probe synthesized in the tube, in CCI of TE buffer (For Example: add CCI primer stock). to obtain the CCI
- to dissolve the lyophilized pellet. 8.1.3.4. Vortex for **CC**
- 8.1.3.5. Spin the probe tubes at CCI in the microcentrifuge
- 8.1.3.6. Aliquot **CC** of probe into **CC** tubes.
- 8.1.3.7. Store the aliquots at CC Assign an expiry date of 1 year from the date of receipt of the lyophilized probe. Place the aliquots in a box and label with the probe name, lot, and expiry.
- 8.1.4. Preparation of Carrier Poly A RNA Dilution Buffer (CC) (In a Negative BSC: BSC-1138-01/BSC-1138-02)
 - 8.1.4.1. Add CC to the 1 CC
 - 8.1.4.2. Vortex for **CCI**
 - 8.1.4.3. Spin the tubes at CC in the microcentrifuge.
 - 8.1.4.4. Aliquot **CCI** tubes and store the aliquots at CCI. Assign an expiry date of 1 year from the dilution date.
- This document cannot be used 8.1.5. Preparation of CC Plasmid Standard (In a Positive BSC)

8.2.



8.2.4.1.2. Mix by pipetting up and down at least times with half the total volume.

Determination of Residual DNA by qPCR in mRNA

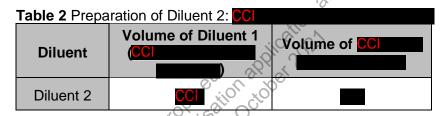


8.2.4.2. Diluent 2 Preparation: CC

Diluent 2 is for the initial dilution of Standard and Sample.

8.2.4.2.1. In a new CCI tube, dilute CCI of Diluent 1) into ((Table 2).

8.2.4.2.2. Mix by pipetting up and down at least times with half the total volume.



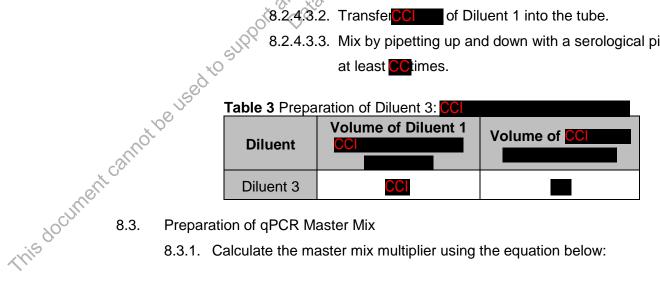
8.2.4.3. Diluent 3 Preparation: CC

Diluent 3 is used for the additional dilutions of Standard and Sample.

8.2.4.3.1. Using a CCI Serological Pipets, add CCI to a new **CCI** tube.

8.2.4.3.2. Transfer of Diluent 1 into the tube.

8.2.4.3.3. Mix by pipetting up and down with a serological pipette at least **CC**times.



- Preparation of qPCR Master Mix
 - 8.3.1. Calculate the master mix multiplier using the equation below:

Determination of Residual DNA by qPCR in mRNA

NOTE: Round up to the nearest whole number

Table 4: qPCR Master Mix Preparation

	$Multiplier = 4.4 \times ($	$8 + 6 \times Numbe$	er of Samples)	
Multiplier	for 1 sample = 62			4
Multiplier	for 2 Samples = 88			ille
Multiplier	for 3 Samples = 115		•.	ons
8.3.2. Using the r	multiplier from Step 8.2	. 5.1 , prepare t	he qPCR Master Mix per	
Table 4 int	o CCI conical tube.		of Jos.	
			Actual Volume (µL) (Column A x Column B)	
Table 4: qPCR Master Mix Pre	paration		ensie	-
	Α	В	Actual Volume (µL)	
Reagent	Volume for 1 well (µL)	Multiplier	(Column A x Column B)	
TaqMan Fast Advanced	CCI		TBD	
Master Mix		Silo		
Forward Primer (CCI		26/10-50/	TBD	
Reverse Primer CC		or oper	TBD	
Probe CCI		on application	TBD	
Exogenous IPC mix (CCI		TBD	TBD	
Exogenous IPC DNACCI			TBD	
CCI			TBD	
Total Volume		,	TBD	

8.3.3. Mix by pipetting up and down at least ctimes with half the total volume.

Divide the master mix into tubes using 8-Tube Strips. 1 8-strip tube (8 tubes) will be needed for the standards and NTC. 1 8-tube strip with 6 tubes will be needed for each sample. Add CCI Master Mix to each tube per Table 5.

