

ViroKey® SARS-CoV-2 RT-PCR Test v2.0

Instructions for Use

For use under an Emergency Use Authorization Only

For Prescription Use Only

For In Vitro Diagnostic Use

IVD

Rx Only



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REF

301068 & 301085



8x48 tests & 4x96 tests

MAT

PS103999M



Consult instructions for use

Version 3.4

Contents

| | |
|--|----|
| Kit contents | 1 |
| Symbols | 2 |
| Storage | 3 |
| Intended use | 4 |
| Warnings and Precautions | 5 |
| Safety information | 6 |
| Quality control | 6 |
| Introduction | 7 |
| Principle | 7 |
| Pathogen information | 8 |
| Limitations | 8 |
| Conditions of Authorization for the Laboratory | 11 |
| Controls | 12 |
| Result interpretation | 13 |
| Performance characteristics | 17 |
| Analytical sensitivity | 17 |
| Analytical reactivity and specificity | 18 |
| FDA SARS-CoV-2 reference panel testing | 24 |
| Clinical performance | 24 |
| Specimen pooling | 27 |
| Sample preparation (for specimen pooling) | 27 |
| Specimen pooling strategy for implementation and monitoring | 28 |
| Result interpretation and test reports (for pooled specimens) | 30 |
| Workflow using ViroKey SARS-CoV-2 RT-PCR Test v2.0 | 31 |
| Sentosa SX101 workflow | 31 |
| KingFisher workflow | 33 |
| Workflow using ViroKey SARS-CoV-2 RT-PCR Test v2.0 | 38 |
| Hamilton workflow | 38 |
| Items to be supplied by user | 40 |
| Important notes | 41 |
| General precautions | 41 |
| Protocol: Automated nucleic acid isolation and detection on the <i>Sentosa SA201</i> / Applied Biosystems 7500 Fast Dx Real-Time PCR Instrument | 42 |
| Sentosa SX101 workflow | 44 |
| 1. <i>Sample preparation and pre-treatment</i> | 44 |
| 2. <i>Automated nucleic acid extraction and RT-PCR set-up on the <i>Sentosa SX101</i> instrument</i> | 46 |
| KingFisher workflow | 57 |
| 3. <i>Buffer, reagent and sample preparation</i> | 57 |
| 4. <i>Automated RT-PCR set-up on the <i>Sentosa SX101</i> instrument</i> | 61 |
| Hamilton workflow | 69 |
| 5. <i>Sample preparation (for individual samples)</i> | 69 |

| | |
|---|------------|
| 6. Automated nucleic acid extraction and RT-PCR set-up on the Hamilton Microlab STAR instrument..... | 72 |
| RT-PCR and data analysis using the Sentosa SA201 Real-Time PCR Instrument and Sentosa SA201 Reporter software..... | 90 |
| 7. PCR on the Sentosa SA201 Real-Time PCR Instrument | 90 |
| 8. Automated data analysis on Sentosa SA201 Reporter | 101 |
| RT-PCR and manual data analysis on the Applied Biosystems 7500 Fast Dx Real-Time PCR System..... | 104 |
| 9. RT-PCR and manual data analysis on the Applied Biosystems 7500 Fast Dx Real-Time PCR System | 104 |
| 10. Manual data analysis on the Applied Biosystems 7500 Fast Dx Real-Time PCR System | 111 |
| Instrument maintenance | 116 |
| Troubleshooting guide..... | 117 |
| Appendix for ViroKey SARS-CoV-2 RT-PCR Test v2.0 on Sentosa SX101 and KingFisher Flex..... | 120 |
| Appendix A : Sentosa SX101 layout for “48-1 ViroKey SARS-CoV-2-v2 v3-3” application..... | 120 |
| Appendix B : Sentosa SX101 layout for “96-1_ViroKey-KF SARS-CoV-2-v2_v3-2” application..... | 121 |
| Appendix for ViroKey SARS-CoV-2 RT-PCR Test v2.0 on Hamilton Microlab STAR | 122 |
| Appendix C : Sample Plate Preparation..... | 122 |
| Appendix D : Viral RNA Extraction..... | 126 |
| Appendix E : Consumable summary..... | 130 |
| Appendix F : HT PCR set-up | 132 |
| References | 136 |
| Contacts | 138 |

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For Prescription Use Only

Kit contents

ViroKey® SARS-CoV-2 RT-PCR Test v2.0

| Kit item no. | Item | Cap color | Description | Quantity (tube) | Volume / tube |
|--------------|------------------|-----------|-------------------------|-----------------|---------------|
| 301068* | SARS-CoV-2 v2 M1 | Green | Mix 1 | 8 | 60 µL |
| | RNA4 M2 | Orange | Mix 2 | 8 | 700 µL |
| | RNA4 M3 | Pink | Mix 3 | 8 | 125 µL |
| | NC5 | Yellow | Negative control (NC) | 8 | 600 µL |
| | SARS-CoV-2 v2 PC | Blue | Positive control (PC) | 8 | 300 µL |
| | EC8 | Red | Extraction control (EC) | 8 | 600 µL |

*Used with ViroKey® SX Virus Total Nucleic Acid Kit (4x48) extraction kit




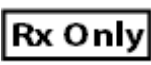

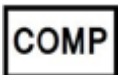
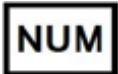









ViroKey® SARS-CoV-2 RT-PCR Test v2.0

| Kit item no. | Item | Cap color | Description | Quantity (tube) | Volume / tube |
|--------------|------------------|-----------|-------------------------|-----------------|---------------|
| 301085* | HT SARS-CoV-2 M1 | Green | Mix 1 | 4 | 115 µL |
| | HT RNA M2 | Yellow | Mix 2 | 4 | 1400 µL |
| | HT RNA M3 | Blue | Mix 3 | 4 | 115 µL |
| | HT NC | Natural | Negative control (NC) | 4 | 300 µL |
| | HT SARS-CoV-2 PC | Purple | Positive control (PC) | 4 | 300 µL |
| | HT EC | Red | Extraction control (EC) | 4 | 1200 µL |

*Used with ViroKey® HT Virus Total Nucleic Acid Kit (4x96) extraction kit

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Symbols

| | |
|---|--|
|  | Contains reagents sufficient for <N> tests |
|  | Use-by date |
|  | In vitro diagnostic medical device |
|  | CAUTION: Federal law restricts this device to sale by or on the order of a licensed healthcare practitioner |
|  | Catalog number |
|  | Component |
|  | Number |
|  | Content |
|  | Lot number |
|  | Control |
|  | Negative control |
|  | Positive control |
|  | Document / label identification number |
|  | Temperature limit |
|  | Manufacturer |
|  | Consult instructions for use |

For a glossary of symbols used in Vela Diagnostics product labeling, refer to:
<https://www.veladx.com/symbol-glossary.html>

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Storage

The components of the ViroKey® SARS-CoV-2 RT-PCR Test v2.0 should be stored at $-20^{\circ}\text{C} \pm 5^{\circ}\text{C}$ and are stable until the expiration date stated on the label. RNA4 M3 / HT RNA M3 is an enzyme, which is in liquid state. Except RNA4 M3 / HT RNA M3, all reagents should be thawed completely before use.

ViroKey® SARS-CoV-2 RT-PCR Test v2.0

| Kit item no. | Item | Quantity (tube) | Volume / tube | Shipping Condition | Storage Condition |
|--------------|------------------|-----------------|-------------------|--------------------|---|
| 301068* | SARS-CoV-2 v2 M1 | 8 | 60 μL | Dry ice | $-25^{\circ}\text{C} - -15^{\circ}\text{C}$ |
| | RNA4 M2 | 8 | 700 μL | Dry ice | $-25^{\circ}\text{C} - -15^{\circ}\text{C}$ |
| | RNA4 M3 | 8 | 125 μL | Dry ice | $-25^{\circ}\text{C} - -15^{\circ}\text{C}$ |
| | NC5 | 8 | 600 μL | Dry ice | $-25^{\circ}\text{C} - -15^{\circ}\text{C}$ |
| | SARS-CoV-2 v2 PC | 8 | 300 μL | Dry ice | $-25^{\circ}\text{C} - -15^{\circ}\text{C}$ |
| | EC8 | 8 | 600 μL | Dry ice | $-25^{\circ}\text{C} - -15^{\circ}\text{C}$ |

*Used with ViroKey® SX Virus Total Nucleic Acid Kit (4x48) extraction kit

ViroKey® SARS-CoV-2 RT-PCR Test v2.0

| Kit item no. | Item | Quantity (tube) | Volume / tube | Shipping Condition | Storage Condition |
|--------------|------------------|-----------------|--------------------|--------------------|---|
| 301085* | HT SARS-CoV-2 M1 | 4 | 115 μL | Dry ice | $-25^{\circ}\text{C} - -15^{\circ}\text{C}$ |
| | HT RNA M2 | 4 | 1400 μL | Dry ice | $-25^{\circ}\text{C} - -15^{\circ}\text{C}$ |
| | HT RNA M3 | 4 | 115 μL | Dry ice | $-25^{\circ}\text{C} - -15^{\circ}\text{C}$ |
| | HT NC | 4 | 300 μL | Dry ice | $-25^{\circ}\text{C} - -15^{\circ}\text{C}$ |
| | HT SARS-CoV-2 PC | 4 | 300 μL | Dry ice | $-25^{\circ}\text{C} - -15^{\circ}\text{C}$ |
| | HT EC | 4 | 1200 μL | Dry ice | $-25^{\circ}\text{C} - -15^{\circ}\text{C}$ |

*Used with ViroKey® HT Virus Total Nucleic Acid Kit (4x96) extraction kit

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Intended use

ViroKey® SARS-CoV-2 RT-PCR Test v2.0 is a real-time RT-PCR test intended for the qualitative detection of nucleic acid from SARS-CoV-2 in nasopharyngeal swabs, oropharyngeal swabs, anterior nasal swabs, mid-turbinate nasal swabs, nasal or nasopharyngeal aspirates, nasal washes and bronchoalveolar lavage samples collected from individuals suspected of COVID-19 by their healthcare provider. Testing is limited to laboratories certified under the Clinical Laboratory Improvement Amendments of 1988 (CLIA), 42 U.S.C. §263a, that meet requirements to perform high complexity tests.

Results are for the identification of SARS-CoV-2 RNA. The SARS-CoV-2 RNA is generally detectable in respiratory specimens during the acute phase of infection. Positive results are indicative of the presence of SARS-CoV-2 RNA. Clinical correlation with patient history and other diagnostic information is necessary to determine patient infection status. Positive results do not rule out bacterial infection or co-infection with other viruses. The agent detected may not be the definite cause of disease. Laboratories within the United States and its territories are required to report all results to the appropriate public health authorities. Negative results do not preclude SARS-CoV-2 infection and should not be used as the sole basis for patient management decisions. Negative results must be combined with clinical observations, patient history, and epidemiological information.

The ViroKey® SARS-CoV-2 RT-PCR Test v2.0 is intended for use by qualified clinical laboratory personnel specifically instructed and trained in the techniques of real-time PCR and in vitro diagnostic procedures. The ViroKey® SARS-CoV-2 RT-PCR Test v2.0 is only for use under the Food and Drug Administration's Emergency Use Authorization.

The following indication is authorized under the FDA's Pooling and Serial Testing [Amendment Letter] for use in laboratories certified under CLIA to perform high complexity tests. The ViroKey® SARS-CoV-2 RT-PCR Test v2.0 test is intended for the qualitative detection of RNA from the SARS-CoV-2 in pooled samples containing aliquots of transport media from up to 3 individual human anterior nasal swab specimens that were collected by a healthcare provider (HCP) or self-collected under the supervision of an HCP from individuals without symptoms or other reasons to suspect COVID-19, and placed in individual vials containing transport media when tested at least once per week as part of a serial testing program.

This indication is authorized with the testing guidelines within this Instructions For Use. Negative results from pooled testing should not be treated as definitive. If a patient's clinical signs and symptoms are inconsistent with a negative result or results are necessary for patient management, then the patient should be considered for individual testing. Specimens included in pools with a positive or invalid result must be reported as presumptive positive or tested individually prior to reporting a result.

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Warnings and Precautions

- This test is for use under Emergency Use Authorization (EUA) only.
- For Prescription Use Only.
- For *in vitro* diagnostic use (IVD).
- This product has not been FDA cleared or approved, but has been authorized for emergency use by FDA under an EUA for use by authorized laboratories.
- This product has been authorized only for the detection of nucleic acid from SARS-CoV-2, not for any other viruses or pathogens.
- The emergency use of this product is only authorized for the duration of the declaration that circumstances exist justifying the authorization of emergency use of in vitro diagnostic for detection and/or diagnosis of COVID-19 under Section 564(b)(1) of the Federal Food, Drug, and Cosmetic Act, 21 U.S.C. §360bbb-3(b)(1), unless the declaration is terminated or authorization is revoked sooner.
- This product is for use in laboratories certified under the Clinical Laboratory Improvement Amendments (CLIA) of 1988, 42 U.S.C. 263a, that meet requirements to perform high complexity tests.
- Testing of pooled samples is limited to laboratories certified under CLIA, 42 U.S.C. §263a, that meet requirements to perform high complexity tests only.
- The performance of these tests was established based on the evaluation of a limited number of clinical specimens. The clinical performance has not been established with all circulating variants but is anticipated to be reflective of the prevalent variants in circulation at the time and location of the clinical evaluation. Performance at the time of testing may vary depending on the variants circulating, including newly emerging strains of SARS-CoV-2 and their prevalence, which change over time.
- The product is to be used by qualified and trained clinical laboratory personnel only.
- Strict compliance with the Instructions for Use (IFU) is required for optimal PCR results.
- For more information about n=3 pooling strategy for implementation and monitoring, see the IFU before proceeding with the PCR workflow.
- ViroKey SX Virus Total Nucleic Acid Kit (4x48) extraction kit (PN: 300677) should only be used with the Sentosa SX101 workflow and the Thermo Fisher KingFisher Flex workflow. ViroKey HT Virus Total Nucleic Acid Kit (4x96) extraction kit (PN: 301088) should only be used with the Hamilton Microlab STAR workflow.
- Do not use expired kit components. Expiration dates are printed on the box and labels of all components. RNA4 M3 / HT RNA M3 is an enzyme, which is in liquid state. Except RNA4 M3 / HT RNA M3, the rest of the ViroKey SARS-CoV-2 RT-PCR Test v2.0 components should be thawed completely at room temperature (approximately 15°C – 25°C) for up to 30 minutes before use.
- RNA4 M3 / HT RNA M3 should be used directly out of the freezer or kept on ice when performing reagent preparation. Handle carefully to avoid contamination and store the remaining RNA4 M3 / HT RNA M3 immediately after use at $\leq -20^{\circ}\text{C}$ for subsequent reactions.

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- All reagents, except RNA4 M2 / HT RNA M2 and RNA4 M3 / HT RNA M3, require thorough mixing by quick vortex. Mix RNA4 M2 / HT RNA M2 and RNA4 M3 / HT RNA M3 by gentle inversion. Centrifuge all tubes briefly to collect the contents at the bottom of the tubes. Avoid foaming of the reagents.
- Mutations that arise within the highly conserved regions of the viral genome covered by the kit's primers and / or probes may result in failure to detect the presence of the virus.
- May cause allergic skin reactions.
- May be harmful if swallowed.
- Use personal protective equipment as required.
- For additional information, please refer to the Safety Data Sheet (SDS).
- All samples and waste should be considered potentially infectious. Clean and disinfect all work surfaces thoroughly with disinfectants recommended by local authorities.
- Do not eat, drink or smoke in the laboratory work area.
- Do not pipette by mouth.
- Wear protective disposable gloves, laboratory coats and eye protection when handling samples and kit reagents.
- Clean and decontaminate work area and instruments, including pipettes, with commercially available decontamination products.
- Avoid microbial and nuclease contamination of reagents when removing aliquots from reagent bottles. Use sterile disposable pipette tips.
- To avoid environmental contamination by amplicons, do not remove the PCR seal after amplification.
- Wash hands thoroughly after handling biological samples and kit reagents.

Safety information

- When working with samples and chemicals, always wear a suitable lab coat, disposable gloves, protective goggles and mask. For more information on the ViroKey SX Virus Total Nucleic Acid Kit (4x48), ViroKey HT Virus Total Nucleic Acid Kit (4x96), and the ViroKey SARS-CoV-2 RT-PCR Test v2.0, please refer to the respective Safety Data Sheets (SDS).
- For more safety information on the instruments, please refer to the relevant instrument IFU.
- Discard samples and waste according to local safety regulations.

Quality control

In accordance with Vela Diagnostics' ISO 13485-certified Quality Management System, each lot of the ViroKey SARS-CoV-2 RT-PCR Test v2.0 is tested against predetermined specifications to ensure consistent product quality.

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Introduction

The ViroKey SARS-CoV-2 RT-PCR Test v2.0 comprises a ready-to-use system for the detection of SARS-CoV-2 RNA extracted with the ViroKey SX Virus Total Nucleic Acid Kit (4x48) on the *Sentosa* SX101 alone, *Sentosa* SX101 and Thermo Fisher KingFisher Flex instrument combination (hereinafter known as KingFisher); or SARS-CoV-2 RNA extracted with ViroKey HT Virus Total Nucleic Acid Kit (4x96) on the Hamilton Microlab STAR instrument. SARS-CoV-2 RNA detection is done via reverse transcription PCR (RT-PCR) on the Applied Biosystems 7500 Fast Dx Real-Time PCR System or the *Sentosa* SA201 Real-Time PCR Instrument (hereinafter known as *Sentosa* SA201, and references to *Sentosa* SA201 in the IFU will also be applicable to the Applied Biosystems 7500 Fast Dx Real-Time PCR System for brevity unless otherwise stated).

The ViroKey SARS-CoV-2 RT-PCR Test v2.0 has specific primers and probes that target the *ORF1a* (FAM reporter dye) and *N* (HEX reporter dye) gene sequences of RNA from SARS-CoV-2 virus for direct detection of the specific amplicons in the same RT-PCR reaction. The genes are detected in the green and orange fluorescence channels respectively, on the *Sentosa* SA201 Real-Time PCR System.

In addition, the ViroKey SARS-CoV-2 RT-PCR Test v2.0 contains a third set of primers and probe designed to detect an extraction control (EC) target in the red fluorescence channel. This extraction control is a non-human synthetic DNA fragment added to all samples to control for the nucleic acid extraction steps, and also function as a PCR inhibition control. The EC amplification system does not compromise the detection limit of the analytical SARS-CoV-2 PCR. The test also contains a negative control (NC5 / HT NC) and a positive control (SARS-CoV-2 v2 PC / HT SARS-CoV-2 PC that allows the user to assess whether the RT-PCR reaction performed correctly. The ViroKey SARS-CoV-2 RT-PCR Test v2.0 does not cross-react with pathogens that cause similar symptoms, such as influenza.

Principle

The ViroKey SARS-CoV-2 RT-PCR Test v2.0 uses TaqMan probe chemistry for real-time RT-PCR detection of viral nucleic acid extracted from respiratory specimens using the ViroKey SX Virus Total Nucleic Acid Kit (4x48) on an automated workflow using the liquid handler *Sentosa* SX101 or *Sentosa* SX101 and Thermo Fisher KingFisher Flex instrument combination; or the ViroKey HT Virus Total Nucleic Acid Kit (4x96) on an automated workflow using the liquid handler Hamilton Microlab STAR instrument. The ViroKey SARS-CoV-2 RT-PCR Test v2.0 contains two primer/probe sets that target the *ORF1a* (FAM reporter dye in the Green fluorescence channel) or *N* (HEX reporter dye in the Orange fluorescence channel) gene sequences of RNA from SARS-CoV-2 virus. The assay also contains primers and a probe to detect an extraction control (EC) sequence, which is a non-human synthetic DNA fragment added to each sample (reporter dye in the Red fluorescence channel).

Nucleic acids extracted from specimens are reverse transcribed into cDNA, and cDNA sequences that are complementary to the oligonucleotide primers are amplified by polymerase chain reaction using the supplied enzyme mixes (tubes RNA4 M2 and RNA4 M3; or tubes HT RNA M2 and HT RNA M3) on the *Sentosa* SA201 Real-Time PCR system with the *Sentosa* SA201 Reporter software.

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If the target nucleic acids are present and amplified, the probe(s) will anneal to specific complementary sequences located between the corresponding forward and reverse primers during the PCR process. During the extension phase of the PCR, the 5' nuclease activity of DNA polymerase degrades the probe bound to the specific target, causing the reporter dye to separate from the quencher dye, generating a fluorescent signal. Probes specific to each target generate a fluorescent signal at different wavelengths, enabling the instrument to differentiate between the signals. With each cycle, additional reporter dye molecules are cleaved from their respective probes, increasing the fluorescence intensity¹. Fluorescence intensity is monitored at each PCR cycle by the *Sentosa* SA201 Real-Time PCR system with the *Sentosa* SA201 Reporter software or the Applied Biosystems 7500 Fast Dx Real-Time PCR System with ABI SDS Software 1.4.1.

Pathogen information

Coronaviruses, which are RNA viruses from the *Coronaviridae* family that are part of the *Coronavirinae* subfamily, cause infectious diseases that mainly infect the respiratory tract, resulting in upper respiratory tract infections (e.g. common cold) in humans². Other symptoms include rhinitis, cough, sore throat, and fever³.

Previously, six coronaviruses that can infect humans were identified—HCoV-229E, HCoV-NL63, HCoV-OC43, HCoV-HKU1, Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV) and Middle East Respiratory Syndrome Coronavirus (MERS-CoV)⁴. In December 2019, a novel coronavirus was discovered in Wuhan, China. The newly discovered coronavirus is the causative agent of the COVID-19 disease. Human-to-human transmission of the virus via respiratory droplets has been confirmed⁵. In February 2020, the International Committee on Taxonomy of Viruses named the novel coronavirus SARS-CoV-2⁶.

Limitations

- All users, analysts, and any person reporting diagnostic results should be trained to perform this procedure by a competent instructor. They should demonstrate their ability to perform the test and interpret the results prior to performing the assay independently.
- The ViroKey SARS-CoV-2 RT-PCR Test v2.0 does not include an Internal Control for RNA extraction/recovery. A known SARS-CoV-2 positive sample should be tested with every batch of patient specimens to monitor the integrity of these process steps.
- The ViroKey SARS-CoV-2 RT-PCR Test v2.0 was validated with nasopharyngeal swabs. Nasal (self-collected under supervision of, or healthcare provider collected), mid-turbinate, and oropharyngeal swab specimens as well as nasopharyngeal wash/aspirate or nasal aspirate specimens, as well as bronchoalveolar lavage samples are also considered acceptable specimen types, but performance has not been established.

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- The ViroKey SARS-CoV-2 RT-PCR Test v2.0 is validated for use for the following combination of extraction kits, instruments and PCR systems:

| Extraction Kit | Extraction Instrument | | | Real Time PCR System |
|----------------------------------|-----------------------|-------------------------|------------------------|------------------------------|
| | Sentosa SX101 | KingFisher ⁱ | Hamilton ⁱⁱ | Sentosa SA201 ⁱⁱⁱ |
| ViroKey SX VTNA ^{iv} | ✓ | ✓ | N/A* | ✓ |
| ViroKey HT VTNA ^v | N/A* | N/A* | ✓ | ✓ |

N/A: Not applicable as workflow combination is not validated.

- The ViroKey SARS-CoV-2 RT-PCR Test v2.0 has not been evaluated for patients receiving intranasally administered influenza vaccine.
- The ViroKey SARS-CoV-2 RT-PCR Test v2.0 may cross-react with human Adenovirus 71 and *Mycoplasma pneumoniae*.
- Negative results do not preclude SARS-CoV-2 virus infection and should not be used as the sole basis for treatment or other patient management decisions.
- A false negative result may occur if a specimen is improperly collected, transported, or handled. False negative results may also occur if amplification inhibitors are present in the specimen or if inadequate numbers of organisms are present in the specimen.
- Positive and negative predictive values are highly dependent on prevalence rates. Positive test results are more likely to represent false positive results during periods of little/no SARS-CoV-2 activity when disease prevalence is low. False negative test results are more likely when prevalence of disease caused by SARS-CoV-2 is high.
- N = 3 Pooling:**
 - Negative results from pooled testing should not be treated as definitive. If a patient's clinical signs and symptoms are inconsistent with a negative result or results are necessary for patient management, then the patient should be considered for individual testing.
 - Specimens included in pools with a positive or invalid result must be reported as presumptive positive or tested individually prior to reporting a result. Individuals included in a pool that returns a positive or invalid result should be treated as a presumptive positive unless or until they receive a negative result when re-tested individually.
 - However, as most individuals in a positive pool will likely receive a negative result when re-tested individually, they should isolate until receiving a negative result when re-tested individually and should not be cohorted with other individuals who have received a positive or presumptive positive result.

ⁱ Sentosa SX101 and Thermo Fisher KingFisher Flex instrument combination

ⁱⁱ Hamilton Microlab STAR instrument

ⁱⁱⁱ Sentosa SA201 Real-Time PCR system

^{iv} ViroKey SX Virus Total Nucleic Acid Kit (4x48) (PN: 300677)

^v ViroKey HT Virus Total Nucleic Acid Kit (4x96) (PN: 301088)

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- Specimens with low viral loads may not be detected with pooled testing due to decreased sensitivity or increased interference from pooled testing.
- Do not use any reagent past the expiration date, as this may affect performance of the assay.
- Optimum specimen types and timing for peak viral levels during infections caused by a SARS-CoV-2 virus have not been determined. Collection of multiple specimens from the same patient may be necessary to detect the virus.
- If SARS-CoV-2 virus mutates in the rRT-PCR target region, the specific novel virus may not be detected or may be detected less predictably. Inhibitors or other types of interference may produce a false negative result. An interference study evaluating the effect of common cold medications was performed.
- The potential for the epidemiology and pathology of disease caused by a specific novel SARS-CoV-2 virus to affect test performance is not fully known. For example, clinicians and laboratories may not know the optimum types of specimens to collect, and when during the course of infection these specimens are most likely to contain levels of virus that can be readily detected.
- Detection of viral RNA may not indicate the presence of infectious virus or that SARS-CoV-2 viruses are the causative agent for clinical symptoms.
- The performance of this test was established based on the evaluation of a limited number of clinical specimens. The clinical performance has not been established with all circulating variants but is anticipated to be reflective of the prevalent variants in circulation at the time and location of the clinical evaluation. Performance at the time of testing may vary depending on the variants circulating, including newly emerging strains of SARS-CoV-2 and their prevalence, which change over time.
- The performance of this assay has not been established for screening of blood or blood products for the presence of SARS-CoV-2.
- This assay cannot rule out diseases caused by other bacterial or viral pathogens.

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Conditions of Authorization for the Laboratory

- The ViroKey SARS-CoV-2 RT-PCR Test v2.0 Letter of Authorization, along with the authorized Fact Sheet for Healthcare Providers, the authorized Fact Sheet for Patients, and other authorized labeling are available on the FDA website: <https://www.fda.gov/medical-devices/coronavirus-disease-2019-covid-19-emergency-use-authorizations-medical-devices/in-vitro-diagnostics-euas>.
- However, to assist clinical laboratories using the ViroKey SARS-CoV-2 RT-PCR Test v2.0 (“your product” in the conditions below), the relevant Conditions of Authorization are listed below:
 - (A) Authorized laboratories^{vi} using your product will include with test result reports, all authorized Fact Sheets. Under exigent circumstances, other appropriate methods for disseminating these Fact Sheets may be used, which may include mass media.
 - (B) Authorized laboratories using your product will use your product as outlined in the authorized labeling. Deviations from the authorized procedures, including the authorized instruments, authorized extraction methods, authorized clinical specimen types, authorized control materials, authorized other ancillary reagents and authorized materials required to use your product are not permitted.
 - (C) Authorized laboratories that receive your product will notify the relevant public health authorities of their intent to run your product prior to initiating testing.
 - (D) Authorized laboratories using your product will have a process in place for reporting test results to healthcare providers and relevant public health authorities, as appropriate.
 - (E) Authorized laboratories using specimen pooling strategies when testing patient specimens with the ViroKey SARS-CoV-2 RT-PCR Test v2.0 must include with negative test result reports for specific patients whose specimen(s) were the subject of pooling, a notice that pooling was used during testing and that “Patient specimens with low viral loads may not be detected in sample pools due to the decreased sensitivity of pooled testing.”
 - (F) Authorized laboratories implementing pooling strategies for testing patient specimens must use the “**Specimen pooling strategy for implementation and monitoring**” recommendations available in the authorized labeling to evaluate the appropriateness of continuing to use such strategies based on the recommendations in the protocol.
 - (G) Authorized laboratories must keep records of specimen pooling strategies implemented including type of strategy, date implemented, and quantities tested, and test result data generated as part of the Protocol for Monitoring of Specimen Pooling Testing Strategies. For the first 12 months from the date of their creation, such records will be made available to FDA within 48 business hours for inspection upon request, and will be made available within a reasonable time after 12 months from the date of their creation.

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For Prescription Use Only

- (H) Authorized laboratories will collect information on the performance of your product and report to DMD/OHT7/OPEQ/CDRH (via email: CDRH-EUA-Reporting@fda.hhs.gov) and to Vela Diagnostics USA, Inc. (via email: support.us@veladx.com or phone: 877.593.7528, in the U.S.) any suspected occurrence of false positive or false negative results and significant deviations from the established performance characteristics of your product of which they become aware.
- (I) All laboratory personnel using your product must be appropriately trained in PCR techniques and use appropriate laboratory and personal protective equipment when handling this kit and use your product in accordance with the authorized labeling.
- (J) Vela Diagnostics, authorized distributors, and authorized laboratories using ViroKey SARS-CoV-2 RT-PCR Test v2.0 will ensure that any records associated with this EUA are maintained until otherwise notified by FDA. Such records will be made available to FDA for inspection upon request.

^{vi} The letter of authorization refers to, “Laboratories certified under the Clinical Laboratory Improvement Amendments of 1988 (CLIA), 42 U.S.C. §263a, that meet requirements to perform high complexity tests” as “authorized laboratories.”

Controls

A tube of Negative Control (NC), which is nucleic acid-free water, is included in the kit for each run.

A tube of Positive Control (PC), consisting of an IVT-RNA fragment that can be amplified by both sets of primer/probes for *Orf1a* and *N* gene, is included in the kit for each run.

An Extraction Control (EC) is spiked into every test sample in every run and is needed to assess the efficacy of the nucleic acid extraction process, as well as test for the presence of inhibitors and validity of a negative result.

The ViroKey SARS-CoV-2 RT-PCR Test v2.0 does not include an Internal Control for RNA extraction/recovery. A known SARS-CoV-2 positive sample should be tested with every run of patients' specimens to monitor the integrity of these process steps.

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Result interpretation

Negative results from pooled testing should not be treated as definitive. If a patient's clinical signs and symptoms are inconsistent with a negative result or results are necessary for patient management, then the patient should be considered for individual testing.

Specimens included in pools with a positive, inconclusive, or invalid result must be tested individually prior to reporting a result.

Specimens with low viral loads may not be detected in sample pools due to the decreased sensitivity of pooled testing.

Negativity / Positivity

The Ct ranges to define negativity / positivity for negative control, positive control and samples for the workflows are listed in the table below. If Ct falls within the range, it is defined as positive (+); if Ct falls out of the range or no Ct is obtained, it is defined as negative (-).

ViroKey SARS-CoV-2 RT-PCR Test v2.0*

| Fluorescence channel | Expected Ct values | | | | | |
|---------------------------------|-------------------------------|-------------|-------------------------------|-------------|-------------------------------|-------------|
| | Negative control | | Positive control | | Samples | |
| | Not detected | Detected | Not detected | Detected | Not detected | Detected |
| Green (ORF1a gene) | < 10.0, > 38.0 or no Ct | 10.0 – 38.0 | < 15.0, > 32.0 or no Ct | 15.0 – 32.0 | < 10.0, > 38.0 or no Ct | 10.0 – 38.0 |
| Orange (N gene) | < 10.0, > 38.0 or no Ct | 10.0 – 38.0 | < 15.0, > 32.0 or no Ct | 15.0 – 32.0 | < 10.0, > 38.0 or no Ct | 10.0 – 38.0 |
| Red (Extraction Control, EC) | < 23.0, > 32.0 or no Ct | 23.0 – 32.0 | < 23.0, > 32.0 or no Ct | 23.0 – 32.0 | < 20.0, > 38.0 or no Ct | 20.0 – 38.0 |

*Used with ViroKey SX Virus Total Nucleic Acid Kit (4x48) extraction kit

ViroKey SARS-CoV-2 RT-PCR Test v2.0*

| Fluorescence channel | Expected Ct values | | | | | |
|------------------------------|-------------------------------|-------------|-------------------------------|-------------|-------------------------------|-------------|
| | Negative control | | Positive control | | Samples | |
| | Not detected | Detected | Not detected | Detected | Not detected | Detected |
| Green (ORF1a gene) | < 10.0, > 40.0 or no Ct | 10.0 – 40.0 | < 15.0, > 32.0 or no Ct | 15.0 – 32.0 | < 10.0, > 40.0 or no Ct | 10.0 – 40.0 |
| Orange (N gene) | < 10.0, > 40.0 or no Ct | 10.0 – 40.0 | < 15.0, > 32.0 or no Ct | 15.0 – 32.0 | < 10.0, > 40.0 or no Ct | 10.0 – 40.0 |
| Red (extraction control, EC) | < 23.0, > 32.0 or no Ct | 23.0 – 32.0 | < 23.0, > 32.0 or no Ct | 23.0 – 32.0 | < 20.0, > 40.0 or no Ct | 20.0 – 40.0 |

*Used with ViroKey HT Virus Total Nucleic Acid Kit (4x96) extraction kit

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Result interpretation of samples

Please refer to the table below for result analysis. All test controls should be examined prior to interpretation of patient results. If the controls are not valid, the patient results cannot be interpreted.

| | Green (ORF1a) | Orange (N) | Red (EC) | Interpretation |
|------------------------------------|------------------|---------------|-------------|---|
| Negative control | - | - | + | Run valid (proceed to PC) |
| | + | - | +/- | Run invalid. Repeat run. |
| | - | + | +/- | |
| | + | + | +/- | |
| | - | - | - | |
| Positive control | + | + | +/- | Run valid (proceed to SARS-CoV-2 positive sample control) |
| | + | - | +/- | Run invalid. Repeat run. |
| | - | + | +/- | |
| | - | - | +/- | |
| SARS-CoV-2 positive sample control | + | + | +/- | Run valid (proceed to result interpretation of samples) |
| | + | - | +/- | Run invalid. Repeat run. |
| | - | + | +/- | |
| | - | - | +/- | |
| Samples | + | + | +/- | SARS-CoV-2 virus detected* |
| | - | + | +/- | |
| | + | - | +/- | |
| | - | - | + | SARS-CoV-2 virus not detected |
| | - | - | - | Sample invalid. Sample should be retested. If result is still invalid, a new specimen should be obtained. |

*For positive samples, the fluorescence channel Cycling Red may be negative due to competition with the target channels.

Run: Whole run on the MicroAmp Fast Optical 96-Well Reaction Plate with Barcode

Test: Test to which the NC / PC belongs

Sample: Single sample in one well of the MicroAmp Fast Optical 96-Well Reaction Plate with Barcode

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Result interpretation of n=3 pooling samples

Please refer to the table below for result analysis. All test controls should be examined prior to interpretation of results. If the controls are not valid, the results cannot be interpreted.

| | Green (ORF1a) | Orange (N) | Red (EC) | Interpretation |
|------------------------------------|---------------|------------|----------|--|
| Negative control | - | - | + | Run valid (proceed to PC) |
| | + | - | +/- | Run invalid. Repeat run. |
| | - | + | +/- | |
| | + | + | +/- | |
| | - | - | - | |
| Positive control | + | + | +/- | Run valid (proceed to SARS-CoV-2 positive sample control) |
| | + | - | +/- | Run invalid. Repeat run. |
| | - | + | +/- | |
| | - | - | +/- | |
| SARS-CoV-2 positive sample control | + | + | +/- | Run valid (proceed to result interpretation of samples) |
| | + | - | +/- | Run invalid. Repeat run. |
| | - | + | +/- | |
| | - | - | +/- | |
| Pooled Samples | + | + | +/- | Presumptive Positive ^{a,b} |
| | - | + | +/- | (Report pooled result to program administrator with notification that subjects in the positive pool should isolate until receiving a negative result when re-tested individually. Individual should not be cohorted with other individuals who have received a positive or presumptive positive result. Individual samples from all subjects in the pool should be re-tested individually.) ^c |
| | + | - | +/- | |
| | - | - | + | SARS-CoV-2 virus not detected ^{a,d} (Report pooled result to program administrator and appropriate public health authorities.) ^c |
| | - | - | - | Sample invalid ^b . Sample should be retested. If result is still invalid, a new specimen should be obtained. (If the result is Negative, report pooled result to program administrator and appropriate public health authorities. If the result is Positive or Invalid, report the result as Presumed Positive to program administrator. A new sample from all subjects in the pool should be run and re-tested individually.) ^c |
| | - | - | - | |

^aPresumptive Positive” and “Negative” are the specific result interpretations for samples tested as part of the 3-swab pooling procedure.

^bIndividuals included in a pool that returns a positive or invalid result should be treated as a presumptive positive unless or until they receive a negative result when re-tested individually. However, as most individuals in a positive pool will likely receive a negative result when re-tested individually, they should isolate until receiving a negative result when re-tested individually and should not be cohorted with other individuals who have received a positive or presumptive positive result. For serial testing programs, additional confirmatory testing for positive results may also be necessary, if there is a low likelihood of COVID-19, such as in individuals without known exposure to COVID-19 or residing in communities with low prevalence of infection.

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°Results of follow-up testing are reported to the program administrator and appropriate public health authorities.

°Specimens with low viral loads may not be detected with pooled testing due to decreased sensitivity or increased interference from pooled testing. For serial testing programs, additional confirmatory testing for negative results may be necessary, if there is a high likelihood of COVID-19, such as an individual with a close contact with COVID-19 or with suspected exposure to COVID-19 or in communities with high prevalence of infection.

Performance characteristics

Analytical sensitivity

ViroKey SARS-CoV-2 RT-PCR Test v2.0 with ViroKey SX Virus Total Nucleic Acid Kit (4x48) extraction kit

The analytical limit of detection (LoD) of ViroKey SARS-CoV-2 RT-PCR Test v2.0 was assessed with the automated *Sentosa* SX101 workflow and automated *Sentosa* SX101 and Kingfisher combination workflow, starting with sample extraction using the ViroKey SX Virus Total Nucleic Acid Kit (4x48) on the *Sentosa* SX101, as well as RT-PCR run on the *Sentosa* SA201. Serial dilutions of the heat-inactivated SARS-CoV-2 in nasopharyngeal matrix were tested to determine the assay LoD. The preliminary LoD was determined by testing three replicates of inactivated virus dilutions between 2.0×10^4 and 50 (GE/mL). The LoD was confirmed by testing at least 20 replicates. If the confirmatory study achieved a positivity of 100%, then a lower concentration was tested (with 20 replicates) until less than 100% positivity was obtained. The overall assay LoD was the lowest dilution giving a final sample detection of $\geq 95\%$ for 20 samples for one of the targets (refer to **Tables 1 and 2**). The overall LoD of the ViroKey SARS-CoV-2 RT-PCR Test v2.0 performed on *Sentosa* SX101 is 200 GE/mL while the overall LoD of the test performed on the *Sentosa* SX101 and KingFisher combination is 250 GE/mL.

Table 1. Results from confirmatory LoD study for the ViroKey SARS-CoV-2 RT-PCR Test v2.0 performed on *Sentosa* SX101.

| Target channel | Genomic equivalents/mL | Detection % | Mean Ct \pm SD |
|-----------------------------------|------------------------|-------------|------------------|
| <i>ORF1a</i> (Green channel) | 200 | 95% (19/20) | 32.27 \pm 1.66 |
| <i>N gene</i> (Orange channel) | 187 | 95% (19/20) | 32.19 \pm 1.90 |

Table 2. Results from confirmatory LoD study for the ViroKey SARS-CoV-2 RT-PCR Test v2.0 performed on *Sentosa* SX101 and KingFisher combination.

| Target channel | Genomic equivalents/mL | Detection % | Mean Ct \pm SD |
|---------------------------------|------------------------|-------------|------------------|
| <i>ORF1a</i> (Green channel) | 250 | 95% (19/20) | 31.22 \pm 2.41 |
| <i>N</i> (Orange channel) | 250 | 95% (19/20) | 33.65 \pm 1.81 |

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ViroKey SARS-CoV-2 RT-PCR Test v2.0 with ViroKey HT Virus Total Nucleic Acid Kit (4x96) extraction kit

The analytical limit of detection (LoD) of ViroKey SARS-CoV-2 RT-PCR Test v2.0 was assessed with the automated Hamilton workflow, starting with sample extraction using the ViroKey HT Virus Total Nucleic Acid Kit (4x96) on the Hamilton Microlab STAR, as well as RT-PCR run on the *Sentosa* SA201. Serial dilutions of the heat-inactivated SARS-CoV-2 in nasopharyngeal matrix were tested to determine the assay LoD. The preliminary LoD was determined by testing three replicates of inactivated virus dilutions between 1.0×10^3 and 125 (GE/mL). The LoD was confirmed by testing at least 20 replicates. If the confirmatory study achieved a positivity of 100%, then a lower concentration was tested (with 20 replicates) until less than 100% positivity was obtained. The overall assay LoD was the lowest dilution giving a final sample detection of $\geq 95\%$ for 20 samples for one of the targets. (**Table 3**). The overall LoD of the ViroKey SARS-CoV-2 RT-PCR Test v2.0 performed on Hamilton Microlab STAR is 200 GE/mL.

Table 3. Results from confirmatory LoD study for the ViroKey SARS-CoV-2 RT-PCR Test v2.0 performed on Hamilton Microlab STAR

| Target channel | Genomic equivalents/mL | Detection % | Mean Ct \pm SD |
|---------------------------------|------------------------|--------------|------------------|
| <i>ORF1a</i> (Green channel) | 187.5 | 95% (19/20) | 34.02 \pm 1.13 |
| <i>N</i> (Orange channel) | 200 | 100% (20/20) | 33.88 \pm 0.57 |

Analytical reactivity and specificity

The analytical reactivity and specificity of the ViroKey SARS-CoV-2 RT-PCR Test v2.0 are ensured by the selection of primers, probes and stringent reaction conditions.

Analytical reactivity

To evaluate the analytical reactivity (inclusivity) of the ViroKey SARS-CoV-2 RT-PCR Test v2.0 for SARS-CoV-2, *in silico* analysis was performed on all sequences available on the National Center for Biotechnology Information (NCBI) GenBank and Global Initiative on Sharing All Influenza Data (GISAID) databases. 2,636,603 complete sequences (401,846 from NCBI GenBank and 2,234,757 from GISAID — sequences downloaded on 4th August 2021) were aligned against primers and probes of ViroKey SARS-CoV-2 RT-PCR Test v2.0. The sequences were aligned with MAFFT (<https://mafft.cbrc.jp/alignment/server/>).

Out of the 401,846 complete SARS-CoV-2 sequences from NCBI GenBank database as of 4th August 2021,

- *ORF1a* primers and probes had 100% match to 396,292 out of 401,846 sequences (98.61%). For the remaining 5554 sequences (1.39%), the primers and probes have at most 1 mismatch with these sequences.

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- *N* gene primers and probes had 100% match to 390,973 out of 401,846 sequences (97.29%). For the remaining 10,873 sequences (2.71%), the primers and probes have at most 1 mismatch with these sequences.

Out of the 2,234,757 complete SARS-CoV-2 sequences from GISAID database as of 4th August 2021,

- *ORF1a* primers and probes had 100% match to 2,202,254 out of 2,234,757 sequences (98.54%). For the remaining 32,503 sequences (1.46%), the primers and probes have at most 1 mismatch with these sequences.
- *N* gene primers and probes had 100% match to 2,163,247, out of 2,234,757 sequences (96.87%). For the remaining 71,510 sequences (3.2%), the primers and probes have at most 1 mismatch with these sequences.

In silico analysis concluded that ViroKey SARS-CoV-2 RT-PCR Test v2.0 will detect all analysed SARS-CoV-2 sequences in the NCBI GenBank (n = 401,846) and in GISAID (n = 2,234,757) databases. None of the mismatching sequences showed mismatches with the other target, therefore the inclusivity of the assay is not expected to be affected.

Analytical specificity (in silico)

To evaluate the analytical specificity (cross-reactivity) of the ViroKey SARS-CoV-2 RT-PCR Test v2.0, in silico analysis was performed on pathogens listed in **Table 4**. NCBI BLAST tool was used to check for cross-reactivity of the different primers and probes of the ViroKey SARS-CoV-2 RT-PCR Test v2.0 against the non-redundant nucleotide database. BLAST tool search default parameters were used except for the “organism.” The search was limited to using the taxonomy ID (taxid/txid) of the respective pathogen. Each primer and probe were compared against all available genome sequences of a certain taxid.

