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## Supplementary appendix for

VALCOR: A protocol for the validation of SARS-corona virus-2 assays

### Information on artificial samples included in the VALCOR panel

Dilutions of artificial RNA specimens to be used for determination of the limit of detection (LOD) on artificial samples.

1. EURM-019 is a solution containing a stabilised in vitro-transcribed (IVT) synthetic single-stranded RNA (ssRNA) of SARS-CoV-2 in buffer, prepared and developed by Joint Research Centre (JRC) for external quality control (EQA)(1). The synthetic RNA is 880 base pairs and contains sequences from the E, RdRP, N & S genes (**Supplementary Figure 1**) that can be transcribed and amplified by RT-PCR assays. The EURM-019 material is provided in vials containing approximately 100  $\mu\text{L}$  of RNA solution at a concentration of about  $7 \times 10^7$  copies/ $\mu\text{L}$ . This reference material needs to be diluted 700 times, in RNase free water (Molecular Biology Grade), added with poly-A carrier RNA at 10 ng/ $\mu\text{L}$ , to achieve a dilution of  $10^5$  copies/ $\mu\text{L}$ . Four subsequent ten-fold serial dilutions can be prepared to achieve a total of 5 working solutions containing approximately:  $10^5$ ,  $10^4$ ,  $10^3$ ,  $10^2$  and 10 copies/ $\mu\text{L}$  to determine the LOD of the evaluated SARS-CoV-2 assays.
2. Research Grade Test Material ID: 10169 is composed of two unique synthetic RNA fragments from the SARS-CoV-2 genome (each ~4kb) in a background of 5 ng/ $\mu\text{L}$  human Jurkat RNA; they are provided in two separate tubes by NIST and include the SARS-Cov-2 sequences 25949-29698 and 12409-15962 from the USA-WA1/2020 isolate, respectively (**Supplementary Figure 2**)(2). The NIST materials cover part of the ORF1ab, E and N target regions and may accommodate a larger number of commercial assays than the EURM-019 material. The concentration of each of the two synthetic RNA fragments, in the two separate tubes, is approximately  $5 \times 10^6$  copies/ $\mu\text{L}$  in a total volume of 110  $\mu\text{L}$ . Both vials of this reference material need to be initially diluted 1:50 in RNase free water (Molecular Biology Grade), added with poly-A carrier RNA at 10 ng/ $\mu\text{L}$ , to achieve a dilution of  $1 \times 10^5$  copies/ $\mu\text{L}$ . Four subsequent ten-fold serial dilutions can be prepared to achieve approximately:  $10^5$ ,  $10^4$ ,  $10^3$ ,  $10^2$  and 10 copies/ $\mu\text{L}$  dilutions to determine the LOD of the evaluated SARS-CoV-2 assays.

## Dilution protocol for the EURM-019

In particular, in order to prepare 2.5 ml volumes of each of the five serial dilutions ( $10^5$ ,  $10^4$ ,  $10^3$ ,  $10^2$  and 10 copies/ $\mu\text{L}$ ) starting from the original EURM-019 material proceed as follows:

