



CleanPlex[®] Respiratory Research Panel v2

User Guide for Early Access

This user guide is for the following products for sequencing on Illumina[®] NGS platforms:

CleanPlex[®] Respiratory Research Panel v2

For other Ready to use Panels not listed, see product document page on the Paragon Genomics website for appropriate user guides

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UG4003-03

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Revision History

Document	Date	Description of Change
UG4003-01	October 2020	<ul style="list-style-type: none">Initial version
UG4003-02	December 2020	<ul style="list-style-type: none">Update User Guide to include new content for Version 2 of panel which now includes RSV primers.
UG4003-03	January 2022	<ul style="list-style-type: none">Updated to reflect most recent language for clarity of procedures. No major changes.Added Ion Torrent compatibility information.

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Overview

Product Information

CleanPlex® Respiratory Research Panel v2 is a fast, robust, and versatile solution for target enrichment and library preparation for next-generation sequencing (NGS) on Illumina® and Ion Torrent sequencing platforms. CleanPlex Respiratory Research Panel v2 generates highly accurate data from minimal RNA input using a fast and simple workflow. CleanPlex Respiratory Research Panel v2 is expertly optimized with predesigned primers to generate valuable insights in the identification of viral RNA from SARS-CoV-2, influenza A H1N1/H1N2/H3N2, influenza B, and respiratory syncytial virus (RSV) A/B in different sample types. This panel can be used as an active research and surveillance tool to interrogate genetic variability of these viruses.

CleanPlex Respiratory Research Panel v2 is powered by Paragon Genomics' proprietary CleanPlex Technology, which combines an advanced primer design algorithm and an innovative background cleaning chemistry to generate best-in-class target enrichment performance and efficient use of sequencing reads. The patented CleanPlex background cleaning chemistry effectively removes non-specific PCR products to enable ultra-high multiplexing of amplicons. More than 20,000 amplicons can be multiplexed per primer pool to build large NGS panels that can interrogate megabase-size genomic regions to unlock new applications using a streamlined workflow.

The CleanPlex Respiratory Research Panel v2 features a fast and simple workflow that can be completed in less than 6 hours from extracted RNA to indexed NGS libraries ready for sequencing. The workflow involves just 4 steps, each consisting of a thermal-cycling or incubation reaction followed by a library purification using magnetic beads. The CleanPlex Respiratory Research Panel v2 has minimal tube-to-tube transfer, offering many benefits of a single-tube workflow such as preservation of nucleotide material and prevention of handling errors and sample mix-up.

The first step of the CleanPlex Respiratory Research Panel v2 workflow is cDNA synthesis and purification from extracted RNA sample. The second step is a multiplex PCR reaction that uses target-specific primers to amplify targets of interest. Independently, Pool 1 of the panel is designed for detection of SARS-CoV-2, influenza A H1N1/H1N2/H3N2, influenza B, and RSV A/B, whereas when including Pool 2 to the library preparation allows for the interrogation of the entire SARS-CoV-2 genome in addition to detection of Influenza A, influenza B, and RSV. The third step is a digestion reaction that performs background cleaning by removing non-specific PCR products. The last step is a PCR reaction that uses CleanPlex Indexed PCR Primers to amplify and add sample-level indexes to the Fusion libraries. CleanMag® Magnetic Beads are recommended for library purification. See the workflow section for a detailed depiction of the CleanPlex workflow.



Respiratory Research Target Enrichment and Library Preparation Workflow

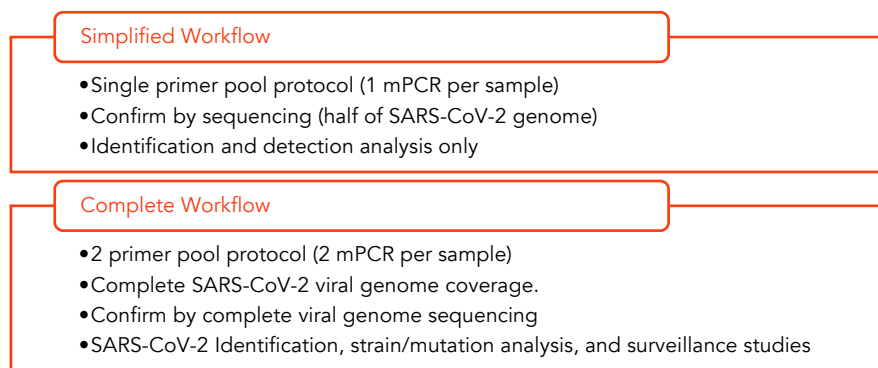
6 hours of total assay time, 60 minutes of hands-on time

Applications

The CleanPlex Respiratory Research Panel v2 can be used to effectively amplify SARS-CoV-2, influenza A H1N1/H1N2/H3N2, influenza B, and RSV RNA in samples using our multiplex PCR technology, enabling reliable results from even low copy numbers.

Our assay produces clean target peaks of defined sizes, which allows for direct detection of the presence of viral genome from the SARS-CoV-2 and viral gene regions from influenza A H1N1, influenza A H1N2, influenza A H3N2, influenzas B, RSV A, and RSV B by electrophoresis. Sequencing is then used to provide confirmation of the species as well as phylogenetic information for specific subtype and potential strain discrimination.

The panel is a two-pool design, with Pool 1 covering the Influenza A/B and RSV A/B gene regions and half of the SARS-CoV-2 genome. The addition of Pool 2 in the workflow completes the coverage of the entire SARS-CoV-2 genome, however for applications that do not require such in-depth study of the entire SARS-CoV-2 genome, just Pool 1 can be used for faster identification and to save on sequencing space. The single-pool application allows a straight forward one mPCR workflow, allowing for faster turnaround, reduced magnetic bead use, and higher sample multiplexing during sequencing.



Organisms	Sample Types	Applications
<ul style="list-style-type: none"> • Virus 	<ul style="list-style-type: none"> • Extracted RNA from bronchoalveolar lavage, tracheal aspirate, sputum, NP/OP swab, nasopharyngeal wash/aspirate or nasal aspirate • Extracted RNA other sources that may contain viral RNA 	<ul style="list-style-type: none"> • Identify the presence of viral RNA from Influenza A H1N1, Influenza A H1N2, Influenza A H3N2, Influenza B, RSV A, RSV B and/or SARS-CoV-2 in a specimen • Confirm specific SARS-CoV-2 strain(s) present in samples through sequencing • Phylogenetic / Surveillance studies for SARS-CoV-2 through in-depth sequence data analysis • High-sensitivity detection

The table below described the content of the panel.

Viruses	Selected Covered Regions	Amplicon Count
SARS-CoV-2	Complete coverage (except 92 bp at the ends of genome)	172 (pool 1) 171 (pool 2)
Influenza A H1N1	Regions in the following genes: HA, M1, NA, NP, NS1, PA, PB1, PB2	18 (pool 1)
Influenza A H1N2	Regions in the following genes: HA, M1, M2, NA, NP, NS1, PB1, PB2	17 (pool 1)
Influenza A H3N2	Regions in the following genes: HA, M1, M2, NA, NP, NS1, PB1, PB2	31 (pool 1)
Influenza B	Regions in the following genes: HA, M1, NA, NS1, PB1, PB2	32 (pool 1)
RSV A	Regions in the following genes: G, F, M, N, NS1, NS2, L, SH, M2-1	21 (pool 1)
RSV B	Regions in the following genes: G, F, M, N, NS1, NS2, P, L, SH, M2-1	30 (pool 1)
Human RNA Primer Control	TBP (House Keeping Gene)	1 (pool 1)

Human RNA Primer Positive Control

The provided control human housekeeping primer pair is present in pool 1 of the panel. This control allows visual (via fragment analysis) confirmation of sample quality and library preparation success—especially for confident negative sample calling. The human RNA amplicon is ~480 bp whereas the viral amplicons are ~250-350bp, allowing an easy sequencing free confirmation of positive vs negative samples. For samples with high viral loads, the human amplicon may not be present in a fragment analysis trace due to the overwhelming amplification of the viral product. This is not an issue as the control is meant for more confident negative sample calling only, by removing concerns about library preparation or sample input concerns.