Table 4. In silico analysis for ViroKey SARS-CoV-2 RT-PCR Test v2.0.

| Microorganism | Genbank Acc No. | In silico analysis for % identity/homology | | | | | |
|---------------------|-----------------|--|----------------|-------|------------------------|----------------|-------|
| | | <i>N</i> | | | <i>ORF1a</i> | | |
| | | Forward Primer | Reverse Primer | Probe | Forward Primer | Reverse Primer | Probe |
| Coronavirus 229E | NC_002645.1 | No alignment was found | | | No alignment was found | | |
| Coronavirus OC43 | NC_006213.1 | No alignment was found | | | No alignment was found | | |
| Coronavirus HKU-1 | NC_006577.2 | No alignment was found | | | No alignment was found | | |
| Coronavirus NL63 | NC_005831.2 | No alignment was found | | | No alignment was found | | |
| SARS-coronavirus | NC_004718.3 | NA | NA | 70% | No alignment was found | | |
| MERS-coronavirus | NC_019843.3 | No alignment was found | | | No alignment was found | | |
| Human adenovirus 2 | AC_000007.1 | No alignment was found | | | No alignment was found | | |
| Human adenovirus 5 | AC_000008.1 | No alignment was found | | | No alignment was found | | |
| Human adenovirus 54 | NC_012959.1 | 65% | NA | NA | No alignment was found | | |
| Human adenovirus A | NC_001460.1 | No alignment was found | | | No alignment was found | | |
| Human adenovirus B1 | NC_011203.1 | No alignment was found | | | No alignment was found | | |

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| Microorganism | Genbank Acc No. | In silico analysis for % identity/homology | | | | | |
|-------------------------------------|------------------|--|----------------|-------|------------------------|----------------|-------|
| | | N | | | ORF1a | | |
| | | Forward Primer | Reverse Primer | Probe | Forward Primer | Reverse Primer | Probe |
| Human adenovirus B2 | NC_011202.1 | No alignment was found | | | No alignment was found | | |
| Human adenovirus C | NC_001405.1 | No alignment was found | | | No alignment was found | | |
| Human adenovirus D | NC_010956.1 | No alignment was found | | | No alignment was found | | |
| Human adenovirus E | NC_003266.2 | No alignment was found | | | No alignment was found | | |
| Human adenovirus F | NC_001454.1 | No alignment was found | | | No alignment was found | | |
| Human adenovirus type 1 | AC_000017.1 | No alignment was found | | | No alignment was found | | |
| Human adenovirus type 35 | AC_000019.1 | No alignment was found | | | No alignment was found | | |
| Human adenovirus type 7 | AC_000018.1 | No alignment was found | | | No alignment was found | | |
| Human metapneumovirus | NC_039199.1 | No alignment was found | | | No alignment was found | | |
| Human parainfluenza virus 1 | NC_003461.1 | No alignment was found | | | No alignment was found | | |
| Human parainfluenza virus 2 | NC_003443.1 | No alignment was found | | | No alignment was found | | |
| Human parainfluenza virus 3 | NC_001796.2 | No alignment was found | | | No alignment was found | | |
| Human parainfluenza virus 4a | NC_021928.1 | No alignment was found | | | No alignment was found | | |
| Influenza A virus H1N1 | GCF_000865725 | No alignment was found | | | No alignment was found | | |
| Influenza A virus H3N2 | GCF_000865085 | No alignment was found | | | No alignment was found | | |
| Influenza A virus H5N1 | GCF_000864105 | No alignment was found | | | No alignment was found | | |
| Influenza A virus H7N9 | GCF_000928555 | No alignment was found | | | No alignment was found | | |
| Influenza B virus | GCF_000820495 | No alignment was found | | | No alignment was found | | |
| Influenza C virus | GCF_000856665.10 | No alignment was found | | | No alignment was found | | |
| Human Parechovirus | NC_001897.1 | No alignment was found | | | No alignment was found | | |
| Enterovirus (e.g. EV68) | NC_038308.1 | No alignment was found | | | No alignment was found | | |
| Human respiratory syncytial virus | NC_001781.1 | No alignment was found | | | No alignment was found | | |
| Human rhinovirus 1 | NC_038311.1 | No alignment was found | | | No alignment was found | | |
| Human rhinovirus 3 | NC_038312.1 | No alignment was found | | | No alignment was found | | |
| Human rhinovirus 14 | NC_001490.1 | No alignment was found | | | No alignment was found | | |
| Human rhinovirus 89 | NC_001617.1 | No alignment was found | | | No alignment was found | | |
| Human rhinovirus C | NC_009996.1 | No alignment was found | | | No alignment was found | | |
| <i>Chlamydomphila pneumoniae</i> | NC_002180.1 | No alignment was found | | | No alignment was found | | |
| <i>Haemophilus influenzae</i> | NZ_LN831035.1 | 65% | NA | NA | NA | NA | 60% |
| <i>Legionella pneumophila</i> | NZ_LR134380.1 | 65% | 68% | NA | 67% | NA | 56% |
| <i>Mycobacterium tuberculosis</i> | NC_000962.3 | No alignment was found | | | 67% | NA | NA |
| <i>Streptococcus pneumoniae</i> * | NZ_LN831051.1 | 80% | 68% | NA | NA | NA | 52% |
| <i>Streptococcus pyogenes</i> | NC_002737.2 | No alignment was found | | | NA | NA | 60% |
| <i>Bordetella pertussis</i> | NC_018518.1 | 65% | NA | NA | 62% | NA | NA |
| <i>Mycoplasma pneumoniae</i> | NZ_CP010546.1 | No alignment was found | | | NA | NA | 52% |
| <i>Pneumocystis jirovecii</i> (PJP) | GCF_001477535.1 | No alignment was found | | | NA | NA | 52% |

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| Microorganism | Genbank Acc No. | In silico analysis for % identity/homology | | | | | |
|--|-----------------|--|----------------|-------|------------------------|----------------|-------|
| | | N | | | ORF1a | | |
| | | Forward Primer | Reverse Primer | Probe | Forward Primer | Reverse Primer | Probe |
| <i>Candida albicans</i> * | GCF_000182965.3 | 65% | 74% | 67% | 62% | NA | 60% |
| <i>Pseudomonas aeruginosa</i> | GCF_000006765.1 | 65% | NA | NA | 67% | NA | 52% |
| <i>Staphylococcus epidermidis</i> | GCF_000007645.1 | NA | 68% | NA | NA | 71% | NA |
| <i>Staphylococcus salivarius</i> | CP013216.1 | NA | 74% | NA | No alignment was found | | |
| <i>Leptospira borgpetersenii</i> | GCF_000013945 | 65% | NA | NA | NA | NA | 56% |
| <i>Leptospira interrogans</i> | GCF_000092565 | 65% | 79% | NA | No alignment was found | | |
| <i>Leptospira santarosai</i> * | GCF_000313175 | 70% | 89% | NA | NA | 62% | NA |
| <i>Chlamydia psittaci</i> | NC_017287.1 | No alignment was found | | | No alignment was found | | |
| <i>Coxiella burnetii</i> (Q-Fever) | NC_002971.4 | NA | 68% | NA | 62% | NA | 60% |
| <i>Staphylococcus aureus</i> | NC_007795.1 | 70% | 68% | NA | No alignment was found | | |
| <i>Klebsiella pneumoniae</i> * | GCF_000240185.1 | 80% | 84% | NA | 62% | NA | 52% |
| <i>Corynebacterium diphtheriae</i> | NZ_LN831026.1 | 65% | 68% | NA | NA | NA | 56% |
| <i>Legionella longbeachae</i> * | GCF_000091785.1 | 65% | 68% | NA | 81% | 67% | 56% |
| <i>Bacillus anthracis</i> (Anthrax) | GCF_000008445.1 | NA | 68% | NA | NA | NA | 56% |
| <i>Moraxella catarrhalis</i> | NC_014147.1 | 85% | NA | NA | NA | 62% | 52% |
| <i>Neisseria elongata</i> | NZ_CP007726.1 | 70% | 68% | NA | 62% | NA | NA |
| <i>Neisseria meningitidis</i> | NZ_LR134525.1 | 65% | 68% | NA | 62% | NA | 52% |
| Pooled human nasal wash - to represent diverse microbial flora in the human respiratory tract* | ZLYEM2C (HMP) | 80% | 74% | 67% | 86% | 71% | 60% |
| Bat coronavirus HKU4-1 | NC_009019.1 | No alignment was found | | | 48% | NA | 40% |
| Bat coronavirus HKU5-1 | NC_009020.1 | No alignment was found | | | NA | 48% | NA |
| Bat coronavirus HKU9-1 | NC_009021.1 | No alignment was found | | | NA | 48% | NA |
| Scotophilus bat coronavirus 512 | NC_009657.1 | No alignment was found | | | NA | NA | 40% |
| Bat coronavirus HKU2 | NC_009988.1 | No alignment was found | | | 48% | 48% | 48% |
| Bat coronavirus 1A | NC_010437.1 | No alignment was found | | | 48% | 48% | NA |
| Bat coronavirus HKU8 | NC_010438.1 | No alignment was found | | | NA | NA | 40% |
| Bat coronavirus BM48-31/BGR/2008 | NC_014470.1 | No alignment was found | | | NA | 57% | NA |
| Rousettus bat coronavirus HKU10 | NC_018871.1 | No alignment was found | | | 48% | NA | 40% |
| Bat coronavirus CDPHE15/USA/2006 | NC_022103.1 | No alignment was found | | | NA | 48% | 40% |
| BtMr-AlphaCoV/SAX2011 | NC_028811.1 | No alignment was found | | | NA | 48% | 48% |

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| Microorganism | Genbank Acc No. | In silico analysis for % identity/homology | | | | | |
|---|-----------------|--|----------------|-------|----------------|----------------|-------|
| | | N | | | ORF1a | | |
| | | Forward Primer | Reverse Primer | Probe | Forward Primer | Reverse Primer | Probe |
| BtRf-AlphaCoV/HuB2013 | NC_028814.1 | No alignment was found | | | NA | 48% | NA |
| BtRf-AlphaCoV/YN2012 | NC_028824.1 | No alignment was found | | | NA | 57% | 48% |
| BtNv-AlphaCoV/SC2013 | NC_028833.1 | No alignment was found | | | NA | 48% | 40% |
| Rousettus bat coronavirus isolate GCCD.1 356 | NC_030886.1 | No alignment was found | | | NA | 48% | NA |
| NL63-related bat coronavirus strain BtKYNL63-9a | NC_032107.1 | No alignment was found | | | NA | NA | 40% |
| Bat coronavirus isolate PREDICT/PDF-2180 | NC_034440.1 | No alignment was found | | | NA | NA | 40% |

Some forward primers, reverse primers, or probes sequences have significant alignments (>80%) with the sequences and these are highlighted in red in **Table 4**. Among those are *Streptococcus pneumoniae*, *Leptospira santarosai*, *Klebsiella pneumoniae*, *Legionella longbeachae* and *Moraxella catarrhalis*. These pathogens were further analyzed and no potential cross-reactivity is expected based on this in silico analysis, as they all do not have nearby or correctly oriented primers or probe with significant alignment (> 80%) to bi-directionally amplify out a PCR product that can be detected on the ViroKey SARS-CoV-2 RT-PCR Test v2.0. In silico analysis of pooled microflora showed potential for cross-reactivity, therefore wet testing was performed (described below).

Analytical specificity (wet testing)

The ViroKey SARS-CoV-2 RT-PCR Test v2.0 was further evaluated for cross-reactivity with respiratory pathogens commonly present in human respiratory specimens, non-targeted coronaviruses as well as pooled human nasal wash representing the diverse microbial flora in the human respiratory tract. Purified and quantified nucleic acid of the pathogens were added directly into the ViroKey SARS-CoV-2 RT-PCR Test v2.0 PCR mix. At least three replicates were tested. All controls performed as expected. The results are presented in **Table 5**.

Table 5. Potential cross-reactivity of the ViroKey SARS-CoV-2 RT-PCR Test v2.0.

| Tested pathogens, strain (RNA) | | Sample input | ORF1a | N | EC |
|--------------------------------|---|---|-------|------|-----|
| Bacteria | <i>Haemophilus influenzae</i> | 5x 10 ⁶ copies (1x 10 ⁶ copies/ reaction) | 0/3 | 0/3 | 3/3 |
| | <i>Mycobacterium tuberculosis</i> , H37Ra | | 0/3 | 0/3 | 3/3 |
| | <i>Streptococcus pneumoniae</i> | | 0/3 | 0/3 | 3/3 |
| | <i>Streptococcus pyogenes</i> Rosenbach | | 0/3 | 0/3 | 3/3 |
| | <i>Mycoplasma pneumoniae</i> | | 1/9* | 1/9* | 9/9 |
| | <i>Legionella pneumophila</i> | | 0/3 | 0/3 | 3/3 |
| | <i>Chlamydophila pneumoniae</i> strain CM-1 | | 0/3 | 0/3 | 3/3 |
| | <i>Bordetella pertussis</i> | | 0/3 | 0/3 | 3/3 |

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| Tested pathogens, strain (RNA) | | Sample input | ORF1a | N | EC |
|---|--|--------------|-------|-----|-----|
| Virus | Human coronavirus 229E | | 0/3 | 0/3 | 3/3 |
| | Human coronavirus OC43 | | 0/3 | 0/3 | 3/3 |
| | Human coronavirus HKU1 | | 0/3 | 0/3 | 3/3 |
| | Human coronavirus NL63 | | 0/3 | 0/3 | 3/3 |
| | Human metapneumovirus (hMPV) | | 0/3 | 0/3 | 3/3 |
| | Human adenovirus 1, Adenoid 71 | | 1/9* | 0/9 | 9/9 |
| | Human parainfluenza virus 2, Greer | | 0/3 | 0/3 | 3/3 |
| | Human parainfluenza virus 3, C243 | | 0/3 | 0/3 | 3/3 |
| | Human parainfluenza virus 4a | | 0/3 | 0/3 | 3/3 |
| | Human parainfluenza virus 4b, CH 19503 | | 0/3 | 0/3 | 3/3 |
| | Influenza A virus (H3N2), A/Aichi/2/68 | | 0/3 | 0/3 | 3/3 |
| | Influenza A virus, A/Cali/07/2009 (H1N1 pdm) | | 0/3 | 0/3 | 3/3 |
| | Influenza B virus, B/Lee/40 | | 0/3 | 0/3 | 3/3 |
| | Enterovirus, H | | 0/3 | 0/3 | 3/3 |
| | Human Respiratory syncytial virus, 18537 | | 0/3 | 0/3 | 3/3 |
| Rhinovirus 57, Ch47 | 0/3 | 0/3 | 3/3 | | |
| Natural human flora – pooled human nasal wash | | NA | 0/3 | 0/3 | 3/3 |

* Initial testing with 3 replicates showed 1/3 positive for one or both targets for *Mycoplasma pneumoniae* and 1/3 positive for ORF1a for human adenovirus 71. Additional 6 replicates were tested.

Cross-reactivity was observed with *Mycoplasma pneumoniae* and adenovirus 71.

Interfering substances

The objective of the study was to verify the effect of potentially interfering substances on the performance of ViroKey SARS-CoV-2 RT-PCR Test v2.0. Base pool of SARS-CoV-2 positive samples were prepared with heat-inactivated SARS-CoV-2 virus (from American Type Culture Collection (ATCC part number VR-1986HK) into negative nasopharyngeal specimens. For each of the interference substances, 10x stock concentrations were added to the SARS-CoV-2 positive samples. The test pool contained the specified test concentrations noted in **Table 6** for each interfering substance. This study demonstrates that the potential interfering substances tested at specific concentrations as stated in **Table 6** have no impact on the performance of ViroKey SARS-CoV-2 RT-PCR Test v2.0.

Table 6. List of potential interfering substances tested with ViroKey SARS-CoV-2 RT-PCR Test v2.0 on Sentosa SX101 .

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| Substance | Active Ingredient(s) | Conc. | Detection % (ORF1a) | Detection % (N) |
|--|---|-----------|---------------------|-----------------|
| Nasal Wash (Flo) | Sodium chloride, potassium chloride, calcium lactate pentahydrate | 15% (v/v) | 100% (3/3) | 100% (3/3) |
| Nasal Spray/drops (Nazolin) | Oxymetazoline HCL | 15% (v/v) | 100% (3/3) | 100% (3/3) |
| Nasal corticosteroids | Fluticasone | 5% (v/v) | 100% (3/3) | 100% (3/3) |
| Systemic antibacterial | Tobramycin | 4 µg/mL | 100% (3/3) | 100% (3/3) |
| Antiviral drugs | Oseltamivir | 3.3 mg/mL | 100% (3/3) | 100% (3/3) |
| Homeopathic relief (Prospan) | Extract from ivy leaf (Hedera helix L. leaf), Potassium sorbate, anhydrous citric acid, xanthan gum, cherry flavour, crystallizing sorbitol syrup | 5% (v/v) | 100% (3/3) | 100% (3/3) |
| Antimicrobial/antiviral/ anesthetic lozenges (Dorithricin) | Benzalkonium, Benzocaine, Tyrothricin | 15% (w/v) | 100% (3/3) | 100% (3/3) |
| Whole blood | NA | 2% (v/v) | 100% (3/3) | 100% (3/3) |
| Mucin | | 60 µg/mL | 100% (3/3) | 100% (3/3) |
| Pooled human nasal wash | | NA | 100% (3/3) | 100% (3/3) |

FLUMIST nasal spray flu vaccine was not tested for its potential interference with ViroKey SARS-CoV-2 RT-PCR Test v2.0.

FDA SARS-CoV-2 reference panel testing

The evaluation of sensitivity and MERS-CoV cross-reactivity was performed using reference material (T1), blinded samples and a standard protocol provided by the FDA. The study included a range finding study and a confirmatory study for LoD. Blinded sample testing was used to establish specificity and to corroborate the LoD. The extraction method and instrument used were ViroKey SX Virus Total Nucleic Acid Kit (4x48) and Sentosa SA201 Real-Time PCR Instrument. The results are summarized in **Table 7**.

Table 7. Summary of LoD confirmation result using the FDA SARS-CoV-2 reference panel.

| Reference Materials Provided by FDA | Specimen Type | Product LoD | Cross-Reactivity |
|-------------------------------------|---------------------|----------------------------|------------------|
| SARS-CoV-2 | Nasopharyngeal Swab | 1.8x10 ⁵ NDU/mL | N/A |
| MERS-CoV | | N/A | ND |

NDU/mL: RNA NAAT detectable units/mL

N/A: Not Applicable

ND: Not Detected

Clinical performance

ViroKey SARS-CoV-2 RT-PCR Test v2.0

The clinical validation study of ViroKey SARS-CoV-2 RT-PCR Test v2.0 was conducted on nasopharyngeal swabs from unaltered patient samples initially tested with an FDA authorized

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molecular assay as a comparator method. All samples were extracted with ViroKey SX Virus Total Nucleic Acid Kit (4x48) on the *Sentosa* SX101 instrument and detected with ViroKey SARS-CoV-2 RT-PCR Test v2.0 on the *Sentosa* SA201.

ViroKey SARS-CoV-2 RT-PCR Test v2.0 performed on Sentosa SX101

A total of 68 nasopharyngeal samples were tested and the results are summarized in **Table 8**. The performance of the ViroKey SARS-CoV-2 RT-PCR Test v2.0 on *Sentosa* SX101 was calculated based on the result interpretation table on page 13, where a sample was considered positive if signals are detected by *ORF1a* and/or *N* target(s), while a sample was considered negative if no signals are detected by both *ORF1a* and *N* targets.

Table 8. Summary of clinical performance results (for *Sentosa* SX101)

| | | Comparator Results | |
|---|----------|--------------------|----------|
| | | Positive | Negative |
| ViroKey SARS-CoV-2 RT-PCR Test v2.0 on <i>Sentosa</i> SX101 | Positive | 33 | 0 |
| | Negative | 1 | 34 |

Positive Percent Agreement: 97.1% (33/34) **95% CI:** 85.1 - 99.5%

Negative Percent Agreement: 100% (34/34) **95% CI:** 89.8 - 100%

Validation of Alternative Workflows

Validation of ViroKey SARS-CoV-2 RT-PCR Test v2.0 performed on Sentosa SX101 and KingFisher combination

A total of 30 positive and 30 negative archived nasopharyngeal samples were tested with the ViroKey SARS-CoV-2 RT-PCR Test v2.0 performed using the *Sentosa* SX101 and KingFisher combination workflow compared to the *Sentosa* SX101 workflow and the results are summarized in **Table 9**. The agreement of the ViroKey SARS-CoV-2 RT-PCR Test v2.0 using *Sentosa* SX101 and KingFisher combination was calculated based on the result interpretation table on page 13 of this IFU.

Table 9. Summary of validation results for *Sentosa* SX101 and KingFisher combination

| | | ViroKey SARS-CoV-2 RT-PCR Test v2.0 On <i>Sentosa</i> SX101 | |
|---|----------|---|----------|
| | | Positive | Negative |
| ViroKey SARS-CoV-2 RT-PCR Test v2.0 on KingFisher | Positive | 30 | 0 |
| | Negative | 0 | 30 |

Positive Percent Agreement: 100% (30/30) **95% CI:** 88.6 - 100%

Negative Percent Agreement: 100% (30/30) **95% CI:** 88.6 - 100%

Validation of ViroKey SARS-CoV-2 RT-PCR Test v2.0 performed on Hamilton Microlab STAR

A total of 30 positive and 30 negative archived nasopharyngeal samples were tested with the ViroKey SARS-CoV-2 RT-PCR Test v2.0 performed using the Hamilton Microlab STAR

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workflow compared to the *Sentosa* SX101 workflow and the results are summarized in **Table 10**. The agreement of the ViroKey SARS-CoV-2 RT-PCR Test v2.0 using the Hamilton Microlab STAR workflow was calculated based on the result interpretation table on page 13 of this IFU.

Table 10. Summary of validation results for Hamilton Microlab STAR instrument.

| | | ViroKey SARS-CoV-2 RT-PCR Test v2.0 on <i>Sentosa</i> SX101 | |
|---|----------|--|----------|
| | | Positive | Negative |
| ViroKey® SARS-CoV-2 RT-PCR Test v2.0 on Hamilton Microlab STAR instrument | Positive | 30 | 0 |
| | Negative | 0 | 30 |

Positive Percent Agreement: 100% (30/30) **95% CI:** 88.6 - 100%

Negative Percent Agreement: 100% (30/30) **95% CI:** 88.6 - 100%

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Specimen pooling

Sample preparation (for specimen pooling)

NOTE: Refer to the “*Sample preparation*” steps for the respective *Sentosa SX101*, *KingFisher* and *Hamilton* workflows.

The following upper respiratory tract specimens, authorized under the Emergency Use Authorization of the ViroKey SARS-CoV-2 RT-PCR Test Kit v2.0, may be tested with sample pooling:

- Nasopharyngeal,
- Oropharyngeal,
- Mid-turbinate and
- Nasal swab specimens collected into VTM / UTM.

NOTE: Only specimens collected into VTM / UTM may be combined for each sample pool.

Up to 3 patient samples can be combined into a single pool before RNA extraction. Each RT-PCR reaction plate can contain pools of different numbers of samples (2 – 3 samples) as well as individual samples. The volume of each individual patient sample or sample pool used in RNA extraction is 230 µL.

NOTE: Laboratories are to use their protocols and systems to name and track the samples in pools throughout the workflow.

IMPORTANT: Pools with test results that are positive, invalid or inconclusive require extraction and testing of the individual patient samples.

Combine equal volumes (of up to 3 patient samples) into a single tube to make up a total volume of ≥ 1,200 µL. Example volumes are shown in the following table.

| Sample | Volume | |
|---------------------|----------|----------|
| | N* = 3 | N* = 2 |
| 1 | 400 µL | 600 µL |
| 2 | 400 µL | 600 µL |
| 3 | 400 µL | – |
| Total volume | 1,200 µL | 1,200 µL |

* N represents the number of samples used.

Store the remaining un-pooled volumes of patient samples according to CDC guidelines.

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Specimen pooling strategy for implementation and monitoring

When considering specimen pooling, laboratories should evaluate the appropriateness of a pooling strategy based on the:

- Positivity rate in the testing population and
- Efficiency of the pooling workflow.

NOTE:

- Individual specimens with low viral loads may **not** be detected due to decreased sensitivity or increased interference when tested with pooled testing.
- The ViroKey SARS-CoV-2 RT-PCR test v2.0 have been validated for n-sample pool sizes up to three samples per pool.

Before implementation of pooling

Determination of appropriate pool size

Before a pooling strategy is implemented, a laboratory should determine the appropriate pool size based on percent positivity rate and desired testing efficiency.

a) If historical laboratory data for individual specimens are available

- If historical data for individual specimens from the previous 7 – 10 days are available, estimate the $P_{individual}$ (percent positivity rate) based on individual results.

$$P_{individual} = (\text{Number of positive specimens over chosen date range} \div \text{Total number of specimens tested over chosen date range}) \times 100\%$$

- Using the calculated $P_{individual}$ and **Table 11**, identify the appropriate $n_{maxefficiency}$ (number of samples to pool for maximum efficiency). If $P_{individual}$ is greater than 25%, pooling of patient specimens will **not** be efficient. Thus, pooling should not be implemented.
- If $P_{individual} < 13\%$, pooling of 3 patient specimens can be tested but pooling efficiency will **not** be maximized.

NOTE: Pooling with greater than 3 patient specimens has **not** been validated and should **not** be performed.

b) If historical laboratory data for individual specimens are unavailable

- If historical data from the previous 7 – 10 days are **unavailable**, 3-specimen pooling may still be implemented.

NOTE: Without calculating $P_{individual}$, the pooling size implemented may **not** maximize pooling efficiency.

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Table 11. Number of samples to pool based on the percent of positive individuals in the population in order to achieve the maximum efficiency.

| P (Percentage of positive individuals in the tested population) | $n_{\text{maxefficiency}}$ (Number of samples to pool for maximum efficiency) | F (Efficiency of pooling n samples) |
|---|---|-------------------------------------|
| 13% – 25% | 3 | 1.48 – 1.10 |

After Implementation of Pooling

Ongoing Monitoring of Pooling Strategy

a) If historical laboratory data for individual specimens is available

- After implementation of a pooling strategy, evaluate the performance of pooled testing by comparing the percent positivity rate of pooled testing to that of individual testing.
- Calculate the P_{pools} (percent positivity rate among patient specimens during specimen pooling) on a daily basis using a moving average of the data from the previous 7 – 10 days of testing.

$$P_{\text{pools}} = \left(\frac{\text{Number of patient specimens with a positive result as determined by individual specimen reflex testing of positive pools over chosen date range}}{\text{Total number of patient specimens tested in pools over chosen date range}} \right) \times 100\%$$

- To ensure the pooling efficiency, it is recommended that P_{pools} be reassessed periodically. P_{pools} should be < 25% while sample pooling is implemented by the laboratory. Otherwise, pooling of patient specimens should be discontinued.

b) If historical laboratory data for individual specimens are unavailable

- After initiating a pooling strategy, evaluate the performance of pooled testing by calculating the $P_{\text{pools-initial}}$ (initial percent positivity rate for pooled specimens).
- $P_{\text{pools-initial}}$ is the percent positivity rate for pooled specimens for the first 7 – 10 days of pooled testing.
- Calculate the $P_{\text{pools-initial}}$ (initial percent positivity rate for individual specimens from pool testing) from the first 7 – 10 days of testing.

$$P_{\text{pools-initial}} = \left(\frac{\text{Number of patient specimens with a positive result as determined by individual specimen reflex testing of positive pools in first 7 – 10 days}}{\text{Total number of patient specimens tested in pools in the first 7 – 10 days}} \right) \times 100\%$$

- If $P_{\text{pools-initial}} > 25\%$, pooling of patient specimens is **not** efficient and should be discontinued until the percent positivity rate decreases.
- If $P_{\text{pools-initial}} \leq 25\%$, pooling of patient specimens can be continued.
- Continue to monitor pooling strategy by calculating the $P_{\text{pools-x}}$ (percent positivity rate among patient specimens during specimen pooling) for subsequent periods of 7 – 10 days. $P_{\text{pools-x}}$ should be updated daily using a moving average.

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- To ensure the pooling efficiency, it is recommended that $P_{pools-x}$ be reassessed periodically and should be < 25% while sample pooling is implemented by the laboratory. Otherwise, pooling of patient specimens should be discontinued.

IMPORTANT:

- Authorized laboratories must keep records of their sample specimen pooling test result data, daily testing totals including number of pooled test results, number of individuals tested and daily running average of percent positive results, as part of monitoring the pooling strategy.
- For the first 12 months from the date of their creation, such records must be made available to FDA upon request within 48 business hours for inspection. After 12 months from the date of their creation, upon FDA request, such records must be made available for inspection within a reasonable time.

NOTE: When resources availability is sufficient to meet testing demand, the FDA recommends that laboratories consider whether the risks of reduced test sensitivity with pooling outweigh the benefits of resource conservation.

Result interpretation and test reports (for pooled specimens)

- The result interpretation for pooled specimen results is the same as individual test results (refer to “**Result interpretation**” section on page 13).
- Authorized laboratories testing pooled specimens with ViroKey SARS-CoV-2 RT-PCR Test v2.0 must include with test result reports for specific individuals whose specimen(s) were the subject of pooling, a notice that their test result is “presumed positive” unless or until they are re-tested individually if the pool in which they were included returns a positive or invalid result.
- The test reports must include instructions to collect a new specimen to be tested individually and must indicate that such individuals should isolate until receiving a negative result when re-tested individually and should not be cohorted with other individuals who have received a positive or presumptive positive result.

Workflow using ViroKey SARS-CoV-2 RT-PCR Test v2.0

Sentosa SX101 workflow

The workflow starts with sample off-board lysis, followed by the extraction of nucleic acids and RT-PCR set-up with the extracted nucleic acids in the MicroAmp Fast Optical 96-Well Reaction Plate using the *Sentosa SX101*.

The ViroKey SX Virus Total Nucleic Acid Kit (4x48) is used for nucleic acid extraction.

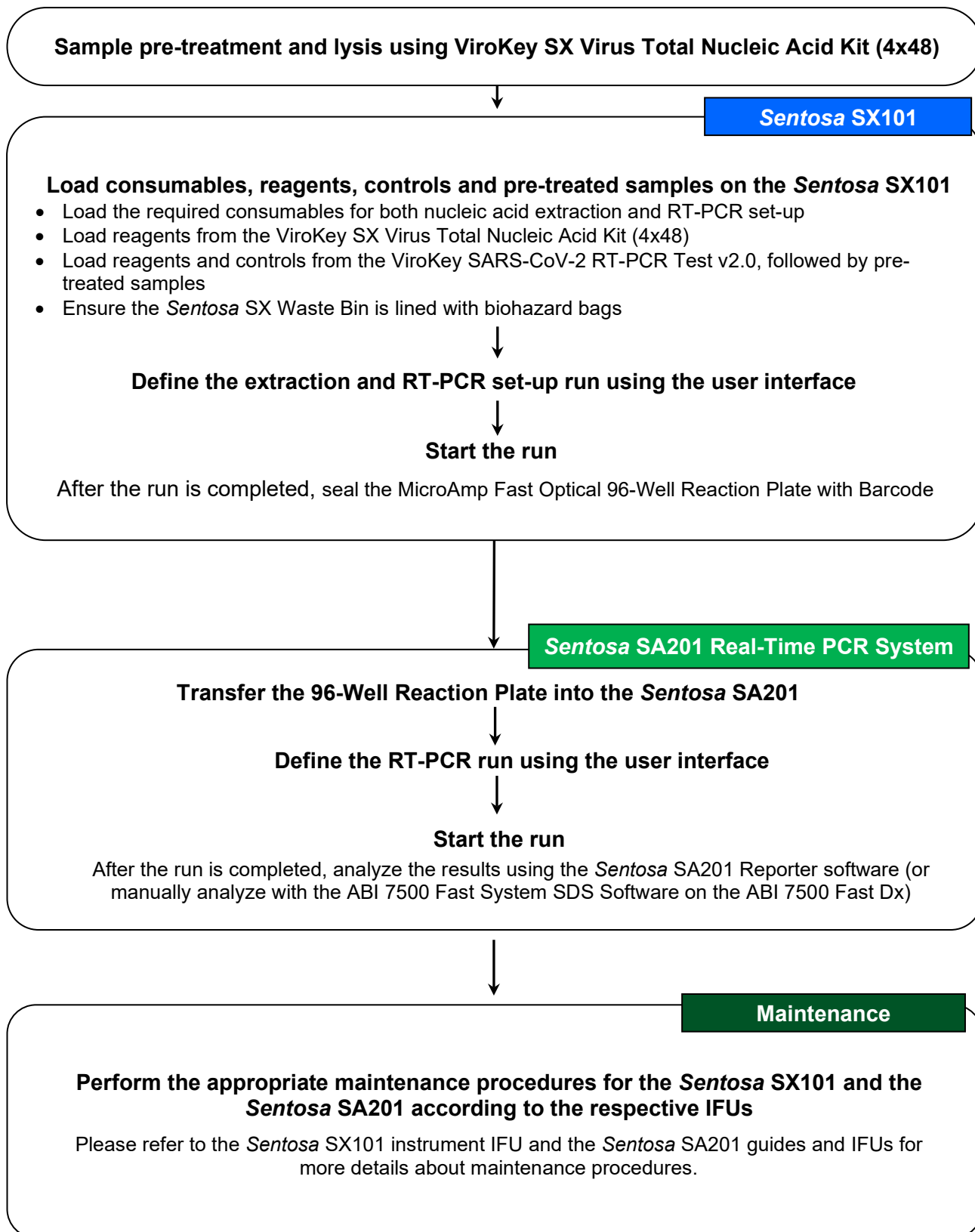
After sample lysis and RT-PCR set-up, the MicroAmp Fast Optical 96-Well Reaction Plate is sealed and then transferred to the *Sentosa SA201* or Applied Biosystems 7500 Fast Dx Real-Time PCR Instrument for PCR amplification followed by data analysis.

The *Sentosa SA201* is a rebranded version of the Applied Biosystems 7500 Fast Dx Real-Time PCR System, thus the workflow is interchangeable between the two instruments. For brevity, only the *Sentosa SA201* workflow will be mentioned in this IFU.

An overview of the workflow is provided (see ***Sentosa SX101 Flowchart***).

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Sentosa SX101 Flowchart: Automated workflow overview



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KingFisher workflow

The workflow starts with sample off-board lysis, followed by lysis incubation and ViroKey SX Virus Total Nucleic Acid Kit (4x48) buffer preparation on the *Sentosa* SX101, nucleic acid extraction on the Thermo Fisher KingFisher Flex instrument, and finally RT-PCR set-up with the extracted nucleic acids in the MicroAmp Fast Optical 96-Well Reaction Plate using the *Sentosa* SX101.

The ViroKey SX Virus Total Nucleic Acid Kit (4x48) is used for nucleic acid extraction.

After sample lysis and RT-PCR set-up, the MicroAmp Fast Optical 96-Well Reaction Plate is sealed and then transferred to the *Sentosa* SA201 for PCR amplification respectively. This is followed by data analysis using *Sentosa* SA201 Reporter or ABI 7500 Fast System SDS Software.

An overview of the workflow is provided (see **KingFisher Flowchart**).

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KingFisher Flowchart: Automated workflow overview

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Sample off-board lysis

Sentosa SX101

Lysis incubation and ViroKey SX Virus Total Nucleic Acid Kit (4x48) buffer preparation

- Set up ID List of samples on *Sentosa SX101* interface
- Load the required consumables for nucleic acid extraction
- Load the off-board lysis + samples DWP
- Load the ViroKey SX Virus Total Nucleic Acid Kit (4x48) reagents
- Load the ViroKey SARS-CoV-2 RT-PCR Test v2.0 reagents
- Start the run

Thermo Fisher KingFisher Flex

Load DWP reagents and samples onto the KingFisher instrument

- Load the prepared DWP with reagents from *Sentosa SX101* onto the KingFisher.
- Load the samples DWP onto the KingFisher.
- Start the run.

Sentosa SX101

Perform RT-PCR set-up run

- Transfer the elution plate from KingFisher to *Sentosa SX101*.
- Click "OK" to begin PCR set-up

After the run is completed, seal the MicroAmp Fast Optical 96-Well Reaction Plate with Barcode

Sentosa SA201 Real-Time PCR System

Transfer the 96-Well Reaction Plate into the *Sentosa SA201*

Define the RT-PCR run using the user interface

Start the run

After the run is completed, analyze the results using the *Sentosa SA201* Reporter software (or manually analyze with the ABI 7500 Fast System SDS Software on the ABI 7500 Fast Dx)

Maintenance

Perform the appropriate maintenance procedures for the *Sentosa SX101*, KingFisher and the *Sentosa SA201* according to the respective IFUs

Please refer to the *Sentosa SX101* instrument, Thermo Fisher KingFisher Flex instrument IFU, and the *Sentosa SA201* guides and IFUs for more details about maintenance procedures.

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Items to be supplied by user

Table 12. List of items to be supplied by user

| Equipment / software | Description / use | Vela item no. |
|---|--|---------------|
| Pipettes (adjustable) ⁱ | For pipetting buffers, reagents and / or samples | N/A |
| Vortex mixer | To mix reagents | N/A |
| Bench top centrifuge ⁱ | To spin down reagents and remove any bubbles | N/A |
| Thermomixer ⁱ | To heat and mix samples | N/A |
| MPS 1000 Mini Plate Spinner, 120V or Eppendorf Centrifuge 5430 / 5430R with Rotor FA-45-24-11 | For PCR plate centrifugation | N/A |
| <i>Sentosa</i> SX101 instrument ⁱ | Automated sample processing system | 400089 |
| Thermo Fisher KingFisher Flex instrument with 96 Deep-well Head ⁱ | Automated sample processing system | 400271 |
| <i>Sentosa</i> SA201 Real-Time PCR Instrument ⁱ | Real-time and end-point thermal cycling using PCR, detection and analysis | 400125 |
| <i>Sentosa</i> SA201 Series Software | To operate <i>Sentosa</i> SA201 Real-time PCR Instrument and to perform PCR data analysis | 460012 |
| <i>Sentosa</i> SA201 Reporter ⁱ | To automate data analysis and result interpretation from <i>Sentosa</i> SA201 | 480142 |
| OR | | |
| ABI 7500 Fast Dx Real-Time PCR instrument | Real-time and end-point thermal cycler for PCR, detection and analysis | N/A |
| ABI 7500 Fast Dx SDS Software | To operate ABI 7500 Fast Dx Real-Time PCR instrument and to perform manual PCR data analysis | N/A |
| Accessories / consumables / reagents | Description / use | Vela item no. |
| ViroKey SX Virus Total Nucleic Acid Kit (4x48) ⁱⁱ | 4x48 tests | 300677 |
| <i>Sentosa</i> SX Magnetic Separator | 1 piece | 400024 |
| <i>Sentosa</i> SX Non-Partition 50 µL Filter Tips (960) | 10 boxes of 96 tips. Alternatively, tips compatible with Eppendorf TM50/TS50 dispensing tool may be used. | 400224 |
| <i>Sentosa</i> SX Non-Partition 1000 µL Filter Tips (960) | 10 boxes of 96 tips. Alternatively, tips compatible with Eppendorf TM1000/TS10000 dispensing tool may be used. | 400223 |
| <i>Sentosa</i> SX 100 mL Reservoir (50) | Set of 50 reservoirs | 400027 |
| <i>Sentosa</i> SX 30 mL Reservoir (50) | Set of 50 reservoirs | 400028 |
| <i>Sentosa</i> SX Deepwell Plate 96/2000 µL (20) | Set of 20 plates | 400068 |
| <i>Sentosa</i> SX Biohazard Bag (100) | 100 pieces | 400033 |
| KingFisher 96-Deepwell Plates (6) | 6 plates | 400294 |
| KingFisher 96-Tip Comb (1) | 1 tip comb | 400295 |

ⁱ Ensure that the instruments have been checked and calibrated according to the manufacturer's recommendations.

ⁱⁱ For nasopharyngeal swabs, use ViroKey SX Virus Total Nucleic Acid Kit (4x48) for virus total nucleic acid extraction.

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| Accessories / consumables / reagents | Description / use | Vela item no. |
|--|---|---------------|
| Sterile pipette tips with filters | For pipetting buffers, reagents and / or samples | N/A |
| Safe-Lock Tubes (1000) | For sample extraction. Alternatively, Sarstedt 1.5 mL screw cap tubes (or tubes of equivalent dimensions) may be used. | 400031 |
| MicroAmp Fast Optical 96-Well Reaction Plate with Barcode, 0.1 mL ⁱⁱⁱ | N/A | N/A |
| MicroAmp Optical Adhesive Film ^{iv} | N/A | N/A |
| MicroAmp Adhesive Film Applicator ^v | For applying the MicroAmp Optical Adhesive Film to seal the MicroAmp Fast Optical 96-Well Reaction Plate with Barcode | N/A |
| Swabs | For collecting nasopharyngeal swab samples | N/A |
| Absolute ethanol | For adding to Buffer D3 in ViroKey SX Virus Total Nucleic Acid Kit (4x48) | N/A |

ⁱⁱⁱ MicroAmp Fast Optical 96-Well Reaction Plate with Barcode, 0.1 mL from Applied Biosystems (Cat. No. 4346906) **MUST** be used. Ensure that the correct plates are used.

^{iv} MicroAmp Optical Adhesive Film from Applied Biosystems (Cat. No. 4311971) **MUST** be used. Use only unexpired films.

^v MicroAmp Adhesive Film Applicator from Thermo Fisher Scientific (Cat. No. 4333183) is recommended.

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Workflow using ViroKey SARS-CoV-2 RT-PCR Test v2.0

Hamilton workflow

The workflow starts with sample plate preparation followed by the lysis and extraction of nucleic acids, and RT-PCR set-up with the extracted nucleic acids in the MicroAmp Fast Optical 96-Well Reaction Plate using the Hamilton Microlab STAR.

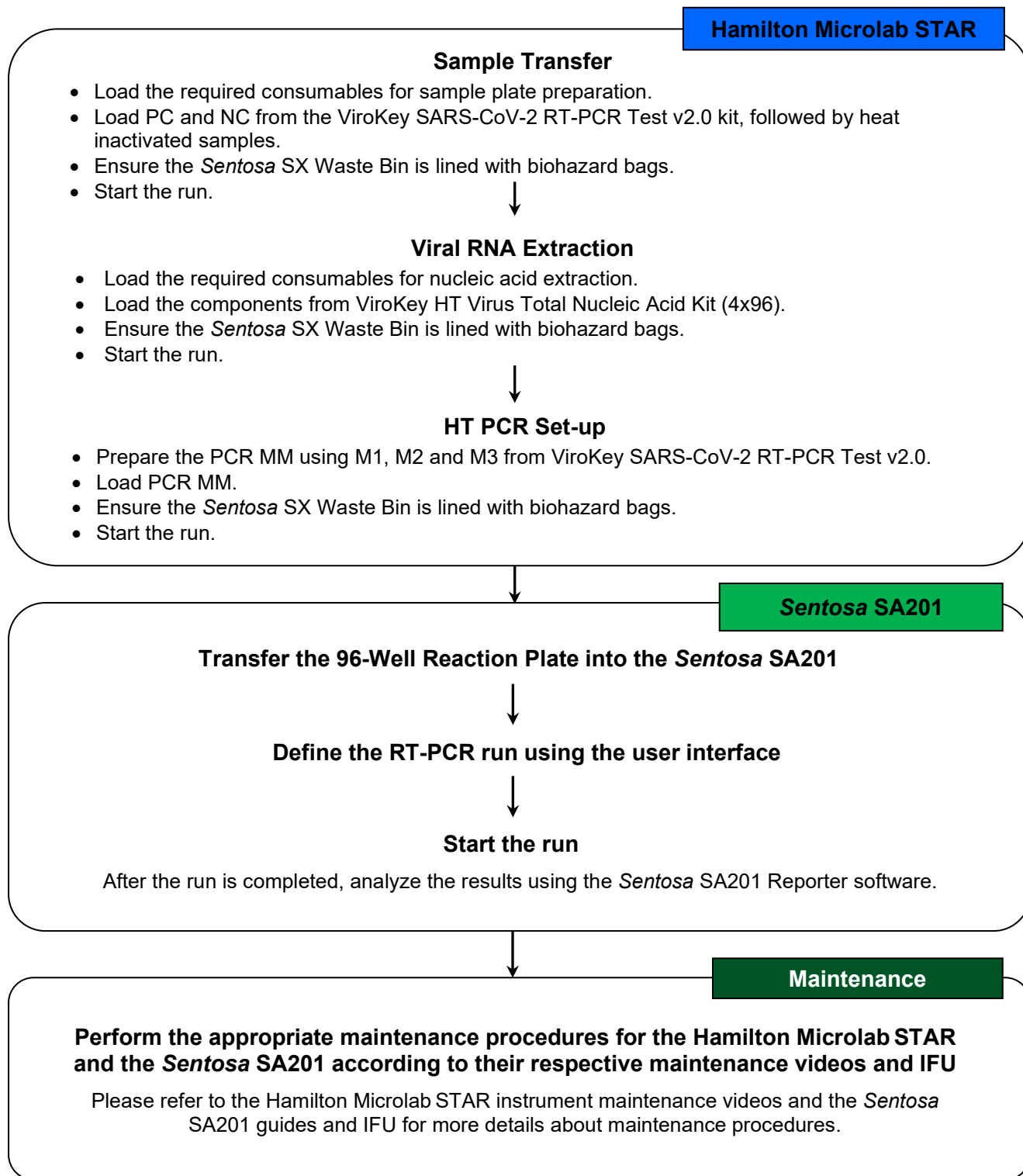
For nasopharyngeal swabs, use the ViroKey HT Virus Total Nucleic Acid Kit (4x96) for nucleic acid extraction.

After sample lysis and RT-PCR set-up, the MicroAmp Fast Optical 96-Well Reaction Plate is sealed, and then transferred to the *Sentosa* SA201 for PCR amplification respectively. This is followed by data analysis using *Sentosa* SA201 Reporter.

An overview of the workflow is provided (see **Hamilton Flowchart**).

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Hamilton Flowchart: Automated workflow overview



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Items to be supplied by user

Table 13. List of items to be supplied by user.

| Equipment / software | Description / use | Vela item no. |
|---|---|---------------|
| Pipettes (adjustable) ⁱ | For pipetting buffers, reagents and / or samples | N/A |
| Vortex mixer | To mix reagents | N/A |
| Bench top centrifuge ⁱ | To spin down reagents and remove any bubbles | N/A |
| Thermomixer ⁱ | To heat and mix samples | N/A |
| Hamilton Microlab STAR | Automated sample processing system | 400316 |
| <i>Sentosa</i> SA201 Real-Time PCR Instrument ⁱ | Real-time and end-point thermal cycling using PCR, detection and analysis | 400125 |
| <i>Sentosa</i> SA201 Series Software | To operate <i>Sentosa</i> SA201 Real-time PCR Instrument and to perform PCR data analysis | 460012 |
| <i>Sentosa</i> SA201 Reporter ⁱ | To automate data analysis and result interpretation from <i>Sentosa</i> SA201 | 480142 |
| Accessories / consumables / reagents | Description / use | Vela item no. |
| ViroKey HT Virus Total Nucleic Acid Kit (4x96) | 4x96 tests | 301088 |
| HT 300 mL Reservoir (40) | To contain the reagents | 400298 |
| PCR Plate 96, 0.2 mL (25) | Mastermix Plate | 400342 |
| HT 8-Strip Tubes, Clear, 0.2 mL (125) | 8-strip tubes (1 PCR Strip) | 400299 |
| HT Reagent Tub with Lid, 60 mL (28) | 60 mL Trough | 400307 |
| HT U Deepwell Plate, Barcoded, 2.2 mL (24) | Deepwell plate | 400308 |
| HT Conductive 1 mL Filter Tips (3840) | For pipetting buffers, reagents and / or samples | 400309 |
| HT Conductive 300 µL Filter Tips (5760) | For pipetting buffers, reagents and / or samples | 400310 |
| HT Conductive 50 µL Filter Tips (5760) | For pipetting buffers, reagents and / or samples | 400311 |
| Sterile pipette tips with filters | For pipetting buffers, reagents and / or samples | N/A |
| MicroAmp Fast Optical 96-Well Reaction Plate with Barcode, 0.1 mL ⁱⁱ | N/A | N/A |
| MicroAmp Optical Adhesive Film ⁱⁱⁱ | N/A | N/A |
| MicroAmp Adhesive Film Applicator ^v | For applying the MicroAmp Optical Adhesive Film to seal the MicroAmp Fast Optical 96-Well Reaction Plate with Barcode | N/A |
| Regular flocked swabs (nasopharyngeal) ^{vi} | For collecting nasopharyngeal swab samples | N/A |
| Absolute ethanol | For adding to Buffer D3 in ViroKey HT Virus Total Nucleic Acid Kit (4x96) | N/A |

ⁱ Ensure that the instruments have been checked and calibrated according to the manufacturer's recommendations.