Determination of Residual DNA by qPCR in mRNA

Table 5 The Master Mix for Controls and Samples

Tube	Standard	& Control Tubes	Sample	e(s) Tubes	Volume
Number	Tube Name	Control	Tube Name	Sample	of Master Mix (µL)
1	STD3	Standard 3	Sample D1	Sample Dilution 1	
2	STD4	Standard 4	Sample D2	Sample Dilution 2	Jaliations
3	STD5	Standard 5	Sample D3	Sample Dilution 3	ailaille
4	STD6	Standard 6	Sample D4	Sample Dilution 4	or <mark>CCI</mark>
5	STD7	Standard 7	Sample D5	Sample Dilution 5	0. 001
6	STD8	Standard 8	Sample D6	Sample Dilution 6	
7	STD9	Standard 9		tel	
8	NTC	No Template Control		70,	

- 8.4.
- 8.4.1. Add of Diluent 3 into the NTC Master Mix tube.

 8.4.2. Mix by pipetting up and down at least 18.4.3. 8.4.2. Mix by pipetting up and down at least times with half the total volume.
 - 8.4.3. Plate CCI of NTC Master Mix into the destination wells of CCI
 - Plate. An example plate map is shown in **Table 6**.

Table 6 Example Plate Lavout

	1	2	3	4	5	6	W 70	8	9	10	11	12
A	STD3	STD3	STD3	Sample1 D1	Sample1 D1	Sample1	Sample2 D1	Sample2 D1	Sample2 D1	Sample3 D1	Sample3 D1	Sample3 D1
В	STD4	STD4	STD4	Sample1 D2	Sample1 D2	Sample1 D2	Sample2 D2	Sample2 D2	Sample2 D2	Sample3 D2	Sample3 D2	Sample3 D2
С	STD5	STD5	STD5	Sample1 D3	Sample1 D3	Sample1 D3	Sample2 D3	Sample2 D3	Sample2 D3	Sample3 D3	Sample3 D3	Sample3 D3
D	STD6	STD6	STD6	Sample1 D4	Sample1 D4	Sample1 D4	Sample2 D4	Sample2 D4	Sample2 D4	Sample3 D4	Sample3 D4	Sample3 D4
E	STD7	STD7	STD7	Sample1 D5	Sample1 D5	Sample1 D5	Sample2 D5	Sample2 D5	Sample2 D5	Sample3 D5	Sample3 D5	Sample3 D5
F	STD8	STD8	STD8	Sample1 D6	Sample1 D6	Sample1 D6	Sample2 D6	Sample2 D6	Sample2 D6	Sample3 D6	Sample3 D6	Sample3 D6
G	STD9	STD9	STD9									
н	NTC	NTC	NTC									

- Plate with Adhesive PCR Film. 8.4.4. Seal the **CC**
- 8.4.5. Cap the tubes containing master mix.
- Plate and the tubes containing master mix into 8.4.6. Move the CC BSC-1138-02.

8.5. Preparation of the test samples (BSC-1138-02).

- 8.5.1. Thaw the sample on Aluminum Bead Bath (the basket of aluminum beads
- 8.5.3. Mix by pipetting up and down at least times with half the total volume.

 8.5.4. Serially dilute (CC) dilutions) Sample Dilution 1 with Diluent 2.

 8.5.4. Strip with Attached Domest C.

 8.5.4.
- - 8.5.4.1. Add CO of **Diluent 3** to tubes 2-6 within the 8-tube stip.
 - 8.5.4.2. Add CC of Sample Dilution 1 to tube 2 and mix by pipetting up and down with at least half the total volume of the tube.
 - 8.5.4.3. Continue diluting CC of the previous dilution tube to the next tube containing **Diluent 3** until all 6 **CC** serial dilutions are complete.
 - 8.5.4.4. When performing serial dilutions, mix by pipetting up and down at least chimes with at least half the total volume before transferring to the next tube.