Other Infectious Disease Applications

For additional SARS-CoV-2 research, we offer a variety of ready to use panels to support host susceptibility studies and co-Infections detection of other respiratory viruses.

Please visit the infectious diseases application page for additional information:

<https://www.paragongenomics.com/applications/infectious-disease/>

All panels can be found under Infectious Diseases Product Category:

<https://www.paragongenomics.com/product-category/products/ready-to-use-panels/infectious-disease/>

SARS-CoV-2 Related Ready to Use Panels		
Panel	SKU	Description
CleanPlex SARS-CoV-2 Research and Surveillance Panel	918011	Original SARS-CoV-2 full viral genome sequencing panel
CleanPlex SARS-CoV-2 FLEX Research and Surveillance Panel	918014	FLEX panel for frontline SARS-CoV-2 mutation research
CleanPlex SARS-CoV-2 Emerging Variants Panel Add-on v2	918023	Panel Add-on primers target emerging variants to maintain high coverage even as the virus evolves
CleanPlex Respiratory Research Panel v2	918303	Respiratory Panel contains additional viral content for concurrent Influenza, RSV, SARS-CoV-2 detection and subtyping
CleanPlex ACE2& TMPRSS2 Panel	916121	Host (human) germline panel for mutation analysis of <i>ACE2</i> and <i>TMPRSS2</i> and associated eQTL for expression level related research, and susceptibility investigations.

Other Applications

For other targeted sequencing applications, Paragon Genomics also offer a while variety of both ready to use panel and custom panels for oncology, drug discovery, and more.

Visit our applications page for additional information: <https://www.paragongenomics.com/applications/>

Other Ready to Use Panels			
Panel	SKU	Application	Description
CleanPlex OncoZoom Cancer HotSpot Panel	916002	Oncology	Target 2,900+ hotspots in 65 genes with known cancer associations.
CleanPlex BRCA1 & BRCA2 Panel v3	916006	Oncology	Target the entire coding region including 20 bases of padding around all targeted coding exons in <i>BRCA1&2</i>
CleanPlex TP53 Panel	916009	Oncology	Target the entire coding region and flanking intronic sequences of <i>TP53</i> for somatic mutations detection low as 1%
CleanPlex UMI Lung Cancer Panel	916066	Oncology	Interrogate 23 genes containing variants that are frequently mutated in lung cancer using a hotspot panel designed to work with cell-free DNA (cfDNA). Detect low-frequency variants below 0.5% MAF.
CleanPlex TMB 500 Panel	916074	Oncology	Interrogate 516 genes associated with the major solid tumor types to assess tumor mutational burden and characterize mutation profile.
OmniFusion™ RNA Lung Cancer Panel	917101	Oncology	Interrogate >530 known RNA fusion and additional novel RNA fusion using a single-primer method.
AccuFusion™ RNA Lung Cancer Panel	917104	Oncology	Interrogate ~280 known RNA fusions using a target specific dual-primer multiplex PCR method.
CleanPlex Mitochondrial Disease Panel	916063	Genetic Disease	Detect and investigate important variants with complete coverage of the entire human mitochondrial genome.
CleanPlex Hereditary Cancer Panel v2	916115	Genetic Disease	Interrogate 37 genes associated with cancers of the breast, ovary, uterus, skin, prostate, and gastrointestinal system, including rs12516 and rs8176318 in <i>BRCA1</i> and Boland inversion in <i>MSH2*</i> .
CleanPlex CFTR Panel	916117	Genetic Disease	Target the entire exon and include 20 bases of padding around all targeted coding exons for <i>CFTR</i> .
CleanPlex Custom NGS Panels	---	Variable	One-on-one service to design a custom panel specific to your applications and needs.

Compatible Sequencing Instruments

CleanPlex Indexed PCR Primers for Illumina are used to generate CleanPlex target-enriched NGS libraries that are compatible with Illumina sequencing platforms, including NovaSeq® 5000/6000 Systems, HiSeq 3000/4000 Systems, HiSeq 2500 System, NextSeq® Series, MiSeq® System, MiniSeq® System, and iSeq® System.

CleanPlex Indexed PCR Primers for Ion Torrent are used to generate CleanPlex target-enriched NGS libraries that are compatible all Ion Torrent sequencing platforms, including Ion PGM System, Ion Proton System, and Ion GeneStudio S5 Series.

Kit Contents

The protocol outlined in the CleanPlex Respiratory Research Panel v2 User Guide requires the following components, which need to be ordered separately:

- CleanPlex Respiratory Research v2 Panel
- CleanPlex Indexed PCR Primers
- CleanMag Magnetic Beads (or equivalent)

Panel Specifications

Panel	Number of Primer Pools	Primer Pool Concentration	Number of Amplicons	Average Amplicon Length	Average Library Length
Respiratory Research Panel v2	2	10X	493 total	105 -196 bp (avg 150 bp)	Viral Targets: 250-350 bp Human Control: 480 bp

CleanPlex NGS Panel — Kit Contents, Store at -20°C

Panel	SKU	Size (Reactions)	Components		
			Primer Pool 1	Primer Pool 2	CleanPlex Targeted Library Kit
CleanPlex Respiratory Research Panel v2	918303	8	8 µl	8 µl	2-pool, 8 rxns
	918304	96	96 µl	96 µl	2-pool, 96 rxns
	918305	384	384 µl	384 µl	2- pool, 384 rxns

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A CleanPlex Targeted Library Kit with RT is included in every CleanPlex Respiratory Research Panel v2 Kit. Please note that the CleanPlex Targeted Library Kit with RT is not sold separately.

CleanPlex Targeted Library Kit with RT — Kit Contents, Store at –20°C (not sold separately)					
Configuration			2-Pool		
Size			8 Rxns	96 Rxns	384 Rxns
Component	Cap Color	SKU	918303	918304	918305
RT Primer Mix DP	Purple Striped		24 µl	288 µl	1152 µl
RT Enzyme	Blue Striped		8 µl	96 µl	384 µl
RT Buffer DP	Green Striped		40 µl	480 µl	1920 µl
5X mPCR Mix	Green		32 µl	384 µl	1536 µl
CP Reagent Buffer	White		16 µl	192 µl	768 µl
CP Digestion Reagent	Yellow		8 µl	96 µl	384 µl
Stop Buffer	Red		64 µl	768 µl	3072 µl
5X 2nd PCR Mix	Blue		64 µl	768 µl	3072 µl
TE Buffer	Clear		500 µl	4 ml	16 ml
DEPC Treated Water (Nuclease-free)	Clear		500 µl	4 ml	16 ml

Required Materials and Equipment Not Included

CleanPlex Indexed PCR Primers (visit www.paragongenomics.com/store for more indexing options)