ⁱⁱ MicroAmp Fast Optical 96-Well Reaction Plate with Barcode, 0.1 mL from Applied Biosystems (Cat. No. 4346906) **MUST** be used. Ensure that the correct plates are used.

ⁱⁱⁱ MicroAmp Optical Adhesive Film from Applied Biosystems (Cat. No. 4311971) **MUST** be used. Use only unexpired films.

^v MicroAmp Adhesive Film Applicator from Thermo Fisher Scientific (Cat. No. 4333183) is recommended.

^{vi} BD Regular flocked swab, sterile single wrapped (Cat. No. 220250) or BD Flexible minitip flocked swab, sterile single wrapped (Cat. No. 220252) in BD Universal viral transport, 3 mL vial (Cat. No. 220220) OR 16 X 100 mm Screw Cap Tube containing 3 mL of UTM Transport and Preservation Medium, 1 Nasopharyngeal Flocked Swab (Cat. No. 305C).

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Important notes

General precautions

- Use sterile pipette tips with filters.
- During manual steps, ensure that the tubes are closed when possible to avoid contamination.
- **Do not mix components from kits with different lot numbers.**
- Proceed continuously from one part of the workflow to the next.

Specimen collection, handling and storage

- Specimen collection:
 - Refer to Interim Guidelines for Collecting, Handling, and Testing Clinical Specimens from Persons for Coronavirus Disease 2019 (COVID-19) <https://www.cdc.gov/coronavirus/2019-ncov/lab/guidelines-clinical-specimens.html>
 - Follow specimen collection device manufacturer instructions for proper collection methods.
- Transporting specimens:
 - Specimens must be packaged, shipped and transported according to the current edition of the International Air Transport Association (IATA) Dangerous Goods Regulation. Follow shipping regulations for UN 3373 Biological Substance, Category B when sending potential SARS-CoV-2 specimens. Store specimens at 2-8°C and ship overnight on ice pack. If a specimen is frozen at $\leq -70^{\circ}\text{C}$, ship overnight on dry ice.
- Storing specimens:
 - After collection and during transport, the specimen should be stored at 2 – 8°C and all laboratory testing must occur within 72 hours of collection. Refrigerated specimens received outside of this 72-hour window should be rejected.
 - If a delay in shipping is expected, store specimens at $\leq -70^{\circ}\text{C}$.
 - Specimens received frozen should be stored at $\leq -70^{\circ}\text{C}$ until processing.
 - Store any residual specimens at $\leq -70^{\circ}\text{C}$.

NOTE: Inadequate specimen collection and / or inappropriate specimen processing, storage and transport may yield false negative results.

Storage of purified nucleic acid

- Purified nucleic acids should be stored at $\leq -70^{\circ}\text{C}$.

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Protocol: Automated nucleic acid isolation and detection on the *Sentosa* SA201 / Applied Biosystems 7500 Fast Dx Real-Time PCR Instrument

ViroKey SARS-CoV-2 RT-PCR Test v2.0 on the *Sentosa* SX101

The ViroKey SX Virus Total Nucleic Acid Kit (4x48) is intended for virus total nucleic acid extraction from respiratory specimens (such as nasal, mid-turbinate, nasopharyngeal, and oropharyngeal swab specimens and nasopharyngeal wash/aspirate or nasal aspirate specimens) and bronchoalveolar lavage samples for use with the ViroKey SARS-CoV-2 RT-PCR Test v2.0.

Important points before starting

- User must be familiar with operating the *Sentosa* SX101 instrument and the *Sentosa* SA201 / Applied Biosystems 7500 Fast Dx Real-Time PCR Instrument. Please refer to the respective IFUs supplied with the instruments for operating instructions.
- Before beginning the procedure, read the “**Important notes**” section, page 40.
- Each tube of reagent in the ViroKey SARS-CoV-2 RT-PCR Test v2.0 is designed for 48 reactions.
- RNA4 M3 is an enzyme, which is in liquid state. Except for RNA4 M3, the rest of the ViroKey SARS-CoV-2 RT-PCR Test v2.0 components should be thawed at room temperature (approximately 15°C – 25°C).
- For software, use current version or higher:

| | |
|--------------------------------------|--|
| <i>Sentosa</i> SX101 | Release 3.0 (Version 41.0.1.5) |
| <i>Sentosa</i> SA201 Series Software | Version 1.0.1 (for use with <i>Sentosa</i> SA201) |
| <i>Sentosa</i> SA201 Reporter | Version 1.5 (for use with <i>Sentosa</i> SA201) |
| ABI SDS Software | Version 1.4.1 (for manual data analysis with ABI 7500 Fast Dx) |
- Screenshots are for illustration purposes, and individual installations may vary.

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ViroKey SARS-CoV-2 RT-PCR Test v2.0 on the Hamilton Microlab STAR

The ViroKey HT Virus Total Nucleic Acid Kit (4x96) is intended for virus total nucleic acid extraction from respiratory specimens (such as nasal, mid-turbinate, nasopharyngeal, and oropharyngeal swab specimens and nasopharyngeal wash/aspirate or nasal aspirate specimens) and bronchoalveolar lavage samples for use with the ViroKey SARS-CoV-2 RT-PCR Test v2.0.

Important points before starting

- User must be familiar with operating the Hamilton Microlab STAR instrument and the *Sentosa* SA201. Please refer to the respective IFUs supplied with the instruments for operating instructions.
- Before beginning the procedure, read the “**Important notes**” section, page 40.
- Each tube of reagent in the ViroKey SARS-CoV-2 RT-PCR Test v2.0 is designed for 96 reactions.
- HT RNA M3 is an enzyme, which is in liquid state. Except for HT RNA M3, the rest of the ViroKey SARS-CoV-2 RT-PCR Test v2.0 components should be thawed at room temperature (approximately 15°C – 25°C).
- For software, use current version or higher:

| | |
|--------------------------------------|--|
| Hamilton Venus software | Release 4.5.0.7977 (for use with Hamilton Microlab STAR) |
| <i>Sentosa</i> SA201 Series Software | Version 1.0.1 (for use with <i>Sentosa</i> SA201) |
| <i>Sentosa</i> SA201 Reporter | Version 1.5 (for use with <i>Sentosa</i> SA201) |
- Screenshots are for illustration purposes, and individual installations may vary.

ViroKey SX Virus Total Nucleic Acid Kit (4x48) / ViroKey HT Virus Total Nucleic Acid Kit (4x96)

Important points before starting

- Ensure that all reagents of the ViroKey SX Virus Total Nucleic Acid Kit (4x48) and ViroKey HT Virus Total Nucleic Acid Kit (4x96) are not precipitated before use. If precipitates are observed, dissolve by incubating in a water bath ($\leq 37^{\circ}\text{C}$).
- The Mag tubes containing magnetic beads require thorough vortexing for 5 minutes before the start of the workflow to ensure proper re-suspension.
- Prior to use, cRNA (lyophilized carrier RNA) must be reconstituted and aliquoted. Refer to detailed procedure for more information.
- Mix the buffers in the bottles by gentle swirling, ensuring no foam or bubbles are present.

Sentosa SX101 workflow

1. Sample preparation and pre-treatment

1.1. Sample preparation (for individual samples)

NOTE: Refer to “**Sample preparation (for specimen pooling)**” section for steps to combine specimens into a pool.

Label empty 1.5 mL Safe-Lock tubes with NC, PC and sample IDs. Up to 46 samples, one positive control (PC) and one negative control (NC) samples can be performed in one run of the ViroKey SARS-CoV-2 RT-PCR Test v2.0.

Fresh samples

- a. Vortex swab in Universal Transport Media (UTM) for 30 seconds.
- b. Remove and discard the swab from the UTM tube according to local safety regulations.
- c. Transfer 230 µL of samples to 1.5 mL Safe-Lock Tubes.

Samples stored at 4°C

- a. Equilibrate to room temperature.
- b. Vortex swab in UTM for 30 seconds.
- c. Remove and discard the swab from the UTM tube according to local safety regulations.
- d. Transfer 230 µL of samples to 1.5 mL Safe-Lock Tubes.

Frozen samples

- a. Thaw samples and equilibrate to room temperature.
- b. Vortex swab in UTM for 30 seconds.
- c. Remove and discard the swab from the UTM tube according to local safety regulations.
- d. Transfer 230 µL of samples to 1.5 mL Safe-Lock Tubes.

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1.2. Sample pre-treatment and lysis

- 1.2.1. Prepare the reagents from the ViroKey SX Virus Total Nucleic Acid Kit (4x48) according to **steps 1.2.2 and 1.2.3**.
- 1.2.2. Reconstitute cRNA (lyophilized carrier RNA) with Buffer D4 as described below.
 - 1.2.2.1. Briefly spin down cRNA for 5 seconds.
 - 1.2.2.2. Add 310 µL of Buffer D4 to cRNA tube.
 - 1.2.2.3. The reconstituted cRNA should be mixed by pulse vortexing for 30 seconds followed by brief centrifugation.
 - 1.2.2.4. Aliquot reconstituted cRNA into 4 tubes of 78 µL and store at -20°C till required.
- 1.2.3. Thaw NC, PC and EC8 completely, vortex for 5 seconds and centrifuge briefly.
- 1.2.4. Prepare the lysis master mix according to the table below.

| Reagents | 48 samples |
|--------------------|------------|
| Buffer D1 | 15 mL |
| Reconstituted cRNA | 75 µL |
| EC8 | 500 µL |

- 1.2.5. Pre-heat the thermomixer to 56°C.
- 1.2.6. Transfer 311 µL of lysis master mix into labeled 1.5 mL Safe-Lock microtubes (sample, NC and PC).
- 1.2.7. Pulse vortex NC and PC for 10 seconds, followed by brief centrifugation to collect the contents at the bottom of the tubes. Transfer 230 µL of NC, PC, and samples into individually labeled 1.5 mL Safe-Lock microtubes containing the lysis master mix (sample, NC and PC).

NOTE: Do not discard the original NC and PC tubes, as they will be required for barcode scanning in **step 2.15**.
- 1.2.8. Pulse vortex the 1.5 mL Safe-Lock microtubes for 10 seconds followed by brief centrifugation to collect the contents at the bottom.
- 1.2.9. Incubate the tubes at 56°C for 8 minutes under 1000 rpm agitation using a thermomixer.
- 1.2.10. Centrifuge the samples briefly to collect the contents at the bottom of the tubes and cool for 3 minutes at room temperature.

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1.2.11. The sample tubes are ready to be loaded onto the *Sentosa* SX101 instrument. Carefully load the sample tubes onto the *Sentosa* SX Rack 0.5 + Adaptor / 1.5 / 2.0 mL in the *Sentosa* SX101 according to the procedure described in the “Automated nucleic acid extraction and RT-PCR set-up on the *Sentosa* SX101 instrument” section, page 46.

2. Automated nucleic acid extraction and RT-PCR set-up on the *Sentosa* SX101 instrument

Figure 1 shows the positions of consumables / labware on the *Sentosa* SX101 platform. Double line the *Sentosa* SX Waste Bin with biohazard bags. Please refer to the layout as indicated by the *Sentosa* SX101 instrument software or the appendix to load all items in the correct positions.

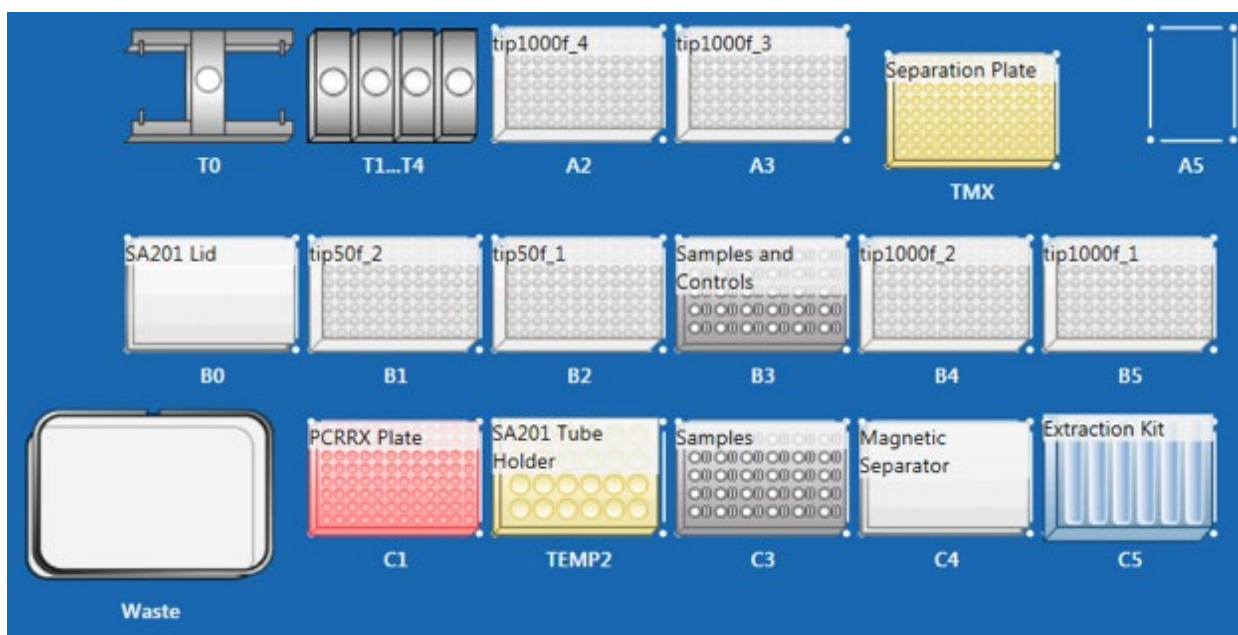



Figure 1. Layout of the *Sentosa* SX101 platform for 96 tests (for *Sentosa* SX101 only workflow)

NOTE:

- Items shown are necessary for nucleic acid extraction and PCR assay set-up for application “48-1 ViroKey SARS-CoV-2-v2 v3-3”.
- Ensure all consumables / labware are properly placed, aligned and secured into their respective positions.
- Ensure that the biohazard bags are properly attached to the *Sentosa* SX Waste Bin before starting a protocol run. For more information, please refer to the *Sentosa* SX101 instrument IFU.

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- 2.1. Switch on the computer, and wait for the initialization procedure to be completed.
- 2.2. On the instrument's computer, launch the *Sentosa SX* software by double-clicking the  icon.

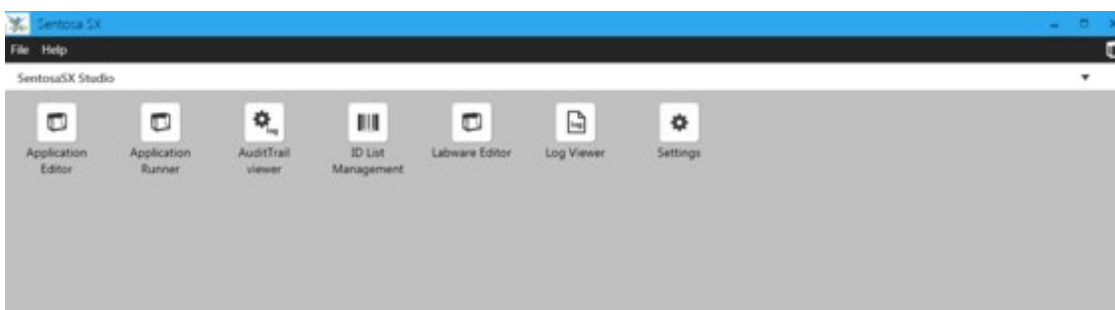
The “Login” window opens.



Type the account name and password, and then click “Login”.

NOTE: Please switch on *Sentosa SX101* instrument after *Sentosa SX* software is launched.

- 2.3. Press / Click on “*Applications Runner*” in the start screen menu to select and open an application.



- 2.4. Select the “*VelaDx*” account and choose the folder “*Sentosa SX Virus*”. Run the suitable application according to the table below.

| Application (v3-3 or higher) | Number of tests | ViroKey SX Virus Total Nucleic Acid Kit (4x48) | ViroKey SARS-CoV-2 RT-PCR Test v2.0 |
|---------------------------------|-----------------|--|-------------------------------------|
| 48-1 ViroKey SARS-CoV-2-v2 v3-3 | Up to 46 tests | 1 set of reagents | 1 set of reagents |

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- 2.5. Place the correct *Sentosa* SX Reservoirs and Modules into positions 1 to 7 of the *Sentosa* SX Reservoir Rack 7 (refer to **Figure 1**, C5) according to the table below.

| Application (v3-3 or higher) | <i>Sentosa</i> SX Reservoir Rack 7 (C5) | | | |
|---------------------------------|---|----------------------|---------------------|-----------------|
| | Position 1 & 5 | Positions 2 to 4 | Position 6 | Position 7 |
| 48-1 ViroKey SARS-CoV-2-v2 v3-3 | Empty | 3 x 100 mL Reservoir | 1 x 30 mL Reservoir | RR Module A1/A2 |

- 2.6. Add 40 mL of absolute ethanol to Buffer D3 and mix well before use.
- 2.7. Transfer all buffers from the ViroKey SX Virus Total Nucleic Acid Kit (4x48) into their respective positions in *Sentosa* SX Reservoir Rack 7 as indicated by the application protocol: 17 mL of D1 in positions 2, 35 mL of D2 in position 3, 50 mL of D3 in position 4 and 4 mL of D4 in position 6.

| Application (v3-3 or higher) | <i>Sentosa</i> SX Reservoir Rack 7 (C5) | | | | | |
|---------------------------------|---|------------|------------|------------|------------|------------|
| | Position 1 | Position 2 | Position 3 | Position 4 | Position 5 | Position 6 |
| 48-1 ViroKey SARS-CoV-2-v2 v3-3 | Empty | D1 | D2 | D3 | Empty | D4 |

NOTE:

- 17 mL of Buffer D1 should be added to position 2, excess buffer may change the beads to sample ratio which may affect its performance for samples at the LoD level.
- All reagents should be gently mixed, without foaming, before use.
- Ensure that all buffers in the bottles are completely transferred into the corresponding reservoir positions.

IMPORTANT: Correct placement of assay components is critical for successful completion of the test. Please follow on-screen prompt carefully for correct placement of components.

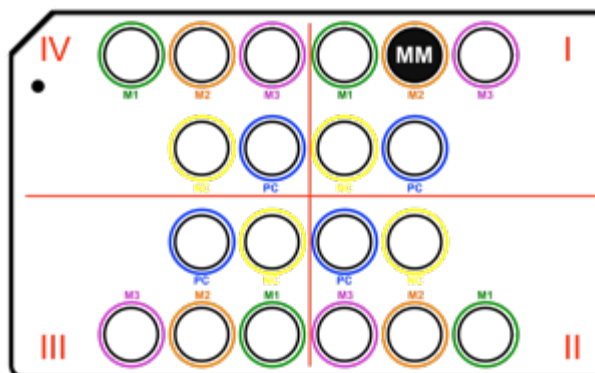
- 2.8. Prepare Reverse Transcription PCR reagents from the ViroKey SARS-CoV-2 RT-PCR Test v2.0. Pulse vortex SARS-CoV-2 v2 M1 (M1) for 5 seconds, and mix RNA4 M2 (M2) and RNA4 M3 (M3) by gentle inversion. Keep the M3 tube on ice for no more than one hour during use.

Pipette 112 µL of M3, 56 µL of M1 into separate tube of M2. Centrifuge reconstituted M1/M2/M3 (MM) briefly to collect the contents at the bottom of the tubes.

Remove the caps of the MM tube (reconstituted M1 / M2 / M3), and load the MM tube into the SA201 Tube Holder rack (Location: TEMP2, C2) at M2 position in Quadrant I.

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NOTE:

- Do not discard the original M1 tube, as it will be required for barcode scanning in **step 2.17**.
- Do **not** mix components from kits with different lot numbers.

2.9. Place the *Sentosa SX RR Module A1/A2*, illustrated in the figure below, on position 7 of the *Sentosa SX Reservoir Rack 7*.



Sentosa SX RR Module A1/A2

Load Mag (magnetic beads) tube from the ViroKey SX Virus Total Nucleic Acid Kit (4x48) on the *Sentosa SX RR Module A1/A2* according to the table below.

| Application (v3-3 or higher) | <i>Sentosa SX Reservoir Rack 7 (C5)</i> | | | |
|---------------------------------|---|-------|-----|-------|
| | 7/A | 7/B | 7/C | 7/D |
| 48-1 ViroKey SARS-CoV-2-v2 v3-3 | Empty | Empty | Mag | Empty |

NOTE:

- Ensure that the magnetic beads in Mag tube from ViroKey SX Virus Total Nucleic Acid Kit (4x48) are fully re-suspended. Vortex the tubes for 1 minute and flick to collect the contents at the bottom of the tube. Ensure that no bubbles or multilayers are observed.
- Ensure that all tubes are uncapped.

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IMPORTANT: Correct placement of assay components is critical for successful completion of the test. Please follow on-screen prompt carefully for correct placement of components.

- 2.10. Set the MicroAmp Fast Optical 96-Well Reaction Plate with Barcode, 0.1 mL on the epMotion Thermoblock for PCR 96 Wells (Thermoblock PCR 96), and place the assembly on position C1 of the *Sentosa* SX101 platform (refer to **Figure 1**).



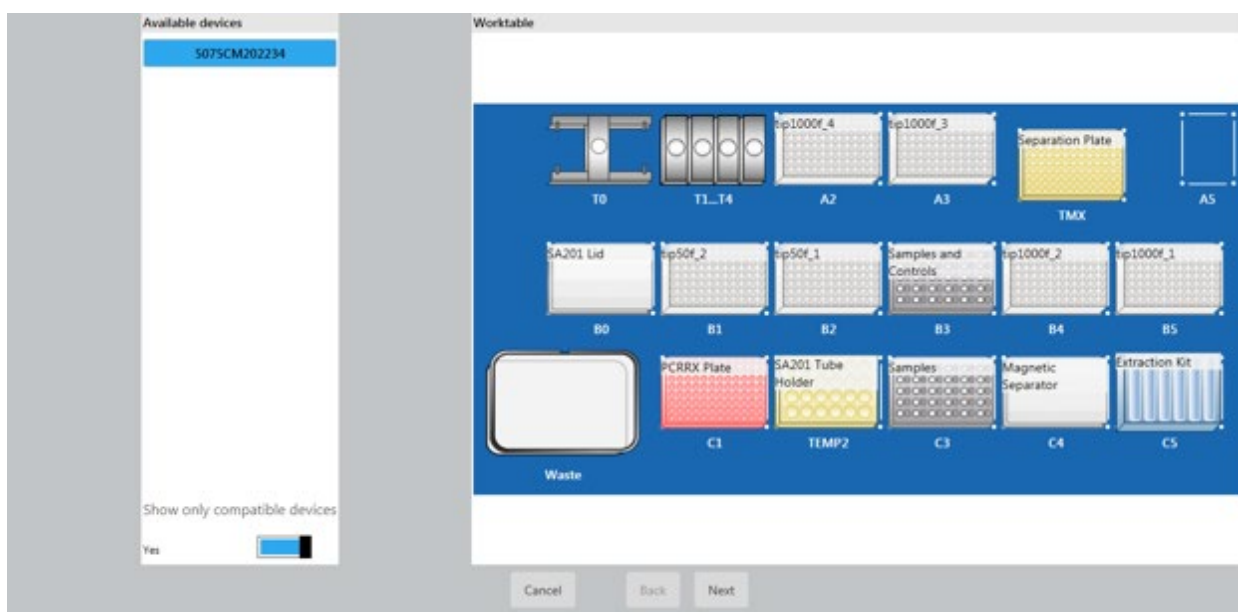
MicroAmp Fast Optical 96-Well Reaction Plate
with Barcode, 0.1 mL



epMotion Thermoblock for PCR 96 Wells

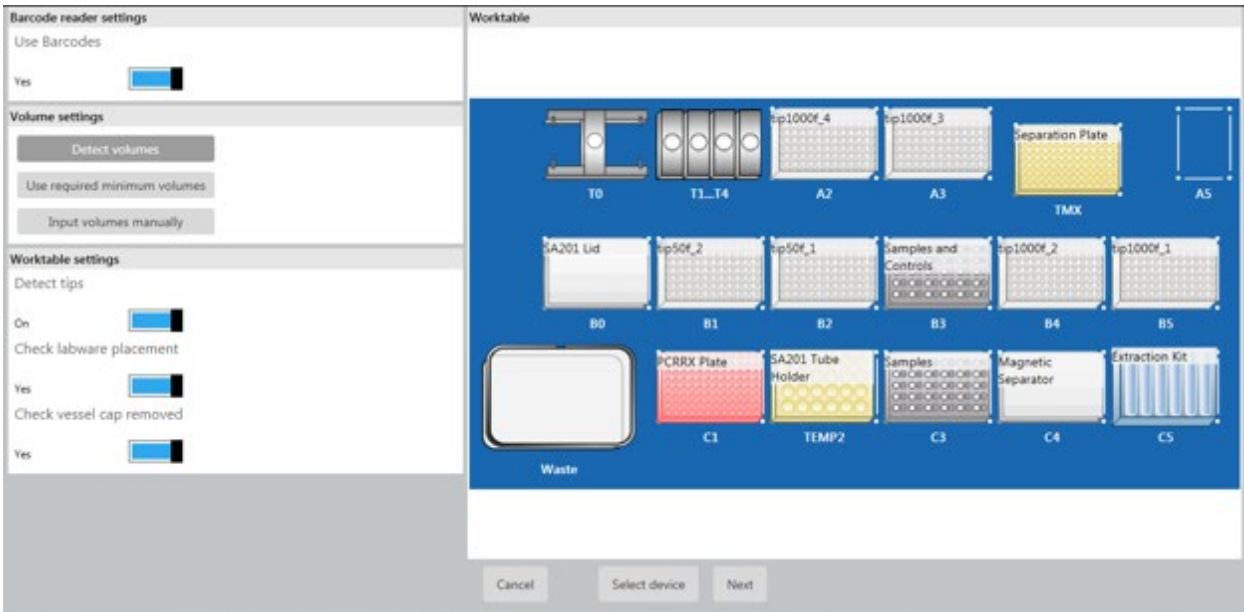
- 2.11. Load the *Sentosa* SX Non-Partition 1000 μ L Filter Tips, *Sentosa* SX Deepwell Plate 96/2000 μ L, *Sentosa* SX Non-Partition 50 μ L Filter Tips and *Sentosa* SX Magnetic Separator on the *Sentosa* SX101 platform. Please refer to the layout as indicated by the *Sentosa* SX101 instrument software (see **Figure 1**) or the appendix to load all items in the correct positions.

- 2.12. In the “Run” tab, select the *Sentosa* SX101 instrument (5075XXXXX, where XXXXX refers to the serial number) under “Available devices” is selected with the “Yes” slider appearing blue. Press / Click “Next”.

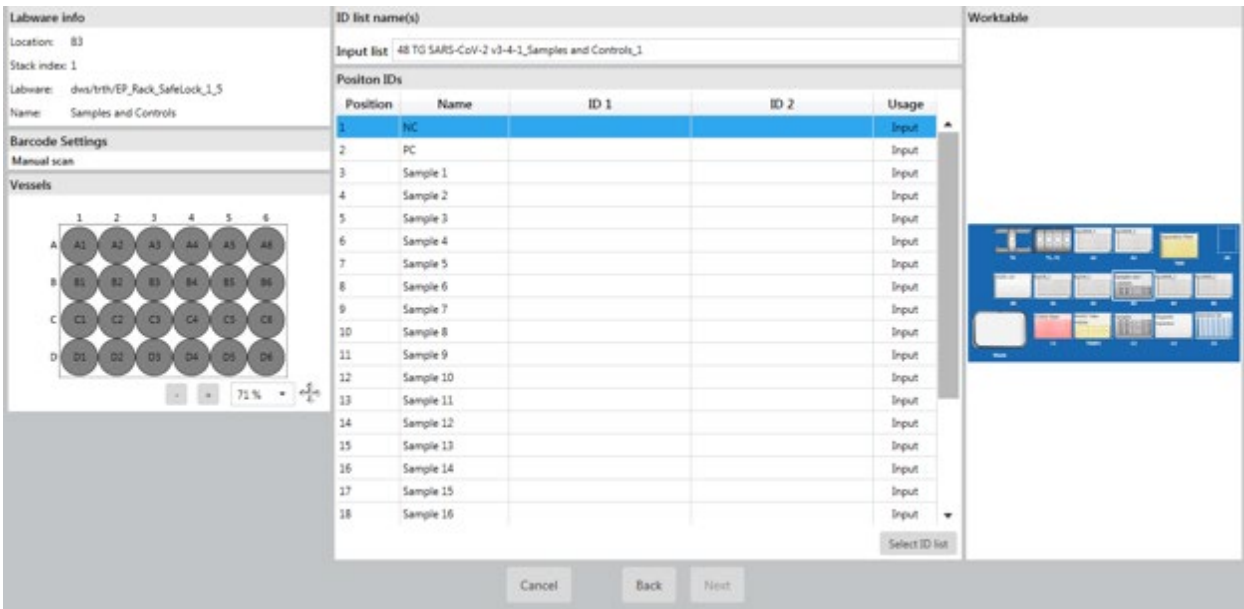


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2.13. Ensure that all options are turned on: all sliders are blue and annotated as “Yes” or “On” under all settings as shown in the following figure. Press / Click “Next”.

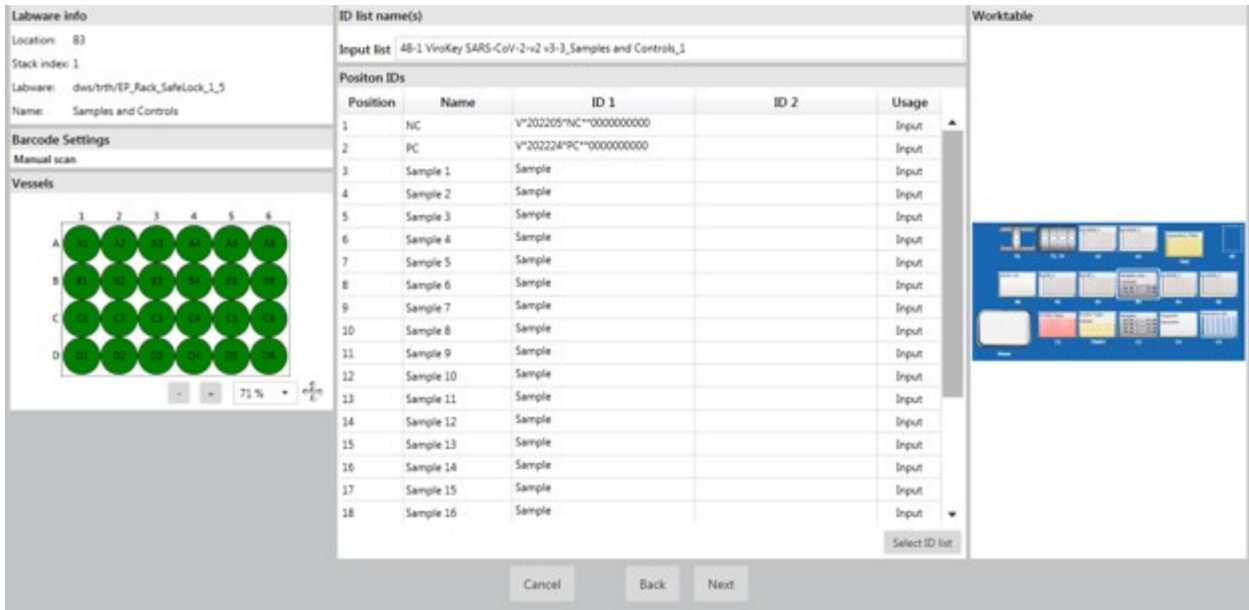


2.14. Enter the run name manually by checking the “Enter manually” check box. Click “OK” and then “Next”.



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2.15. Scan the NC, PC and samples' ID barcodes according to the table below. If the samples do not have ID barcodes, enter the sample IDs manually by checking the "Enter manually" check box.

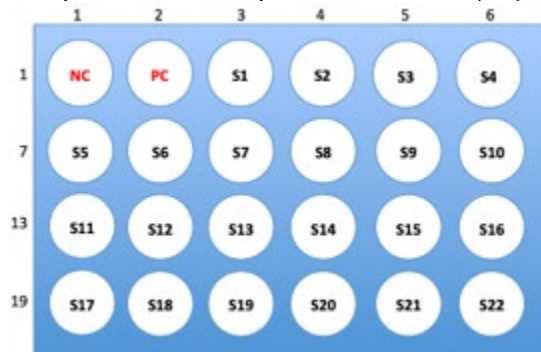


| Application (v3-3 or higher) | Sentosa SX Rack 0.5 + Adaptor / 1.5 / 2.0 mL | | |
|------------------------------------|--|------------|-----------------|
| | Sample rack (B3) | | |
| | Position 1 | Position 2 | Position 3 – 24 |
| 48-1 ViroKey SARS-CoV-2-v2 v3-3 | NC | PC | Samples |

Once all samples are identified, click "OK" and then "Next".

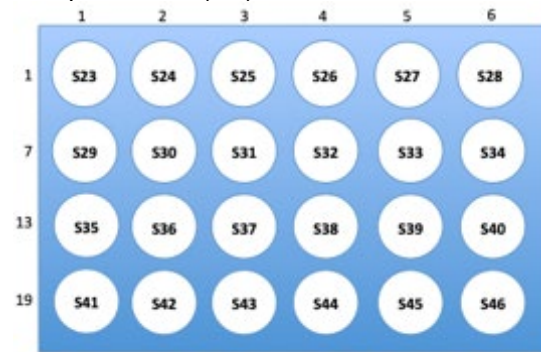
2.16. Load NC, PC and samples onto the Sentosa SX Rack 0.5 + Adaptor / 1.5 / 2.0 mL (refer to **Figure 1**, B3 and C3) as illustrated below.

Sample Rack 1: Samples and Controls (B3)



*NC – Negative Control, PC – Positive Control, S – Sample

Sample Rack 2 (C3)

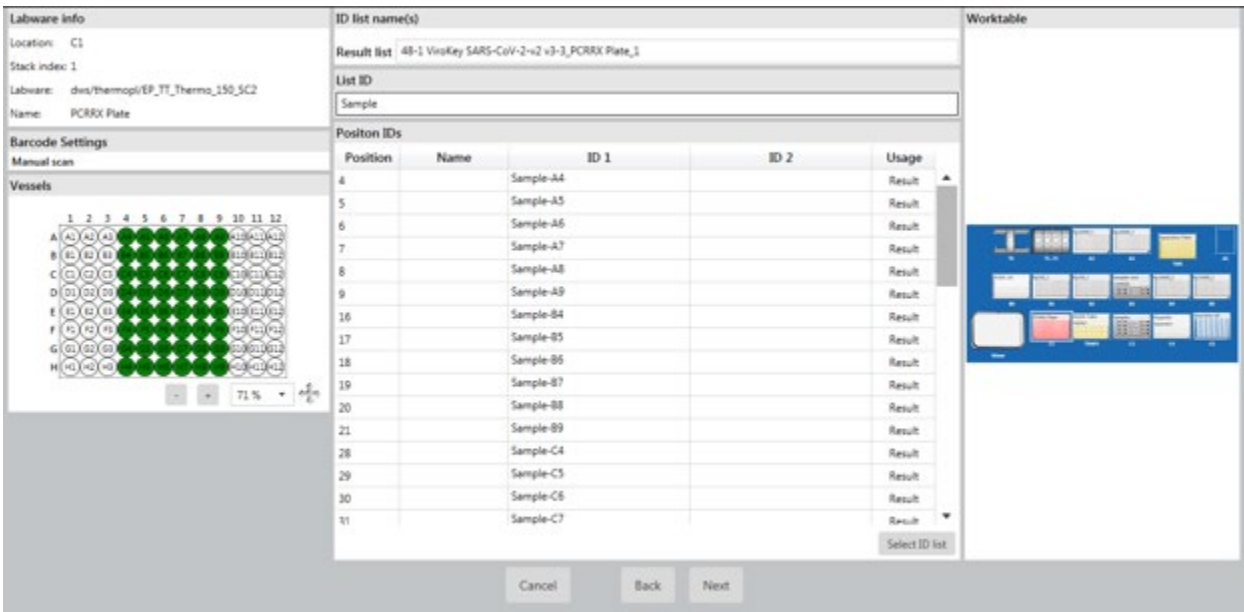


S – Sample

NC – Negative control, PC – Positive control, S – Sample

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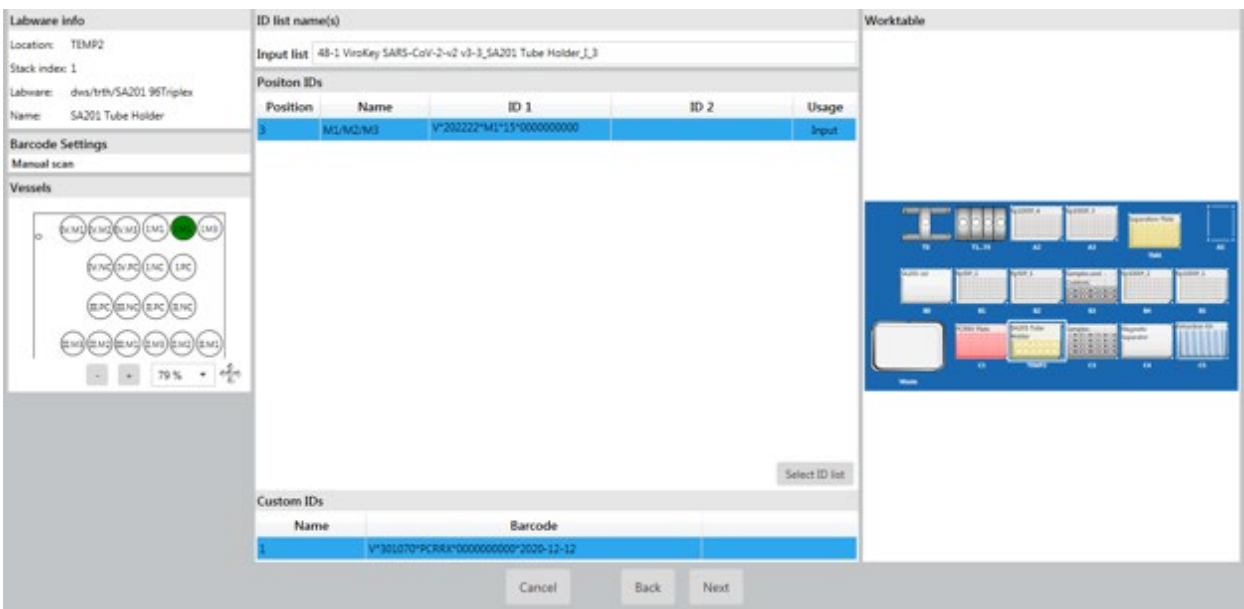
2.17. Scan the barcode on the *Sentosa SX* Barcoded PCR Plate 96 (reaction plate) or enter the ID manually under “List ID”. Press / Click “Next”.



After scanning, place the reaction plate back onto the *Sentosa SX* Thermoblock PCR 96 OC (refer to **Figure 1**, Location: C1). The reaction plate should be oriented with the barcode label facing towards the user.

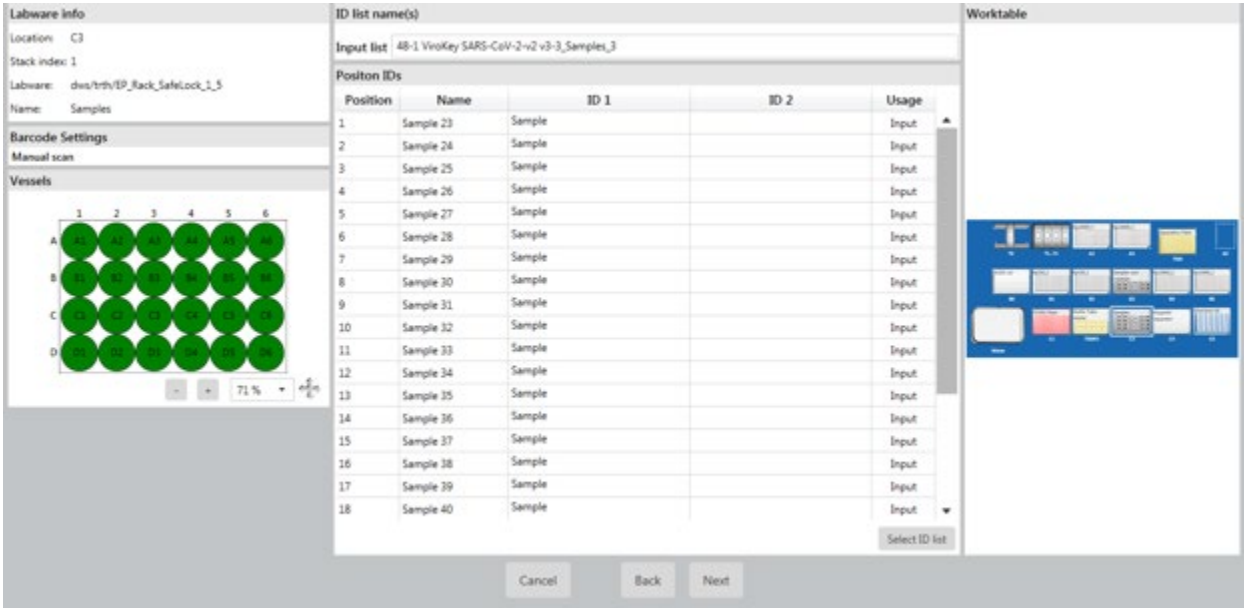
IMPORTANT: Correct placement of assay components is critical for successful completion of the test. Please follow on-screen prompt carefully for correct placement of components.

2.18. For the reconstituted M1 / M2 / M3 mixture stored in the M2 tube (MM), scan the empty M1 tube ID barcode to ensure the correct test kit is used. Click “OK” and then “Next”.

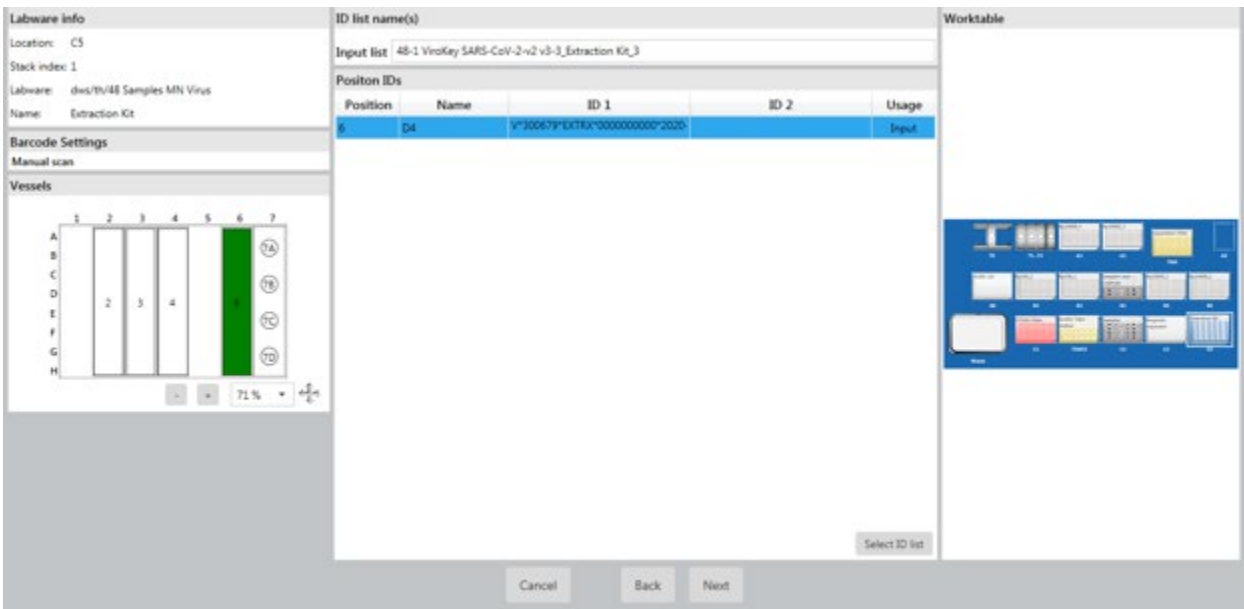


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2.19. Scan samples' ID barcodes according to the table below for the last 24 samples. If the samples do not have ID barcodes, enter the sample IDs manually by checking the “*Enter manually*” check box.



2.20. Scan the 2-D barcode on the ViroKey SX Virus Total Nucleic Acid Kit (4x48) box that will be used in the run. Press / Click “*Next*”.



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2.21. The software conducts a volume check for each item; click “Next” for each “*volume check*” window.

- *Sentosa SX* Deepwell Plate 96/2000 µL (Location: TMX)
- *Sentosa SX* Rack 0.5 + Adaptor / 1.5 / 2.0 mL (Location: B3 and C3)
- SA201 Tube Holder Rack (Location: TEMP2 (C2))
- *Sentosa SX* Reservoir Rack 7 (Location: C5)

At the last window, press / click “Run”.

| Please enter Reason | |
|---------------------|---|
| Type | Application Started |
| Creation Date | 5/6/2020 12:44 PM |
| User | service |
| Software Version | 41.0.1.5 |
| Device | 5075CN202247 |
| Application | Vela DiXiqPCR SARS-CoV-2/48 ViroKey SARS-CoV-2 v3-S Rev 1 |
| Database Version | 4.0.0.0 |
| Reason | <input type="text"/> |

In the “*Please enter Reason*” pop-up window, enter a reason for the run in the textbox if applicable, if not, enter any alphanumeric character / symbol key and press / click “Save” to continue.

2.22. Nucleic acid extraction and PCR set-up steps are performed automatically. At the end of the protocol, the status of the run changes from “*running*” to “*completed*”.