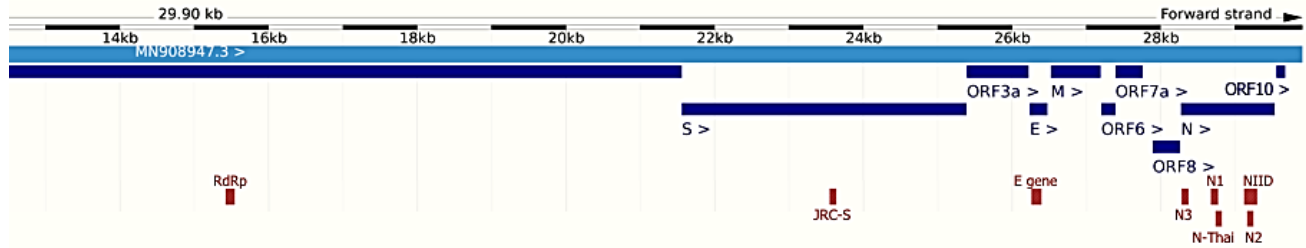
- **1st step:** 10  $\mu\text{L}$  of original EURM-019 material ( $7 \times 10^7$  copies/ $\mu\text{L}$ ) + 690  $\mu\text{L}$  RNase free water with poly-A carrier RNA (1:70 dilution) =  $10^6$  copies/ $\mu\text{L}$ ;
- **2nd step:** 250  $\mu\text{L}$  of  $10^6$  copies/ $\mu\text{L}$  dilution + 2250  $\mu\text{L}$  RNase free water with poly-A carrier RNA =  $10^5$  copies/ $\mu\text{L}$ ;
- **3rd step:** 250  $\mu\text{L}$  of  $10^5$  copies/ $\mu\text{L}$  dilution + 2250  $\mu\text{L}$  RNase free water with poly-A carrier RNA =  $10^4$  copies/ $\mu\text{L}$ ;
- **4th step:** 250  $\mu\text{L}$  of  $10^4$  copies/ $\mu\text{L}$  dilution + 2250  $\mu\text{L}$  RNase free water with poly-A carrier RNA =  $10^3$  copies/ $\mu\text{L}$ ;
- **5th step:** 250  $\mu\text{L}$  of  $10^3$  copies/ $\mu\text{L}$  dilution + 2250  $\mu\text{L}$  RNase free water with poly-A carrier RNA =  $10^2$  copies/ $\mu\text{L}$ ;
- **6th step:** 250  $\mu\text{L}$  of  $10^2$  copies/ $\mu\text{L}$  dilution + 2250  $\mu\text{L}$  RNase free water with poly-A carrier RNA =  $10^1$  copies/ $\mu\text{L}$

## Dilution protocol for the NIST materials

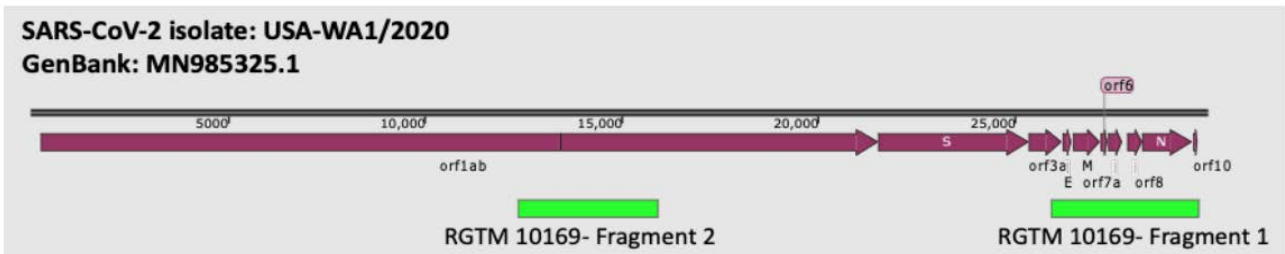
In particular, in order to prepare 2.5 ml volumes for each of the five serial dilutions ( $10^5$ ,  $10^4$ ,  $10^3$ ,  $10^2$  and 10 copies/ $\mu\text{L}$ ) of both fragments of RGTM 10169 original material proceed as follows:

- **1st step:** 50  $\mu\text{L}$  of original RGTM 10169 material ( $5 \times 10^6$  copies/ $\mu\text{L}$ ) + 2450  $\mu\text{L}$  RNase free water with poly-A carrier RNA (1:50 dilution) =  $1 \times 10^5$  copies/ $\mu\text{L}$ ;
- **2nd step:** 250  $\mu\text{L}$  of  $10^5$  copies/ $\mu\text{L}$  dilution + 2250  $\mu\text{L}$  RNase free water with poly-A carrier RNA =  $10^4$  copies/ $\mu\text{L}$ ;
- **3rd step:** 250  $\mu\text{L}$  of  $10^4$  copies/ $\mu\text{L}$  dilution + 2250  $\mu\text{L}$  RNase free water with poly-A carrier RNA =  $10^3$  copies/ $\mu\text{L}$ ;
- **4th step:** 250  $\mu\text{L}$  of  $10^3$  copies/ $\mu\text{L}$  dilution + 2250  $\mu\text{L}$  RNase free water with poly-A carrier RNA =  $10^2$  copies/ $\mu\text{L}$ ;
- **5th step:** 250  $\mu\text{L}$  of  $10^2$  copies/ $\mu\text{L}$  dilution + 2250  $\mu\text{L}$  RNase free water with poly-A carrier RNA =  $10^1$  copies/ $\mu\text{L}$ .