CleanPlex Dual-Indexed PCR Primers for Illumina — Store at –20°C			
	SKU	Size (Reactions)	Format
CleanPlex Dual-Indexed PCR Primers for Illumina Set T	716021	9	Random 3 i7 indexes + 3 i5 indexes (9 tubes)
CleanPlex Dual-Indexed PCR Primers for Illumina Set A	716006 716017	96 384	12 i7 indexes + 8 i5 indexes (20 tubes)
CleanPlex Dual-Indexed PCR Primers for Illumina Set B	716018 716019	96 384	12 i7 indexes + 8 i5 indexes (20 tubes)

CleanPlex Single-Indexed PCR Primers for Ion Torrent — Store at –20°C			
	SKU	Size (Reactions)	Format
CleanPlex® Single-Indexed PCR Primers v2 for Ion Torrent Set T	716016	8	8 tubes
CleanPlex® Plated Single-Indexed PCR Primers v2 for Ion Torrent Set C	716053	192	96 indexes, (96-well plate)
CleanPlex® Plated Single-Indexed PCR Primers v2 for Ion Torrent Set D	716054	192	96 indexes (96-well plate)
CleanPlex® Plated Single-Indexed PCR Primers v2 for Ion Torrent Set E	716055	192	96 indexes (96-well plate)
CleanPlex® Plated Single-Indexed PCR Primers v2 for Ion Torrent Set F	716056	192	96 indexes (96-well plate)

- CleanMag Magnetic Beads, or equivalent — eg. Agencourt™ AMPure™ XP Kit (Beckman Coulter, A63880, A63881, or A63882)

CleanMag Magnetic Beads — Store at 2–8°C			
	SKU	Size (Volume)	Reactions 1-pool panels
CleanMag Magnetic Beads, 1 ml	718001	1 ml	~5
CleanMag Magnetic Beads, 5 ml	718002	5 ml	~25
CleanMag Magnetic Beads, 20 ml	718005	20 ml	~100
CleanMag Magnetic Beads, 60 ml	718003	60 ml	~300
CleanMag Magnetic Beads, 450 ml	718004	450 ml	~2,250

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- For PCR tubes or strips, CleanMag Magnetic Rack (SKU 719001) or equivalent magnetic racks designed for PCR strip workflows
- For 96-well PCR plates, CleanMag Magnetic Plate (SKU 719002) or equivalent magnetic plates designed for PCR plate workflows

CleanMag Magnetic Rack & Plate		
	SKU	Compatibility
CleanMag Magnetic Rack	719001	2 rows of 12 tubes each for PCR strip tubes
CleanMag Magnetic Plate	719002	96 well PCR plates, full or semi- skirted compatible

- 70% ethanol (freshly prepared)
- Nuclease-free water
- Nuclease-free, low bind, thin-wall PCR strip tubes with attached caps, or 96-well PCR plate with adhesive film
- Pipettors and low-retention filtered pipette tips
- Thermal cycler
- Mini-centrifuge, 96-well plate centrifuge
- Qubit® Fluorometer and dsDNA HS (high sensitivity) Assay Kit, or equivalent
- Agilent® 2100 Bioanalyzer® Instrument and Agilent High Sensitivity DNA Kit, or equivalent

Storage, Handling, and Usage

CleanPlex Respiratory Research Panel and CleanPlex Indexed PCR Primers are shipped on blue ice (ice packs). Upon receipt, immediately store the library kit and CleanPlex Indexed PCR Primers at -20°C in a constant-temperature freezer. Do not store in a freezer with auto-defrost or frost-free features. Do not store at -80°C.

CleanMag Magnetic Bead solution is shipped at room temperature or on blue ice (ice packs). **CleanMag Magnetic bead may be frozen during transit.** This single freeze thaw will not affect the performance of the beads. Upon receipt, immediately store CleanMag Magnetic Beads at 2°C to 8°C in a constant-temperature refrigerator. Do not freeze. Do not store at -20°C.

Always ensure that all frozen components are fully thawed and have been vortexed and spun down to bring all liquids to the bottom of the tubes prior to use.

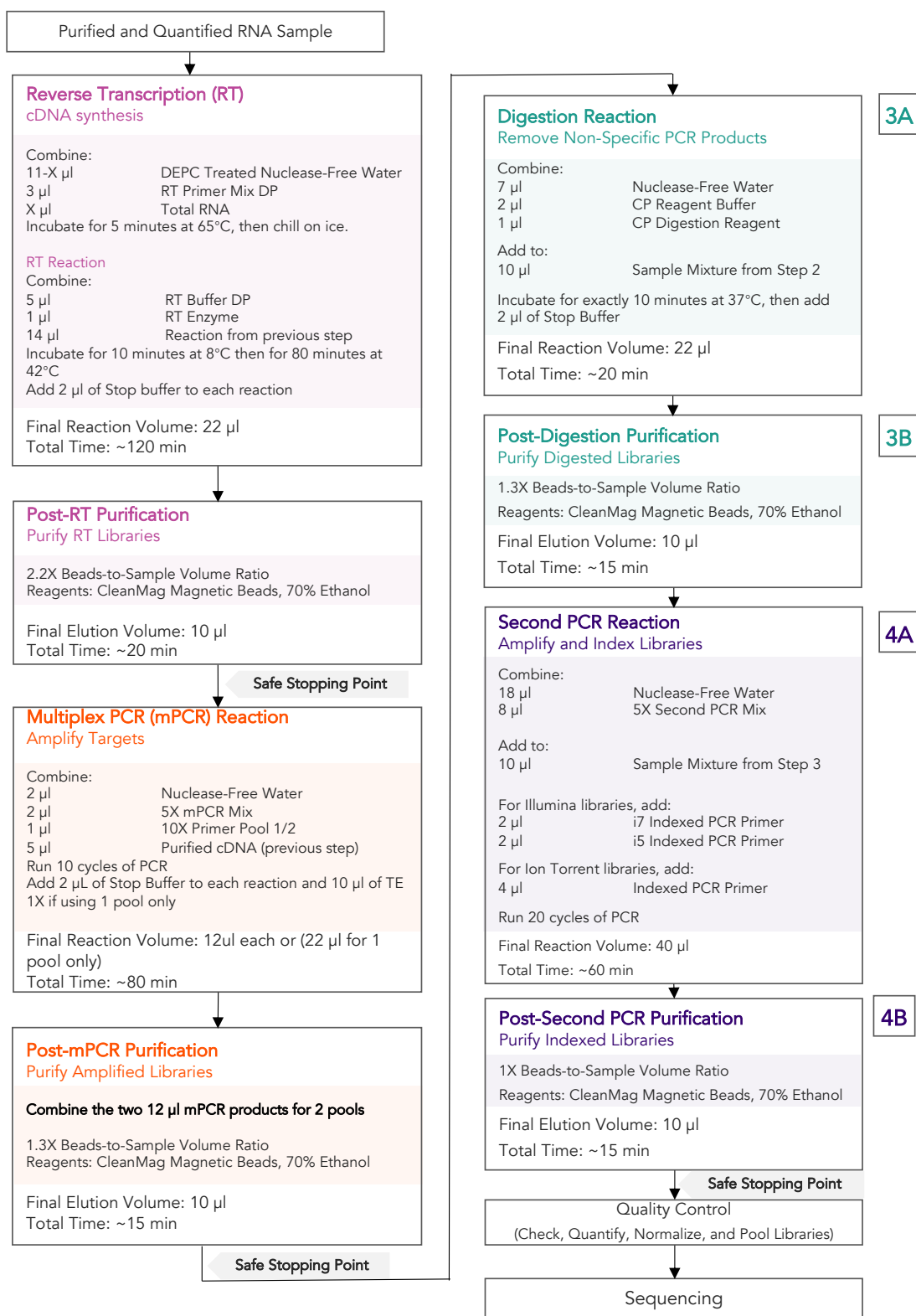
The components containing enzymes are viscous (10X Respiratory Panel v2 pools, RT Enzyme Mix, 5X mPCR Mix, CP Digestion Reagent, 2nd PCR Mix) and specially formulated for storage at -20°C without freezing to avoid freeze-thaw cycles to retain their full activity. Please avoid storing these components below -23°C.