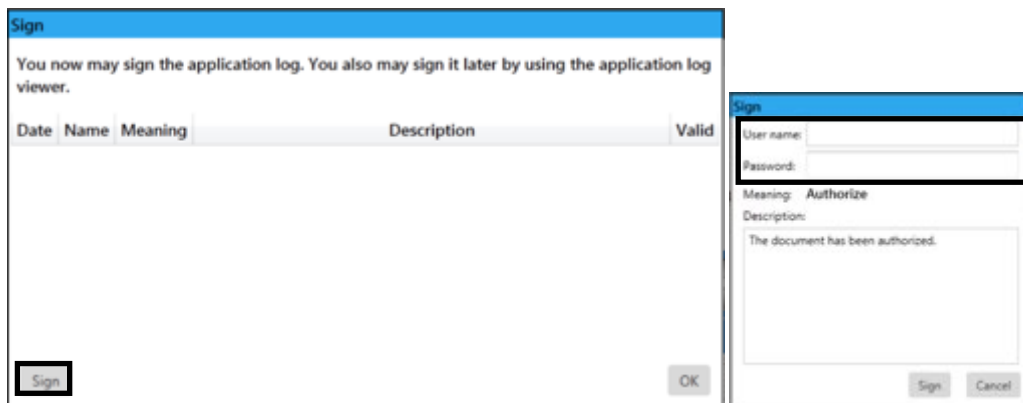
After the run is completed, carefully remove the MicroAmp Fast Optical 96-Well Reaction Plate. Apply the MicroAmp Optical Adhesive Film over the plate and seal the plate tightly to prevent contamination. Briefly spin down the PCR plate and load it onto the *Sentosa SA201* Real-Time PCR Instrument or the Applied Biosystems 7500 Fast Dx Real-Time PCR Instrument.



Proceed to RT-PCR and data analysis using the *Sentosa SA201* Real-Time PCR Instrument and *Sentosa SA201* Reporter (pages 90 to 103) or Applied Biosystems 7500 Fast Dx Real-Time PCR Instrument with the ABI SDS Software for manual data analysis (pages 104 to 115).

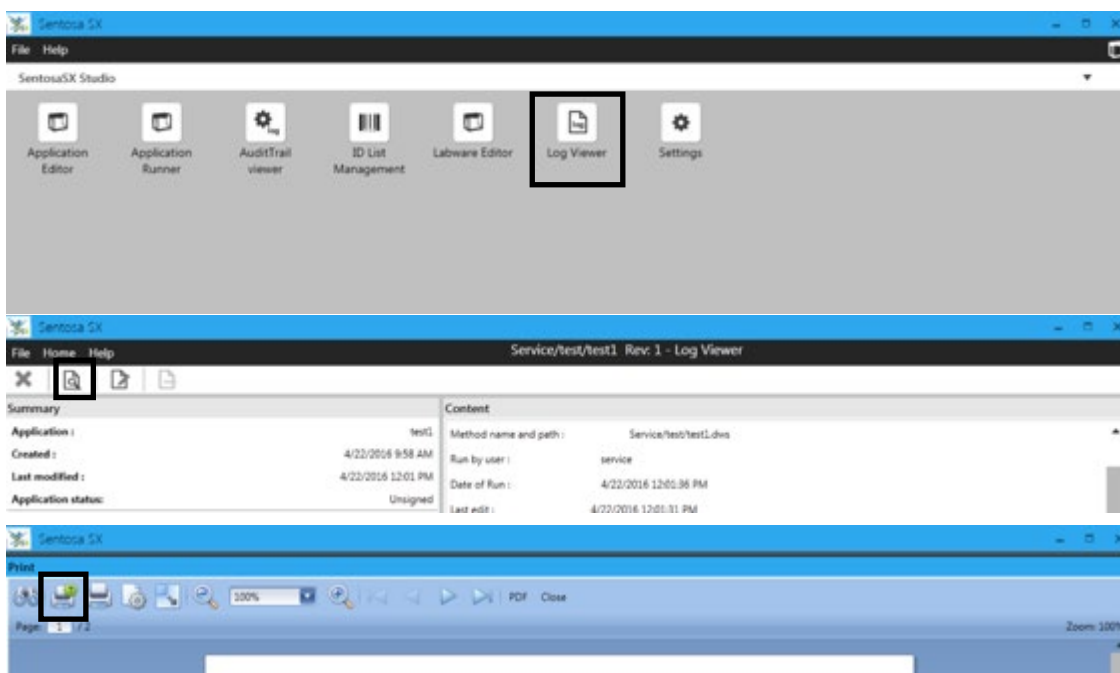
After RT-PCR and data analysis are complete, proceed to page 13 for “**Result interpretation**” section.

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2.23. Log file of the run is automatically generated which is then electronically signed by the operator by clicking “Sign”.



2.24. To print the log file, press / click on “Log Viewer” in the start screen, select the respective log and press / click the  icon followed by the  icon.



2.25. Clean and disinfect the *Sentosa SX101* instrument after each run. For instrument maintenance, please refer to the *Sentosa SX101* instrument IFU.

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KingFisher workflow

3. Buffer, reagent and sample preparation

3.1. Buffer and reagent preparation:

Remove the following reagents from the ViroKey SX Virus Total Nucleic Acid Kit (4x48) and prepare according to the instructions.

| Storage | Reagents | Quantity | Preparation |
|---------|--------------------------------|----------|--|
| RT | D1 (Lysis buffer) | 2 | Gently invert to mix. |
| | D2 (Wash buffer 1) | 2 | Mix by gentle inversion, briefly spin down. |
| | D3 (Wash buffer 2) | 2 | Add 40 mL of molecular grade absolute ethanol to the D3 bottle. Mix well. |
| | D4 (ddH ₂ O) | 2 | a. Briefly spin down. Reconstitute cRNA with 310 µL of D4. |
| | cRNA (lyophilized carrier RNA) | 2 | b. Vortex and spin down. c. Aliquot reconstituted cRNA into 4 tubes of 78 µL. |
| | Magnetic Beads | 2 | d. Store cRNA at -20°C until use. Vortex for 5 minutes to fully resuspend magnetic beads. |

Remove the following reagents from the ViroKey SARS-CoV-2 RT-PCR Test Kit v2.0 and prepare according to the instructions.

| Storage | Reagent | Quantity | Preparation |
|---------|---------|----------|---|
| -20°C | NC | 1 | Thaw completely, vortex for 5 seconds and spin down |
| | PC | 1 | |
| | EC8 | 2 | |

Prepare Lysis master mix with the following volumes.

| Reagents | 96 samples |
|--------------------|------------|
| Buffer D1 | 34.0 mL |
| Reconstituted cRNA | 156 µL |
| EC8 | 1.2 mL |

NOTE:

- All reagents should **not** be subjected to more than five repeated freeze-thaw cycles.

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3.2. Sample preparation (for individual patient samples)

NOTE: Refer to “**Sample preparation (for specimen pooling)**” section for steps to combine specimens into a pool.

Fresh samples

- a. Vortex swab in Universal Transport Media (UTM) for 30 seconds.
- b. Remove and discard the swab from the UTM tube according to local safety regulations.
- c. Transfer 230 μ L of samples to the KingFisher 96-Deepwell Plate (DWP) according to **Figure 2**.

Samples stored at 4 °C

- a. Equilibrate to room temperature.
- b. Vortex swab in UTM for 30 seconds.
- c. Remove and discard the swab from the UTM tube according to local safety regulations.
- d. Transfer 230 μ L of the sample to the DWP according to **Figure 2**.

Frozen samples

- a. Thaw samples and equilibrate to room temperature.
- b. Vortex swab in UTM for 30 seconds.
- c. Remove and discard the swab from the UTM tube according to local safety regulations.
- d. Transfer 230 μ L of the sample to the DWP according to **Figure 2**.

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3.3. Transfer of samples to the Deepwell Plate—for both individual patient samples and pooled samples

3.3.1. Add 230 μ L of NC and PC to well A1 and B1 in the DWP.

3.3.2. Dispense 309 μ L of Lysis master mix (LMM) into each well of the Sample Deep Well Plate to inactivate the virus.

3.3.3. Add samples according to **Figure 2** below.

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 |
|---|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| A | NC | S7 | S15 | S23 | S31 | S39 | S47 | S55 | S63 | S71 | S79 | S87 |
| B | PC | S8 | S16 | S24 | S32 | S40 | S48 | S56 | S64 | S72 | S80 | S88 |
| C | S1 | S9 | S17 | S25 | S33 | S41 | S49 | S57 | S65 | S73 | S81 | S89 |
| D | S2 | S10 | S18 | S26 | S34 | S42 | S50 | S58 | S66 | S74 | S82 | S90 |
| E | S3 | S11 | S19 | S27 | S35 | S43 | S51 | S59 | S67 | S75 | S83 | S91 |
| F | S4 | S12 | S20 | S28 | S36 | S44 | S52 | S60 | S68 | S76 | S84 | S92 |
| G | S5 | S13 | S21 | S29 | S37 | S45 | S53 | S61 | S69 | S77 | S85 | S93 |
| H | S6 | S14 | S22 | S30 | S38 | S46 | S54 | S62 | S70 | S78 | S86 | S94 |

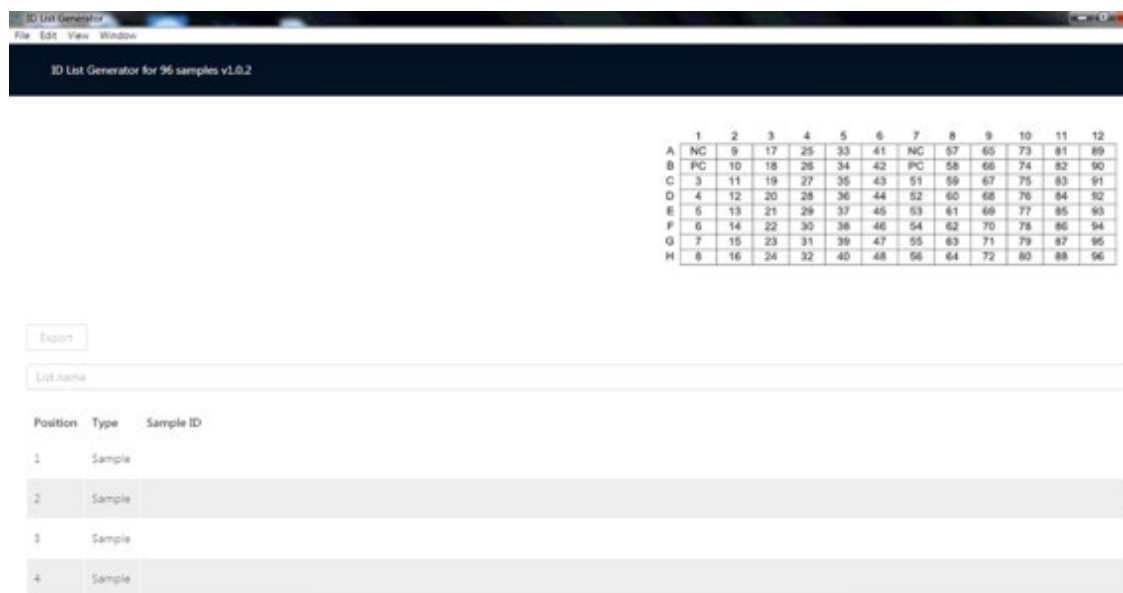
Figure 2. Layout of samples in the KingFisher 96-Deepwell Plate.

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3.4. Set up ID List of samples on the *Sentosa SX101*

3.4.1. Start the “*ID List Generator*” software and log in to your account.

3.4.2. Scan NC tube’s barcode in position 1 and PC tube’s barcode in position 2, followed by Sample Name of each sample.



3.4.3. Export Sample ID list (e.g. *SampleList.xml*) for import into the *Sentosa SX101*.

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4. Automated RT-PCR set-up on the Sentosa SX101 instrument

Figure 3 shows the positions of consumables / labware on the *Sentosa* SX101 platform. Double line the *Sentosa* SX Waste Bin with biohazard bags. Please refer to the layout as indicated by the *Sentosa* SX101 instrument software or the appendix to load all items in the correct positions.

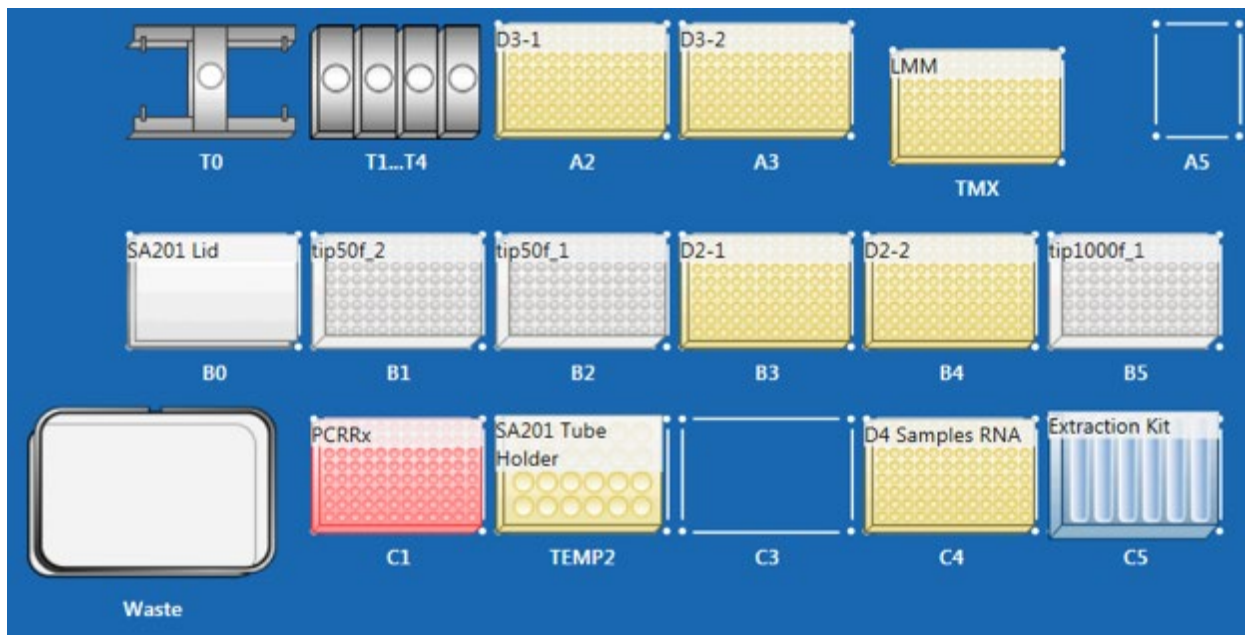


Figure 3. Layout of the *Sentosa* SX101 platform for 96 tests with ViroKey SX Virus Total Nucleic Acid Kit (4x48) (for *Sentosa* SX101 and KingFisher combination workflow).

NOTE:

- Items shown are necessary for PCR assay set-up for application “**96-1_ViroKey-KF SARS-CoV-2-v2_v3-2**”.
- Ensure all consumables / labware are properly placed, aligned and secured into their respective positions.
- Ensure that the biohazard bags are properly attached to the *Sentosa* SX Waste Bin before starting a protocol run. For more information, please refer to the *Sentosa* SX101 instrument IFU.

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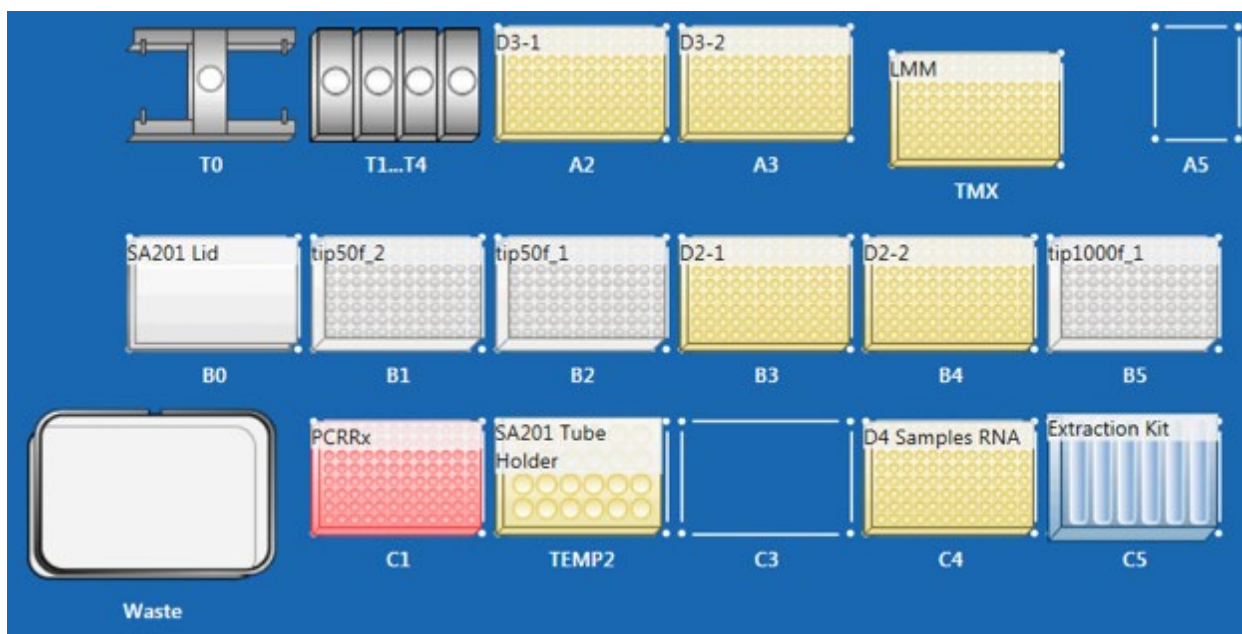
4.1. Start the Sentosa SX software and log in to your account.

4.2. Click on “*Application Runner*” on the start screen.

4.3. Perform the following steps:

- Select VelaDx Account.
- Open “**qPCR ViroKey**” folder.
- Launch “**96-1_ViroKey-KF SARS-CoV-2-v2_v3-2**” application.

4.4. Prepare worktable according to the layout below.



4.5. Place the correct *Sentosa SX* Reservoirs and Modules into positions 1 to 7 of the *Sentosa SX* Reservoir Rack 7 (C5) according to the table below.

| Application (v3-1 or higher) | <i>Sentosa SX</i> Reservoir Rack 7 (C5) | | | |
|---|---|-----------------|-------------------|-----------------|
| | Positions 1 to 3 | Position 5 | Positions 4 and 6 | Position 7 |
| 96-1_ViroKey-KF SARS-CoV-2-v2_v3-2 | 3 x 100 mL Reservoir | RR Module A1/A2 | Empty | 30 mL Reservoir |

4.6. Add 40 mL of absolute ethanol to each of the 2 bottles Buffer D3 and mix well before use.

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- 4.7. Transfer all buffers from the ViroKey SX Virus Total Nucleic Acid Kit (4x48) into their respective positions in *Sentosa* SX Reservoir Rack 7 as indicated by the application protocol (refer to the table below).

| Buffer | Position | Volume (mL) |
|--------|----------|-------------|
| 1x D1 | 1 | 35 |
| 2x D2 | 2 | 70 |
| 2x D3 | 3 | 100 |
| 2x D4 | 7 | 12 |

| Application (v3-1 or higher) | <i>Sentosa</i> SX Reservoir Rack 7 (C5) | | | | | |
|---------------------------------------|---|------------|------------|------------|------------|------------|
| | Position 1 | Position 2 | Position 3 | Position 4 | Position 6 | Position 7 |
| 96-1_ViroKey-KF SARS-CoV-2-v2_v3-2 | D1 | 2x D2 | 2x D3 | Empty | Empty | 2x D4 |

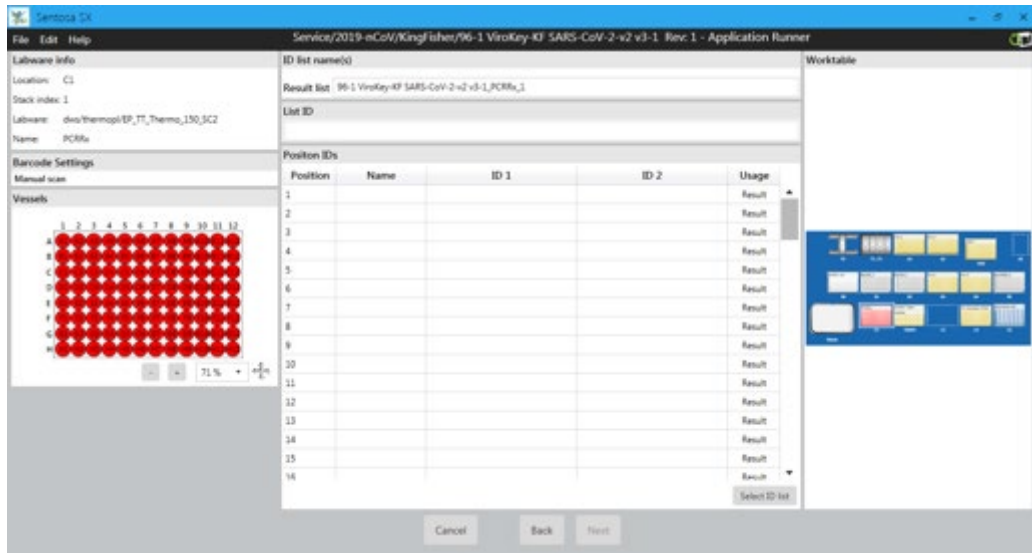
- 4.8. Place the *Sentosa* SX RR Module A1/A2 on position 5 of the *Sentosa* SX Reservoir Rack 7.
- 4.9. Load Mag (magnetic beads) tubes from the ViroKey SX Virus Total Nucleic Acid Kit (4x48) on the *Sentosa* SX RR Module A1/A2 according to the table below.

| Application (v3-1 or higher) | <i>Sentosa</i> SX Reservoir Rack 7 (C5) | | | |
|--|---|-------|-------|-------|
| | 5/A | 5/B | 5/C | 5/D |
| 96-1_ViroKey-KF SARS- CoV-2-v2_v3-2 | Mag | Empty | Empty | Empty |

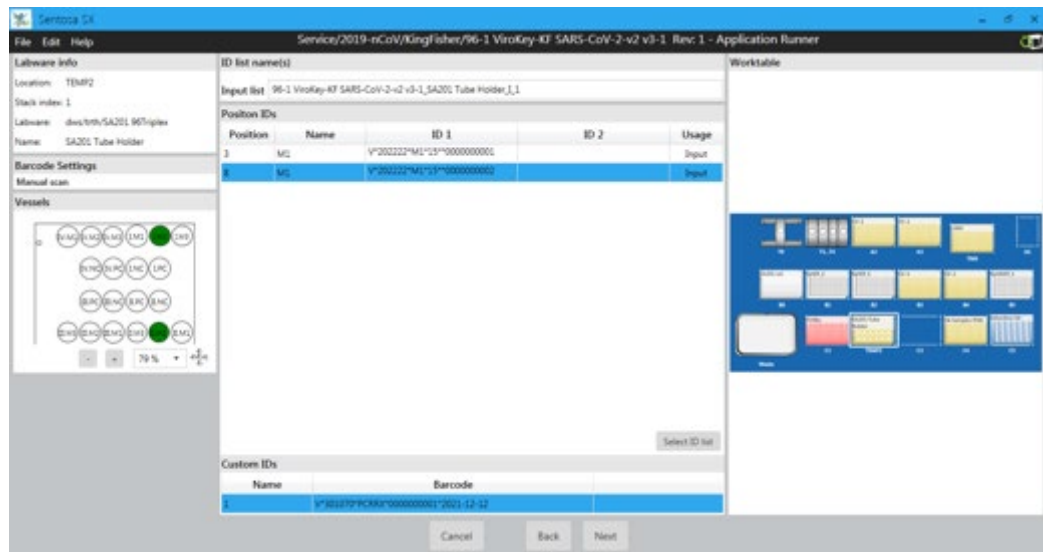
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4.10. Start the run

- 4.10.1. Proceed to the “Run” tab when all the labware, consumables and reagents are in place. Click “Next”.
- 4.10.2. Make sure all of the levels checked are blue. Click “Next”.
- 4.10.3. When prompted, scan the barcodes of the following labware:
 - a. PCR plate (Position C1) — click “Next”.

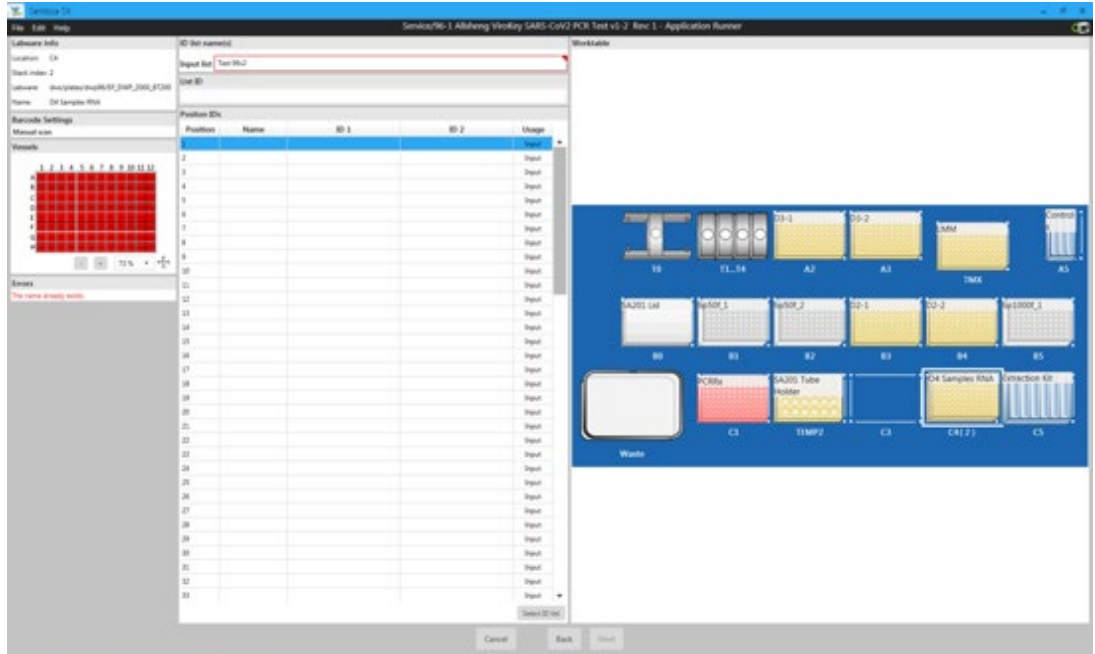


- b. 2-D barcodes of M1 tubes.
- c. 2-D barcode on the PCR kit box — click “Next”.

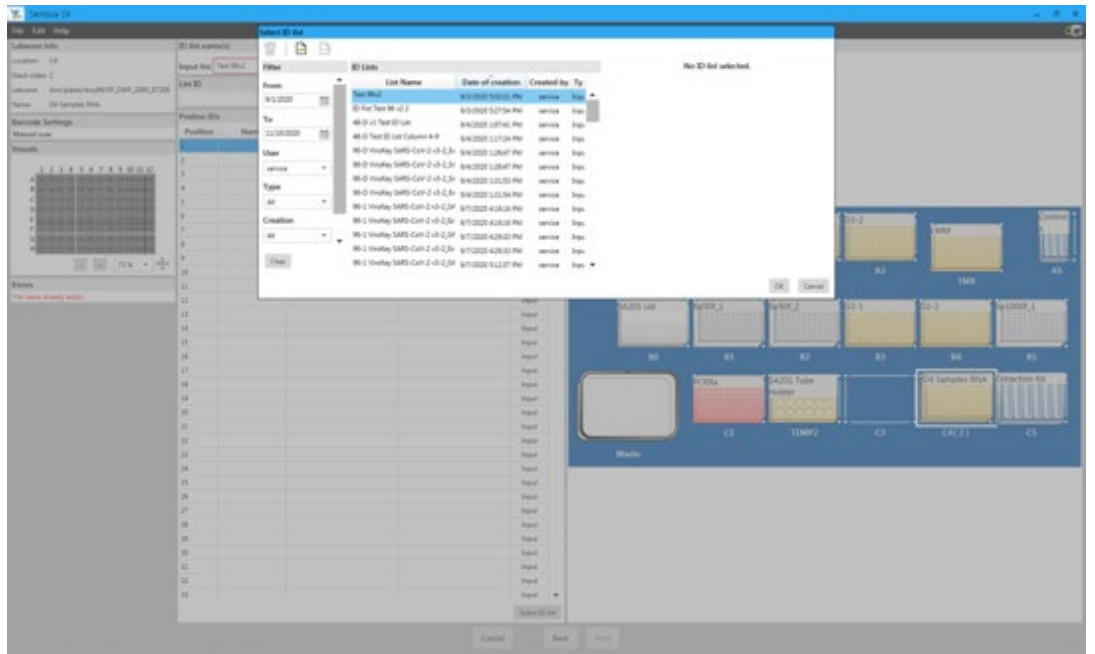


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d. Click on “Select ID List”.

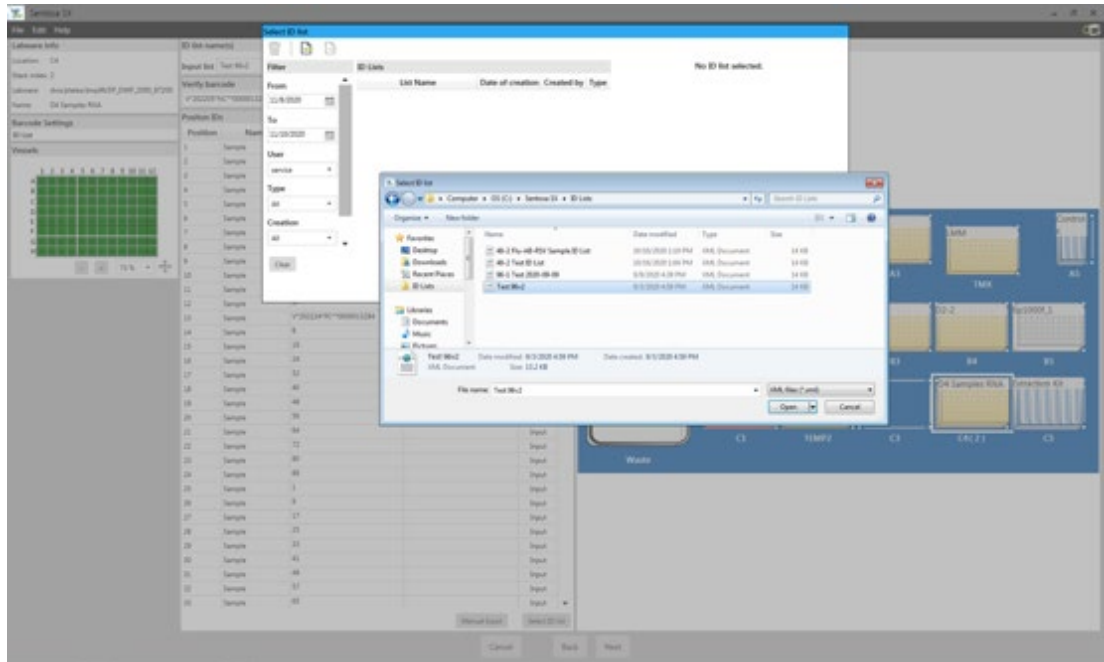


e. Click on “Import file” icon.

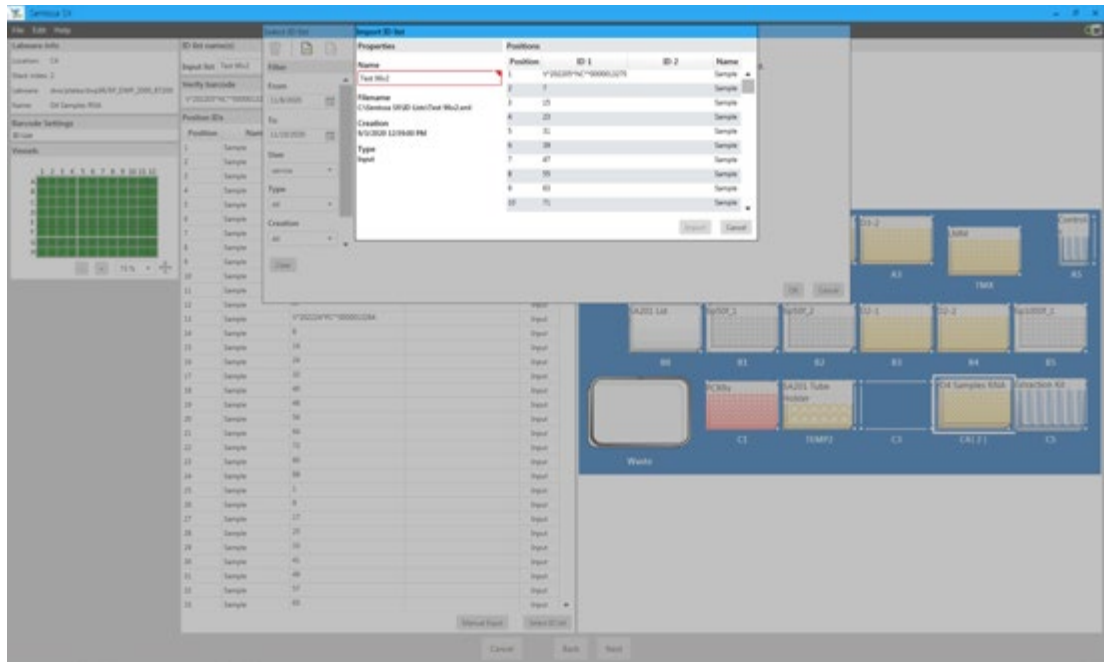


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f. Select .xml file to import from folder.

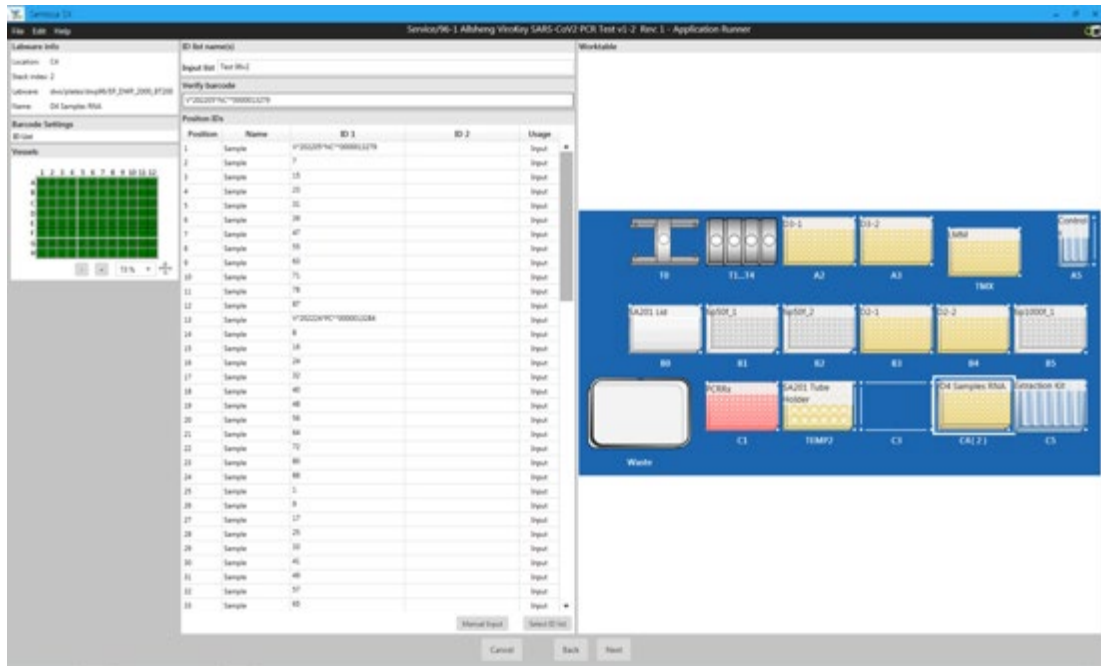
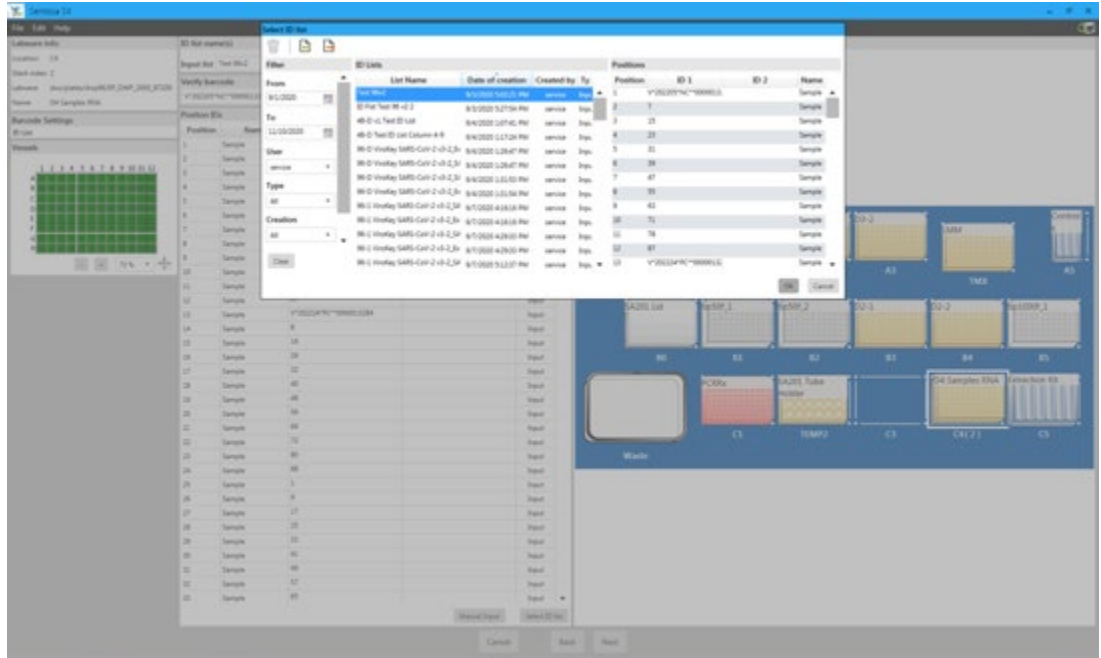


g. Click "Import".



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h. Select the ID list and click “OK”.



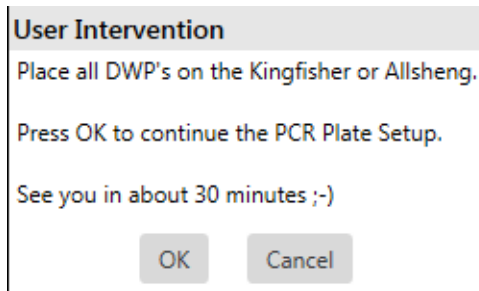
4.10.4. Click “Next” for all the volume-check windows.

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4.11. User Interventions and Run completion

4.11.1. First User Intervention

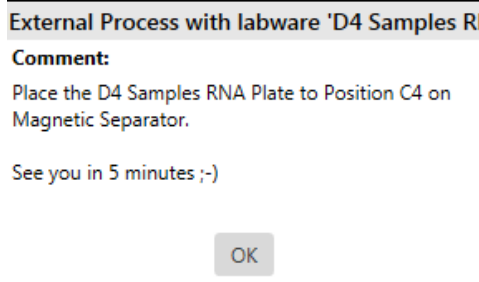
- a. At the first User Intervention window, open the *Sentosa SX101* and place all DWP's reagents and samples onto the KingFisher instrument. Then, run the KingFisher application "**96-1_ViroKey_VTNA_v1-1**".



- b. Click "OK" to begin the extraction on the KingFisher instrument. Once the extraction has completed, proceed to click "OK" on the *Sentosa SX101* to initiate the transfer of the PCR MM into the PCR Plate.

4.11.2. Second User Intervention

- a. At the second User Intervention window, remove the D4-Samples plate from the KingFisher instrument and place onto the position C4 on the *Sentosa SX101*.



- b. Click "OK" to begin the sample transfer to the PCR plate on *Sentosa SX101*.
- c. At the end of the run, click "Exit". A *.smp* file will be generated in the following directory "*C:\Sentosa SX\SMP*".
- d. Save the *.smp* file in a thumb drive.
- e. Seal the Reaction Plate accordingly with Optical Adhesive Seal and briefly spin down.
NOTE: Ensure the plate is well sealed.

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Hamilton workflow

5. Sample preparation (for individual samples)

NOTE: Refer to “**Sample preparation (for specimen pooling)**” section for steps to combine specimens into a pool.

Sample in Universal Transport Medium (UTM) or Viral Transport Medium (VTM) tubes **must** be heat-inactivated at 75°C for 30 minutes before placing onto the Hamilton Microlab STAR instrument with the cap and swab removed for sample transfer⁷.

Up to 376 samples, four positive control (PC) and four negative control (NC) samples can be performed in one run of the ViroKey SARS-CoV-2 RT-PCR Test v2.0, resulting in four PCR plates.

Fresh samples

- a. Vortex swab in Universal Transport Media for 30 seconds.
- b. Remove swabs from the tubes and discard the swabs according to the local safety regulations.
- c. Inactivate the SARS-CoV-2 virus in samples in an oven / a water bath at 75°C for 30 minutes.

Samples stored at 4°C


- a. Equilibrate to room temperature.
- b. Vortex swab in Universal Transport Media for 30 seconds.
- c. Remove swabs from the tubes and discard the swabs according to the local safety regulations.
- d. Inactivate the SARS-CoV-2 virus in samples in an oven / a water bath at 75°C for 30 minutes.

Frozen samples

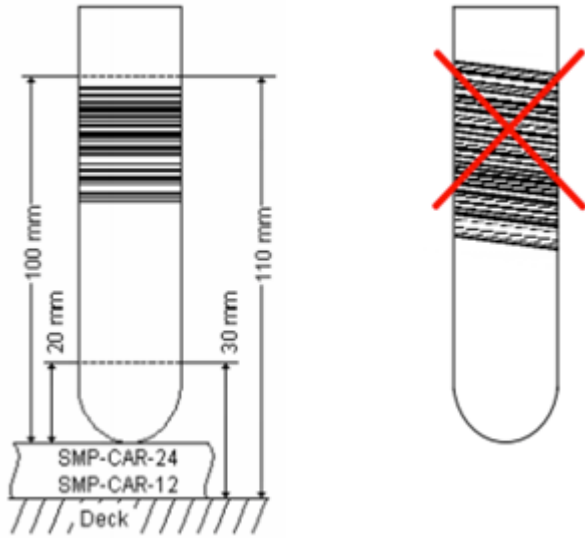

- a. Thaw samples and equilibrate to room temperature.
- b. Vortex swab in Universal Transport Media for 30 seconds.
- c. Remove swabs from the tubes and discard the swabs according to the local safety regulations.
- d. Inactivate the SARS-CoV-2 virus in samples in an oven / a water bath at 75°C for 30 minutes.

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Sample Tube Criteria for Hamilton Microlab STAR instrument

| Sample Tube Criteria | Description | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|--------------------------|--|----------------|----------------|----------------|----------------|----------|--------------|-----|-------|----------|-------------|-----|-------|----------|------------|------|-----|----------|-------------|-------|-----|----------|------------|-------|-----|----------|---|-----|------|
| Specifications | <ul style="list-style-type: none"> • Diameter: Between 14.5 mm to 18 mm • Height: Between 60 mm to 120 mm | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Sample tube ID (Barcode) | <ul style="list-style-type: none"> • Maximum of 20 characters • Only alphanumeric characters are allowed (i.e. no symbols are allowed) for sample tube ID barcodes. • Symbols are allowed for ID barcodes for kits, NC and PC. | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Barcode labels | <ul style="list-style-type: none"> • High quality print (ANSI / CEN / ISO grade A or B quality) is required for the barcode label. • Ensure that the barcode specifications and positioning meet the requirements in the table and figure below. <div style="text-align: center;">  <p>Label specifications</p> <table border="1"> <thead> <tr> <th colspan="2">Dimension</th> <th>Minimum length</th> <th>Maximum length</th> </tr> </thead> <tbody> <tr> <td>A</td> <td>Label length</td> <td>N/A</td> <td>80 mm</td> </tr> <tr> <td>B</td> <td>Code length</td> <td>N/A</td> <td>74 mm</td> </tr> <tr> <td>C</td> <td>Quiet zone</td> <td>3 mm</td> <td>N/A</td> </tr> <tr> <td>D</td> <td>Label width</td> <td>12 mm</td> <td>N/A</td> </tr> <tr> <td>E</td> <td>Code width</td> <td>12 mm</td> <td>N/A</td> </tr> <tr> <td>F</td> <td>Distance from the barcode to the label edge</td> <td>N/A</td> <td>1 mm</td> </tr> </tbody> </table> </div> | Dimension | | Minimum length | Maximum length | A | Label length | N/A | 80 mm | B | Code length | N/A | 74 mm | C | Quiet zone | 3 mm | N/A | D | Label width | 12 mm | N/A | E | Code width | 12 mm | N/A | F | Distance from the barcode to the label edge | N/A | 1 mm |
| Dimension | | Minimum length | Maximum length | | | | | | | | | | | | | | | | | | | | | | | | | | |
| A | Label length | N/A | 80 mm | | | | | | | | | | | | | | | | | | | | | | | | | | |
| B | Code length | N/A | 74 mm | | | | | | | | | | | | | | | | | | | | | | | | | | |
| C | Quiet zone | 3 mm | N/A | | | | | | | | | | | | | | | | | | | | | | | | | | |
| D | Label width | 12 mm | N/A | | | | | | | | | | | | | | | | | | | | | | | | | | |
| E | Code width | 12 mm | N/A | | | | | | | | | | | | | | | | | | | | | | | | | | |
| F | Distance from the barcode to the label edge | N/A | 1 mm | | | | | | | | | | | | | | | | | | | | | | | | | | |

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| Sample Tube Criteria | Description |
|----------------------|---|
| | <ul style="list-style-type: none"><li data-bbox="446 298 1474 361">• Glue barcode label within a range of between 20 mm to 100 mm from the bottom of the tube and at an angle of 90° to the tube (refer to figure below). <div data-bbox="646 394 1226 928" style="text-align: center;"><p data-bbox="820 949 1117 982">Position of the barcode</p></div> <ul style="list-style-type: none"><li data-bbox="446 1033 1458 1096">• Ensure that the orientation of the sample tube allows the barcode label to be seen through the gap as shown in the figure below.<li data-bbox="446 1102 1458 1165">• This is to ensure that the barcode can be successfully scanned by the automated barcode scanner on the Hamilton Microlab STAR instrument. <div data-bbox="734 1186 1205 1606" style="text-align: center;"><p data-bbox="782 1621 1166 1654">Orientation of the sample tube</p></div> |

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6. Automated nucleic acid extraction and RT-PCR set-up on the Hamilton Microlab STAR instrument

The workflow on the Hamilton Microlab STAR instrument is split into three stages:

- Sample transfer,
- Viral RNA Extraction, and
- RT-PCR set-up.

6.1. Sample transfer

Figure 4 shows the positions of consumables / labware on the Hamilton Microlab STAR platform. Double line the waste bin with biohazard bags. Please refer to the layout as indicated by the Hamilton Microlab STAR instrument software or the appendix to load all items in the correct positions.