Table 7: Sample Serial Dilutions

Dilution Name	Final Dilution	Volume of Previous Dilution (μL)	Volume of Diluent 3 (µL)
Sample Dilution 1	CCI		
Sample Dilution 2		JCI	
Sample Dilution 3			
Sample Dilution 4			
Sample Dilution 5			
Sample Dilution 6			

- Add CC of each Testing sample dilution into destination tube containing Master Mix from Table 5.
- 8.5.6. Mix by pipetting up and down at least times with half the total volume.
- 8.5.7. Plate CC of Sample Master Mix into the destination wells of the CC plate (Table 6).
- 8.5.8. Seal the **CCI** plate with Adhesive PCR film. Move the CCI plate and the tubes containing the Standard Master Mix into BSC-1139-01/BSC-1139-02.

Determination of Residual DNA by qPCR in mRNA

- 8.6. Preparation of the Standard Curve (BSC-1139-01/BSC-1139-02)
 - 8.6.1. Remove one tube of aliquoted CCI standard from CCI

 - 8.6.3. Mix by pipetting up and down at least times with half the total volume.
 - 8.6.4. Dilution of Standard samples
 - 8.6.4.1. Serially dilute the plasmid **Stock 1** (CCI) using Diluent 3 in a new 8-tube strip per **Table 8.**
 - **NOTE:** 2 8-tube strips will be needed as there are 9 total standard dilutions.
 - 8.6.4.2. Prepare Standard 1 by diluting CC of Stock 1 into CC of Diluent 3.
 - 8.6.4.3. Mix by pipetting up and down at least times with half the total volume.
 - 8.6.4.4. Add CC of Diluent 3 to tubes 2-9 within the 8-tube stip.
 - 8.6.4.5. Add CC of Standard 1 to tube 2 and mix by pipetting up and down with at least half the total volume of the tube.
 - 8.6.4.6. Continue diluting College of the previous dilution tube to the next tube containing **Diluent 3** until all 9 College serial dilutions are complete.
 - 8.6.4.7. When performing serial dilutions, mix by pipetting up and down at least crimes with at least half the total volume before transferring to the next tube.

Table 8 Standard Dilutions

Dilution Na	ame	Number of Copies/ µL	Volume of Previous Dilution (µL)	Volume of Diluent 3 (µL)
Standard	1	CCI		
Standard	2			
Standard	3			
Standard	4			
Standard	5			
Standard	6			
Standard	7			
Standard	8			
Standard	9			

Number: SOP-1020 Effective Date: 09 Oct 2020 Version: 1.0

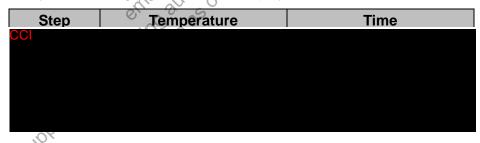
Determination of Residual DNA by qPCR in mRNA

8.6.5. Add CCI of Standard 3 – Standard 9 into their corresponding destination tubes containing Master Mix per Table 5.

- 8.6.6. Mix by pipetting up and down at least times with half the total volume.
- 8.6.7. Plate CCI of Standard Master Mix (Standard 3 Standard 9) into the destination wells per Table 6.
- Optical Adhesive 8.6.8. Seal the plate with CC Film.
- Repeat as needed until all 8.6.9. Centrifuge the plate at CC bubbles are gone and the contents are at the base of the wells

8.7. Running the Assay

- 8.7.1. Start the QuantStudio[™] 7 per SOP-0451.
- 8.7.2. Select Method "SOP-1020 Residual plasmid" from Run template.
- 8.7.3. Ensure all wells containing material are selected.
- 8.7.4. Ensure all wells are named according to plate map (Table 6).
- 8.7.5. Ensure standard curve concentrations are assigned appropriately.
- 8.7.6. Ensure replicates are assigned appropriately.
- 8.7.7. Verify the following parameters are displayed:



- 8.7.8. Load plate on to QuantStudio™ 7.
- Start run.

Data Analysis

- 8.8.1. When the run is complete, go to the Analysis screen.
- 8.8.2. Select the Standard Curve.
- 8.8.3. Select the wells that include the samples, NTC wells, and standards 3-9
- 8.8.4. Select "Target 1" to record the R^2 , Slope and C_T .