The Respiratory Research Panels is developed, designed and sold exclusively for **research use only**. None of the products or their individual components have been tested for use in diagnostic procedures.

For hazard information, please refer to the Safety Data Sheet (SDS), which is available upon request.

Workflow

The following diagram illustrates the Respiratory Panel's targeted NGS library preparation workflow.



Protocol

General Best Practices

- When using the kit for the first time, briefly vortex and spin the tubes in the kit to bring the liquid to the bottom of the tubes. Store the tubes containing (10X Respiratory Panel v2 pools, RT Enzyme Mix, 5X mPCR Mix, CP Digestion Reagent, 2nd PCR Mix) on ice during their respective procedures. All other components, including primer pools, may be thawed at room temperature, mixed thoroughly by vortexing and spun-down before use.
- Use good laboratory practices to minimize cross-contamination. If possible, perform PCR setup in an isolated area or room to minimize cross-contamination between samples, multiplex PCR (mPCR) primers, or indexed PCR primers. Always change pipette tips between samples and change gloves frequently. Clean all workstations and tools with 10% bleach followed by water, then alcohol at the end of each work day.
- Use a calibrated PCR thermal cycler as specified by the manufacturer's user guide. Validated thermal cyclers include Bio-Rad C1000, Eppendorf Mastercycler series, and Applied Biosystems GeneAmp PCR System 9700. Generally, a thermal cycler set with the highest ramp speed, such as 5°C/second and higher, is not recommended. For thermal cyclers with adjustable ramp speed, we recommend 3°C/second up and 2°C/second down speed, or use the default setting (no ramp adjustment).
- To ensure accurate assembly of reactions, withdraw (10X Respiratory Panel v2 pool(s), RT Enzyme Mix, 5X mPCR Mix, CP Digestion Reagent, 2nd PCR Mix) slowly from containers and dispense it slowly into the reaction mixtures. A good practice is to remove excess from outside of tip and rinse the tip by pipetting up and down several times after dispensing viscous solutions into aqueous mixture. Thoroughly mix each assembly to ensure solutions are homogenous prior to PCR and incubations. Remember to briefly spin the PCR tubes or 96-well PCR plate after mixing.
- Always keep working solutions and PCR products on ice until needed. Combine PCR mixes just immediately prior to use and do not prolong storage of combined PCR mixes and PCR products.
- The protocol is designed to minimize the number of tube-to-tube transfer in order to avoid or reduce sample loss. Except for the transfer of RT products to the multiplexing PCR step and the pooling of mPCR products, the entire protocol is performed following a single-tube workflow, with no tube-to-tube transfers.
- When working with 96-well PCR plates, take extra care to ensure thorough mixing of all samples and proper sealing to avoid cross contamination between samples.
- Magnetic bead purification steps should be performed carefully to minimize residual supernatant and ethanol washes, and to minimize bead loss. Using a strong magnetic rack or plate specifically designed for manual handling of PCR tubes or 96-well PCR plates is critical for a successful bead purification

- Always pre-warm thermal cycles, pre-warm a water bath or heat block to 65°C or 37°C as described in the protocol.
- Assign sample indexes to specific samples before starting the protocol.
- Always prepare a master mix of reagents when working with multiplex reactions. Prepare ~5% excess of each master mix to allow for pipetting losses. A master mix calculation sheet can be downloaded from the Product Documents page on the Paragon Genomics website at www.paragongenomics.com/product_documents/.

RNA Best Practices

- RNA is a single stranded polynucleotide that is incredibly susceptible to degradation by base- or enzyme-catalyzed hydrolysis. This means that working with RNA can be more demanding than its double stranded, counterpart, DNA due to the chemical instability of RNA and because of the pervasive presence of RNases. Furthermore, unlike DNases, RNases have no requirement for metal ion co-factors and can remain active even after prolonged boiling or autoclaving.
- When working with RNA, wear gloves at all times. After putting on gloves, avoid touching contaminated surfaces and equipment with the gloved hands. Even if all the reagents have been decontaminated, RNases can be reintroduced by contact with ungloved hands or with unfiltered air.
- Use sterile, disposable plasticware whenever possible. These require no treatment and are considered to be RNase-free.
Note: *Autoclaving without DEPC/DMPC treatment is insufficient for inactivating RNases.*
- If possible, designate a special area for RNA work only. Treat surfaces of benches, glassware, and pipettes with commercially available RNase inactivating agents such as RNase Zap® or equivalent agent.
- Also, wipe benches with a three-wash method, using 10% bleach, followed by water, and finish with 90-100% ethanol **each time** prior to use, in order to rid the area of microorganisms.
- Whenever possible, purchase reagents that are free of RNases. Be sure to separate reagents used for RNA work from "general use reagents" in the laboratory and use only for RNA processing.
- Prior to processing, store RNA at -70 to -80°C, as aliquots in ethanol, isopropanol or lysis buffer as indicated by extraction method. Most RNA is relatively stable at this temperature. Centrifuge the RNA and resuspend in an appropriate RNase-free buffer before use. Use autoclaved DEPC water to elute and resuspend RNA or alternatively use molecular grade water certified as RNase and DNase free
- Although DNA is relatively stable at elevated temperatures (+100°C), most RNA is not. Therefore, avoid high temperatures (above +65°C) since these affect the integrity of the RNA. This means it is critical to handle solutions of RNA on ice when using, this includes thawing and processing RNA Samples and related reactions on ice.

Input RNA Requirements

Refer to the following chart for the amounts of input DNA.

Panel	RNA Input Range)	Recommended RNA Input (per pool)
CleanPlex Respiratory Research Panel v2	50–100 ng Or 5-11 µl of extracted RNA	50 ng Or 11 uL of extracted RNA

- The maximum volume of RNA input per RT Reaction is 11 µl. An input of more than 5 µl of extracted and purified RNA (10-15ng/ µl concentration) is recommended per pool. When working with low viral load samples or unknown viral load samples, use the full 11 µl RNA input or best chances of detection.
- Qubit RNA HS Assay Kit (Thermo Fisher, Cat. No. Q32851 or Q32854) or an equivalent fluorometric method is recommended for measuring RNA concentration. UV spectrophotometry methods (e.g. NanoDrop™ spectrophotometer) are not recommended because it can significantly overestimate the RNA concentration.
- If sample quality is questionable, more RNA can be used for best results.
- Some recommended RNA extractions kits include: QIAamp® Viral RNA Mini Kit, QIAamp® MinElute Virus Spin Kit or RNeasy® Mini Kit (QIAGEN), EZ1 DSP Virus Kit (QIAGEN), Roche MagNA Pure Compact RNA Isolation Kit, Roche MagNA Pure Compact Nucleic Acid Isolation Kit, Roche MagNA Pure 96 DNA and Viral NA Small Volume Kit.
- After RNA extraction, avoid diluting RNA samples to < 10 ng/µl when possible for prolonged storage since RNA is less stable in solution at lower concentrations.
- Avoid freeze-thawing RNA samples when possible. Use freshly extracted RNA when possible.
- RNA Input is based off of tested conditions using Universal Human Reference RNA; actual optimal input may vary based on actual RNA sample quality and viral load.
- Compatible RNA buffering systems are Tris HCl or TE.