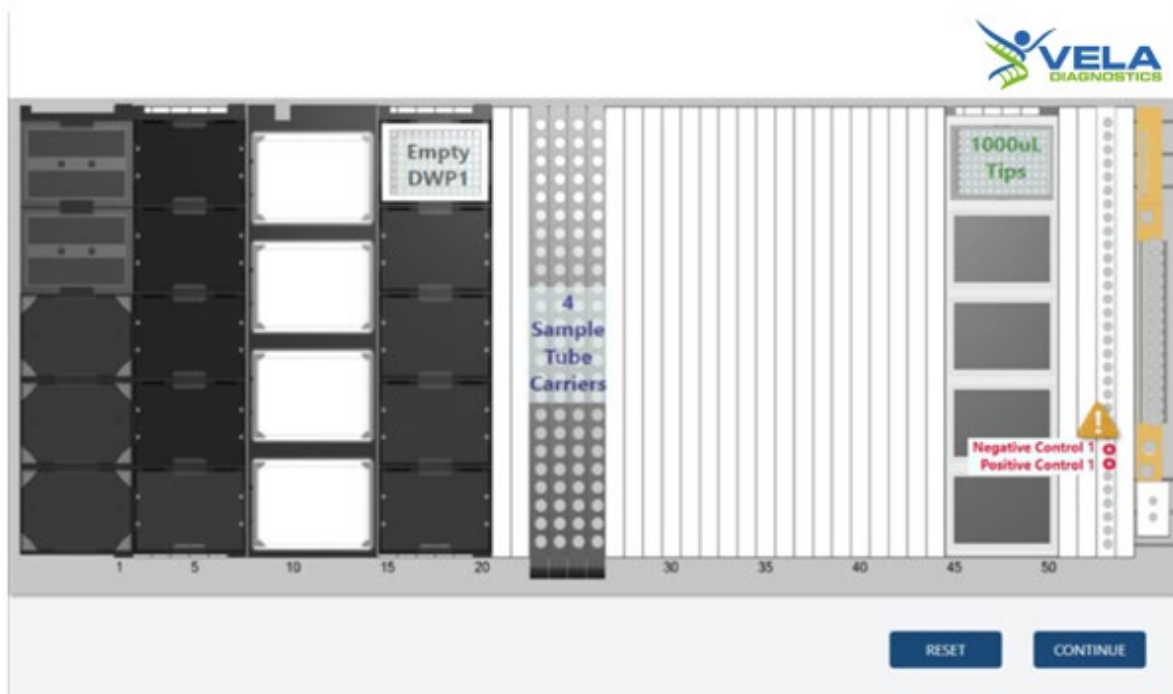



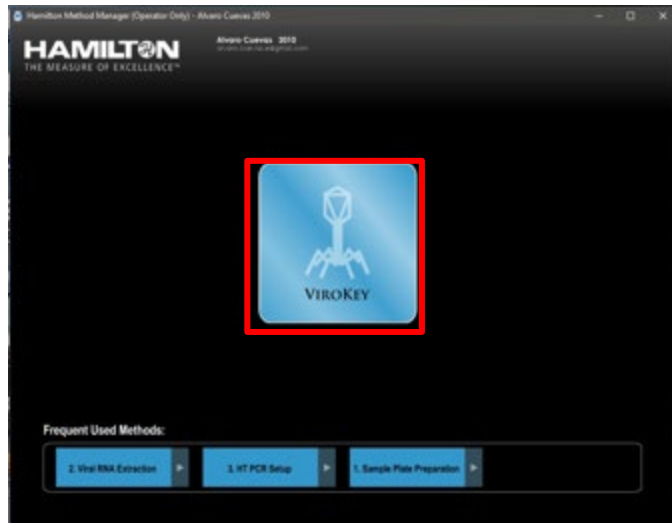
Figure 4. Layout of the Hamilton Microlab STAR platform for 1 deepwell plate (1x96 tests) for sample plate preparation (refer to Appendix for 2 to 4 deepwell plates layout).

NOTE:

- Items shown are necessary for nucleic acid extraction and PCR assay set-up for application “*STAR8AL96 Vela_SampleTransfer_V1.2.med*”.
- Ensure all consumables / labware are properly placed, aligned and secured into their respective positions.
- Ensure that the biohazard bags are properly attached to the waste bin before starting a protocol run. For more information, please refer to the Hamilton Microlab STAR instrument IFU.

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- 6.1.1. Switch on the computer, and wait for the initialization procedure to be completed.
- 6.1.2. On the instrument's computer, launch the Hamilton Microlab STAR software by double-clicking the  icon.
NOTE: Please switch on Hamilton Microlab STAR instrument after Hamilton Microlab STAR software is launched.
- 6.1.3. Press / Click “VIROKEY” button.



- 6.1.4. Press / Click “Run” under “1. Sample Plate Preparation” to launch the sample plate preparation application.



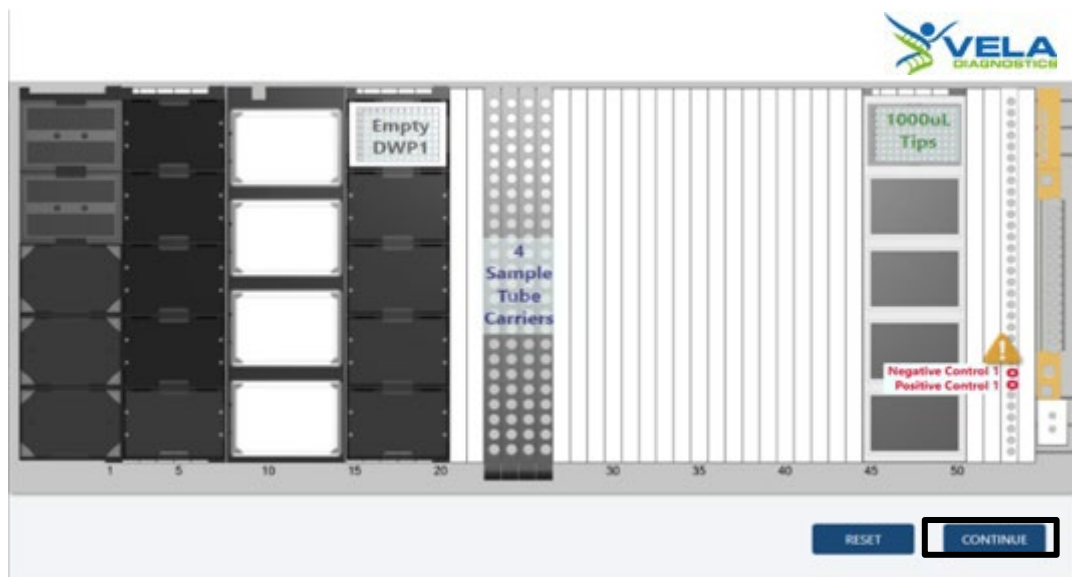
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- 6.1.5. Input values 1 to 4 (minimum: 1, maximum: 4) for the “*NUMBER OF DEEPWELL PLATES*”. Load the empty deepwell plates onto the Hamilton Microlab STAR worktable (refer to **Figure 4** in **step 6.1**). Press / Click “*CONTINUE*” when done.



- 6.1.6. Press / Click “*CONTINUE*” to proceed to scanning of NC and PC tubes.



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- 6.1.7. Scan the 2-D barcodes on the NC and PC for **Control Set 1 (NC1 and PC1)**. Load the **Control Set 1** onto **Tube Carrier Track 53**. Press / Click “**CONTINUE**” when done.



NOTE: Ensure that the NC and PC tubes are uncapped before loading.

- 6.1.8. [If applicable] Repeat **step 6.1.6** for **Control Sets 2 to 4** if performing for 2x96 to 4x96 tests respectively.

NOTE: Each control set corresponds to each sample set in the table below. Each control set consists of 1 NC and 1 PC and each sample set consists of 94 samples.

| Track Carrier | Control Set | Sample Set |
|---------------|-------------|------------|
| 53 | 1 | 1 |
| | 2 | 2 |
| | 3 | 3 |
| | 4 | 4 |

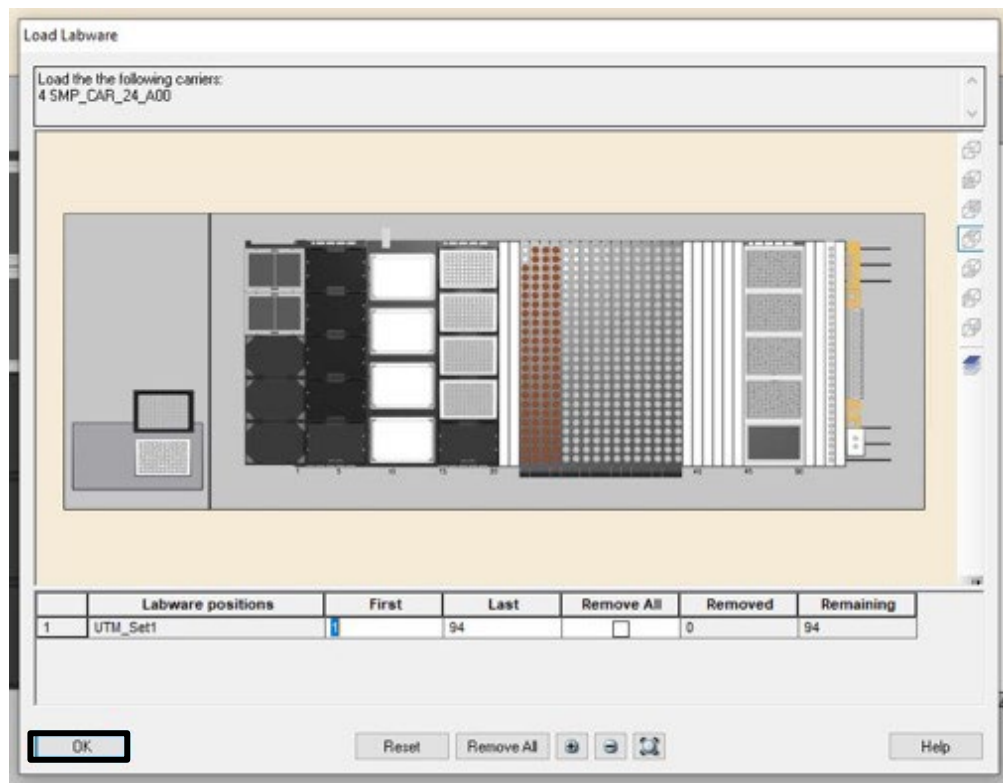
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6.1.9. Load the sample tubes onto the sample tube carriers.

Input the number of samples used under the “*First*” and “*Last*” columns or select the area where the “*First*” and “*Last*” samples are placed using the cursor (by “*clicking*” and “*dragging*” over an area). Press / Click “OK” when done.

NOTE:

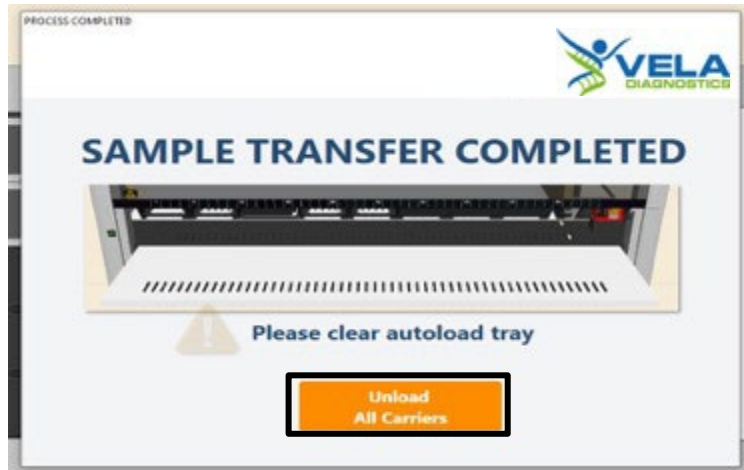
- Ensure that the sample tubes are uncapped before loading.
- User can run less than 94 samples in each run by indicating the first and last sample in the carrier.
- After the user has indicated the “*First*” and “*Last*” samples, location of the samples are shown as “brown circles”.



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- 6.1.10. Press / Click *“Unload All Carriers”* after the run is completed. Unload all carriers, clean and disinfect the Hamilton Microlab STAR instrument after each run. For instrument maintenance, please refer to the Hamilton Microlab STAR instrument maintenance videos.



Proceed to *“2. Viral RNA Extraction”*, on the *“Hamilton Method Manager”* user interface, after the run is completed.

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6.2. Viral RNA Extraction

Figure 5 shows the positions of consumables / labware on the Hamilton Microlab STAR platform. Double line the waste bin with biohazard bags. Please refer to the layout as indicated by the Hamilton Microlab STAR instrument software or the appendix to load all items in the correct positions.

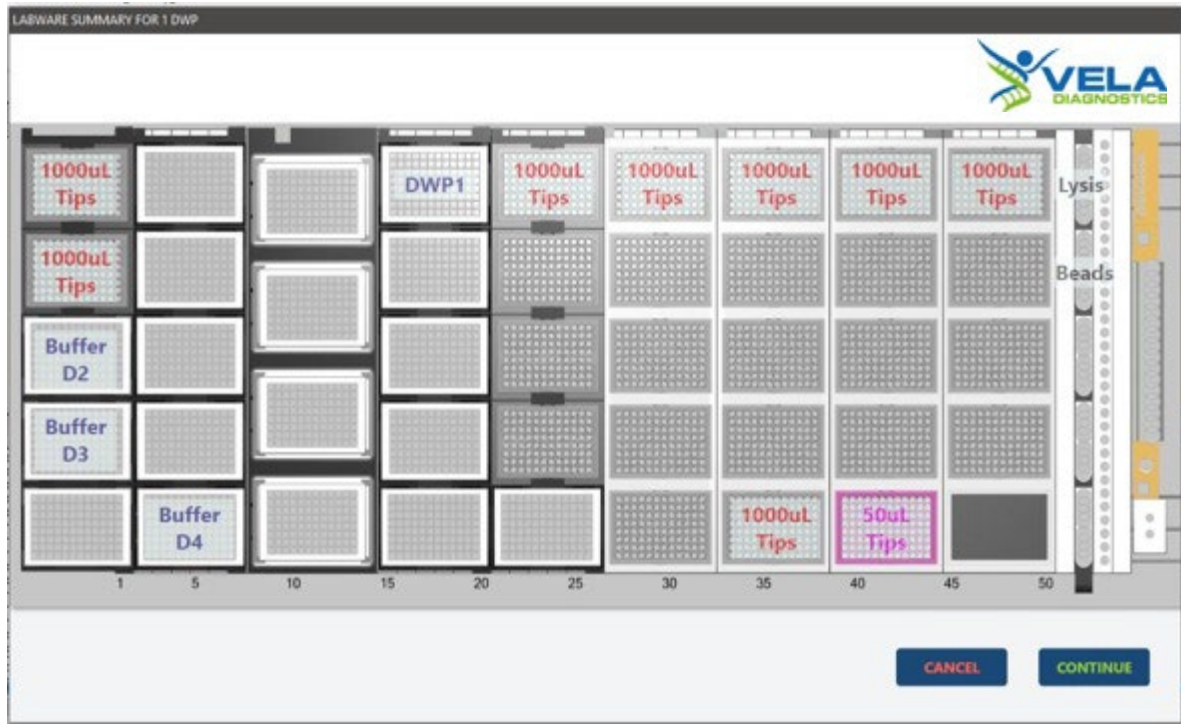


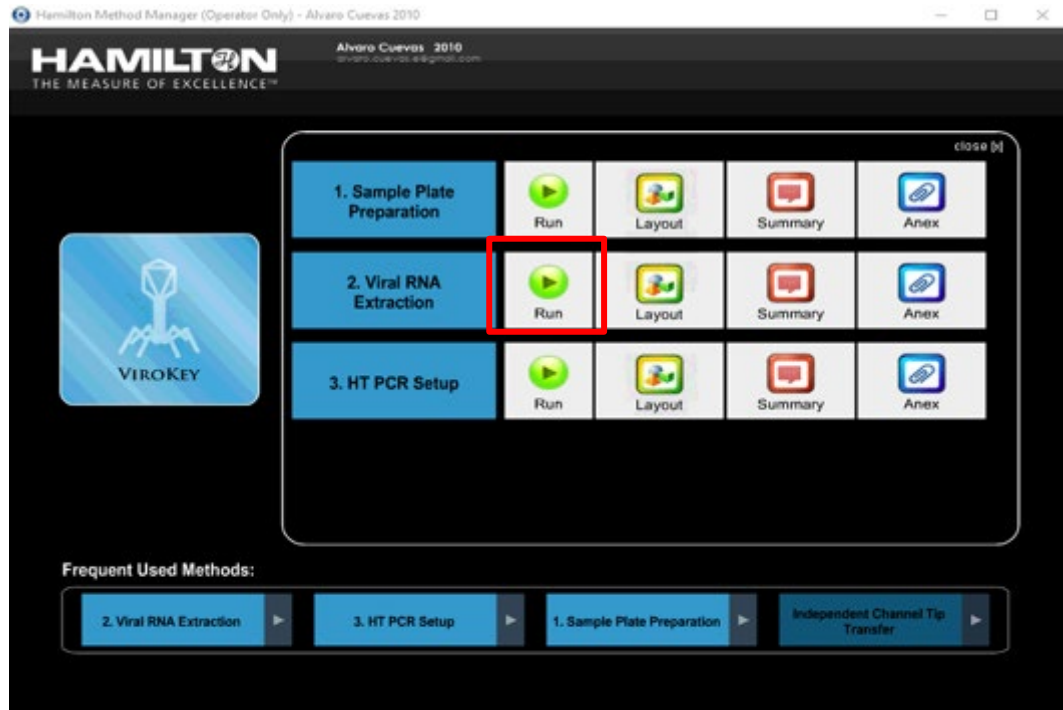
Figure 5. Layout of the Hamilton Microlab STAR platform for 1 deepwell plate for viral RNA extraction (refer to Appendix for 2 to 4 deepwell plate layouts).

NOTE:

- Items shown are necessary for nucleic acid extraction for application **"STAR8AL96 Vela_ViroKey_V3.10.med"**.
- Ensure all consumables / labware are properly placed, aligned and secured into their respective positions.
- Ensure that the biohazard bags are properly attached to the waste bin before starting a protocol run. For more information, please refer to the Hamilton Microlab STAR instrument IFU.

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6.2.1. Press / Click “Run” under “2. Viral RNA Extraction”.



6.2.2. Empty the liquid waste bottle. Press / Click “DONE” after placing back the empty waste bottle.



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- 6.2.3. Input values 1 to 4 (minimum: 1; maximum: 4) for the “NUMBER OF DEEPWELL PLATES”. Press / Click “CONTINUE” when done.



ViroKey HT Total Nucleic Acid Kit

VELA DIAGNOSTICS

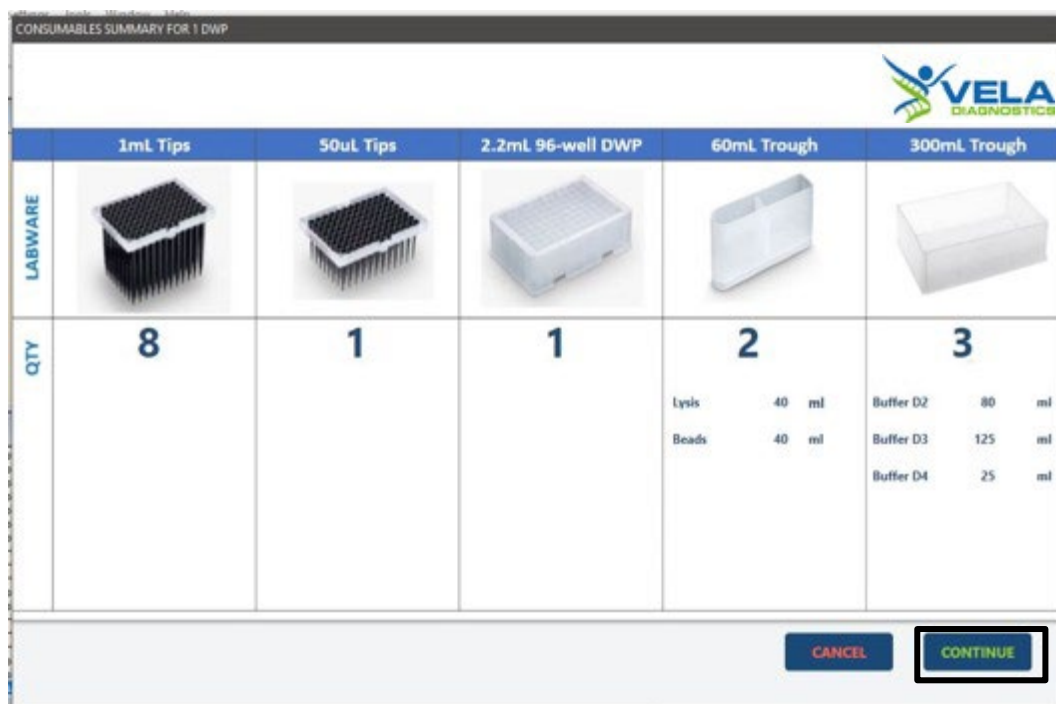
Throughput

NUMBER OF DEEPWELL PLATES: 4

Min: 1 Max: 4

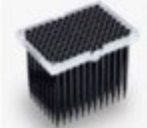
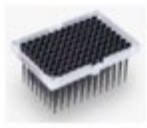



CANCEL CONTINUE

- 6.2.4. Prepare the reagents and consumables (Buffer D2 to D4, lysis master mix, 1,000 μ L tips and 50 μ L tips and beads). Press / Click “CONTINUE” when done. Refer to Appendix for Consumables Summary for 2 to 4 deepwell plates.



CONSUMABLES SUMMARY FOR 1 DWP

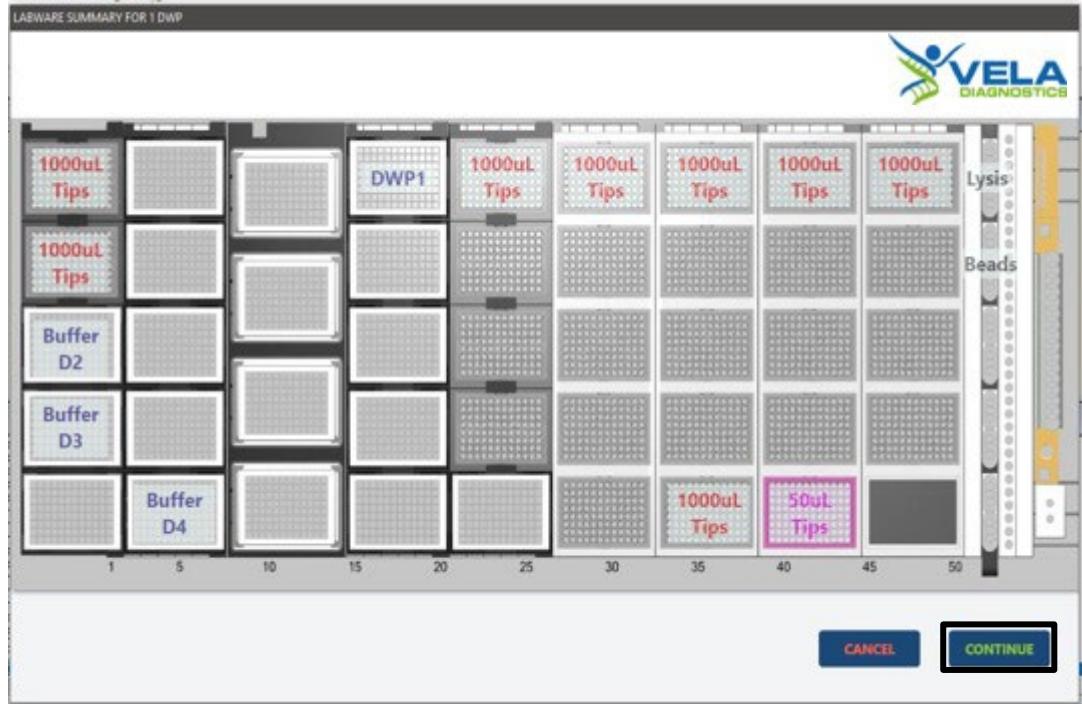
VELA DIAGNOSTICS

| | 1mL Tips | 50uL Tips | 2.2mL 96-well DWP | 60mL Trough | 300mL Trough |
|---------|---|---|---|---|---|
| LABWARE |  |  |  |  |  |
| QTY | 8 | 1 | 1 | 2 | 3 |
| | | | | Lysis 40 ml Beads 40 ml | Buffer D2 80 ml Buffer D3 125 ml Buffer D4 25 ml |

CANCEL CONTINUE

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- 6.2.5. Load the reagents and consumables based on the layout below. Press / Click “CONTINUE” when done. Refer to Appendix to view layout with 2 to 4 deepwell plates.



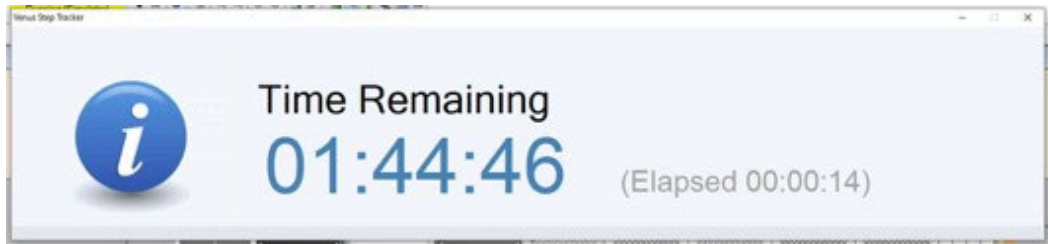
- 6.2.6. Scan the ViroKey HT Total Nucleic Acid Kit label. Press / Click “CONTINUE” when done.



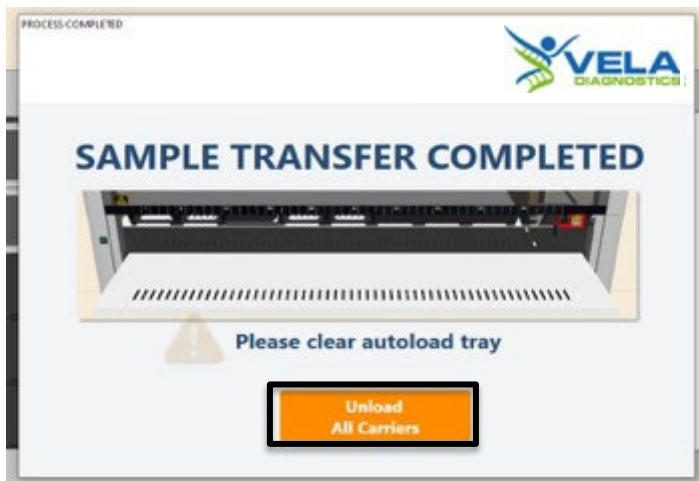
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- 6.2.7. Wait for extraction to be completed. Extraction takes approximately 1 hour 45 minutes to complete.



- 6.2.8. Press / Click “Unload All Carriers” after the run is completed. Unload all carriers, clean and disinfect the Hamilton Microlab STAR instrument after each run. For instrument maintenance, please refer to the Hamilton Microlab STAR instrument maintenance videos.



Proceed to “3. HT PCR Setup”, on the “Hamilton Method Manager” user interface, after the run is completed.

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6.3. HT PCR set-up

Figure 6 shows the positions of consumables / labware on the Hamilton Microlab STAR platform. Double line the waste bin with biohazard bags. Please refer to the layout as indicated by the Hamilton Microlab STAR instrument software or the appendix to load all items in the correct positions.

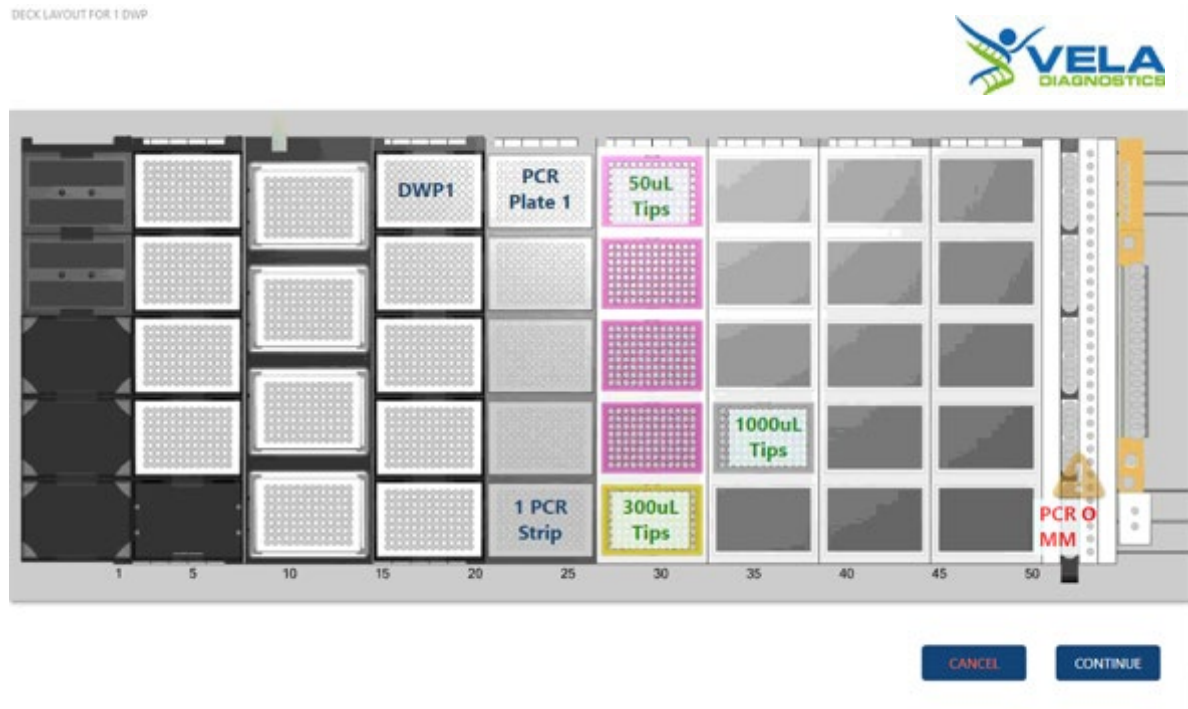


Figure 6. Layout of the Hamilton Microlab STAR platform for 1 sample plate for HT PCR set-up (refer to Appendix for 2 to 4 sample plate layouts).

NOTE:

- Items shown are necessary for PCR assay set-up for application “**STAR8AL96 Vela_PCRsetup_V1.3.med**”.
- Ensure all consumables / labware are properly placed, aligned and secured into their respective positions.
- Ensure that the biohazard bags are properly attached to the waste bin before starting a protocol run. For more information, please refer to the Hamilton Microlab STAR instrument IFU.

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6.3.1. Press / Click “Run” under “3. HT PCR Setup”.



6.3.2. Input values 1 to 4 (minimum: 1; maximum: 4) for the “Number of Sample Plate”.



Press / Click “CONTINUE” when done.

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- 6.3.3. Load the reagents and consumables based on the layout below. Press / Click “CONTINUE” when done. Refer to Appendix to view layout with 2 to 4 sample plates.



NOTE: PCR Strip in the layout refers to HT 8-Strip Tubes.

- 6.3.4. Scan the PCR Kit 1 (HT M1 of ViroKey SARS-CoV-2 RT-PCR Test v2.0 (4x96)) label. Press / Click “CONTINUE” when done.



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- 6.3.5. Scan the PCR Plate 1 label. Place plate on PCR plate carrier, Track 21 – 26, Position 1. Press / Click “CONTINUE” when done.



- 6.3.6. [If applicable] Repeat **steps 6.3.1 to 6.3.5** and for **PCR Plates 2 to 4** if performing for 2x96 to 4x96 tests respectively.

NOTE:

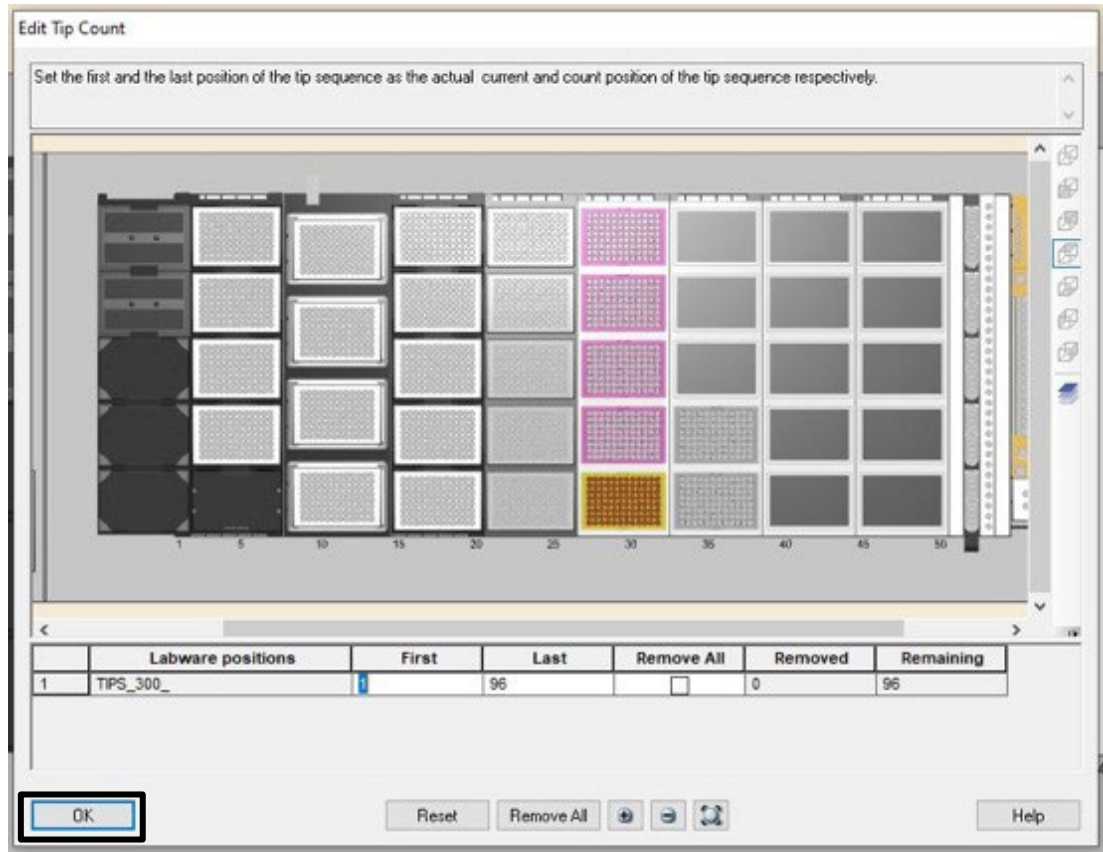
| Track | PCR Plate | Position |
|---------|-----------|----------|
| 21 – 26 | 1 | 1 |
| | 2 | 2 |
| | 3 | 3 |
| | 4 | 4 |

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6.3.7. Input the number of 300 μ L tips used under the “*First*” and “*Last*” columns or select the area where the “*First*” and “*Last*” samples are placed using the cursor (by “*clicking*”, “*holding*” and “*dragging*” over an area). Press / Click “OK” when done.

NOTE:

- After the user has indicated the “*First*” and “*Last*” samples, location of the samples are shown as “brown circles”.
- Remove the leftover tips (if any) and use them for the next PCR set-up.

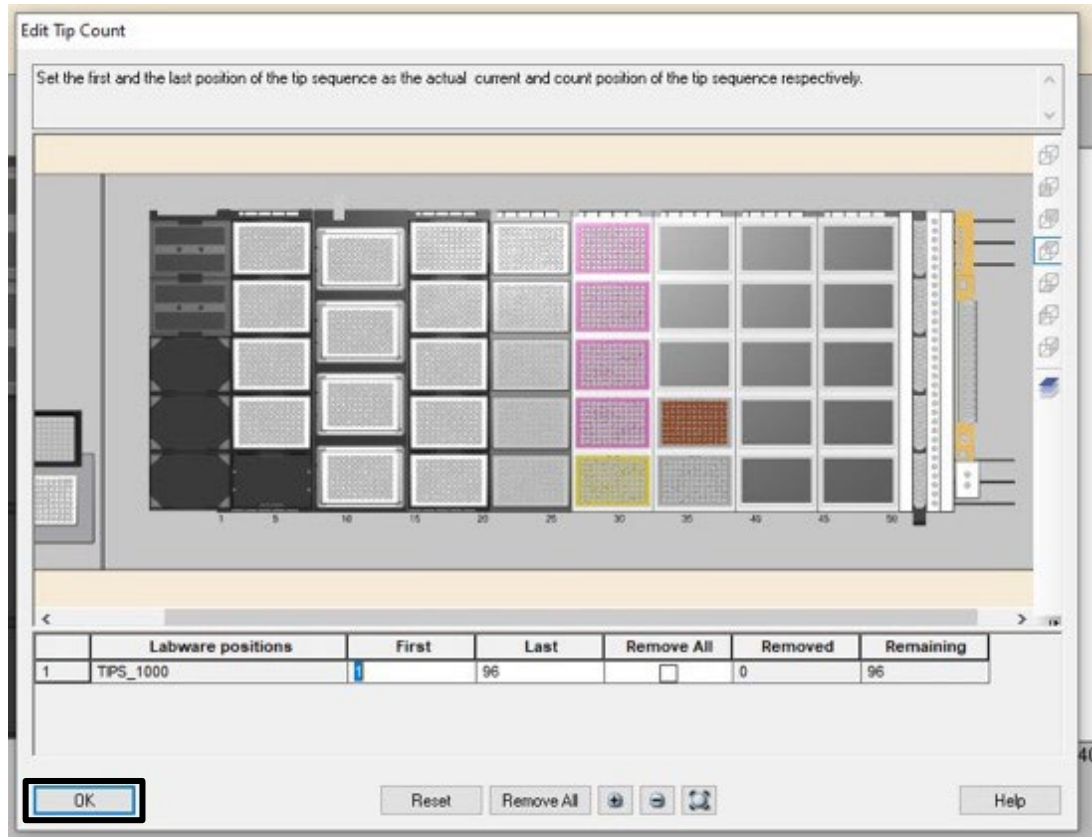


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6.3.8. Input the number of 1,000 μ L tips used under the “*First*” and “*Last*” columns or select the area where the “*First*” and “*Last*” samples are placed using the cursor (by “*clicking*” and “*dragging*” over an area). Press / Click “OK” when done.

NOTE:

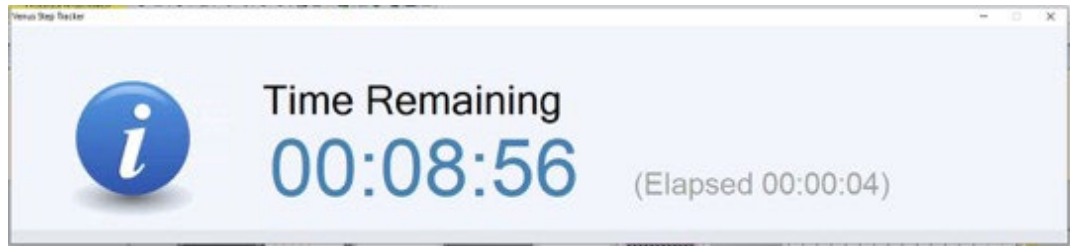
- After the user has indicated the “*First*” and “*Last*” samples, location of the samples are shown as “brown circles”.
- Remove the leftover tips (if any) and use them for the next PCR set-up.



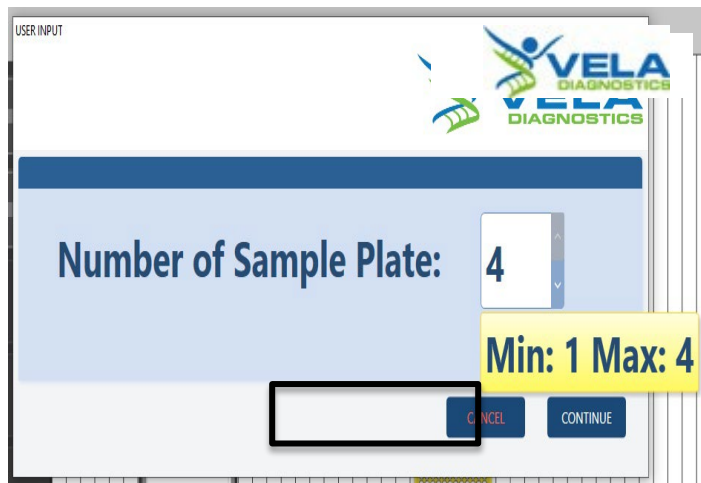
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- 6.3.9. Wait for PCR set-up to be completed. PCR set-up takes approximately 9 minutes to complete.



- 6.3.10. Press / Click “Unload All Carriers” after the run is completed. Unload all carriers, clean and disinfect the Hamilton Microlab STAR instrument after each run. For instrument maintenance, please refer to the Hamilton Microlab STAR instrument maintenance videos.



- 6.3.11. After the run is completed, carefully remove the MicroAmp Fast Optical 96-Well Reaction Plate. Apply the MicroAmp Optical Adhesive Film over the plate and seal the plate tightly to prevent contamination. Briefly spin down the PCR plate and load it onto the *Sentosa* SA201 Real-Time PCR Instrument.

Proceed to RT-PCR and data analysis using the *Sentosa* SA201 Real-Time PCR Instrument and *Sentosa* SA201 Reporter (pages 90 to 103).

After RT-PCR and data analysis are complete, proceed to page 13 for “**Result interpretation**” section.

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RT-PCR and data analysis using the *Sentosa SA201* Real-Time PCR Instrument and *Sentosa SA201 Reporter* software

7. *PCR on the Sentosa SA201 Real-Time PCR Instrument*

- 7.1. Switch on the *Sentosa SA201* Real-Time PCR Instrument by pressing the power button on the instrument.

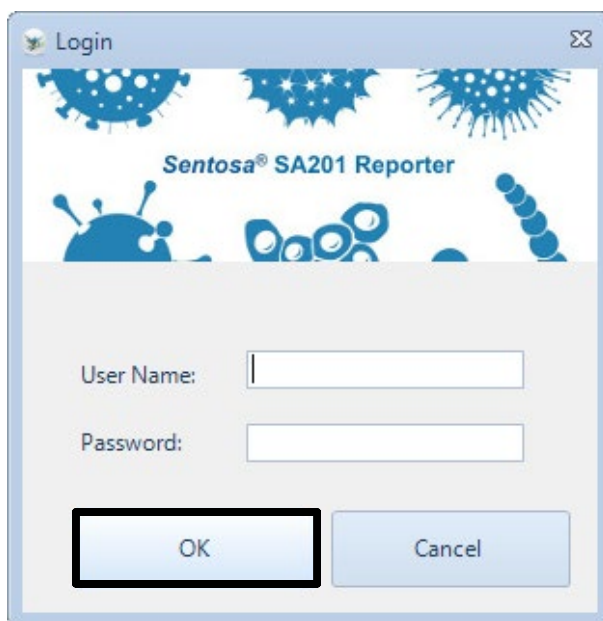
NOTE: Ensure the green indicator is lit and not flashing.



- 7.2. Launch the *Sentosa SA201 Reporter* software by double-clicking on the icon.



Type the user name and password, and then click “OK”.



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7.3. After logging in, “Access Mode” pop-up dialog is displayed.

Click “Import ID List” under “Access Mode” pop-up dialog to import the required “.smp” file generated by the Sentosa SX101 instrument (**Figure 7**) / Hamilton Microlab STAR instrument (**Figure 8**).



7.3.1. Import “.smp” file generated by the Sentosa SX101 instrument

Select “.smp” file to import from “Sentosa SA > SMP” folder. Click “Open” to import the selected file.

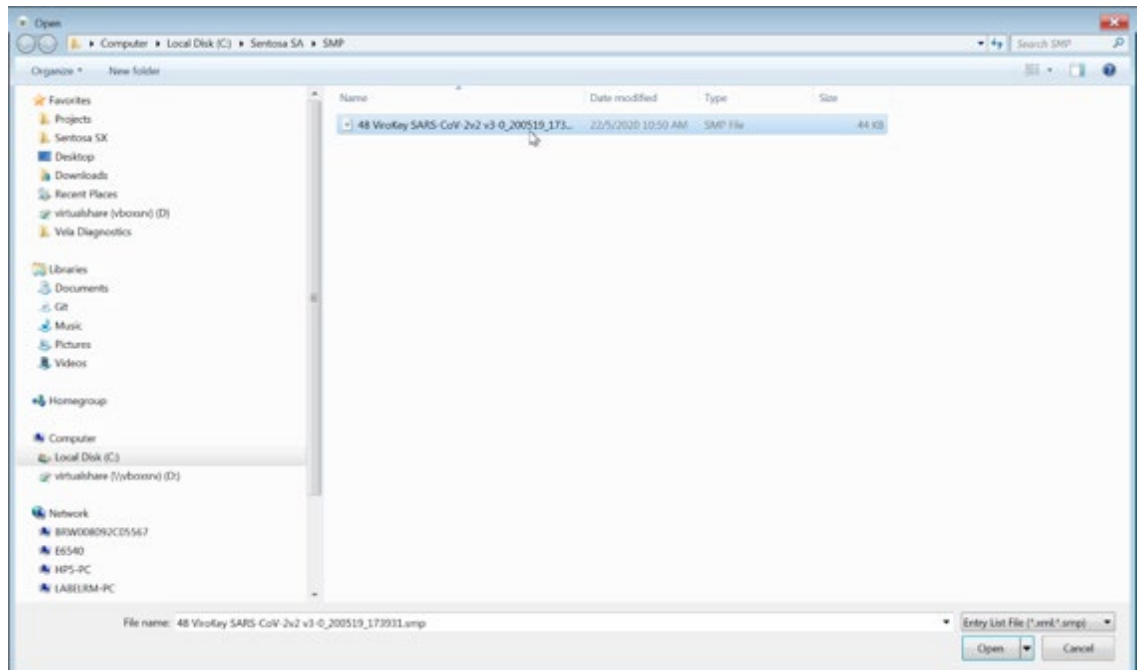


Figure 7. “.smp” file generated by Sentosa SX101 instrument is found in “Sentosa SA > SMP” folder.

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7.3.2. Import “.smp” file generated by the Hamilton Microlab STAR instrument

Select “.smp” file to import from “Veladx” folder. Click “Open” to import the selected file.