NOTE: Target 1 detects the residual DNA in the samples.

The standard curve of Target 2 will generate a blank graph in the report because Target 2 is Internal Positive Control (IPC).

- 8.8.5. Save the PDF report to the SDMS folder.
- 8.8.6. Open the PDF report from the SDMS folder and print it out.
- 8.8.7. Using the excel version of FRM-0795 "SOP-1020 Residual DNA Calculation Sheet", calculate the standard curve and sample concentrations. All excel formulas may be found on Attachment 1.
- 8.8.8. The copies/µL of each point of the standard curve and each sample dilution are calculated using the following equation: inputting the C_T, slope, and y-intercept of the standard curve.

Copies/
$$\mu$$
L = $10^{(Ct - y - intercept)/Slope}$

- 8.8.9. The copies/µL of each sample dilution is then multiplied by the corresponding dilution factor to determine the neat copies/µL.
- 8.8.10. The % (g/L DNA)/(g/L RNA) (%w/w) of the sample is then calculated using the following equations:

NOTE: The Plasmid MW can be found within the Validation Report of the test construct.

$$(g/LDNA) = \frac{(\frac{copies}{\mu L})(Plasmid\ MW\ (Da))(1 \times 10^{6}(\frac{\mu L}{L}))}{(6.022 \times 10^{23}\ molecules/mole)}$$

$$\% W/_W = \frac{g/L \text{ DNA}}{g/L \left(\frac{mg}{mL}\right) \text{ RNA}}$$

- 8.8.11. The % (g/L DNA)/(g/L RNA) (%w/w) of the sample dilutions in which the C_T was within the C_T range of the standard curve are then averaged to determine the %w/w of the sample.
- 8.8.12. Save the calculation sheet **FRM-0795**, print the calculation sheet with and without formulas showing, and attach to the APW.
- 8.9. System and Sample Suitability Criteria
 - 8.9.1. R² must be CC
 - 8.9.2. The slope of the standard curve must be between CCI inclusive
 - 8.9.3. Amplification must be observed in at least 2 of 3 replicates for 10^2 standard.

Determination of Residual DNA by qPCR in mRNA

8.9.4. The Average C_T value observed in NTC must be above the average C_T of the lowest point of standard curve.

- 8.9.5. IPC must be amplified in NTC wells.
- 8.9.6. The %RSD of each sample dilution's software calculated concentration (copies/ μ L) for all standards and samples within the quantitative range of the standard curve must have a %RSD of CCI III If the average C_T value of a sample is higher than the average C_T of the lowest standard (10²) of the standard curve, the %RSD criteria does not apply.
- 8.9.7. If all system and sample suitability criteria are met, the sample is valid. If the criteria are not met the assay is invalid. Proceed with the invalid assay procedure, SOP-0409.

8.10. Results Reporting

- 8.10.1. Have FRM-0736 reviewed per SOP-0082 and report results. The reviewer must review the formulas of the attached calculation sheet to ensure correct calculations.
- 8.10.2. Report the result (% w/w). If the value is less than the LOQ %w/w then report <(LOQ %w/w).
- 8.10.3. Refer to the specification of the test sample to determine if the %w/w is within specification. If the residual plasmid %w/w is out of specification, refer to the OOS procedure, SOP-0033.
- 8.10.4. Have **FRM-0736** reviewed per **SOP-0082** and report results. The reviewer must review the formulas of the attached calculation sheet to ensure correct calculations.

9.0 ATTACHMENTS

- 9.1. Attachment 1: SOP-1020 Residual DNA Calculation Formula Sheet (Electronically attached in Veeva)
- 9.2. Attachment 2: BSC Placement

10.0 REVISION HISTORY

1.0 Refer to Veeva Header for Effective Date New Document PPD PPD Autoritation and any extensions of validation and extensions of validatio	Revision # Effective Date Change Details Author Refer to Veeva Header for Effective Date New Document PPD The Date of the Date Set of Effective Date Set
av sapplication and any extensions of validation and extensions of validations of validat	osupport any marketing date as of 29 October 202.
iologication octob	Support any marketing at the date as of 29

ATTACHMENT 2: BSC Placement

(Page 1 of 1)