Set up and Preparations

- When working with multiple samples with the same input, prepare a master mix of RT Primer Annealing Reaction Mixture for RT. Mix well, aliquot into individual tubes, then add the recommended RNA input to each reaction.
- Bring Magnetic bead solution to room temperature for at least 30 minutes before use. Replace in 2-8 °C storage at the end of the day.
- Freshly prepare 12mL (per 8 reactions) of 70% Ethanol by combining 8.4mL of 100% ethanol and 3.6mL nuclease-free water at volume ratios of 7 to 3 respectively. Do not top off one liquid with the other in a volumetric container because the volumetric ratio will not be accurate. When water and ethanol are mixed, the final volume will be less than the sum of individual volumes. Lower concentration of ethanol will affect final library yield.
- For all samples to be sequenced together, assign a specific index combination (CleanPlex Dual-Indexed PCR Primers for Illumina) to each sample.
- **Note:** Use the 1-Pool method for quick detection, reduced hands on time, and reduced total sequencing reads. However, for complete genome sequencing of SARS-CoV-2, use the 2-Pool method for in-depth analysis.
- **Note** the safe stopping points after Post-RT Purification, Post-mPCR Purification, and Post-2nd PCR purification. After starting Digestion Step, samples must be carried through to 2nd PCR purification without stopping. Plan accordingly.

1A. Reverse Transcription (RT) Reaction

- 1A.1. Thaw RT primer Mix and RT Buffer tubes and keep all Reverse Transcription reagents on ice. Before use, vortex and quick spin all reagents. Using thin-wall PCR strip tubes (or a 96-well PCR plate), prepare the Reverse Transcription Primer Annealing Reaction Mixture by adding components in the following order on ice or a cold block

Note: When working with multiple samples with same input volumes, prepare a master mix of RT Primer Annealing Reaction Mixture. Mix well, aliquot into individual tubes, then add RNA samples to each reaction.

Note: Pre-warm a thermal cycler or heating unit to 65°C before beginning the RT Primer Annealing Reaction.



Important! Use RNA Best Practices by performing all reactions on a cold block on ice and diligently avoid contamination and introduction of RNases until RT step (1A) and RT Purification (1B) are complete.

RT Primer Annealing Reaction Mixture		
Reagent	Cap Color	Volume per reaction
DEPC Treated Nuclease-Free Water	—	11 – X μ l
RT Primer Mix DP	Purple Striped	3 μ l
Total RNA	—	X μ l
Total Volume per reaction		14 μl

- 1A.2. Close the caps of the PCR tubes or seal the PCR plate with adhesive film, spin briefly to bring down the liquid, mix thoroughly by pipetting up and down at least 5 times or by vortexing vigorously for at least 5 seconds until homogenous. Avoid unnecessarily prolonged vortexing. Spin briefly for 3 seconds to collect the liquid.

Note: It is crucial that the reaction mixture is homogenous prior to thermal cycling. Incomplete mixing can cause decreased yield and increase nonspecific product formation.

Note: If using a PCR plate, use an applicator tool to firmly secure each reaction well and around the perimeter of the plate to prevent evaporation during thermal cycling.

- 1A.3. Load the tubes/plate in the thermal cycler and run the following thermal cycling protocol to anneal RT Primers.

RT Primer Annealing Reaction Incubation Protocol			
Step	Temperature	Time	Preheat
Incubation	65 °C	5 min	65 °C
Hold	4 °C	∞	-



Important! Do not stop and store samples. Immediately after RT primer annealing, continue to Reverse transcription Reaction

- 1A.4. Keep the tubes/plate on ice. Open the tubes or carefully remove the adhesive film from the PCR plate. Prepare the Reverse Transcription (RT) Reaction Mixture by adding components in the following order on ice or a cold block.

Note: When working with multiple samples, prepare a master mix of Reverse Transcription Reaction Mixture. Mix well, aliquot into individual tubes.

RT Reaction Mixture		
Reagent	Cap Color	Volume per reaction
RT Buffer DP	Green Striped	5 µl
RT Enzyme	Blue Striped	1 µl
Previous Reaction	—	14 µl
Total Volume per reaction		20 µl

- 1A.5. Close the caps of the PCR tubes or seal the PCR plate with adhesive film, spin briefly to bring down the liquid, mix thoroughly by pipetting up and down at least 5 times or by vortexing vigorously for at least 5 seconds until homogenous. Avoid unnecessarily prolonged vortexing. Spin briefly for 3 seconds to collect the liquid.

Note: It is crucial that the reaction mixture is homogenous prior to thermal cycling. Incomplete mixing can cause decreased yield and increase nonspecific product formation.

Note: Avoid over vortexing, RNA is single stranded and susceptible to manual shearing and excessive fragmentation

- 1A.6. Set up the temperature as shown below. Allow the cycler to reach 8 °C prior to loading the tubes/plate in the thermal cycler. Run the following thermal cycling protocol.

Step	Temperature	Time	Preheat
Equilibration	8 °C	10 min	8 °C
Incubation	42 °C	80 min	
Hold	4 °C	∞	

1A.7. When the incubations are complete, immediately add 2 µl of Stop Buffer (red cap) into each tube/well and mix by spinning briefly then vortexing. Spin again briefly to collect the liquid. The volume of each sample is now approximately 22 µl.



Important! Do not stop and store samples after reverse transcription. Add stop buffer then proceed to Step 1B, Post-RT Purification immediately.

1B. Post-RT Purification



Important! Ensure the Magnetic Bead Solution has come to room temperature before use.



Important! Use freshly prepared 70% ethanol. Lower concentration ethanol may result in lower yields.

- 1B.1. Vortex the magnetic beads suspension vigorously until homogenous. Perform a **2.2X** bead-based purification by adding 48 μ l of magnetic beads to each sample as described in the table below. Mix by pipetting up and down at least 5 times or vortex vigorously for at least 5 seconds until homogenous.

Post Reverse Transcription Purification — 2.2X Beads-to-Sample Volume Ratio

Reagent	Volume per reaction
Reverse Transcription Product	22 μ l
Magnetic Beads	48 μ l



Important! Magnetic bead volume is critical to the purification process. Always dispense slowly and carefully. Keep the outside of the pipette free from droplets, **AND** make sure the entire volume is added to the sample (residual from inside pipette tips) before discarding the tip.

Ensure the bead + sample solution is thoroughly mixed before incubation, especially when working in a 96-well PCR plate format. Inadequate mixing can result in lowered yields and/or increased background in the final library.

- 1B.2. Incubate the mixture for **10 minutes** at room temperature.
- 1B.3. Briefly spin the tubes/plate. Place the tubes/plate on a magnetic rack and incubate for at least **2 minutes until the liquid is clear**. The beads will be drawn onto one side of each tube/well. While keeping the tubes/plate on the magnetic rack, carefully remove and discard the supernatant without disturbing the beads.

Note: If the magnetic beads are aspirated into the pipette tip at any point during the purification process, dispense the solution back into tube, remove the tip, allow the beads to migrate toward the magnet again, then repeat.

