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LAMP/RT-LAMP COVID positive control

In 1 collection

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Works for me

dx.doi.org/10.17504/protocols.io.bsknncve

Laboratorio de Tecnologias Libres

Reclone.org (The Reagent Collaboration Network)

Tamara Matute

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ABSTRACT

This protocol explains how to prepare dsDNA and ssRNA target positive control for LAMP and RT-LAMP reactions. Particularly it describes the pipeline for SARS-CoV-2 Nucleocapsid (N) gene positive control which is included in the ReClone collection. The general procedure involves amplifying the gene of interest with primers which add T7 promoter and T7 terminator to its sequence followed by T7 in vitro transcription to obtain the ssRNA.

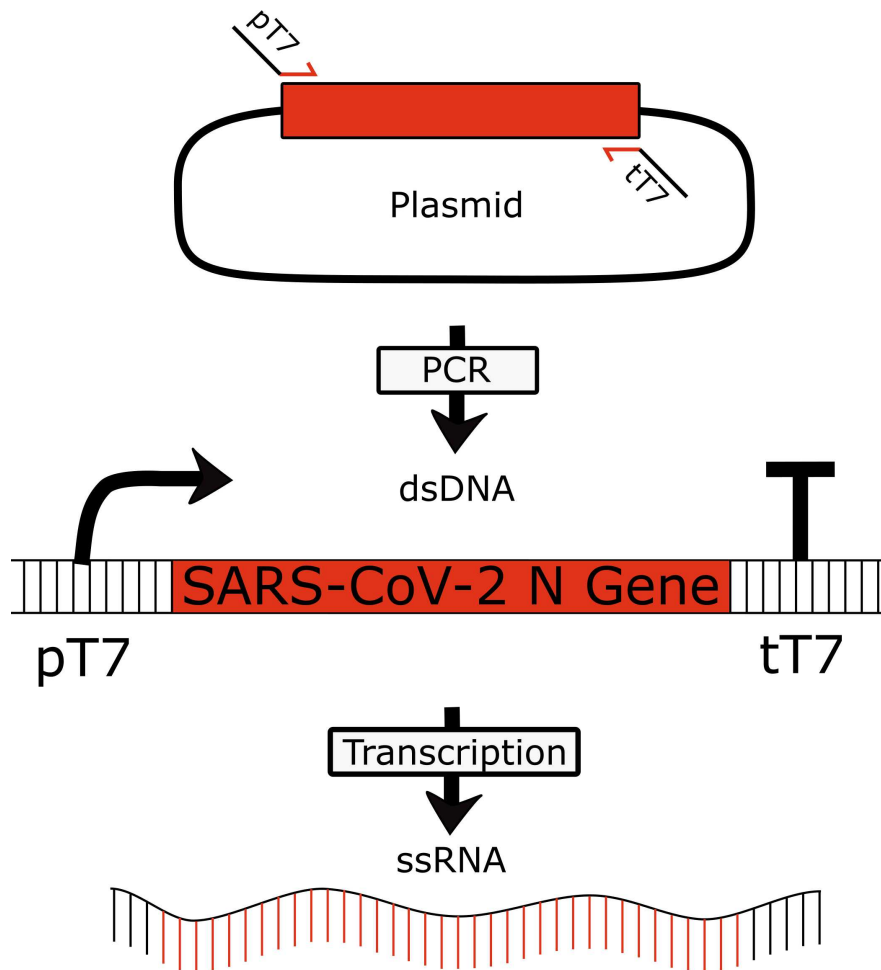


Figure 1: General pipeline. It shows how dsDNA is amplified from control plasmid at the time pT7 and tT7 are incorporated to its sequence which is used to perform the ssRNA T7 in vitro transcription.

Sequence elaboration:

Sequence [OrfN_5](#) was designed and synthesized based on IDT SARS-CoV-2 positive control plasmid ([CAT#10006625_2019](#)).

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PROTOCOL CITATION

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COLLECTIONS ⓘ



Low Cost LAMP and RT-LAMP

KEYWORDS

COVID, SARS-Cov-2, ssRNA, dsDNA, positive control, ReClone, in vitro transcription, Reverse Transcription

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IMAGE ATTRIBUTION

Isaac Núñez. GNU General Public License v3.0.

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47470

PARENT PROTOCOLS

Part of collection

[Low Cost LAMP and RT-LAMP](#)

MATERIALS TEXT

Materials and Tools:

- Pipettes p2, p10, p200
- Pipette tips
- PCR tubes (0.2 uL)
- rNTPS

Kits and enzymes:

- [Promega Wizard® SV Gel and PCR Clean-Up System](#)
- [Qiagen RNeasy Kit](#)
- HiScribe™ ([NEB E2040S](#))
- PPI ([NEB M0361S](#))
- RNasin® ([Promega N2111](#))
- DNase I ([NEB M0303S](#))

Equipment:

- Thermocycler
- Centrifuge
- spin
- Nano-Spectrophotometer

N gene Amplification

- 1 Amplify SARS-Cov-2 Nucleocapsid (N) gene fragment dsDNA from ReClone or IDT positive control plasmid with the *ultramers* indicated in Table 1.