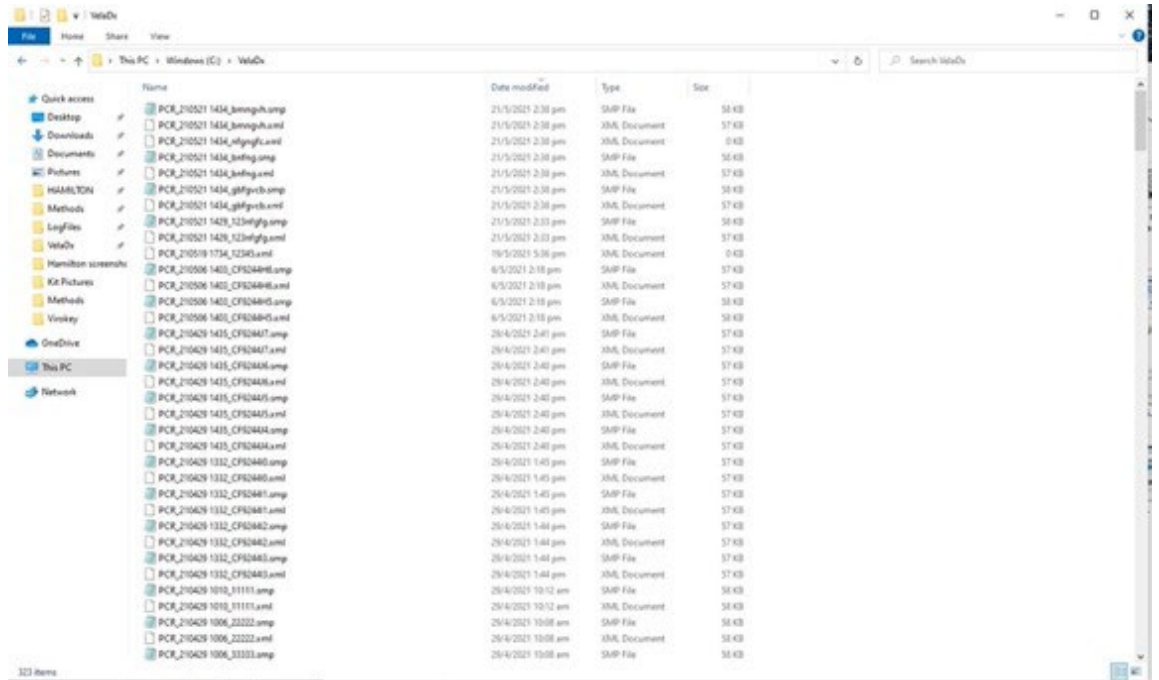
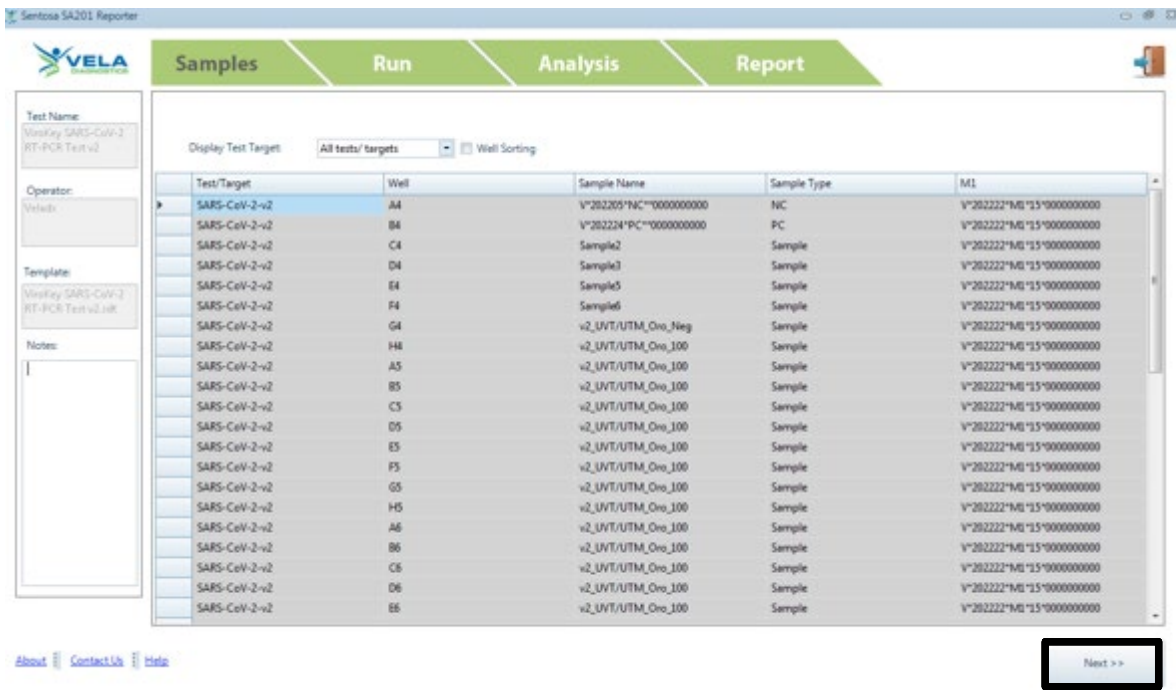
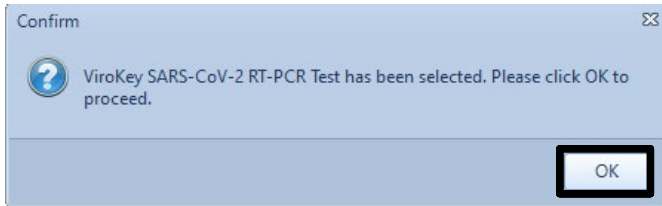


Figure 8. “.smp” file generated by Hamilton Microlab STAR instrument is found in “Veladx” folder.

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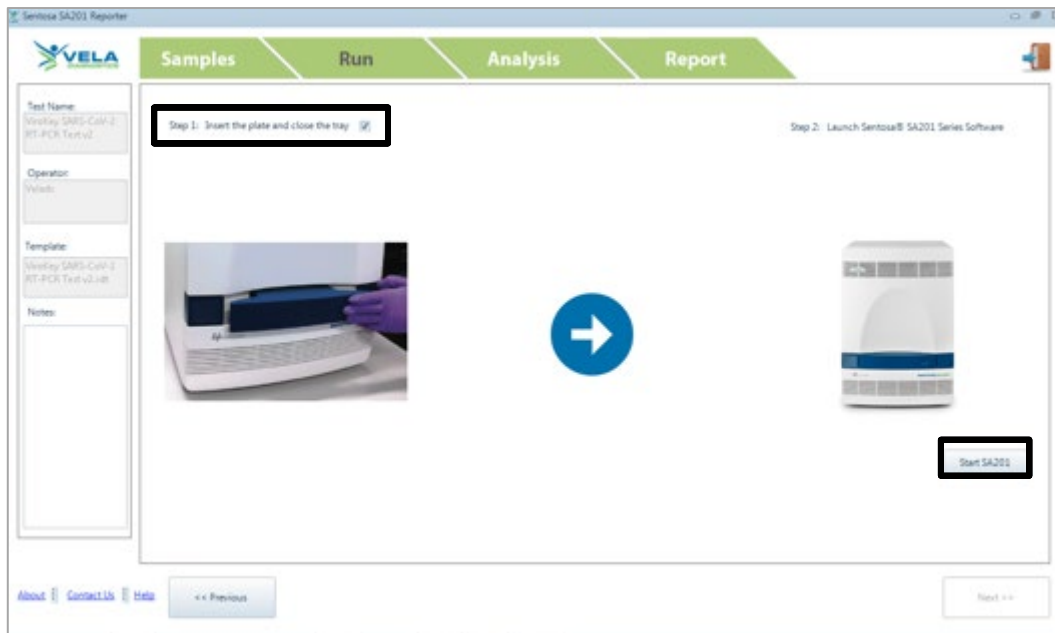
7.4. After the “.smp” file has been imported, the software will require a confirmation on the selected assay. Click “OK” to confirm the sample layout and the information displayed from the “.smp” file.



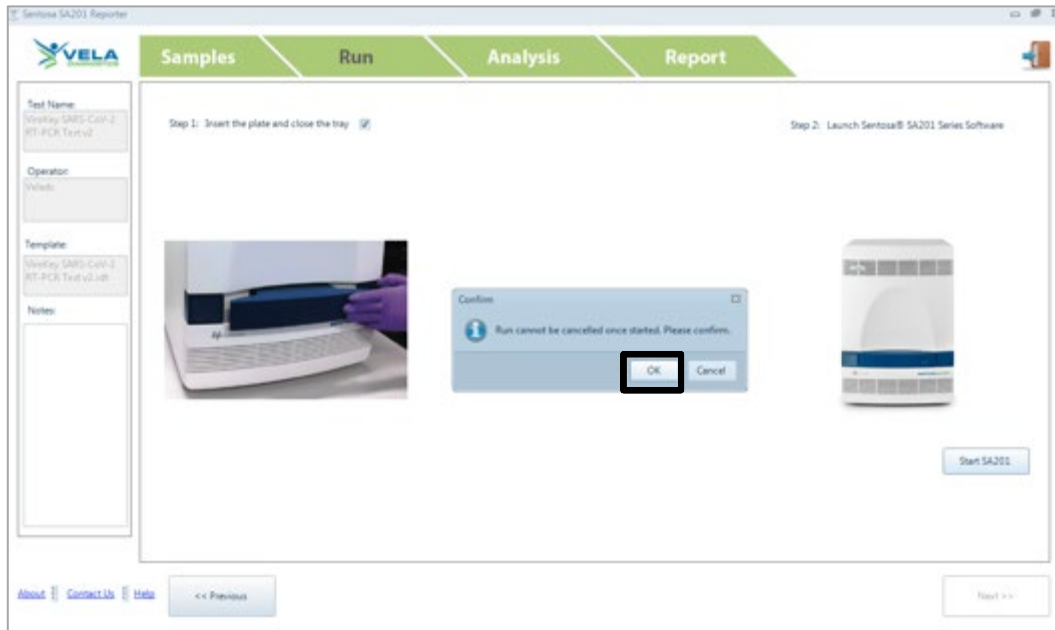
Click “Next”.

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7.5. Activate “Insert the plate and close the tray” checkbox to activate “Step 2: Launch Sentosa SA201 Series Software”. Click “Start SA201” button.

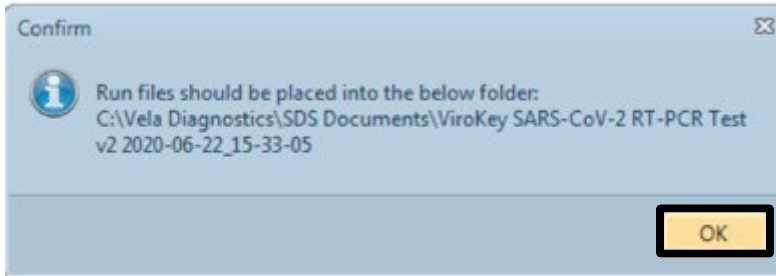


7.6. A “Confirm” dialog box will be displayed. Click “OK”.

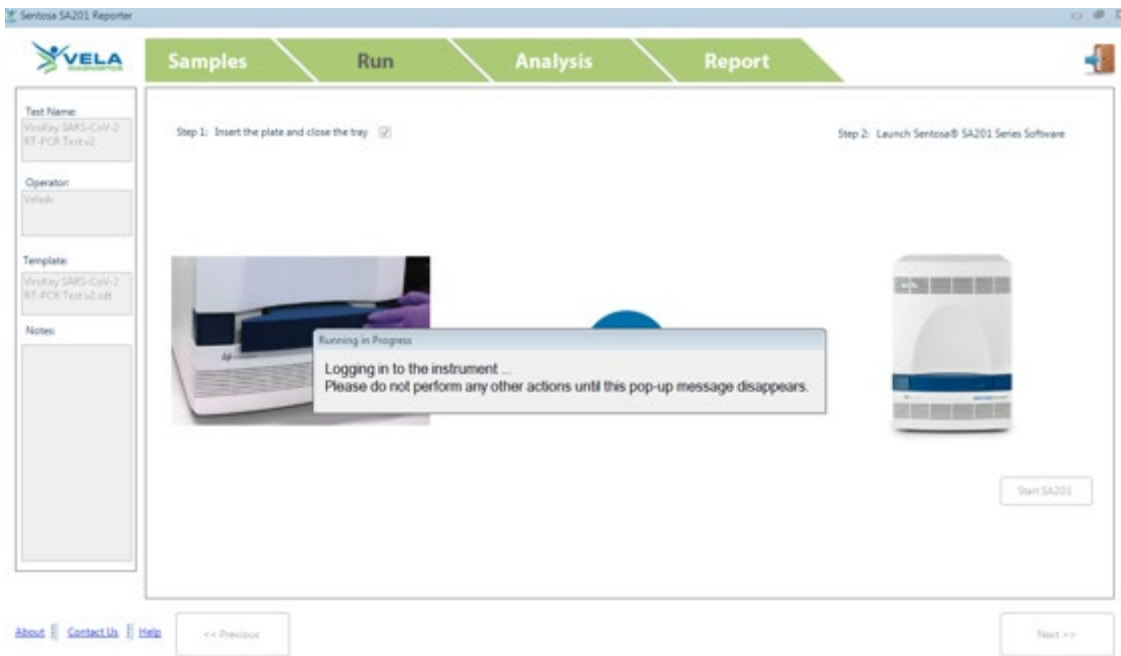


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7.7. Another “Confirm” dialog box will be displayed. Click “OK”.



7.8. The *Sentosa SA201 Reporter* will begin the process (automatically) of logging in to the *Sentosa SA201 Series Software* and running a series of steps on it to start the new run. A pop-up window titled “*Running in Progress*” will be displayed throughout this process, reminding the user not to perform any other actions. The pop-up window will also indicate the individual specific steps that are being performed in the background.

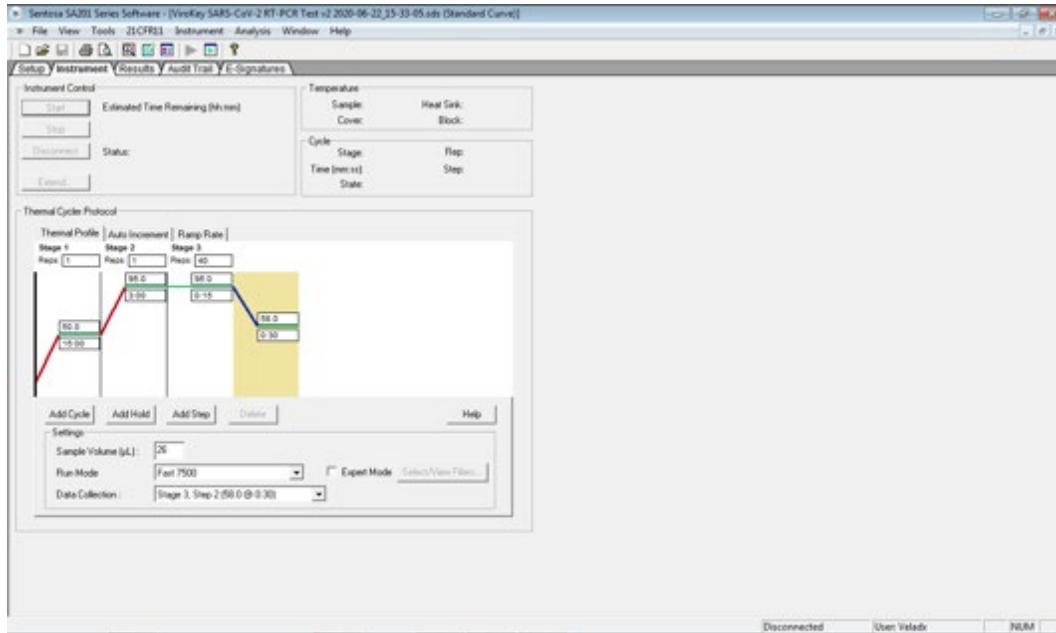


The following is the list of automated steps that will be performed on the *Sentosa SA201 Series Software*:

- I. Logging in to the *Sentosa SA201 Series Software* using the same user account credentials that were used to log in to the *Sentosa SA201 Reporter*.
- II. Importing the sample set-up file which was generated by the *Sentosa SA201 Reporter*.
- III. Saving the run document (“*.sds*”) file.
- IV. Starting the run.

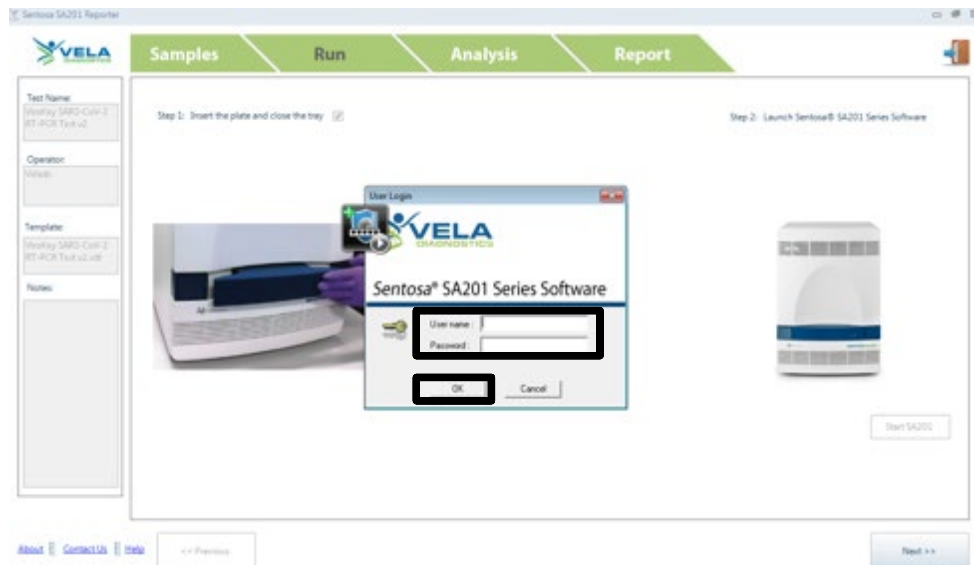
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Please do not perform any other action during the automated process. The run will be started on the *Sentosa SA201* instrument at the end of the process. This can be verified by selecting the “*Instrument*” tab and checking the “*Instrument Control*” panel on the *Sentosa SA201* Series Software.



7.9. [Optional] If the automated process is stopped or interrupted due to any unforeseen circumstances, the run can be resumed manually by following the steps listed below. Please skip any steps that have already been completed by the automated process before the interruption occurs.

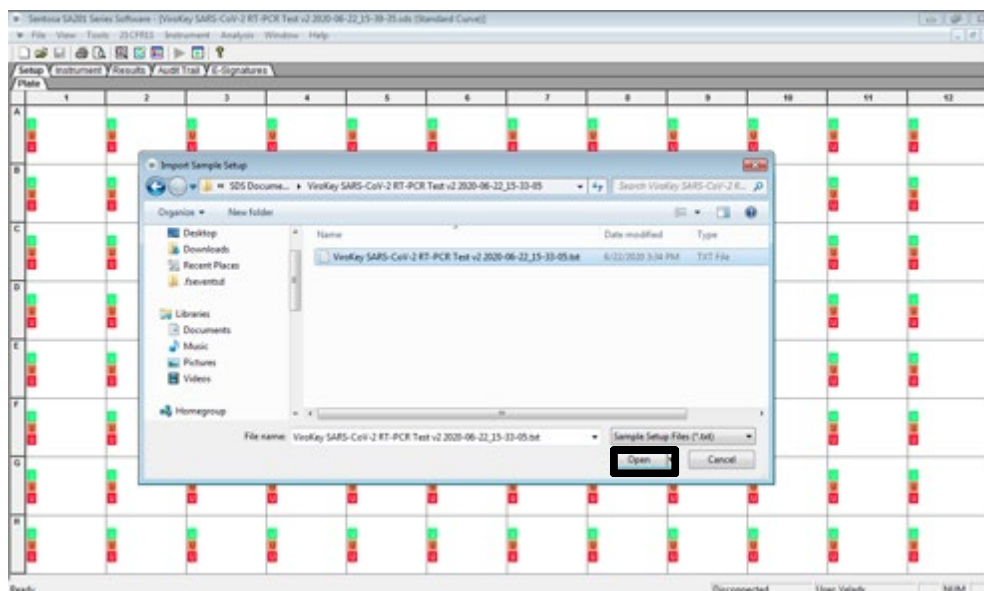
7.9.1. Log in to the *Sentosa SA201* Series Software by typing the user name and password in the “*User Login*” pop-up window. Click “*OK*”.



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- 7.9.2. Select “File” from the main menu and “Import Sample Setup” from the drop-down list. “Import Sample Setup” pop-up window will be displayed. The sample file is given a default file name (“Sentosa SA201 Assay name PCR/RT-PCR Test YYYY-MM-DD_HH-MM-SS.txt”). Select the “.txt” file and click “Open”.

NOTE: DO NOT modify the generated “.txt” file as this will result in an error.



The sample layout will change according to the imported sample set-up file.

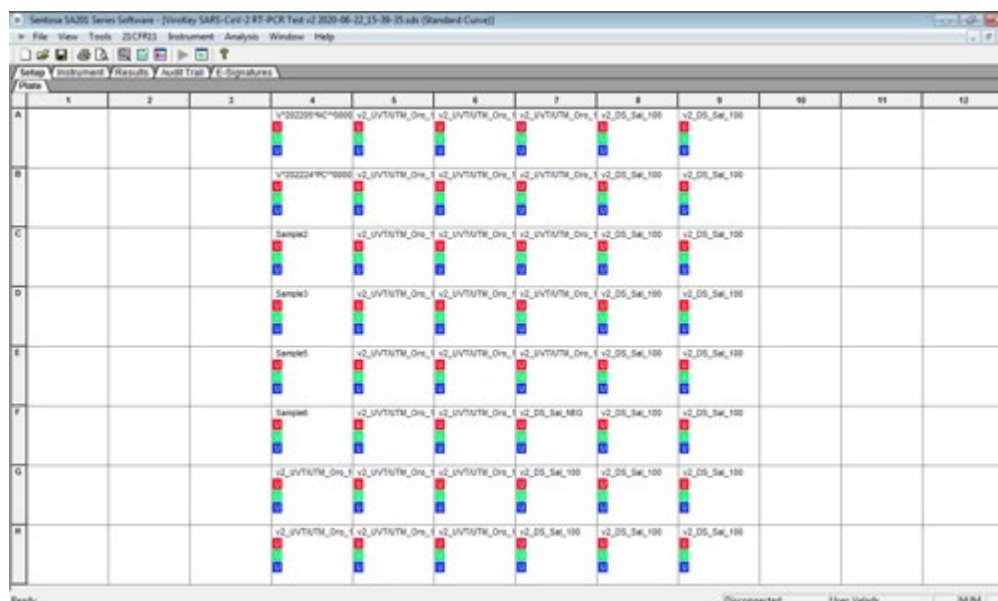


Figure 9. Imported sample set-up file for ViroKey SARS-CoV-2 RT-PCR Test v2.0 ran on Sentosa SX101 instrument.

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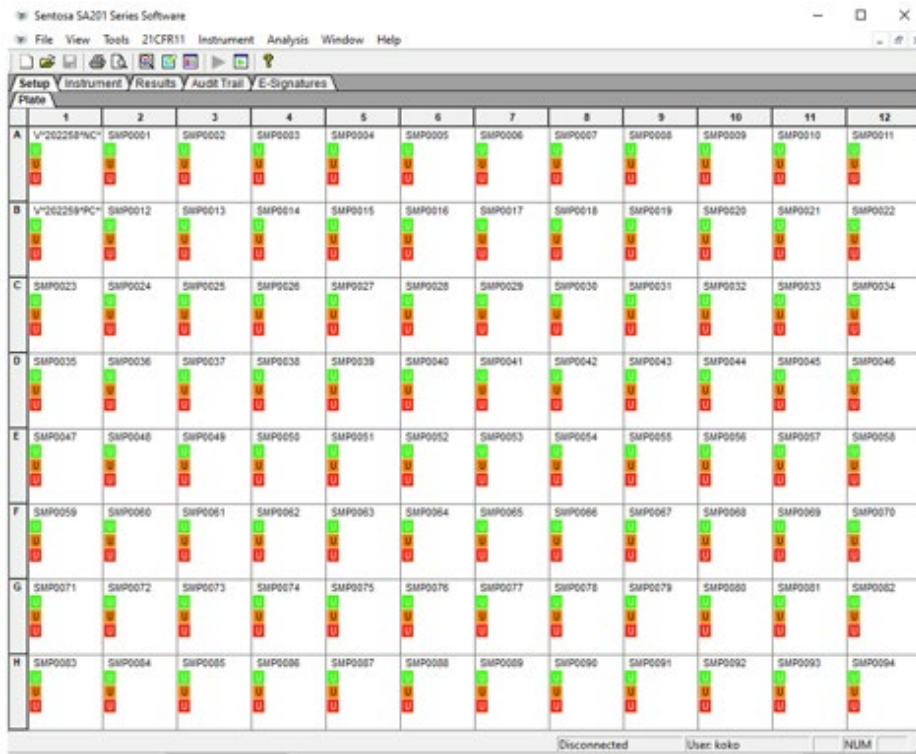
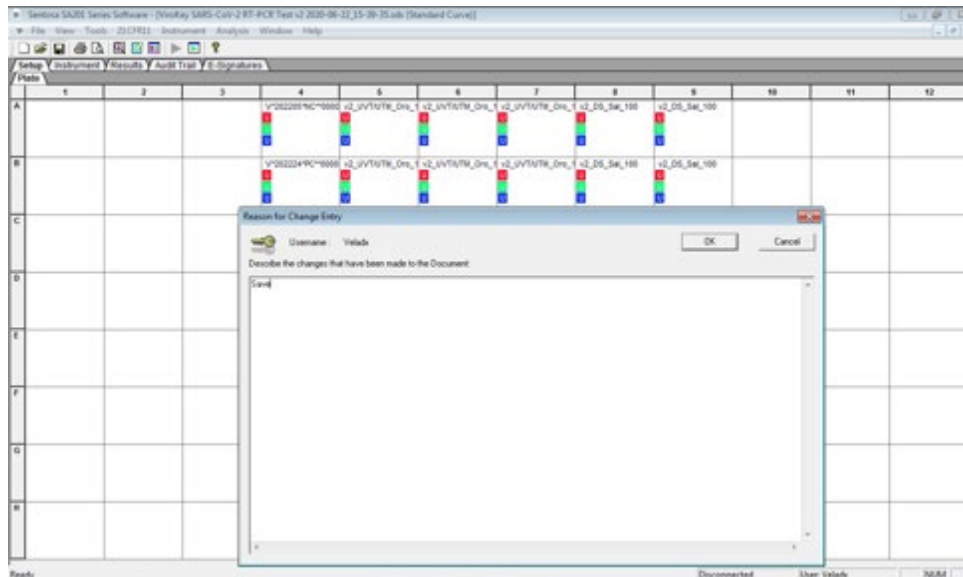


Figure 10. Imported sample set-up file for ViroKey SARS-CoV-2 RT-PCR Test v2.0 ran on Hamilton Microlab STAR instrument.

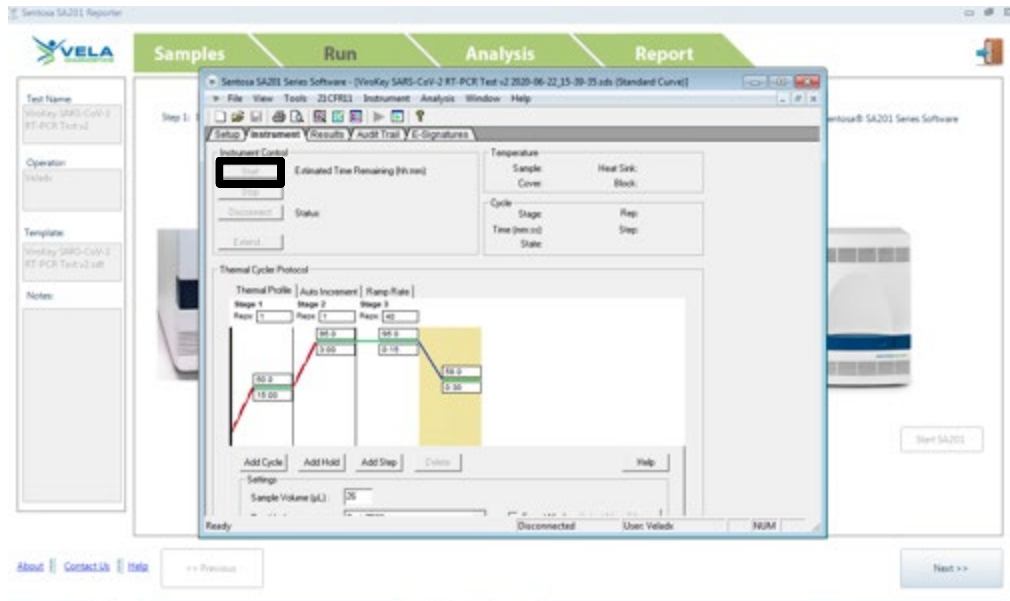
- 7.9.3. Select “File” from the main menu and “Save” from the drop-down list. “Reason for Change Entry” window will be displayed. Describe the changes made in the document or simply enter “Save file” or any other suitable text in the textbox and click “OK” to save the run document (“.sds”) file.

NOTE: DO NOT modify the generated “.sds” file as this will result in an error.

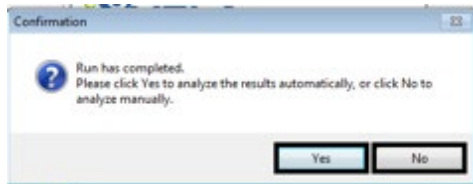


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7.9.4. Select the “Instrument” tab and click “Start” to start the run.



7.10. At the end of the run, a confirmation pop-up window will be displayed indicating that the run has completed. A window will prompt the user if result analysis on the Sentosa SA201 Series Software is to be performed automatically or manually.



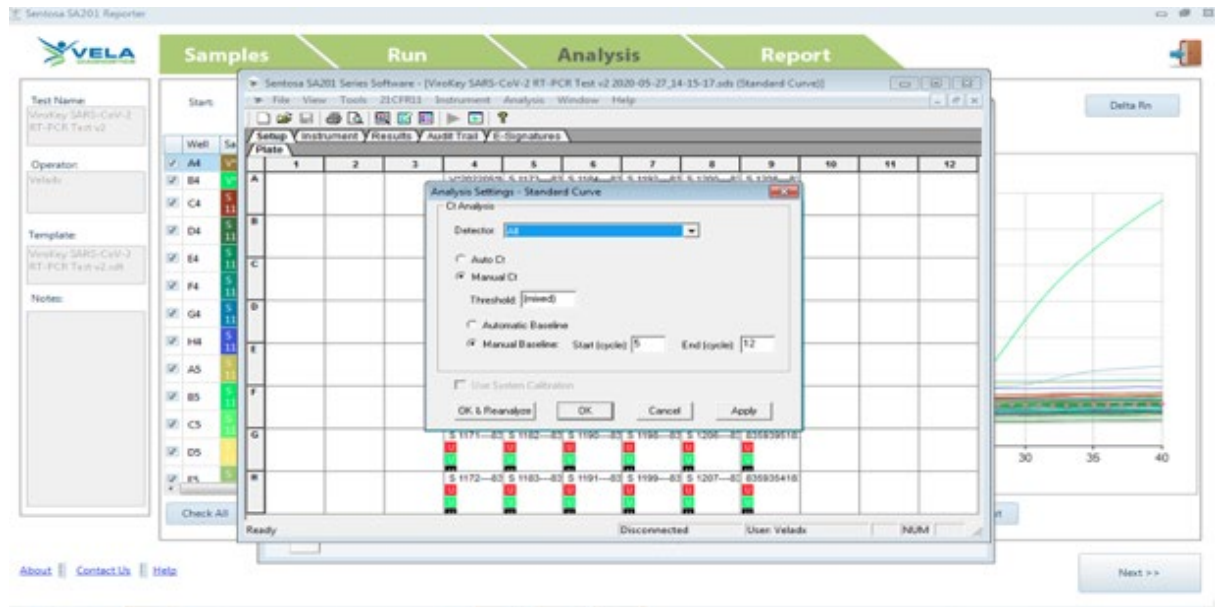
Click “Yes” to perform the result analysis automatically by using preconfigured analysis settings. A pop-up window titled “Analysis in Progress” will be displayed briefly, reminding the user not to perform any other actions.


The pop-up window will disappear when the result analysis has completed successfully. The *Sentosa* SA201 Series Software may now be closed by clicking the close button “” on the title bar. On the *Sentosa* SA201 Reporter, click “Next” to proceed to data analysis.

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7.11. [Optional] In the previous step, click “No” if the user wishes to make changes to preconfigured analysis setting(s) before performing the result analysis. Click “OK” on the pop-up window with the message “The run completed successfully”. Log in to the Sentosa SA201 Series Software if “Idle Timeout re-authentication required” pop-up window is prompted.

On the Sentosa SA201 Series Software, change the analysis setting(s) as necessary. Select “Analysis” from the main menu and “Analyze” from the drop-down list. “Reason for Change Entry” window will be displayed. Enter “Analysis” or any other suitable text in the text box and click “OK” to perform the result analysis.



The Sentosa SA201 Series Software may now be closed by clicking the close button “” on the title bar. On the Sentosa SA201 Reporter, click “Next” to proceed to data analysis.

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8. Automated data analysis on Sentosa SA201 Reporter

Ct values for each channel will be displayed under “Analysis” tab. Click “Next” to switch to “Report” tab to generate report.




Under “Analysis” tab, there are other functions available as described below:

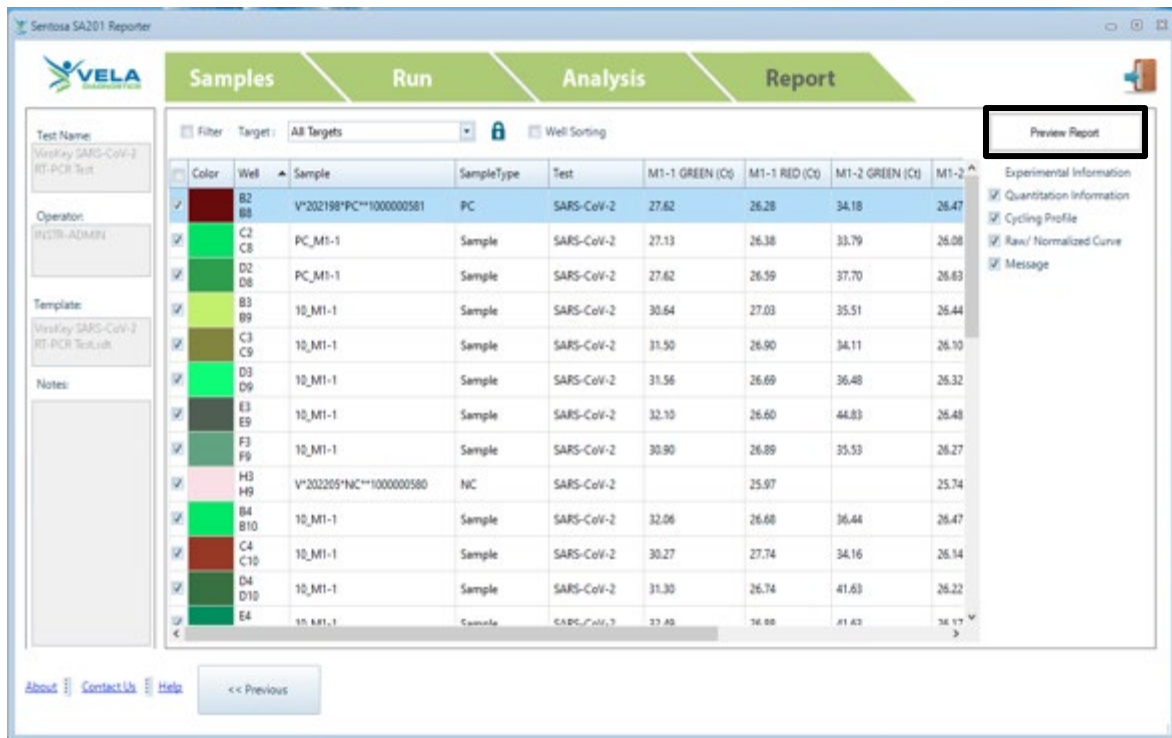
- Delta Rn is the magnitude of the fluorescence signal generated during the PCR at each time point. Delta Rn curve represents the signal processed from the raw data.
- Click “Linear Scale” to display the Y-axis in linear scale.
- Click “Log Scale” to display the Y-axis in log scale.
- Click “Check All” / “Uncheck All” to select / unselect all samples from the list. Only the selected sample curves will be displayed.
- To enlarge a particular area of a sample curve, click “Zoom In” and select the area of interest. Click “Zoom Out” to decrease the magnification of the curve.
- Click “Auto-Scale” to display all selected sample curves automatically to a standard size.

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8.1. Report generation

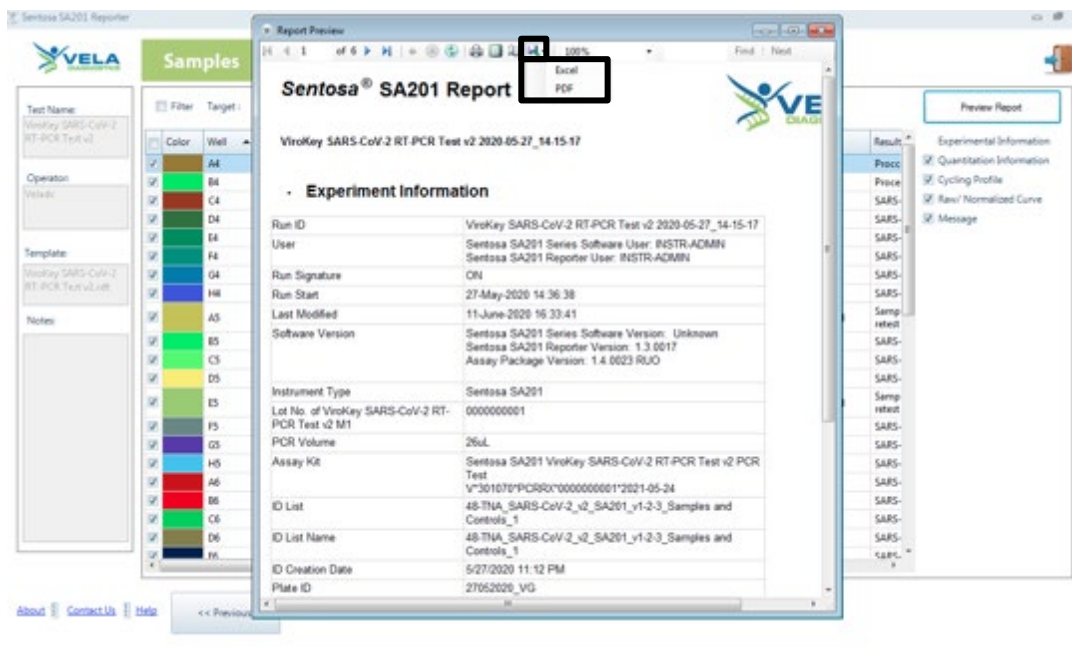
Under “Report” tab, there are other functions available as mentioned below:

- Activate “Filter” checkbox to display the selected samples, or deactivate “Filter” checkbox to hide the selected samples. User can also select individual samples by activating the checkbox for each sample. Only selected samples will be displayed in the report.
- Click “” icon to group the samples with same sample ID. If user selects one sample ID, all the grouped samples will be selected together.
- Activate the checkboxes under “Experimental Information” to allow the user to customize the report.
- Activate “Quantitation Information” checkbox to display assay analysis settings for each fluorescence channel.
- Activate “Cycling Profile” checkbox to display the run parameter settings.
- Activate “Raw / Normalized Curve” checkbox to display both raw and normalized curves for each fluorescence channel.
- Activate “Message” checkbox to display any pre-defined message for the run.
- “Result” column will display the test result of the samples for the run.
- “Validity” column will display the validity of the sample for the run.
- “Fluorescence channels Ct” column will display the Ct value for the samples.
- Click “Preview Report” to preview the report.

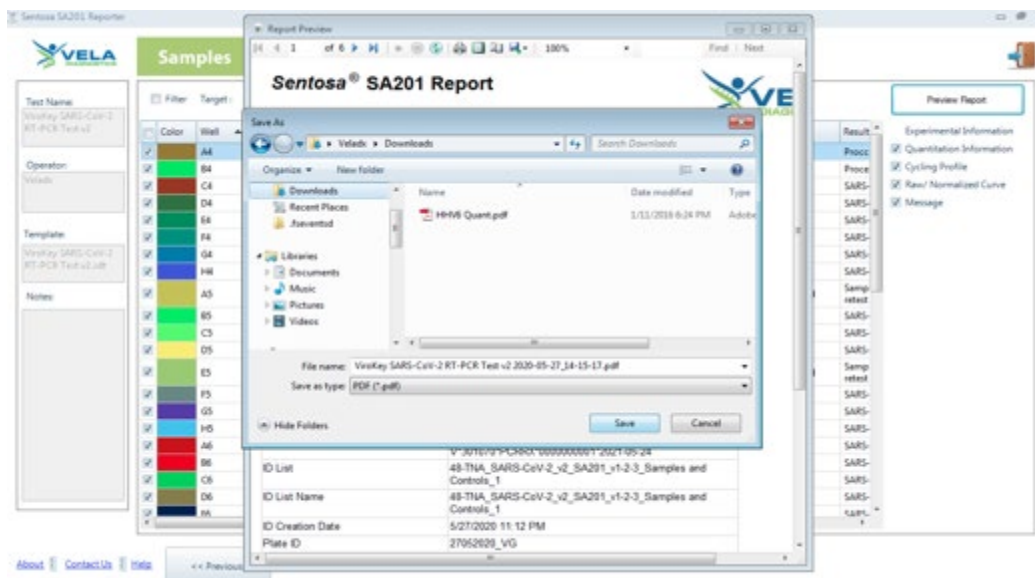


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8.2. The “Report Preview” pop-up window will be displayed. The report can be saved, printed and / or exported to PDF or Excel.



8.3. Click the “” icon and select “PDF”. The “Save As” pop-up window will be displayed. Select a location and click “Save” to save the report.



After the run is completed, proceed to “**Result interpretation**” section on page 13.


RT-PCR and manual data analysis on the Applied Biosystems 7500 Fast Dx Real-Time PCR System

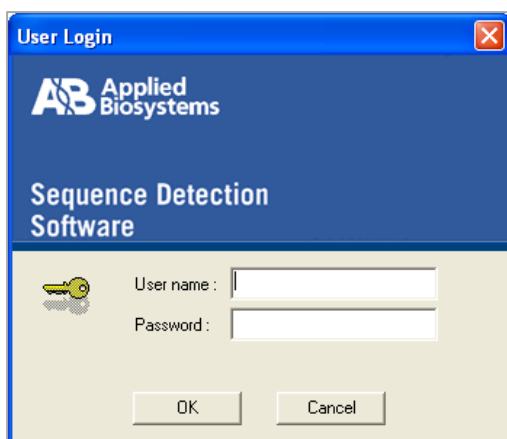
9. *RT-PCR and manual data analysis on the Applied Biosystems 7500 Fast Dx Real-Time PCR System*

- 9.1. Turn on the Applied Biosystems 7500 Fast Dx Real-Time PCR System by pressing the power button on the instrument, and wait for the initiation procedure to be completed.

NOTE: Ensure the green indicator is lit and not flashing.

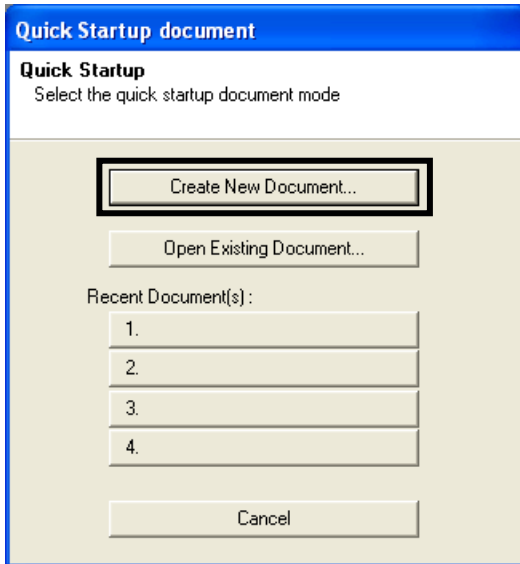


- 9.2. On the instrument's computer, launch the ABI 7500 Fast System SDS Software by double-clicking the  icon. The "Login" window opens, type the account name and password, and then click on "OK".

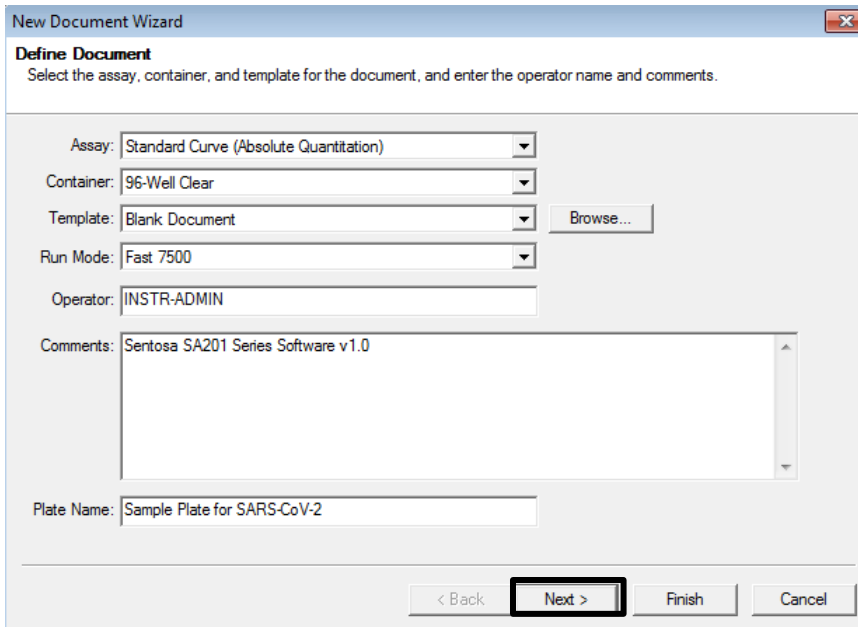


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9.3. In the “Quick Startup document” dialog box, select “Create New Document”.