- 1B.4. Cap/seal the tubes/plate, and briefly spin again to bring down the remaining liquid. Place the tubes/plate on the magnetic rack to gather the beads. Using a 10 µl pipette tip, carefully remove all residual supernatant from the bottom of the tube/well without disturbing the beads.



Important! Removing all residual supernatant from the Post RT Cleanup *prior* to ethanol washing is critical to obtaining a clean, high-quality library. The above spin and remove step ensure complete removal of supernatant.

Note: A strong compatible magnetic rack is essential. If your magnetic rack or plate cannot collect the magnetic beads effectively, please look into a replacement.

- 1B.5. Add 180 µl of freshly prepared 70% ethanol to each tube/well. Reposition the tubes/plate on the magnetic rack by placing the clear side of the tubes/wells (the side without beads) against the magnet. Allow the beads to completely migrate through the ethanol to the other side. **Do not vortex.** Carefully remove and discard the supernatant without disturbing the beads.
- 1B.6. Repeat step 1B.5.
- 1B.7. After the second wash, briefly spin the tubes/plate to bring down all remaining liquid. Place the tubes/plate on the magnet rack to gather the beads. Carefully remove the residual ethanol in each tube/well. Keeping the tubes/plate on the magnetic rack, air-dry the beads at room temperature for 5 minutes. **Do not over or under dry.**

Note: Over-dried beads can dislodge from the side of the tube and lead to cross contamination. They are also more difficult to resuspend during elution. Residual ethanol inhibits PCR and will result in reduced yield. Especially when working with 96-well PCR plates, make sure all residual ethanol is dried (may take longer than 5 minutes) before going to the next step.

- 1B.8. Remove tubes/wells from the magnetic rack and add 10 µl TE buffer directly onto the pellet for each tube/well. Briefly spin and vortex to resuspend the dried beads completely. The DNA will be immediately released from the beads as long as all beads are in solution. Spin briefly to collect the liquid to the bottom. There is no need to remove the beads.
- 1B.9. Proceed to Step 2A. Multiplex PCR Reaction.



Safe Stopping Point. Purified products may be stored at 10°C for up to 1 hour or at –20°C for up to 24 hours.

2A. Multiplex PCR (mPCR) Reaction



Important: Each primer pool requires one mPCR and 5 µl of the purified RT reaction product. When working with a 1-pool workflow, the remaining 5 µl of the purified RT reaction can be stored at -20°C for future use or discarded. When working with the 2-pool workflow, split the 10 µl of the purified RT reaction into two 5 µl tubes (1 for each pool), beads included.

Note: for increased sensitivity for 1 pool workflow, 7 µL of purified RT reaction product can be used in place of the additional 2 µL nuclease-free water.

- 2A.1. Thaw 10x Respiratory Panel v2 Primer Pool(s) and vortex thoroughly before use. Prepare the mPCR Reaction Master Mixture by adding components in the following order on ice or a cold block.

Note: Use the 1-Pool method for quick detection of SARS-CoV-2 and Influenza A/B and reduced turnaround time. However, if in-depth sequencing is desired for SARS-CoV-2, use the 2-Pool method for a more complete coverage. See application section for additional information. Pool 2 **does not** contain influenza A/B targets; use Pool 1 for interrogation of influenza A/B.

Note: When working with multiple reactions, prepare a master mix. Mix well, then add 5 µl of master mix to 5 µl of each sample. 2-pool workflow requires 2 mPCR reactions per sample.

mPCR Reaction Master Mix		
Reagent	Cap Color	Volume per reaction
Nuclease-Free Water	—	2 µl
5X mPCR Mix	Green	2 µl
10X Respiratory Panel v2 Primer Pool 1 or 10X Respiratory Panel v2 Primer Pool 2	—	1 µl
Total Volume		5 µl



Important! 5X mPCR Mix and 10X Primer Pool(s) are viscous. Pipette slowly, remove any excess reagent on the outside of the pipette tip, and rinse tip in solution when handling these reagents.

mPCR Reaction Mixture	
Reagent	Volume per reaction
Purified RT sample from 1B	5 µl
mPCR Master mix	5 µl
Total Volume per reaction	10 µl

- 2A.2. Close the caps of the PCR tubes or seal the PCR plate with adhesive film, spin briefly to bring down the liquid, mix thoroughly by vigorously for at least 5 seconds until homogenous. Avoid prolonged vortexing. Spin briefly for 3 seconds to collect the liquid.

Note: It is crucial that the reaction mixture is homogenous prior to thermal cycling. Incomplete mixing can cause decreased yield and increase nonspecific product formation.

Note: If using a PCR plate, use an applicator tool to firmly secure each reaction well and around the perimeter of the plate to prevent evaporation during thermal cycling.

Load the tubes/plate in the thermal cycler and run the following thermal cycling protocol.

Note: For applications the strictly work with very low viral count samples, an additional 2-4 mPCR cycles can be added to increase sensitivity.

mPCR Thermal Cycling Protocol				
Step	Temperature	Time	Ramping*	Cycles
Initial Denaturation	95 °C	10 min	-	-
Denaturation	98 °C	15 sec	3 °C/s	10**
Annealing/Extension	60 °C	5 min	2 °C/s	
Hold	10 °C	∞		

* For thermal cyclers without adjustable ramp speed, the default setting can be used if max ramping speed is ≤5°C/S.

** for applications strictly detecting low viral counts, an additional 2-4 mPCR cycles can be added to increase sensitivity.

- 2A.3. Immediately add 2 µl of Stop Buffer (red cap) into each tube/well and mix by spinning briefly then vortexing. Spin again briefly for 3 seconds to collect the liquid. The volume of each sample is now approximately 12 µl.

Note: Do not allow samples to hold at 10 °C for longer than 30 minutes before adding Stop Buffer.

- 2A.4. Proceed to Step 2B. Post-mPCR Purification.



Important! Do not stop and store samples after the mPCR Reaction. Add Stop buffer then proceed to Step 2B, Post-mPCR Purification immediately.

2B. Post-mPCR Purification



Important! Ensure the Magnetic Bead Solution has come to room temperature before use.



Important! Use freshly prepared 70% ethanol. Lower concentration ethanol may result in lower yields.

- 2B.1. Open the tubes or carefully remove the adhesive film from the PCR plate.
- When using 1-pool workflow, add 10 µl of TE Buffer to each sample for a total of 22 µl volume.
 - When using 2-pool workflow, combine the 12 µl multiplex PCR products for each sample for a total of 24 µl volume.
- 2B.2. Vortex the magnetic beads suspension vigorously until homogenous. Perform a **1.3X** bead-based purification by adding magnetic beads to each sample as described in the table below. Mix by pipetting up and down at least 5 times or vortex vigorously for at least 5 seconds until homogenous.

Post-mPCR Purification — 1.3X Beads-to-Sample Volume Ratio		
Reagent	1-Pool workflow	2-Pool workflow
Total Sample Volume	22 µl (12 µl of sample + 10 µl of TE)	24 µl
Magnetic Beads to add	29 µl	31 µl



Important! Magnetic bead volume is critical to the purification process. Always dispense slowly and carefully. Keep the outside of the pipette free from droplets, **AND** make sure the entire volume is added to the sample (residual from inside pipette tips) before discarding the tip.

Ensure the bead + sample solution is thoroughly mixed before incubation, especially when working in a 96-well PCR plate format. Inadequate mixing can result in lowered yields and/or increased background in the final library.