## Schematic diagram of the artificial samples



**Supplementary Figure 1.** Schematic of EURM-019 synthetic RNA fragments  
(Published with permission from JRC)



**Supplementary Figure 2.** Schematic of RTGM 101069 synthetic RNA fragments  
(Published with permission from NIST)

## Standard datasheet used for the transmission of clinical and testing data

### Datasheet\_provider\_v1

| label   | legend  |
|---------|---|
| panel   | VALCOR panel (ex. VALCOR_BE1, VALCOR_DK1, ...)  |
| num     | Sample number (newly generated)   |
| mat     | Material <ol style="list-style-type: none"><li>1 extracted RNA</li><li>2 rough residual material</li></ol>  |
| extract | RNA extraction procedure used for test1   |
| anat    | Anatomical site where the specimen was taken, or material <ol style="list-style-type: none"><li>1 nasopharynx</li><li>2 oropharynx</li><li>3 oral cavity</li><li>4 sputum</li><li>5 saliva</li><li>6 deep respiratory airway (trachea or deeper)</li><li>9 unknown</li></ol>                          |
| dis     | Disease status at moment of collection <ol style="list-style-type: none"><li>1 very severe, needing admission at intensive care unit</li><li>2 severe, needing hospitalisation</li><li>3 moderate or mild disease, needing to stay isolated at home</li><li>4 no symptoms</li><li>9 unknown</li></ol> |
| place   | Place or service where specimen collection took place <ol style="list-style-type: none"><li>1 IC unit</li><li>2 emergency unit of hospital</li><li>3 preadmission/triage centre for COVID-19 disease</li><li>4 visit at cabinet of a doctor</li></ol>   |

|         |     |  |
|---------|-----|--|
|         | 5   | contact tracing  |
|         | 6   | elsewhere  |
|         | 9   | unknown  |
| coldev  |     | Device used to collect specimen  |
|         | 1   | nasopharyngeal swab  |
|         | 2   | oropharyngeal swab   |
|         | 3   | lavage (fi for bronchoalveolar collection)                                       |
|         | 5   | oral swab  |
|         | 8   | vial to collect saliva   |
|         | 9   | unknown  |
| col_d   |     | Date of collection of specimen (format dd/mm/yyyy)                               |
| age     |     | Age of patient in years  |
|         | 999 | unknown  |
| sex     |     | Sex of patient   |
|         | 1   | male   |
|         | 2   | female   |
|         | 3   | other  |
|         | 9   | unknown  |
| test1   |     | first test used for identifying SARS-CoV-2                                       |
| genes1  |     | Genes targeted for RNA SARS-CoV-2 testing  |
| load_x1 |     | Viral load or signal strength output for test1<br>(to be repeated for each gene) |

## Datasheet\_client

| label     | legend  |
|-----------|---|
| panel     | VALCOR panel (ex. VALCOR_BE1, VALCOR_DK1, ...)  |
| num       | Sample number (newly generated by provider)   |
| receive_d | Date of reception of VALCOR panel at client lab<br>format: dd/mm/yyyy                                   |
| mat       | Material<br>1 extracted RNA<br>2 rough residual material  |
| extract   | RNA extraction procedure used for test, if client received rough residual material                      |
| test      | Test used by client laboratory for identifying SARS-CoV-2 (to be detailed in form Test characteristics) |
| result    | Result<br>0 negative<br>1 positive<br>8 invalid<br>9 unknown  |
| genes     | Genes targeted for RNA SARS-CoV-2 testing   |
| load_x    | Viral load or signal strength output for test1<br>(to be repeated for each gene)                        |
| test_d    | Date of testing of VALCOR panel at client lab<br>format: dd/mm/yyyy                                     |

## References

1. Joint Research Centre (JRC). EURM-019 single stranded RNA (ssRNA) fragments of SARS-CoV-2 [Available from: <https://crm.jrc.ec.europa.eu/p/EURM-019> Accessed 10 August 2020.
2. National Institute of Standards and Technology (NIST). SARS-CoV-2 Research Grade Test Material [Available from: <https://www.nist.gov/programs-projects/sars-cov-2-research-grade-test-material> Accessed 10 August 2020.