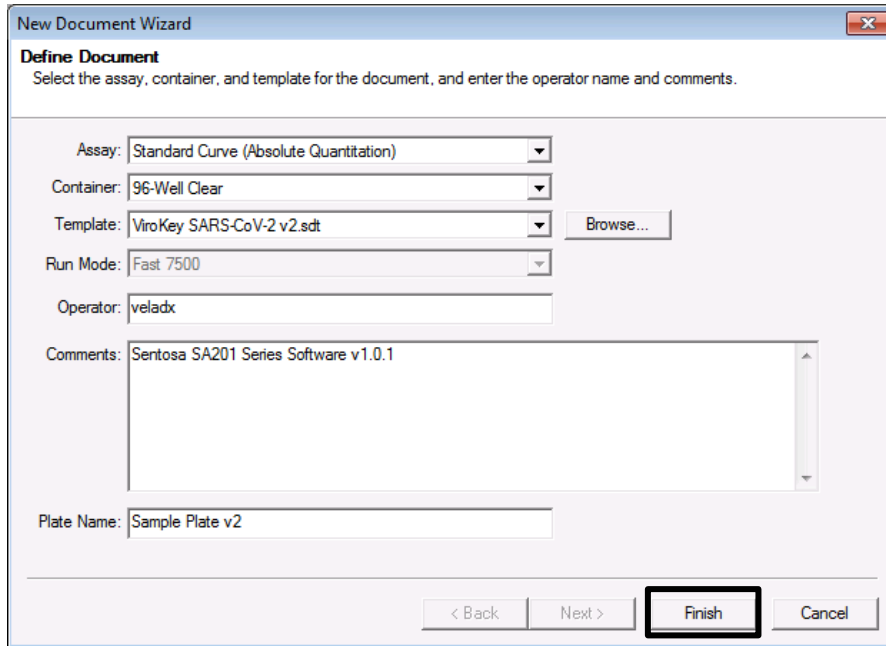


A “New Document Wizard” window appears for “Define Document”. In the “Assay” drop-down list, select “Standard Curve (Absolute Quantitation)”. The default setting for “Container” should be “96-Well Clear”. The default setting for “Template” should be “Blank Document” for the first run. In the “Run Mode” drop-down list, select “Fast 7500”. Enter the name of the operator and the plate in the “Operator” and “Plate Name” fields respectively. Click “Next”.



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If a template was created before, for “*Template*” select “*ViroKey SARS-CoV-2 v2*”. In the “*Run Mode*” drop-down list, select “*Standard 7500*”. Enter the name of the operator and the plate in the “*Operator*” and “*Plate Name*” fields respectively. Click “*Finish*”.



9.4. A “*New Document Wizard*” window appears for “*Select Detectors*”. Click “*New Detector*” to create new “*Green – ORF1a*”, “*Orange – N*” and “*Red - EC*” detectors, if needed, according to the table below:

| Detector Name | Reporter Dye | Quencher Dye |
|---------------|--------------|--------------|
| Green – ORF1a | FAM | (none) |
| Orange – N | VIC* | (none) |
| Red – EC | CY5 | (none) |

*VIC Reporter Dye is used in place of HEX Reporter Dye due to similar excitation and emission wavelength, and the lack of HEX Reporter Dye in the ABI7500 list.

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Select the “Reporter Dye” from the drop-down list. Select the “Quencher Dye” as “None”. Select the “Color” to match the detector. Click “Create Another” to specify new detector “Name”, “Reporter Dye” and “Quencher Dye”. Click “OK” after all detectors are created.

New Detector

Name: Green - ORF1a

Description:

Reporter Dye: FAM

Quencher Dye: (none)

Color: ■

Notes:

Create Another OK Cancel

- 9.5. The “New Document Wizard” window for “Select Detectors” appears. Select the detectors and click “Add”. In the “Passive Reference” drop-down list, select “ROX”. Click “Next”.

New Document Wizard

Select Detectors
Select the detectors you will be using in the document.

Find:

Passive Reference: ROX

| Detector Name | Description | Reporter | Quencher |
|---------------|-------------|----------|----------|
| Green - ORF1a | | FAM | (none) |
| Orange - N | | VIC | (none) |
| Red - EC | | CYS | (none) |

Add >>

<< Remove

Detectors in Document

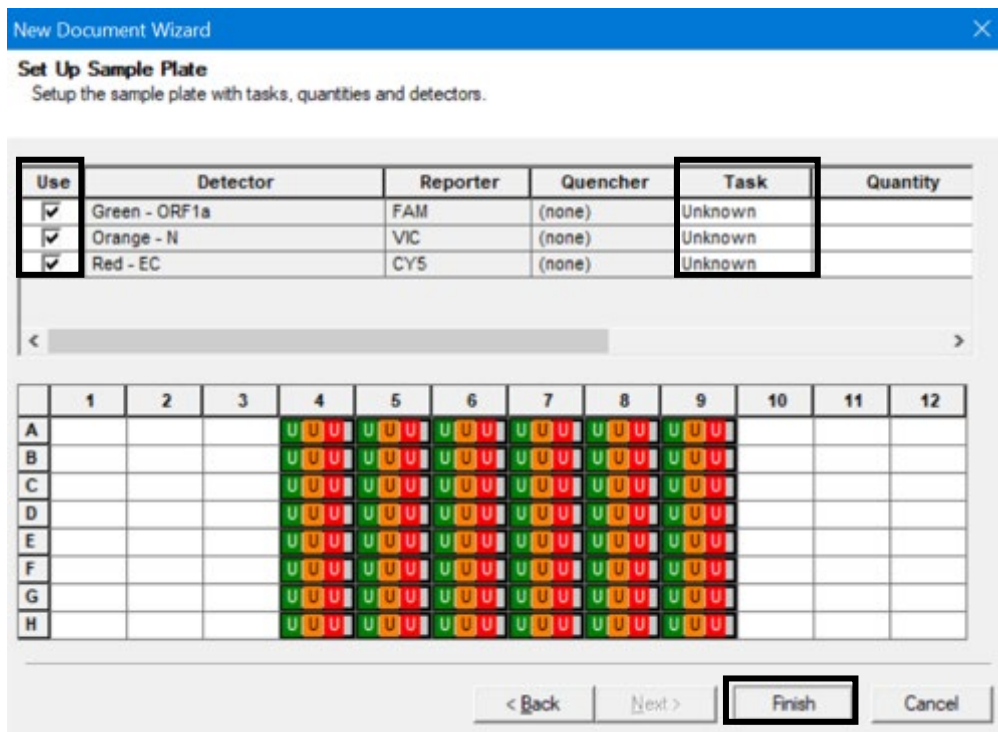
- Green - ORF1a
- Orange - N
- Red - EC

New Detector...

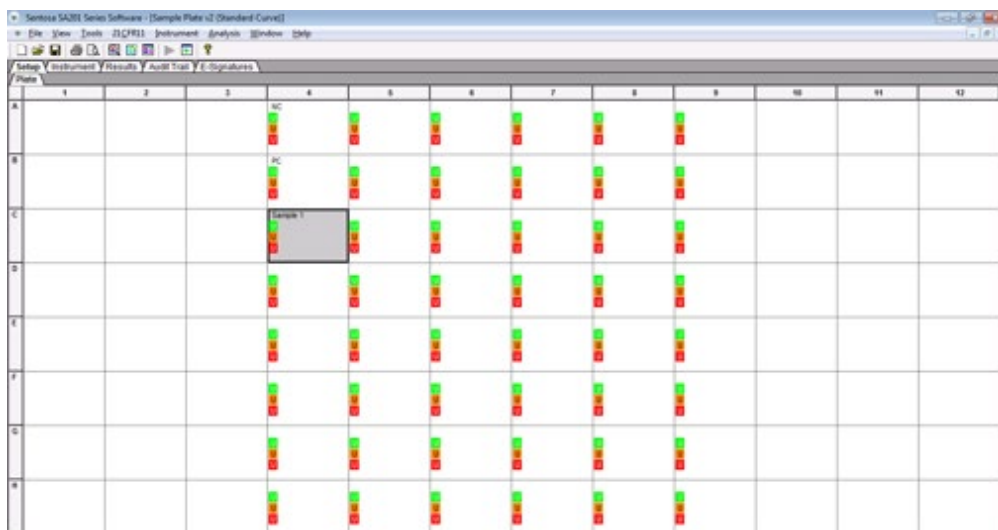
< Back **Next >** Finish Cancel

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- 9.6. A “New Document Wizard” window for “Set Up Sample Plate” appears. Select wells “A4” to “H9” (all wells from columns 4 to 9) and check the “Use” boxes for the detectors. The default setting for “Task” should be “Unknown”. Click “Finish”. The SDS Software will create the plate document.



- 9.7. A window for plate document appears. In the window, select “Setup” tab, and the “Plate” tab should be displayed. Name the wells of the plate by selecting them, then click on “View” menu, followed by “Well Inspector”.



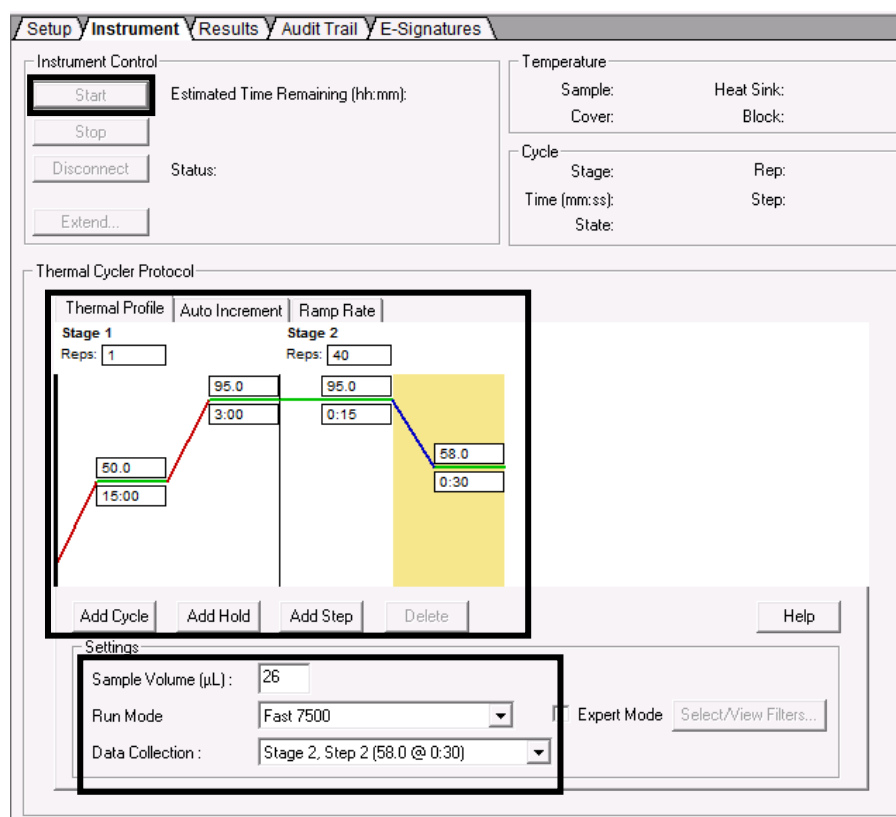
Enter the sample name by typing or barcode entry for each and verify the information of the well(s).

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9.8. The thermal cycling conditions need to be manually specified according to the table below.

| Stage | Reps | Temperature (°C) | Duration (min) |
|-------|------|------------------|----------------|
| 1 | 1 | 50 | 15:00 |
| | | 95 | 3:00 |
| 2 | 40 | 95 | 0:15 |
| | | 58 | 0:30 |

Under the “*Instrument*” tab, enter the thermal cycling condition values in the boxes. Accept the default settings for “*Auto Increment*” and “*Ramp Rate*” for all stages.

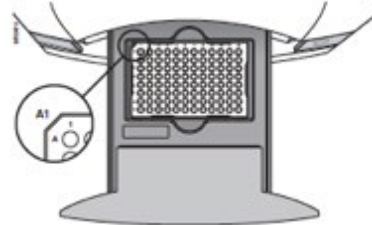


Specify the “*Sample Volume*” as 26 µL. The default setting for “*Run Mode*” should be “*Fast 7500*”. In the “*Data Collection*” drop-down list, select “*Stage 2, Step 2 (58.0 @ 0:30)*”.

9.9. Save the run file in “*sds*” format. The plate document can also be saved as a template document for future use. To do this, save the template file in “*sdt*” format in a preferred folder.

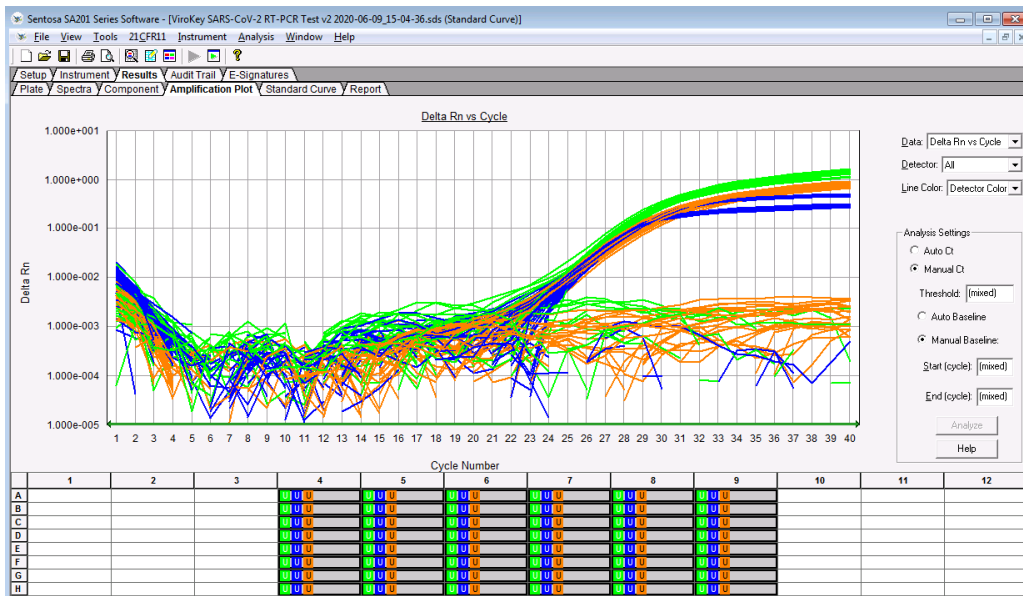
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9.10. At the front of the Applied Biosystems 7500 Fast Dx Real-Time PCR System, push to open the plate holder tray and load the plate into the precision plate holder. Ensure that the plate is properly aligned in the holder.

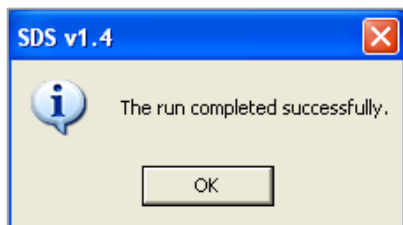


9.11. Under “Instrument Control” on the “Instrument” tab, click “Start”.

9.12. Information on real-time status of the run based on fluorescence emissions is displayed in the “Results” tab, under “Amplification Plot”.



9.13. At the end of the run, a message appears indicating whether or not the run is successful. All data generated is saved in the “.sds” file specified in **step 9.9**.

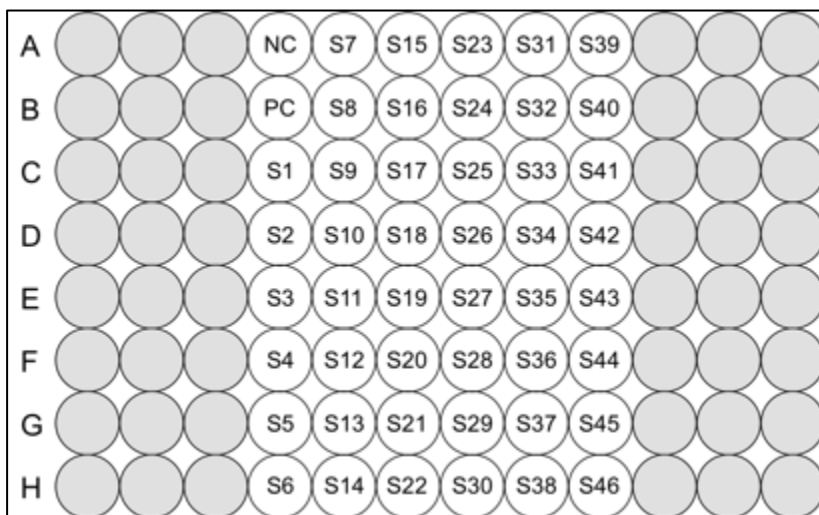


9.14. After the run is completed, proceed to manual data analysis on the Applied Biosystems 7500 Fast Dx Real-Time PCR System (pages 111 to 115).

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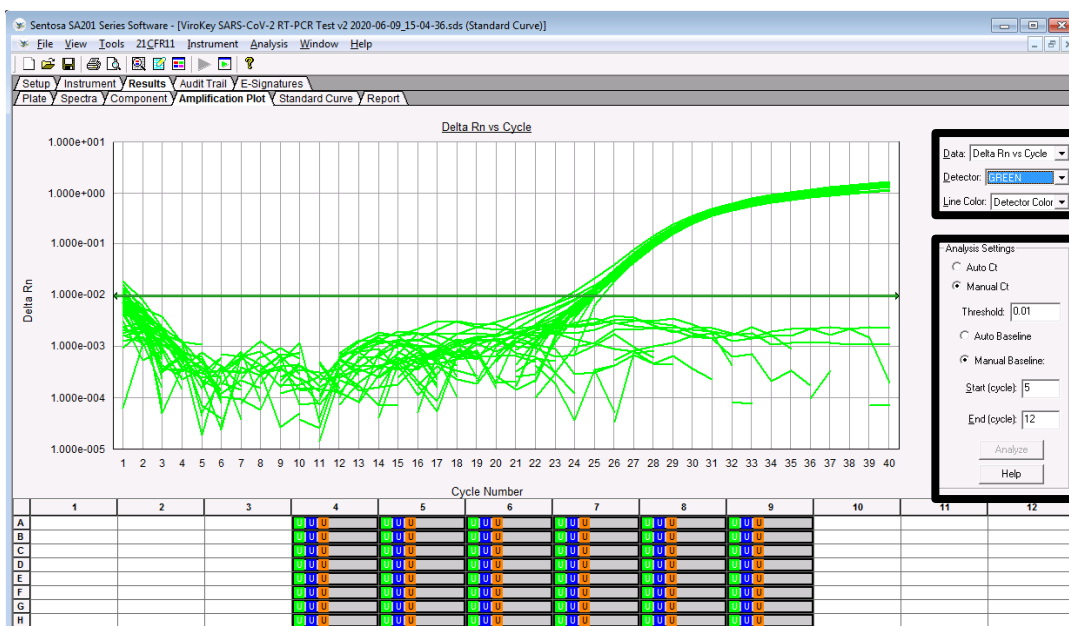
10. Manual data analysis on the Applied Biosystems 7500 Fast Dx Real-Time PCR System

For the automated workflow runs, please refer to the plate layout below and analyze the results accordingly.



NC – Negative control, PC – Positive control, S – Sample

10.1. In the run window, select the “Results” tab, followed by the “Amplification Plot” tab. Select “Delta Rn vs Cycle” in the “Data” drop-down list. In the “Detector” drop-down list, select a detector (“Green – ORF1a”, “Orange – N”, or “Red – EC”).



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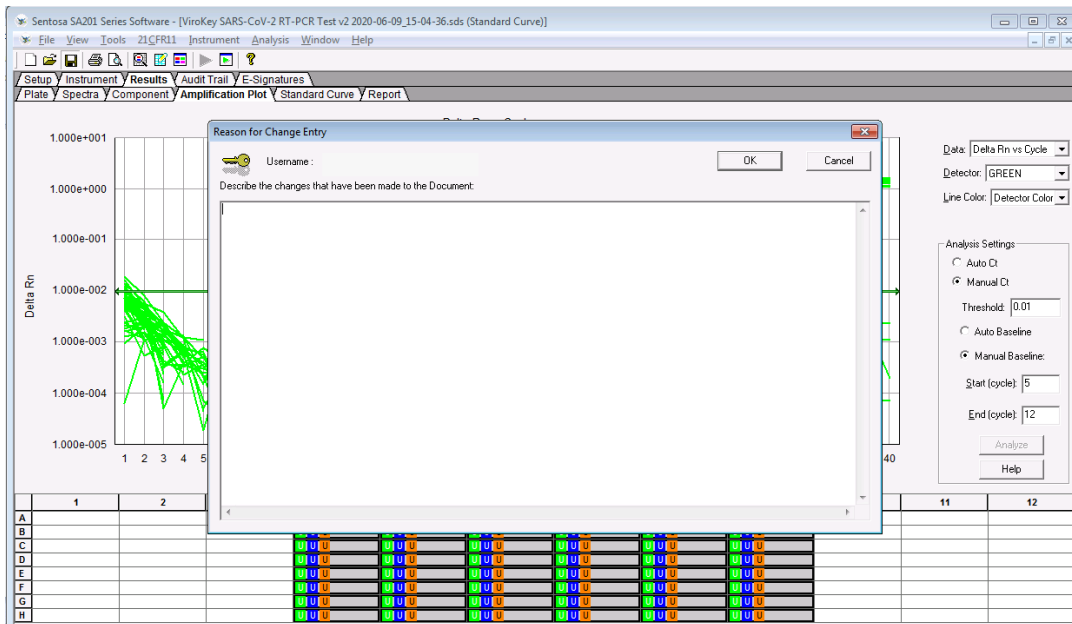
Set the threshold and baseline for the detectors according to the table below:

| Detector | Threshold | Baseline | |
|---------------|-----------|---------------|-------------|
| | | Start (cycle) | End (cycle) |
| Green – ORF1a | 0.01 | 5 | 12 |
| Orange – N | 0.007 | 5 | 12 |
| Red – EC | 0.01 | 5 | 12 |

To set the threshold for the detector, select “Manual Ct” under “Analysis Settings” and enter the value. To set the baseline for the detector, select “Manual Baseline” under “Analysis Settings” and enter the values. Click “Analyze”. After which, the red threshold line turns green.

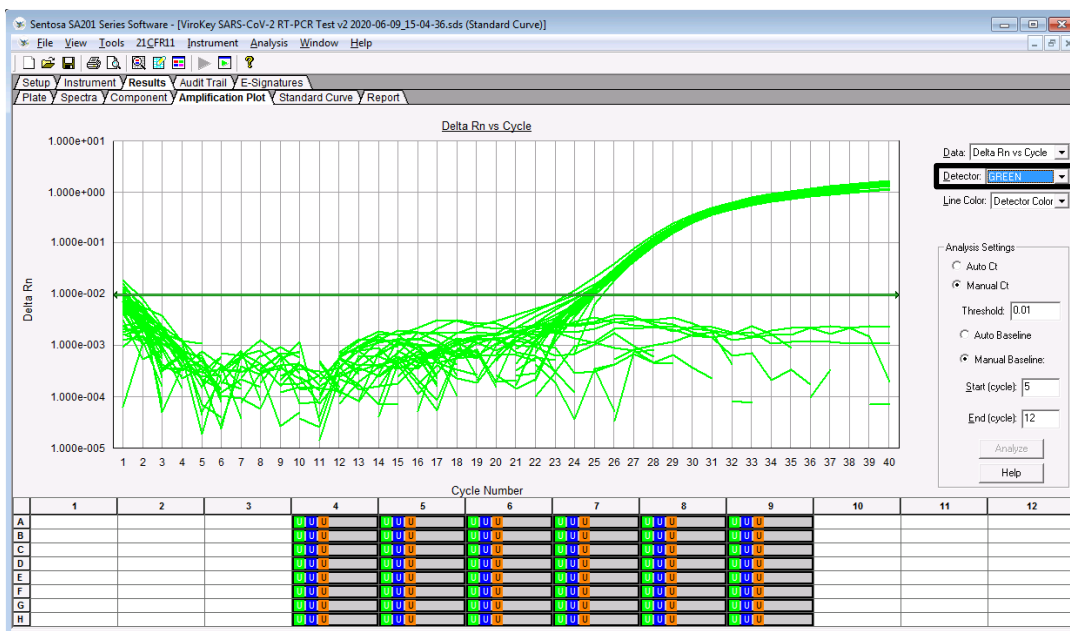
Repeat these steps to set the threshold and baseline values for all detectors.

- 10.2. Select “File” from the main menu and “Save” from the drop-down list. “Reason for Change Entry” window will be displayed. Describe the changes made in the document or simply enter “Save file” or any other suitable text in the textbox and click “OK” to save the run document (“.sds”) file.

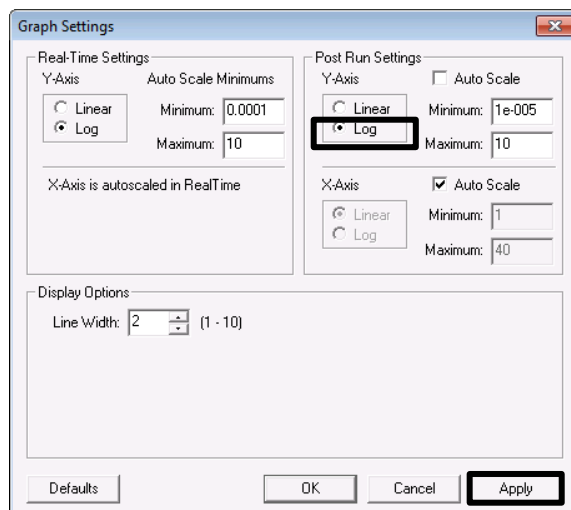


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10.3. To generate graphs for specific samples or target channel, select the corresponding sample wells at the bottom of the window, then choose the desired target channel from the “Detector” drop-down list. Select “GREEN” for the analysis of the SARS-CoV-2 target *ORF1a*, “ORANGE” for the analysis of the SARS-CoV-2 target *N*, and “RED” for the analysis of the extraction control.

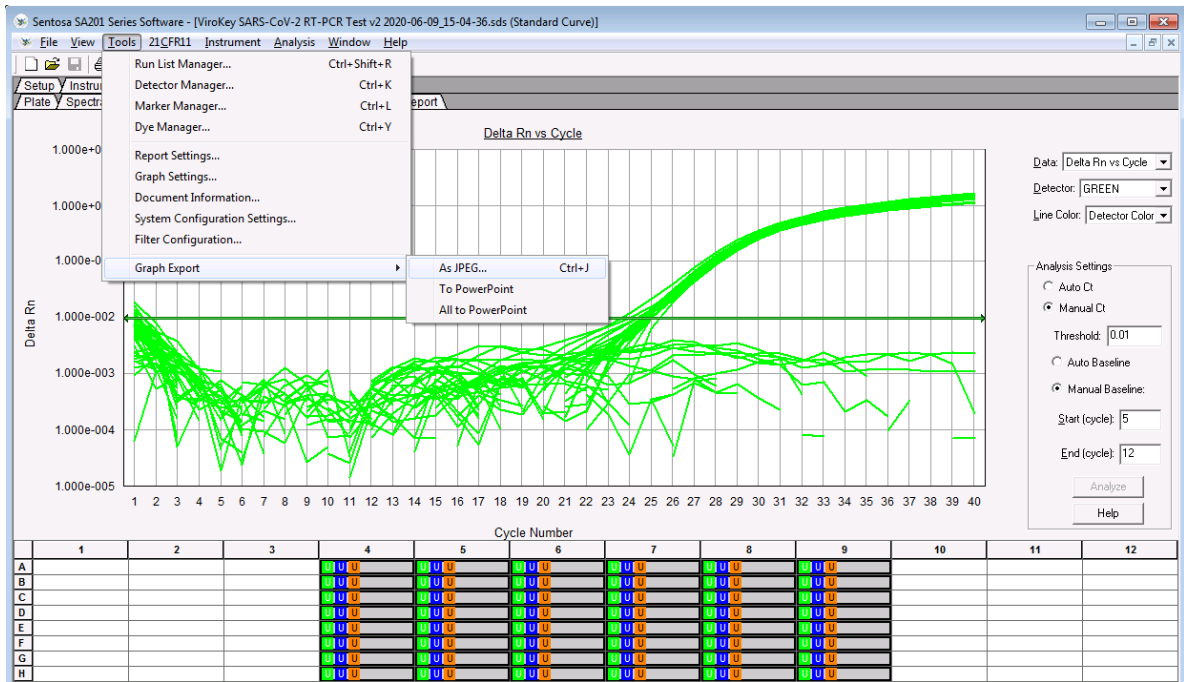


Right click on the graph to select “Graph setting”. In “Post Run setting” category, choose “Log” for Y-axis. Click “Apply”.

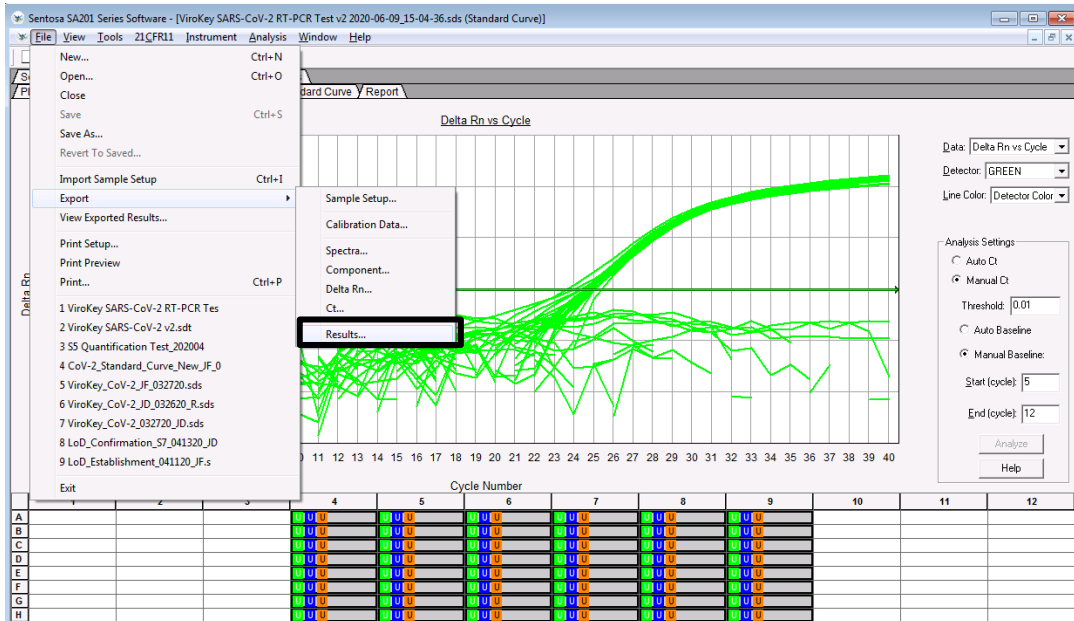


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10.4. To export the graphs for the run, select “Tools” menu -> “Graph Export”, then choose the desired format to export the graph in.

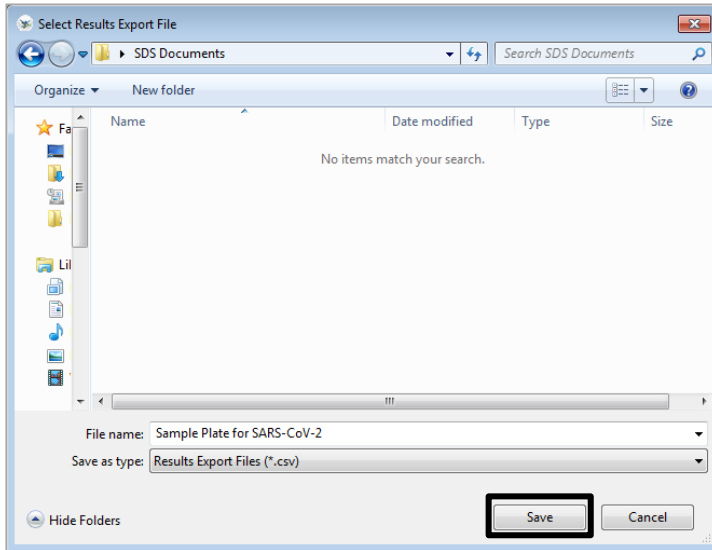


10.5. To export results, save the “.sds” file first. Select “File” menu -> “Export”, then choose the desired information to export.



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10.6. The “*Select Results Export*” pop-up window appears. Accept the default setting for “*Save as type*”. Navigate to the desired folder and enter the name of the result export file (“.csv”). Click “*Save*”.



After the run is completed, proceed to “**Result interpretation**” section on page 13.

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Instrument maintenance

After every run, discard used sample tubes, plates, reagents and tips according to the local safety regulations. All samples and waste should be considered potentially infectious.

A reservoir collects liquid waste generated during the nucleic acid extraction procedure. Dispose the liquid waste according to the local safety and environment regulations. Dispose the biohazard bags after each run.

Perform regular cleaning of the instruments *Sentosa* SX101, Thermo Fisher KingFisher Flex, Hamilton Microlab STAR, and *Sentosa* SA201 after each run. Refer to the respective instrument IFUs or maintenance videos for detailed procedures.

Ensure that maintenance is performed regularly to minimize the risk of error.

Always wear the appropriate personal protective equipment (PPE: lab coat, gloves, goggles, mask) during cleaning / maintenance procedures.

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Troubleshooting guide

The troubleshooting guide may be helpful in solving any problems that may arise. For more information, please contact the authorized Vela Diagnostics representative. Vela Diagnostics Service and Support is always ready to answer any questions about the information and protocols in this IFU or sample and assay technologies (for contact information, refer to the back cover).

Comments and recommended actions

1. General handling

- | | |
|--|--|
| a) Error message displayed on the screen | When an error message is displayed during a protocol run, please refer to the instrument IFUs. |
|--|--|

2. Precipitates in the reagents of the ViroKey SX Virus Total Nucleic Acid Kit (4x48) / ViroKey HT Virus Total Nucleic Acid Kit (4x96)

- | | |
|------------------------|--|
| a) Storage of reagents | Reagents might precipitate upon storage. If required, shake vigorously to dissolve the precipitates. |
|------------------------|--|

3. Consistent high Ct values observed for samples

- | | |
|--|--|
| a) Magnetic beads were not completely re-suspended | Mag (magnetic beads) requires thorough vortexing before use to ensure proper resuspension. |
|--|--|

- | | |
|---|--|
| b) Frozen samples were not mixed properly after thawing | Thaw frozen samples with mild agitation to ensure thorough mixing. |
|---|--|

- | | |
|---------------------------|--|
| c) Degraded nucleic acids | Ensure that samples are stored correctly and not subjected to multiple freeze-thaw cycles. Repeat the extraction procedure with new samples. |
|---------------------------|--|

- | | |
|----------------------------|---|
| d) Incomplete sample lysis | Ensure that Buffer D1 (lysis buffer) does not contain precipitates. If required, shake vigorously to dissolve the precipitates. |
|----------------------------|---|

- | | |
|---|--|
| e) Clogging of pipette tip due to insoluble material in the samples | Insoluble material was not removed from the sample prior to starting the extraction procedure on the <i>Sentosa</i> SX101 instrument. To remove insoluble material, centrifuge the diluted sample suspension at 3,000 x g for 1 minute, and transfer the supernatant to a fresh sample tube. |
|---|--|

4. No signal with positive control (PC) in the Green, Orange or Red fluorescence channels

- | | |
|---|--|
| a) PCR conditions do not comply with the protocol | Ensure that the correct thermal cycling conditions are input into the <i>Sentosa</i> SA201 Series Software or ABI 7500 Fast System SDS Software. |
|---|--|
-

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Comments and recommended actions

Comments and recommended actions

-
- | | |
|---|---|
| b) Incorrect PCR configuration | Ensure that the correct thermal cycling conditions are input into the <i>Sentosa</i> SA201 Series Software Software or ABI 7500 Fast System SDS Software. |
| c) Storage conditions for one or more components did not comply with the instructions given in the “ Storage ” section | Check the storage condition (refer to the kit label) of the reagents and use a new kit, if necessary. |
| d) Extraction / assay kit has expired | Check the expiration date (refer to the kit label) of the reagents and use a new kit, if necessary. |
| e) Incorrect passive reference setting | Check the passive reference setting is set correctly to ROX in the well inspector and reanalyze. |
-

5. Weak or no signal of the extraction control (EC) in the Red fluorescence channel subjected to extraction using the ViroKey SX Virus Total Nucleic Acid Kit (4x48) / ViroKey HT Virus Total Nucleic Acid Kit (4x96)

- | | |
|---|---|
| a) PCR conditions do not comply with the protocol | Ensure that the correct thermal cycling conditions are input into the <i>Sentosa</i> SA201 Series Software Software or ABI 7500 Fast System SDS Software. For PCR configuration, please refer to Section 4 of the troubleshooting guide . |
| b) PCR inhibition | Dilute the extraction eluent 10 times and repeat the PCR. Collect new sample and repeat the workflow. |
| c) EC is not added into the sample | Ensure that EC was added during the sample pre-treatment and lysis steps. |
| d) Loss of nucleic acid during extraction | No signal of the extraction control may indicate the loss of nucleic acid during the extraction. Ensure the correct SX101 application is used and follow the instructions closely. Refer to Section 3 of the troubleshooting guide . |
| e) Storage conditions for one or more kit components did not comply with the instructions given in the “ Storage ” section | Check the storage condition (refer to the kit label) of the reagents and use a new kit if necessary. |
-

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Comments and recommended actions

Comments and recommended actions

-
- | | |
|---------------------------------------|--|
| f) Extraction / assay kit has expired | Check the expiration date (refer to the kit label) of the reagents and use a new kit if necessary. |
|---------------------------------------|--|

6. Signals with the negative control in the Green and Orange fluorescence channels of the analytical PCR

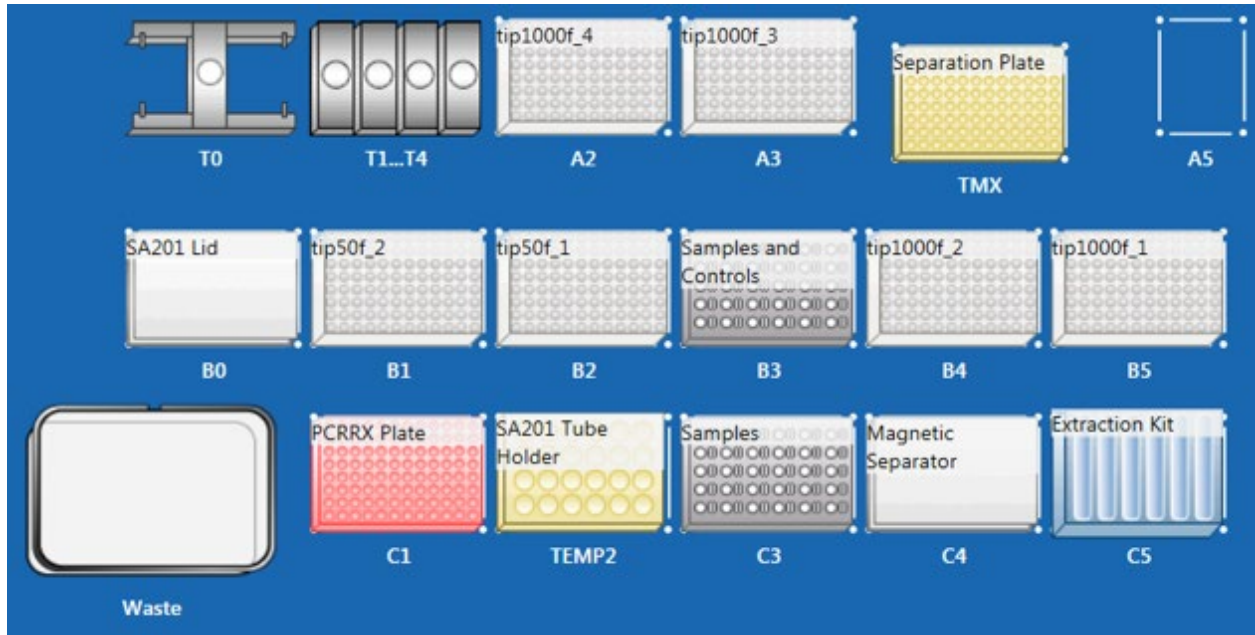
- | | |
|--|---|
| a) Contamination occurred during extraction / PCR set-up | Repeat the extraction and PCR protocols with new reagents. Ensure that the workspace and instruments are decontaminated as recommended. First check the Rn for true amplification profile and rule out baseline issues. |
| b) Baseline issue | Check the raw (Rn) signal of the green channel of the NC. Sudden jumps in baseline can become false positive call in the dRn. |
-

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Appendix for ViroKey SARS-CoV-2 RT-PCR Test v2.0 on Sentosa SX101 and KingFisher Flex

Appendix A: Sentosa SX101 layout for “48-1 ViroKey SARS-CoV-2-v2 v3-3” application

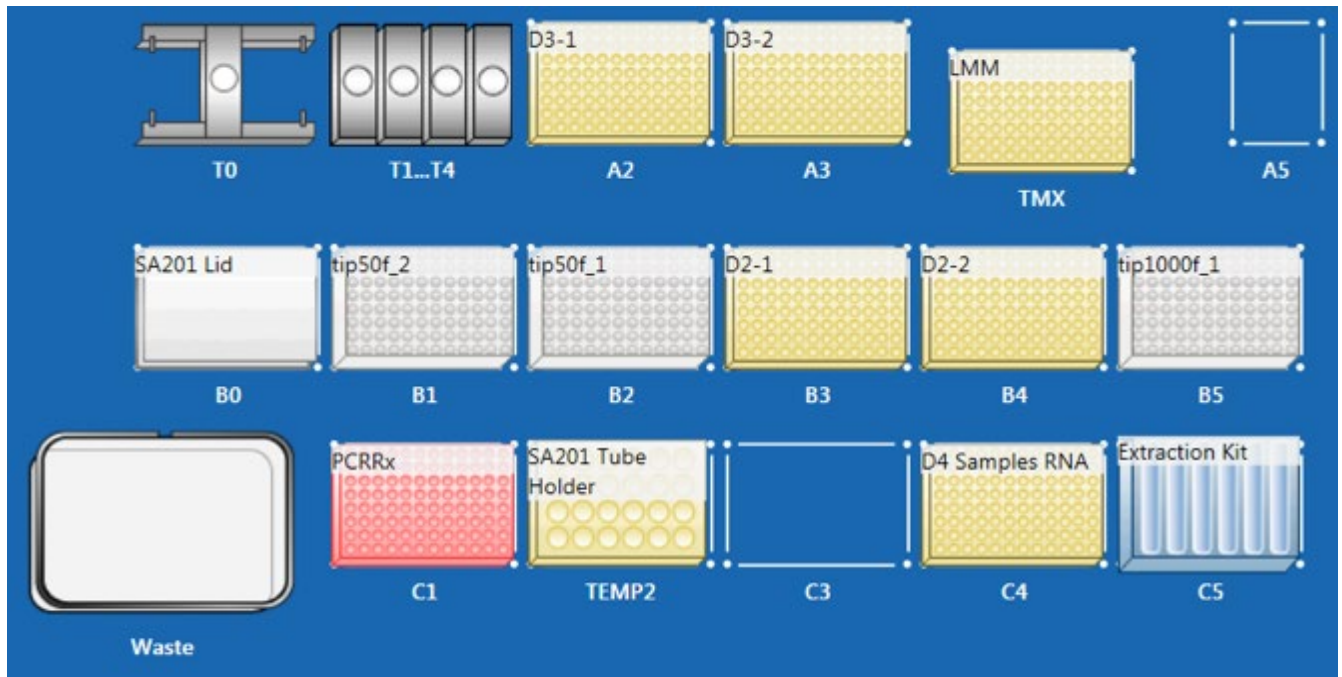


| Position | Labware |
|-----------|--|
| T0 | Sentosa SX Gripper |
| T1 to T4 | Sentosa SX Dispensing Tools |
| A2 | Sentosa SX Non-Partition 1000 μ L Filter Tips |
| A3 | Sentosa SX Non-Partition 1000 μ L Filter Tips |
| TMX | Sentosa SX Deepwell Plate 96/2000 μ L |
| A5 | Empty |
| B0 | SA201 Lid |
| B1 | Sentosa SX Non-Partition 50 μ L Filter Tips |
| B2 | Sentosa SX Non-Partition 50 μ L Filter Tips |
| B3 and C3 | Sentosa SX Rack 0.5 + Adaptor / 1.5 / 2.0 mL |
| B4 | Sentosa SX Non-Partition 1000 μ L Filter Tips |
| B5 | Sentosa SX Non-Partition 1000 μ L Filter Tips |
| C1 | MicroAmp Fast Optical 96-Well Reaction Plate, 0.1 mL |
| TEMP2 | Sentosa SA201 Tube Holder Rack |
| C4 | Sentosa SX Magnetic Separator |
| C5 | Sentosa SX Reservoir Rack 7 |

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Appendix B: Sentosa SX101 layout for “96-1_ViroKey-KF SARS-CoV-2-v2_v3-2” application

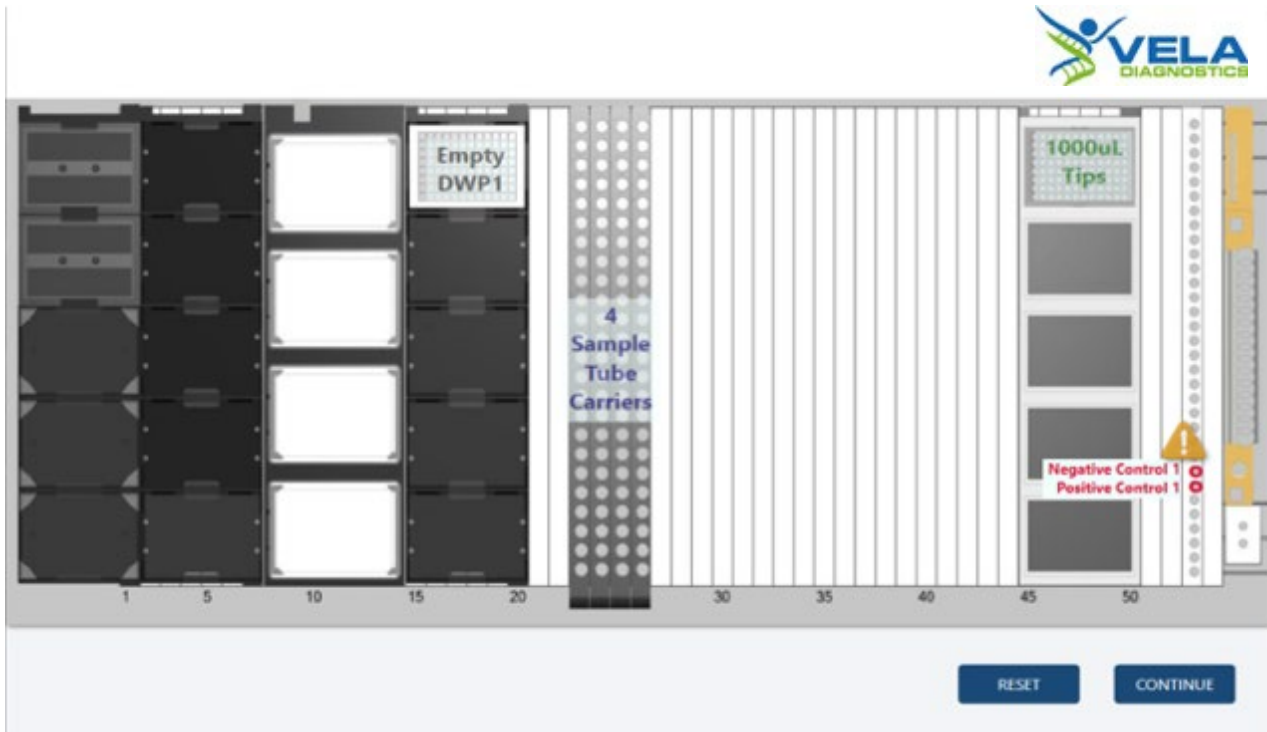


| Position | Labware |
|----------|--|
| T0 | Sentosa SX Gripper |
| T1 to T4 | Sentosa SX Dispensing Tools |
| A2 | KingFisher 96-Deepwell Plate |
| A3 | KingFisher 96-Deepwell Plate |
| TMX | KingFisher 96-Deepwell Plate |
| A5 | Empty |
| B0 | SA201 Lid |
| B1 | Sentosa SX Non-Partition 50 µL Filter Tips |
| B2 | Sentosa SX Non-Partition 50 µL Filter Tips |
| B3 | KingFisher 96-Deepwell Plate |
| B4 | KingFisher 96-Deepwell Plate |
| B5 | Sentosa SX Non-Partition 1000 µL Filter Tips |
| C1 | MicroAmp Fast Optical 96-Well Reaction Plate, 0.1 mL |
| TEMP2 | Sentosa SA201 Tube Holder Rack |
| C3 | Empty |
| C4 | KingFisher 96-Deepwell Plate |
| C5 | Sentosa SX Reservoir Rack 7 |