- 2B.3. Incubate the mixture for **5 minutes** at room temperature.
- 2B.4. Briefly spin the tubes/plate. Place the tubes/plate on a magnetic rack and incubate for at least **2 minutes until the liquid is clear**. The beads will be drawn onto one side of each tube/well. While keeping the tubes/plate on the magnetic rack, carefully remove and discard the supernatant without disturbing the beads.

Note: If the magnetic beads are aspirated into the pipette tip at any point during the purification process, dispense the solution back into tube, remove the tip, allow the beads to migrate toward the magnet again, then repeat.

- 2B.5. Cap/seal the tubes/plate, and briefly spin again to bring down the remaining liquid. Place the tubes/plate on the magnetic rack to gather the beads. Using a 10 µl pipette tip, carefully remove all residual supernatant from the bottom of the tube/well without disturbing the beads.



Important! Removing all residual supernatant from the Multiplex PCR Reaction *prior* to ethanol washing is critical to obtaining a clean, high-quality library. The above spin and remove step ensure complete removal of supernatant.

Note: A strong compatible magnetic rack is essential. If your magnetic rack or plate cannot collect the magnetic beads effectively, please look into a replacement.

- 2B.6. Add 180 µl of freshly prepared 70% ethanol to each tube/well. Reposition the tubes/plate on the magnetic rack by placing the clear side of the tubes/wells (the side without beads) against the magnet. Allow the beads to completely migrate through the ethanol to the other side. **Do not vortex.** Carefully remove and discard the supernatant without disturbing the beads.

- 2B.7. Repeat step 2B.6

- 2B.8. After the second wash, briefly spin the tubes/plate to bring down all remaining liquid. Place the tubes/plate on the magnet rack to gather the beads. Carefully remove the residual ethanol in each tube/well. Keeping the tubes/plate on the magnetic rack, air-dry the beads at room temperature for 5 minutes. **Do not over or under dry.**

Note: Over-dried beads can dislodge from the side of the tube and lead to cross contamination. They are also more difficult to resuspend during elution. Residual ethanol inhibits PCR and will result in reduced yield. Especially when working with 96-well PCR plates, make sure all residual ethanol is dried (may take longer than 5 minutes) before going to the next step.

- 2B.9. Remove tubes/wells from the magnetic rack and add 10 µl TE buffer directly onto the pellet for each tube/well. Briefly spin and vortex to resuspend the dried beads completely. The DNA will be immediately released from the beads as long as all beads are in solution. Spin briefly to collect the liquid to the bottom. There is no need to remove the beads.

- 2B.10. Proceed to Step 3A. Digestion Reaction.



Safe Stopping Point. Purified products may be stored at 10°C for up to 1 hour or at -20°C for up to 24 hours.

3A. Digestion Reaction

Note: After starting the Digestion Reaction, the samples cannot be stored and must continue to Post-Digestion Purification, then Second PCR Reaction. Plan accordingly.

Note: When thawing CP Reagent Buffer, bring the tube to room temperature. Ensure all visible precipitate is dissolved by vortexing as needed.

Note: Pre-warm a thermal cycler or heating unit to 37°C before beginning the Digestion Reaction.

- 3A.1. Prepare Digestion Reaction Master Mix and add to each purified sample from Step 2B. The magnetic beads in the sample mixture do not affect the Digestion Reaction.

Note: When working with multiple reactions, prepare a master mix. Mix well, then add 10 µl of master mix to each sample.

Digestion Reaction Master Mix		
Reagent	Cap Color	Volume per reaction
Nuclease-Free Water	—	7 µl
CP Reagent Buffer	White	2 µl
CP Digestion Reagent	Yellow	1 µl
Total Volume per reaction		10 µl

Digestion Reaction Mixture	
Reagent	Volume per reaction
Digestion Reaction Master Mix	10 µl
Purified Sample from Step 2B	10 µl
Total Volume per reaction	20 µl

- 3A.2. Mix by pipetting up and down at least 5 times or vortexing vigorously for at least 5 seconds until homogenous. Avoid unnecessarily prolonged vortexing. Spin briefly for 3 seconds to collect the liquid.

Note: It is crucial that the reaction mixture is homogenous prior to incubation. Incomplete mixing can cause digestion of the library or under-digestion of nonspecific products.

Note: If using a PCR plate, use an applicator tool to firmly secure each reaction well and around the perimeter of the plate to prevent evaporation during incubation.

- 3A.3. Incubate at 37°C for exactly 10 minutes. **Do not** incubate shorter or longer than 10 minutes.
- 3A.4. Immediately add 2 µl of Stop Buffer (red cap) to each tube/well and mix by spinning briefly then vortexing. Spin again briefly for 3 seconds to collect the liquid. The volume of each sample is approximately 22 µl.
- 3A.5. Proceed to Step 3B. Post-Digestion Purification immediately.



Important! Do not stop and store samples after the Digestion Reaction. Proceed to Step 3B. Post-Digestion Purification immediately.

3B. Post-Digestion Purification

- 3B.1. Vortex the magnetic beads suspension to disperse beads. Perform a **1.3X** bead-based purification by adding **29 µl** of magnetic beads to each sample. Mix by pipetting up and down at least 5 times or vortex vigorously for at least 5 seconds until homogenous.

Post-Digestion Purification — 1.3X Beads-to-Sample Volume Ratio	
Reagent	Volume per reaction
Digestion Reaction Product	22 µl
Magnetic Beads	29 µl



Important! Magnetic bead volume is critical to the purification process. Always dispense slowly and carefully. Keep the outside of the pipette free from droplets, **AND** make sure the entire volume is added to the sample (residual from inside pipette tips) before discarding the tip.

Ensure the bead + sample solution is thoroughly mixed before incubation, especially when working in a 96-well PCR plate format. Inadequate mixing can result in lowered yields and/or increased background in the final library.

- 3B.2. Incubate the mixture for **5 minutes** at room temperature.
- 3B.3. Briefly spin the tubes/plate. Place the tubes/plate on a magnetic rack and incubate for at least **2 minutes until the liquid is clear**. The beads will be drawn onto one side of each tube/wall. While keeping the tubes/plate on the magnetic rack, carefully remove and discard the supernatant without disturbing the beads.
- 3B.4. Cap/seal the tubes/plate and briefly spin again to bring down the remaining liquid. Place the tubes/plate on the magnetic rack to gather the beads. Using a 10 µl pipette tip, carefully remove all residual supernatant from the bottom of the tube/well without disturbing the beads.



Important! Removing all residual supernatant from the Digestion Reaction *prior* to ethanol washing is critical to obtaining a clean, high-quality library. The above spin and remove step ensure complete removal of supernatant.

- 3B.5. Add 180 µl of freshly prepared 70% ethanol to each tube/well. Reposition the tubes/plate on the magnetic rack by placing the clear side of the tubes/wells (the side without beads) against the magnet. Allow the beads to completely migrate through the ethanol to the other side. **Do not vortex**. Carefully remove and discard the supernatant without disturbing the beads.

3B.6. Repeat step 3B.5.