Name	Sequence
NT7_Fw	CGA AAT TAA TAC GAC TCA CTA TAG GGG CAA CGC GAT GAC GAT GGA TAG
T7_Nter_Rv	ACT GAT CAA AAA ACC CCT CAA GAC CCG TTT AGA GGC CCC AAG GGG TTA TGC TAG TTA GGC CTG AGT TGA GTC AG

Table 1 : Primers/Ultramers used to amplify N-gene positive control

The amplification can be carried out using any standard PCR reaction formulation (e.g. Phusion DNA polymerase with HF buffer), adding **0.01 ng** to **1 ng** of the plasmid template and **1 µl** of each primer at 10 µM concentration and following this thermocycler program:

Initial denaturation at 98 °C for 00:00:30

Followed by 35 cycles of:

98 °C per 00:00:05

57 °C per 00:00:15

extension at 72 °C per 00:01:00

End by a final extension at 72 °C per 00:05:00

dsDNA positive control

2 dsDNA purification

Perform PCR reaction purification with any commercially available kit.

We use [Promega Wizard® SV Gel and PCR Clean-Up System](#)



Typical yields are around **25 µl** at 30 - 100 ng/µL.

- 3 Store sample under **-20 °C**

In case you are not making RT-LAMP positive control **go to step 10**.

ssRNA positive control

4 In vitro transcription preparation

In vitro transcription has to be done from previously prepared dsDNA. We do it using HiScribe™ ([NEB E2040S](#)) system plus PPI ([NEB M0361S](#)) and RNasin® ([Promega N2111](#)):

Compound	Volume (μ L)
rATP	2,0
rUTP	2,0
rGTP	2,0
rCTP	2,0
Buffer 10X	2,0
T7 pol	2,0
RNAsin	0,5
PPI (NEB)	0,5
DNA (from PCR)	7,0
Total	20,0

Table 2: *In vitro* transcription formulation.

- Incubate reaction at 37°C Overnight
- Treat the reaction with DNase I ([NEB M0303S](#)) by diluting the reaction with $70\ \mu\text{l}$ H_2O (molecular grade) and $10\ \mu\text{l}$ 10X buffer DNase I.
- Incubated at 37°C per 00:15:00 .

Heat inactivation of DNase is not recommended because it can harm RNA.

- Perform RNA purification with any available kit. We use [Qiagen RNeasy Kit](#).



Typical yields are around $50\ \mu\text{l}$ at 1000ng/ μL .

- Perform aliquots and store the samples at -80°C

Copy number computation and dilutions

- In order to compute the sample **copy number concentration**, it's necessary to measure its **mass concentration** in a nano-spectrophotometer, plate reader, or estimate it by gel electrophoresis imaging.

NanoDrop™ 3300 Fluorospectrometer
Fluorospectrometer

NanoDrop™ 3300 nd-3300 [↗](#)



Repeat steps 8 to 10 for ssRNA each time you perform experimentation because samples and aliquots concentration is not stable even though keeping them frozen.

- 11 Compute the sample copy number concentration [copies/?L] by replacing the length [bp] (**Table 3**) and mass concentration [ng/?L] (C_{mass}) in the next mathematical expressions :

$$(1.a) \ Z_{\text{mol } dsDNA} \frac{g}{\text{mol}} = \text{length } dsDNA[bp] * 617.96 \frac{g}{\text{mol} * bp} + 36.04 \frac{g}{\text{mol}}$$

$$(1.b) \ Z_{\text{mol } ssRNA} \frac{g}{\text{mol}} = \text{length } ssRNA[bp] * 321.47 \frac{g}{\text{mol} * bp} + 18.02 \frac{g}{\text{mol}}$$

$$(2) \ Y_{\frac{\text{copies}}{ng}} = \left(Z_{\text{mol } ssRNA} \frac{g}{\text{mol}} * \frac{10^9 ng}{g} \right)^{-1} * 6,02210^{23} \frac{\text{copies}}{\text{mol } dsDNA}$$

$$(3) \ X_{\frac{\text{copies}}{\mu L}} = C_{mass} \frac{ng}{\mu L} * Y_{\frac{\text{copies}}{ng}}$$

	Length [bp]
dsDNA	1427
ssRNA	1374

Table 3: dsDNA and ssRNA fragment sizes.

use eq. 1.a for dsDNA and eq. 1.b for ssRNA.



Typical amounts are:

dsDNA: $10^8 - 10^9$ copies/ng

ssRNA: $10^9 - 10^{10}$ copies/ng

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Make serial dilutions with molecular grade H₂O to reach the target $\frac{\text{copies}}{\mu\text{L}}$ concentration.

As positive control we typically use  1 μL of sample at $10.000 \frac{\text{copies}}{\mu\text{L}}$

You can store aliquots of dsDNA samples at targets concentrations at $-20\text{ }^{\circ}\text{C}$ or $-80\text{ }^{\circ}\text{C}$.
Freezing and thawing cycles may affect the concentration then use each aliquot just one time.