Appendix for ViroKey SARS-CoV-2 RT-PCR Test v2.0 on Hamilton Microlab STAR

Appendix C: Sample Plate Preparation

C.1. Layout of the Hamilton Microlab STAR platform for sample plate preparation (with 1 deepwell plate) using “STAR8AL96 Vela_SampleTransfer_V1.2.med” application

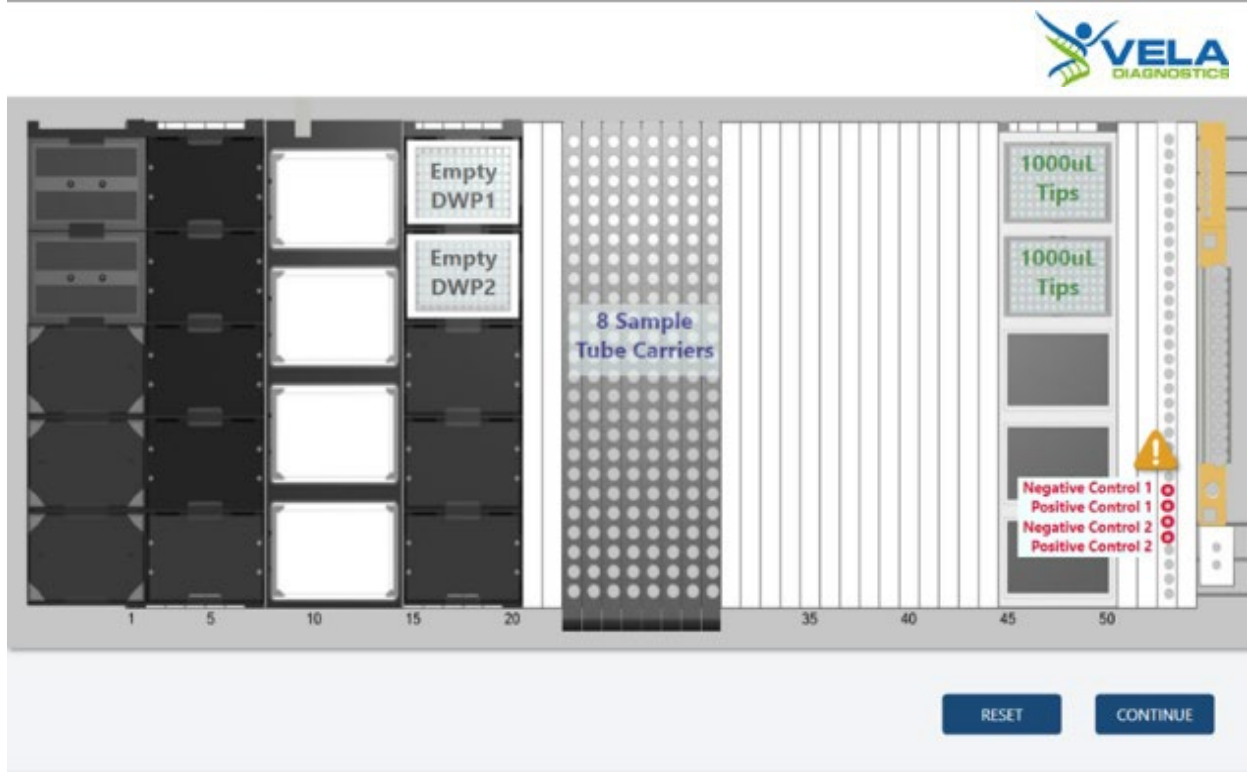


| Track(s) | Description |
|----------|---------------------------------------|
| 1 | Empty |
| 2 to 7 | Empty |
| 8 to 14 | Empty |
| 15 to 20 | HT U Deepwell Plate, Barcoded, 2.2 mL |
| 23 to 26 | 4 Sample Tube Carriers |
| 45 to 50 | HT Conductive 1 mL Filter Tips (96) |
| 53 | NC and PC (Positions 25 and 26) |

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C.2. Layout of the Hamilton Microlab STAR platform for sample plate preparation (with 2 deepwell plates) using “STAR8AL96 Vela_SampleTransfer_V1.2.med” application

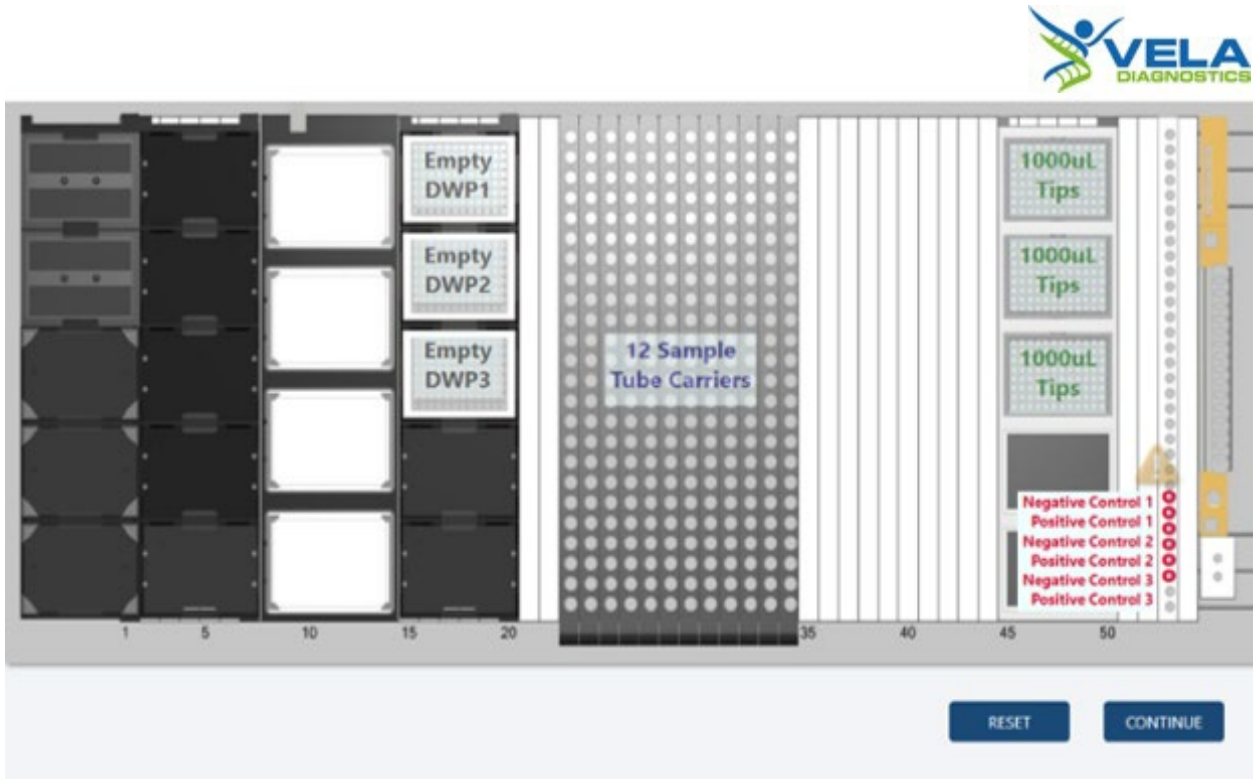


| Track(s) | Description |
|----------|--|
| 1 | Empty |
| 2 to 7 | Empty |
| 8 to 14 | Empty |
| 15 to 20 | 2x HT U Deepwell Plate, Barcoded, 2.2 mL |
| 23 to 30 | 8 Sample Tube Carriers |
| 45 to 50 | HT Conductive 1 mL Filter Tips (2x96) |
| 53 | 2x NC and 2x PC (Positions 25 to 28) |

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C.3. Layout of the Hamilton Microlab STAR platform for sample plate preparation (with 3 deepwell plates) using “STAR8AL96 Vela_SampleTransfer_V1.2.med” application

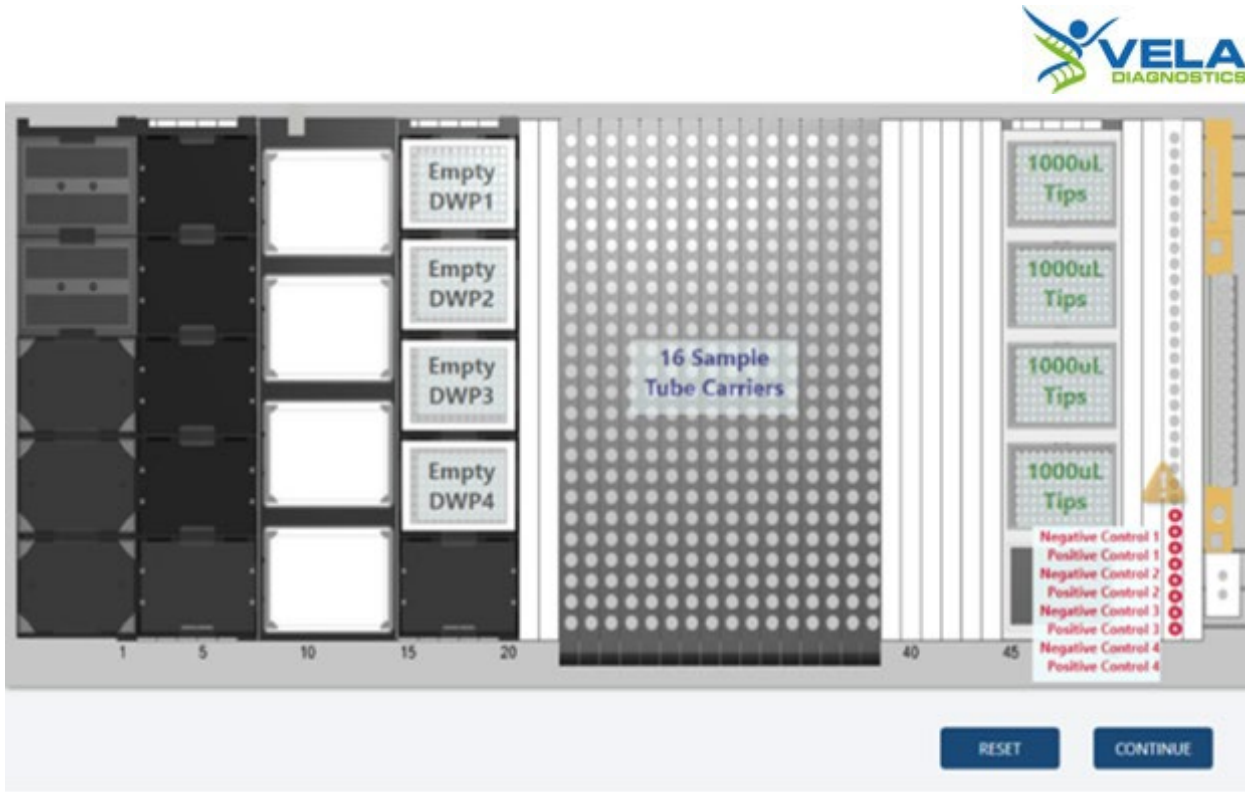


| Track(s) | Description |
|----------|--|
| 1 | Empty |
| 2 to 7 | Empty |
| 8 to 14 | Empty |
| 15 to 20 | 3x HT U Deepwell Plate, Barcoded, 2.2 mL |
| 23 to 34 | 12 Sample Tube Carriers |
| 45 to 50 | HT Conductive 1 mL Filter Tips (3x96) |
| 53 | 3x NC and 3x PC (Positions 25 to 30) |

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C.4. Layout of the Hamilton Microlab STAR platform for sample plate preparation (with 4 deepwell plates) using “STAR8AL96 Vela_SampleTransfer_V1.2.med” application



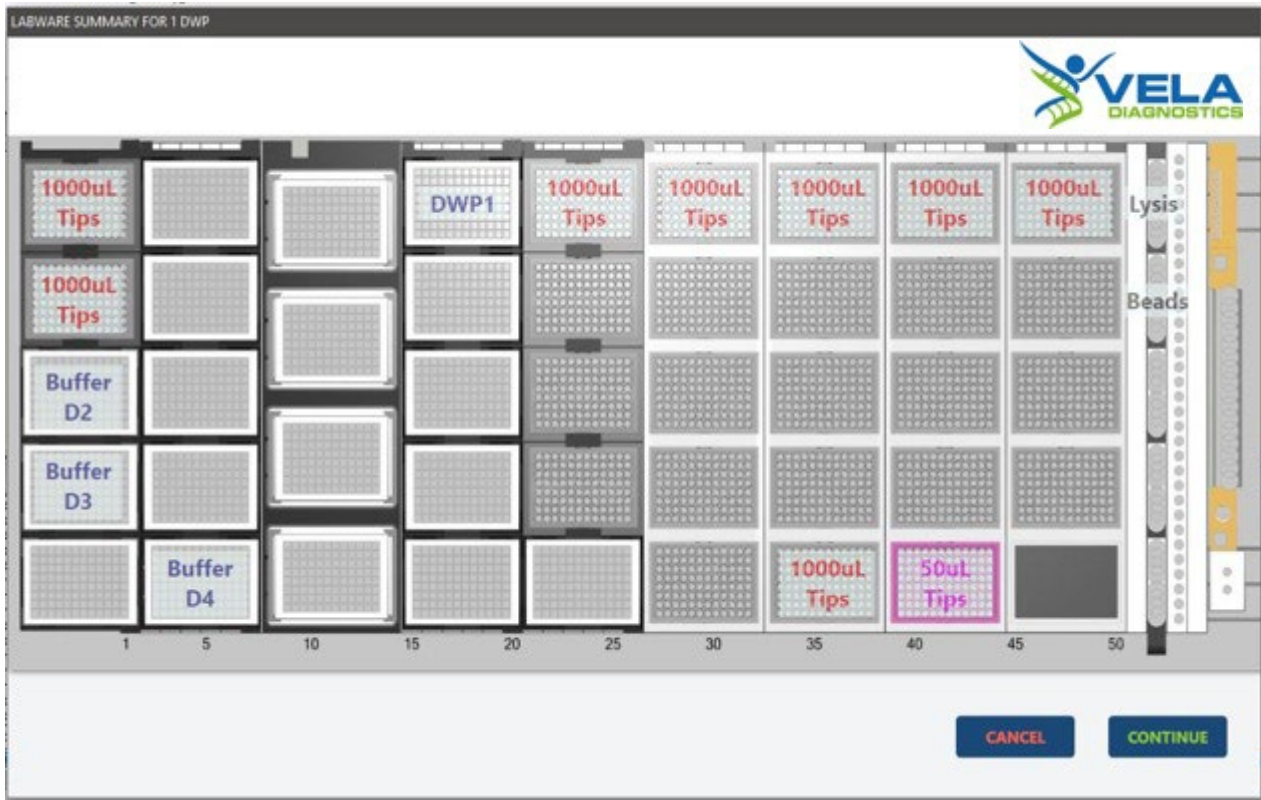
| Track(s) | Description |
|----------|--|
| 1 | Empty |
| 2 to 7 | Empty |
| 8 to 14 | Empty |
| 15 to 20 | 4x HT U Deepwell Plate, Barcoded, 2.2 mL |
| 23 to 38 | 16 Sample Tube Carriers |
| 45 to 50 | HT Conductive 1 mL Filter Tips (4x96) |
| 53 | 4x NC and 4x PC (Positions 25 to 32) |

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Appendix D: Viral RNA Extraction

D.1. Layout of the Hamilton Microlab STAR platform for viral RNA extraction (with 1 deepwell plate) using “STAR8AL96 Vela_ViroKey_V3.10.med” application

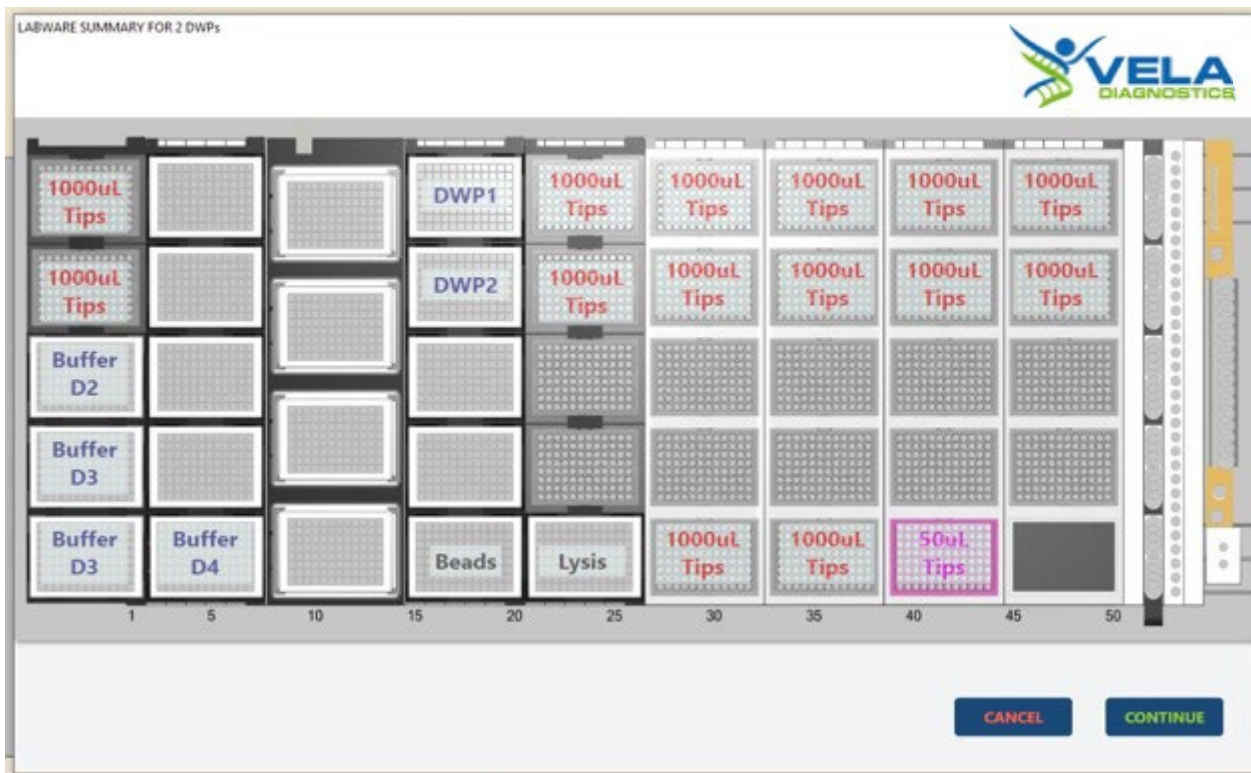


| Track(s) | Description |
|----------|---|
| 1 | <ul style="list-style-type: none"> HT Conductive 1 mL Filter Tips (2x96) 2x HT 300 mL Reservoir |
| 2 to 7 | HT 300 mL Reservoir |
| 8 to 14 | Empty |
| 15 to 20 | HT U Deepwell Plate, Barcoded, 2.2 mL |
| 21 to 26 | HT Conductive 1 mL Filter Tips (96) |
| 27 to 32 | HT Conductive 1 mL Filter Tips (96) |
| 33 to 38 | HT Conductive 1 mL Filter Tips (2x96) |
| 39 to 44 | <ul style="list-style-type: none"> HT Conductive 1 mL Filter Tips (96) HT Conductive 50 µL Filter Tips (96) |
| 45 to 50 | HT Conductive 1 mL Filter Tips (96) |
| 52 | 2x HT Reagent Tub with Lid, 60 mL |

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D.2. Layout of the Hamilton Microlab STAR platform for viral RNA extraction (with 2 deepwell plates) using “STAR8AL96 Vela_ViroKey_V3.10.med” application

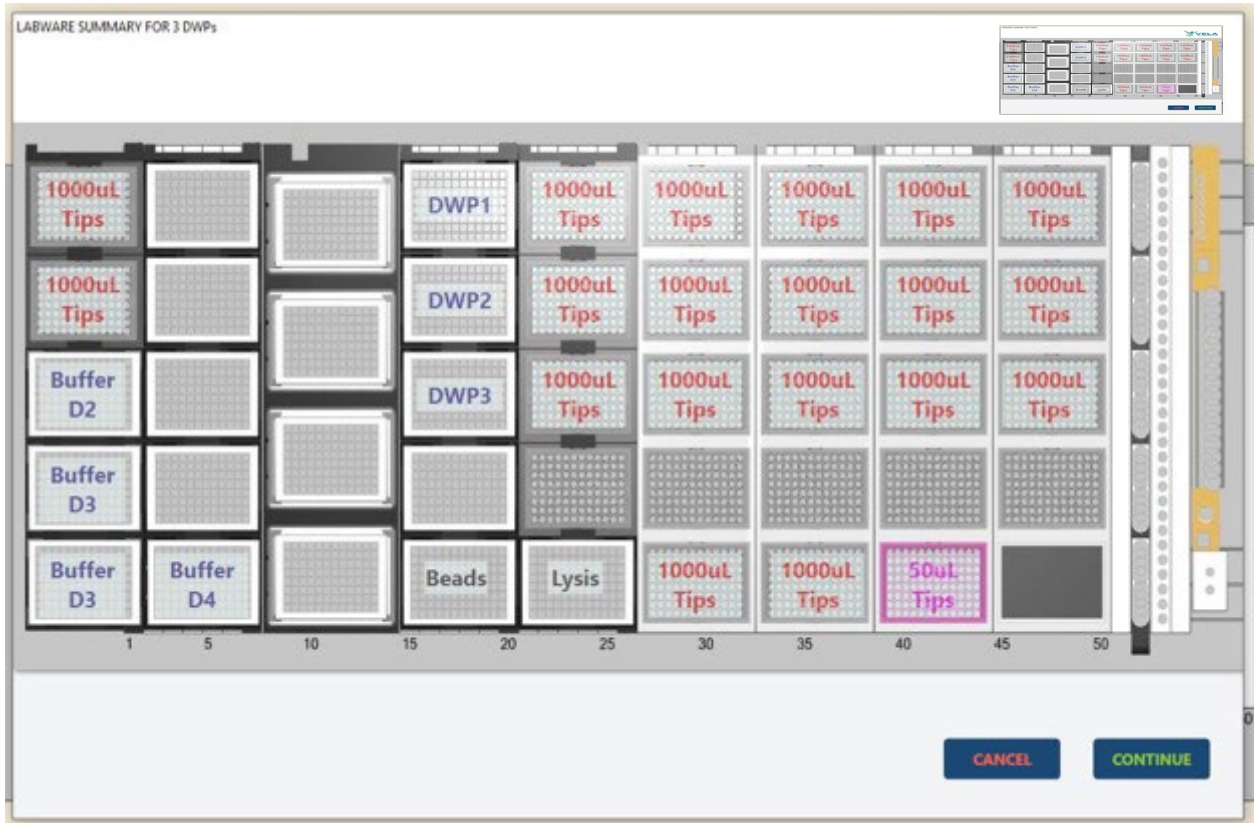


| Track(s) | Description |
|----------|---|
| 1 | <ul style="list-style-type: none"> HT Conductive 1 mL Filter Tips (2x96) 3x HT 300 mL Reservoir |
| 2 to 7 | HT 300 mL Reservoir |
| 8 to 14 | Empty |
| 15 to 20 | <ul style="list-style-type: none"> 2x HT U Deepwell Plate, Barcoded, 2.2 mL HT 300 mL Reservoir |
| 21 to 26 | <ul style="list-style-type: none"> HT Conductive 1 mL Filter Tips (2x96) HT 300 mL Reservoir |
| 27 to 32 | HT Conductive 1 mL Filter Tips (3x96) |
| 33 to 38 | HT Conductive 1 mL Filter Tips (3x96) |
| 39 to 44 | <ul style="list-style-type: none"> HT Conductive 1 mL Filter Tips (2x96) HT Conductive 50 µL Filter Tips (96) |
| 45 to 50 | HT Conductive 1 mL Filter Tips (2x96) |

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D.3. Layout of the Hamilton Microlab STAR platform for viral RNA extraction (with 3 deepwell plates) using “STAR8AL96 Vela_ViroKey_V3.10.med” application

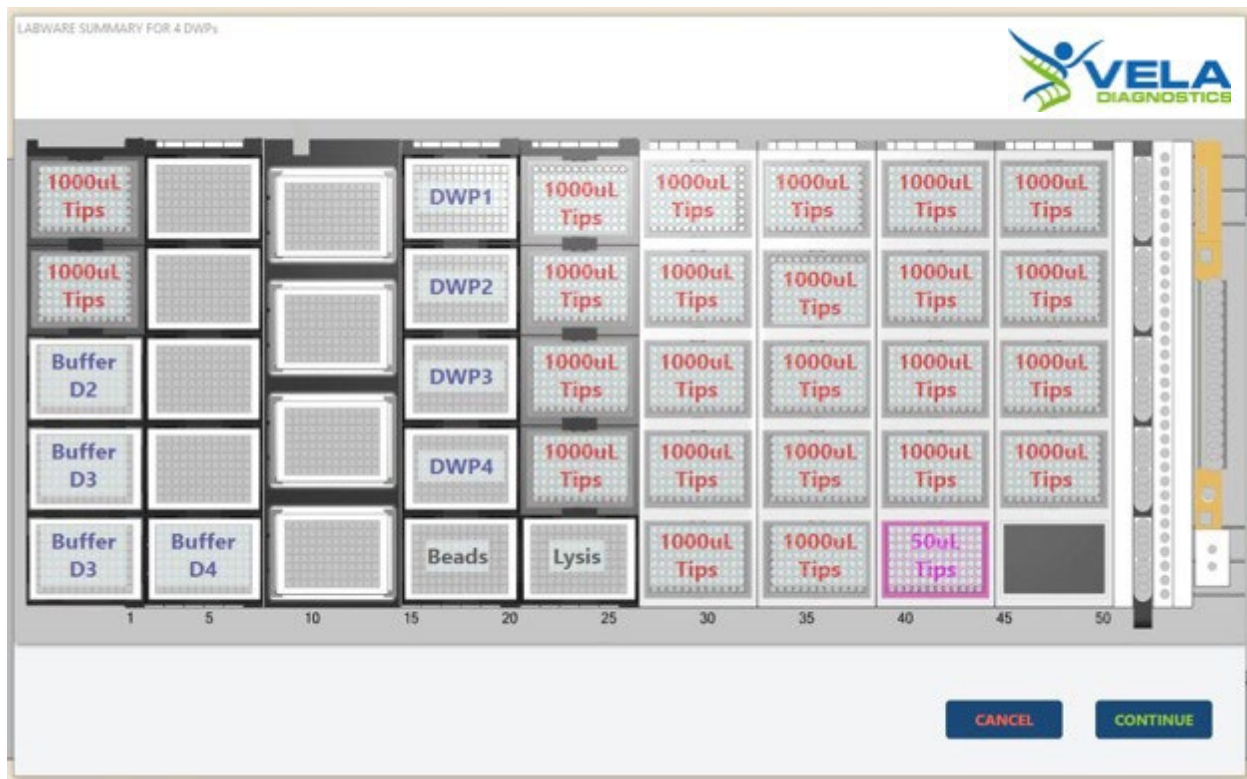


| Track(s) | Description |
|----------|--|
| 1 | <ul style="list-style-type: none"> HT Conductive 1 mL Filter Tips (2x96) 3x HT 300 mL Reservoir |
| 2 to 7 | HT 300 mL Reservoir |
| 8 to 14 | Empty |
| 15 to 20 | <ul style="list-style-type: none"> 3x HT U Deepwell Plate, Barcoded, 2.2 mL HT 300 mL Reservoir |
| 21 to 26 | <ul style="list-style-type: none"> HT Conductive 1 mL Filter Tips (3x96) HT 300 mL Reservoir |
| 27 to 32 | HT Conductive 1 mL Filter Tips (4x96) |
| 33 to 38 | HT Conductive 1 mL Filter Tips (4x96) |
| 39 to 44 | <ul style="list-style-type: none"> HT Conductive 1 mL Filter Tips (3x96) HT Conductive 50 μL Filter Tips (96) |
| 45 to 50 | HT Conductive 1 mL Filter Tips (3x96) |

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D.4. Layout of the Hamilton Microlab STAR platform for viral RNA extraction (with 4 deepwell plates) using “STAR8AL96 Vela_ViroKey_V3.10.med” application



| Track(s) | Description |
|----------|--|
| 1 | <ul style="list-style-type: none"> HT Conductive 1 mL Filter Tips (2x96) 3x HT 300 mL Reservoir |
| 2 to 7 | HT 300 mL Reservoir |
| 8 to 14 | Empty |
| 15 to 20 | <ul style="list-style-type: none"> 4x HT U Deepwell Plate, Barcoded, 2.2 mL HT 300 mL Reservoir |
| 21 to 26 | <ul style="list-style-type: none"> HT Conductive 1 mL Filter Tips (4x96) HT 300 mL Reservoir |
| 27 to 32 | HT Conductive 1 mL Filter Tips (5x96) |
| 33 to 38 | HT Conductive 1 mL Filter Tips (5x96) |
| 39 to 44 | <ul style="list-style-type: none"> HT Conductive 1 mL Filter Tips (4x96) HT Conductive 50 μL Filter Tips (96) |
| 45 to 50 | HT Conductive 1 mL Filter Tips (4x96) |

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Appendix E: Consumable summary

E.1. Consumable summary for 1 deepwell plate


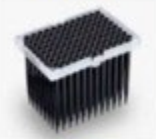
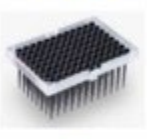



| CONSUMABLES SUMMARY FOR 1 DWP | | | | | |
|---|---|---|---|--|---|
|  | | | | | |
| | 1mL Tips | 50uL Tips | 2.2mL 96-well DWP | 60mL Trough | 300mL Trough |
| LABWARE |  |  |  |  |  |
| QTY | 8 | 1 | 1 | 2 | 3 |
| | | | | Lysis 40 ml Beads 40 ml | Buffer D2 80 ml Buffer D3 125 ml Buffer D4 25 ml |
| <input type="button" value="CANCEL"/> <input type="button" value="CONTINUE"/> | | | | | |

E.2. Consumable summary for 2 deepwell plates


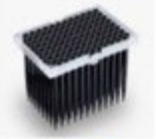
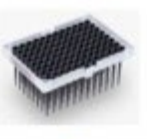



| CONSUMABLES SUMMARY FOR 2 DWP | | | | | |
|---|---|---|---|--|---|
|  | | | | | |
| | 1mL Tips | 50uL Tips | 2.2mL 96-well DWP | 60mL Trough | 300mL Trough |
| LABWARE |  |  |  |  |  |
| QTY | 14 | 1 | 2 | 0 | 6 |
| | | | | | Lysis 80 ml Beads 80 ml Buffer D2 160 ml Buffer D3A 125 ml Buffer D3B 125 ml Buffer D4 50 ml |
| <input type="button" value="CANCEL"/> <input type="button" value="CONTINUE"/> | | | | | |

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E.3. Consumable summary for 3 deepwell plates

| CONSUMABLES SUMMARY FOR 3 DWP | | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|--|--|-------|-----|----|-------|-----|----|-----------|-----|----|------------|-------|----|------------|-------|----|-----------|----|----|
|  | | | | | | | | | | | | | | | | | | | | | | | |
| | 1mL Tips | 50uL Tips | 2.2mL 96-well DWP | 60mL Trough | 300mL Trough | | | | | | | | | | | | | | | | | | |
| LABWARE |  |  |  |  |  | | | | | | | | | | | | | | | | | | |
| QTY | 19 | 1 | 3 | 0 | 6 | | | | | | | | | | | | | | | | | | |
| | | | | | <table border="0"> <tr><td>Lysis</td><td>120</td><td>ml</td></tr> <tr><td>Beads</td><td>120</td><td>ml</td></tr> <tr><td>Buffer D2</td><td>240</td><td>ml</td></tr> <tr><td>Buffer D3A</td><td>187.5</td><td>ml</td></tr> <tr><td>Buffer D3B</td><td>187.5</td><td>ml</td></tr> <tr><td>Buffer D4</td><td>50</td><td>ml</td></tr> </table> | Lysis | 120 | ml | Beads | 120 | ml | Buffer D2 | 240 | ml | Buffer D3A | 187.5 | ml | Buffer D3B | 187.5 | ml | Buffer D4 | 50 | ml |
| Lysis | 120 | ml | | | | | | | | | | | | | | | | | | | | | |
| Beads | 120 | ml | | | | | | | | | | | | | | | | | | | | | |
| Buffer D2 | 240 | ml | | | | | | | | | | | | | | | | | | | | | |
| Buffer D3A | 187.5 | ml | | | | | | | | | | | | | | | | | | | | | |
| Buffer D3B | 187.5 | ml | | | | | | | | | | | | | | | | | | | | | |
| Buffer D4 | 50 | ml | | | | | | | | | | | | | | | | | | | | | |
| | | | | <input type="button" value="CANCEL"/> | <input type="button" value="CONTINUE"/> | | | | | | | | | | | | | | | | | | |

E.4. Consumable summary for 4 deepwell plates

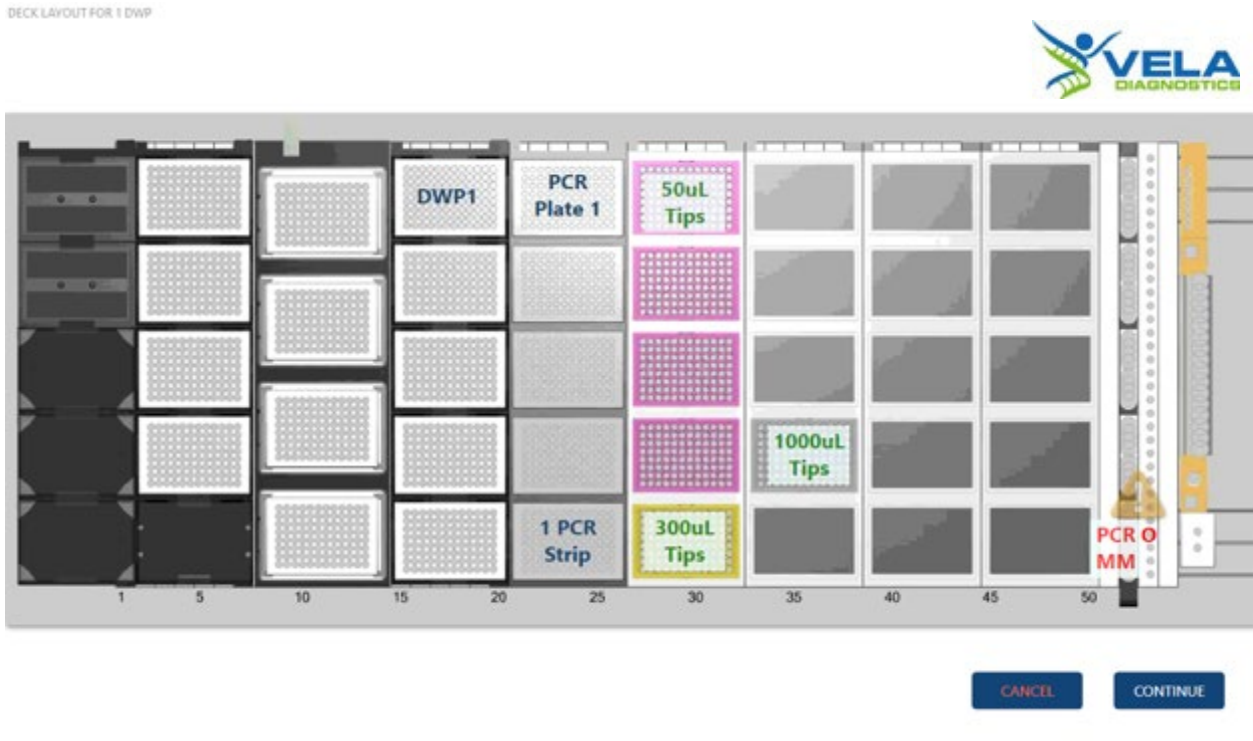
| CONSUMABLES SUMMARY FOR 4 DWP | | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|--|--|-------|-----|----|-------|-----|----|-----------|-----|----|------------|-----|----|------------|-----|----|-----------|----|----|
|  | | | | | | | | | | | | | | | | | | | | | | | |
| | 1mL Tips | 50uL Tips | 2.2mL 96-well DWP | 60mL Trough | 300mL Trough | | | | | | | | | | | | | | | | | | |
| LABWARE |  |  |  |  |  | | | | | | | | | | | | | | | | | | |
| QTY | 24 | 1 | 4 | 0 | 6 | | | | | | | | | | | | | | | | | | |
| | | | | | <table border="0"> <tr><td>Lysis</td><td>160</td><td>ml</td></tr> <tr><td>Beads</td><td>160</td><td>ml</td></tr> <tr><td>Buffer D2</td><td>300</td><td>ml</td></tr> <tr><td>Buffer D3A</td><td>250</td><td>ml</td></tr> <tr><td>Buffer D3B</td><td>250</td><td>ml</td></tr> <tr><td>Buffer D4</td><td>50</td><td>ml</td></tr> </table> | Lysis | 160 | ml | Beads | 160 | ml | Buffer D2 | 300 | ml | Buffer D3A | 250 | ml | Buffer D3B | 250 | ml | Buffer D4 | 50 | ml |
| Lysis | 160 | ml | | | | | | | | | | | | | | | | | | | | | |
| Beads | 160 | ml | | | | | | | | | | | | | | | | | | | | | |
| Buffer D2 | 300 | ml | | | | | | | | | | | | | | | | | | | | | |
| Buffer D3A | 250 | ml | | | | | | | | | | | | | | | | | | | | | |
| Buffer D3B | 250 | ml | | | | | | | | | | | | | | | | | | | | | |
| Buffer D4 | 50 | ml | | | | | | | | | | | | | | | | | | | | | |
| | | | | <input type="button" value="CANCEL"/> | <input type="button" value="CONTINUE"/> | | | | | | | | | | | | | | | | | | |

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Appendix F: HT PCR set-up

F.1. Layout of the Hamilton Microlab STAR platform for HT PCR set-up (with 1 sample plate) using “STAR8AL96 Vela_PCRsetup_V1.3.med” application

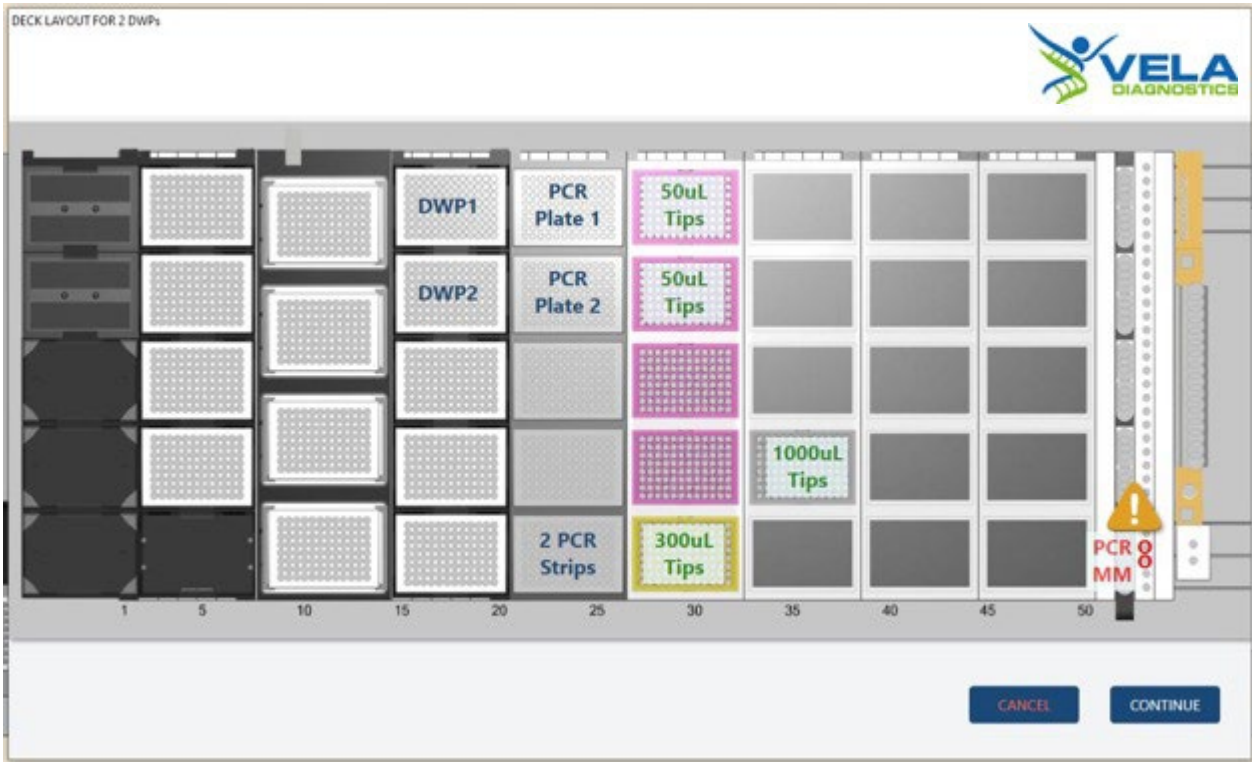


| Track(s) | Description |
|----------|---|
| 1 | Empty |
| 2 to 7 | Empty |
| 8 to 14 | Empty |
| 15 to 20 | <ul style="list-style-type: none"> HT U Deepwell Plate, Barcoded, 2.2 mL |
| 21 to 26 | <ul style="list-style-type: none"> MicroAmp Fast Optical 96-Well Reaction Plate with Barcode, 0.1 mL 1x HT 8-Strip Tubes, Clear, 0.2 mL |
| 27 to 32 | <ul style="list-style-type: none"> HT Conductive 50 μL Filter Tips (96) HT Conductive 300 μL Filter Tips (96) |
| 33 to 38 | HT Conductive 1 mL Filter Tips (96) |
| 39 to 44 | Empty |
| 45 to 50 | Empty |
| 53 | PCR MM (Position 29) |

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F.2. Layout of the Hamilton Microlab STAR platform for HT PCR set-up (with 2 sample plates) using “STAR8AL96 Vela_PCRsetup_V1.3.med” application



| Track(s) | Description |
|----------|--|
| 1 | Empty |
| 2 to 7 | Empty |
| 8 to 14 | Empty |
| 15 to 20 | <ul style="list-style-type: none"> • 2x HT U Deepwell Plate, Barcoded, 2.2mL |
| 21 to 26 | <ul style="list-style-type: none"> • 2x MicroAmp Fast Optical 96-Well Reaction Plate with Barcode, 0.1 mL • 2x HT 8-Strip Tubes, Clear, 0.2 mL |
| 27 to 32 | <ul style="list-style-type: none"> • HT Conductive 50 µL Filter Tips (2x96) • HT Conductive 300 µL Filter Tips (96) |
| 33 to 38 | HT Conductive 1 mL Filter Tips (96) |
| 39 to 44 | Empty |
| 45 to 50 | Empty |
| 53 | 2x PCR MM (Positions 29 and 30) |

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F.3. Layout of the Hamilton Microlab STAR platform for HT PCR set-up (with 3 sample plates) using “STAR8AL96 Vela_PCRsetup_V1.3.med” application



| Track(s) | Description |
|----------|---|
| 1 | Empty |
| 2 to 7 | Empty |
| 8 to 14 | Empty |
| 15 to 20 | <ul style="list-style-type: none"> 3x HT U Deepwell Plate, Barcoded, 2.2mL |
| 21 to 26 | <ul style="list-style-type: none"> 3x MicroAmp Fast Optical 96-Well Reaction Plate with Barcode, 0.1 mL 3x HT 8-Strip Tubes, Clear, 0.2 mL |
| 27 to 32 | <ul style="list-style-type: none"> HT Conductive 50 μL Filter Tips (3x96) HT Conductive 300 μL Filter Tips (96) |
| 33 to 38 | HT Conductive 1 mL Filter Tips (96) |
| 39 to 44 | Empty |
| 45 to 50 | Empty |
| 53 | 3x PCR MM (Positions 29 to 31) |

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F.4. Layout of the Hamilton Microlab STAR platform for HT PCR set-up (with 4 sample plates) using “STAR8AL96 Vela_PCRsetup_V1.3.med” application



| Track(s) | Description |
|----------|---|
| 1 | Empty |
| 2 to 7 | Empty |
| 8 to 14 | Empty |
| 15 to 20 | <ul style="list-style-type: none"> 4x HT U Deepwell Plate, Barcoded, 2.2mL |
| 21 to 26 | <ul style="list-style-type: none"> 4x MicroAmp Fast Optical 96-Well Reaction Plate with Barcode, 0.1 mL 4x HT 8-Strip Tubes, Clear, 0.2 mL |
| 27 to 32 | <ul style="list-style-type: none"> HT Conductive 50 μL Filter Tips (4x96) HT Conductive 300 μL Filter Tips (96) |
| 33 to 38 | HT Conductive 1 mL Filter Tips (96) |
| 39 to 44 | Empty |
| 45 to 50 | Empty |
| 53 | 4x PCR MM (Positions 29 to 32) |

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2023-05-10

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