3B.7. After the second wash, briefly spin the tubes/plate to bring down all remaining liquid. Place the tubes/plate on the magnetic rack to gather the beads. Carefully remove the residual ethanol left behind in each tube/well. Keeping the tubes/plate on the magnetic rack, air-dry the beads at room temperature for 5 minutes. **Do not over or under dry.**

Note: *Over-dried beads can dislodge from the side of the tube and lead to cross contamination, and they are also more difficult to resuspend during elution. Residual ethanol inhibits PCR and will result in reduced yield. Especially when working with 96-well PCR plates, make sure all residual ethanol is dried (may take longer than 5 minutes) before going to the next step.*

3B.8. Remove tubes/wells from the magnetic rack and add 10 µl TE buffer directly onto the pellet for each tube/well. Briefly spin and vortex to resuspend the dried beads completely. The DNA will be immediately released from the beads as long as all beads are in solution. Spin briefly to collect the liquid to the bottom. There is no need to remove the beads.

3B.9. Proceed to Step 4A. Second PCR Reaction immediately.



Important! Do not stop and store samples after Post-Digestion Purification. Proceed to Step 4A. Second PCR Reaction immediately.

4A. Second PCR Reaction

Note: Remember to assign a specific index or unique combination of dual index to each sample before starting this step.

- 4A.1 Thaw Indexed PCR Primers, vortex thoroughly, then spin briefly to collect the liquid. Prepare Second PCR Reaction Master Mix and add to each purified sample from Step 3B. Then add a unique (combination of) Indexed PCR Primer(s) to each sample.

Note: When working with multiple samples, prepare a master mix. Mix well, then add 26 μ l of master mix to each sample.

Second PCR Reaction Master Mix

Reagent	Cap Color	Volume per reaction
Nuclease-Free Water	—	18 μ l
5X 2nd PCR Mix	Blue	8 μ l
Total Volume per reaction		26 μl

Second PCR Reaction Mixture

Reagent	Illumina Volume per reaction	Ion Torrent Volume per reaction
Second PCR Reaction Master Mix	26 μ l	26 μ l
Purified Sample from Step 3B	10 μ l	10 μ l
i5 Dual-Indexed PCR Primer for Illumina	2 μ l	—
i7 Dual-Indexed PCR Primer for Illumina	2 μ l	—
Single-Indexed PCR Primer for Ion Torrent	—	4 μ l
Total Volume per reaction	40 μl	40 μl

Note: For Illumina indexes in plates, the i5 and i7 indexes are already combined. Use 4 μ l of the pooled index per sample. For separate indexes in tubes, use 2 μ l each as shown above.

Note: For Illumina indexes in plates, the i5 and i7 index sequence information (plate maps) can be downloaded from [Product Document Page](#) under Indexes and Useful Tools.



Important! When handling Indexed PCR Primers, take extra care to prevent cross contamination by opening one tube at a time and changing pipette tips and gloves as necessary. Avoid touching the opening and inside of the tubes with your hands, pipette channel, or anything non-disposable.

- 4A.2 Close the caps of the PCR tubes or seal the PCR plate with adhesive film. Spin briefly to collect the liquid, then mix thoroughly by pipetting up and down at least 5 times or vortexing vigorously for at least 5 seconds until homogenous. Avoid unnecessarily prolonged vortexing. Spin briefly for 3 seconds to collect the liquid.

Note: It is crucial that the reaction mixture is homogenous prior to thermal cycling. Incomplete mixing can cause decreased yield and increase non-specific product formation.

Note: If using a PCR plate, use an applicator tool to firmly secure each reaction well and around the perimeter of the plate to prevent evaporation during thermal cycling.

- 4A.3 Load the tubes/plate in the thermal cycler, and run the following thermal cycling protocol to amplify and index the libraries. Use the three tables below for thermal cycling protocol and cycle number suggestions for the Ready-to-Use NGS Panels and Custom NGS Panels.

Note: The Second PCR thermal cycling protocol depends on the starting RNA input amount and RNA quality. Generally, lower quality RNA, lower RNA input amount, or fewer amplicons in a panel requires more PCR cycles.

Second PCR Reaction — Thermal Cycling Protocol				
Step	Temperature	Time	Ramping*	Cycles
Initial Denaturation	95 °C	10 min	-	1
Denaturation	98 °C	15 sec	3 °C/s	See table below
Annealing/Extension	60 °C	75 sec	2 °C/s	
Hold	10 °C	∞		

* For thermal cyclers without adjustable ramp speed, the default setting can be used if max ramping speed is ≤5°C/S.

CleanPlex Respiratory Research Panels — Second PCR Cycle Number	
Application	Number of Cycles
1 or 2 pool Workflows	20

* For optimal yield, Respiratory Research panel may benefit from adjustment to Second PCR cycle numbers based on the sample quality, viral input (when known), and application.

* For applications that specialize in very low viral count detection based on the Ct values, you can make the following adjustments:

For example: to accommodate an increased 2 - 4 mPCR cycles (Step 2A.2) to a total of 12 -14 mPCR cycles you can reduce the 2nd PCR cycle number by 2 - 4 cycles i.e. reduce from 20 cycles to 16 - 18 2nd PCR cycles.

4A.4 Proceed to Step 4B, Post- Second PCR Purification, immediately after cycle completion. Do not allow PCR product to hold at 10 °C for more than 30 minutes.



Important! Important! Do not stop and store samples after the Second PCR Reaction. Proceed to Step 4B. Post-Second PCR Purification immediately.

4B. Post-Second PCR Purification

- 4B.1. Vortex the magnetic beads suspension to disperse beads. Perform a **1X** bead-based purification by adding **40 µl** of magnetic beads to each sample. Mix by pipetting up and down at least 5 times or by vortexing vigorously for at least 5 seconds until homogenous.

Post-Second PCR Purification — 1X Beads-to-Sample Volume Ratio	
Reagent	Volume per reaction
Magnetic Beads	40 µl
Second PCR Reaction Product	40 µl



Important! Magnetic bead volume is critical to the purification process. Always dispense slowly and carefully. Keep the outside of the pipette free from droplets, **AND** make sure the entire volume is added to the sample (residual from inside pipette tips) before discarding the tip.

Ensure the bead + sample solution is thoroughly mixed before incubation, especially when working in a 96-well PCR plate format. Inadequate mixing can result in lowered yields and/or increased background in the final library.

- 4B.2. Incubate the mixture for 5 minutes at room temperature.
- 4B.3. Briefly spin the tubes/plate. Place the tubes/plate on a magnetic rack and incubate for at least **2 minutes until the liquid is clear**. The beads will be drawn onto one side of each tube/wall. While keeping the tubes/plate on the magnetic rack, carefully remove and discard the supernatant without disturbing the beads.
- 4B.4. Cap/seal the tubes/plate, and briefly spin again for to bring down the remaining liquid. Place the tubes/plate on the magnetic rack to gather the beads. Using a 10 µl pipette tip, carefully remove all residual supernatant from the bottom of the tube/well without disturbing the beads.



Important! Removing all residual supernatant from the Multiplex PCR Reaction *prior* to ethanol washing is critical to obtaining a clean, high-quality library. The above spin and remove step ensure complete removal of supernatant.

- 4B.5. Add 180 µl of freshly prepared 70% ethanol to each tube/well. Reposition the tubes/plate on the magnetic rack by placing the clear side of the tubes/wells (the side without beads) against the magnet. Allow the beads to completely migrate through the ethanol to the other side. **Do not vortex**. Carefully remove and discard the supernatant without disturbing the beads.
- 4B.6. Repeat step 4B.5.

- 4B.7. After the second wash, briefly spin the tubes/plate to bring down all remaining liquid. Place the tubes/plate on the magnetic rack to gather the beads. Carefully remove the residual ethanol left behind in each tubes/well. Keeping the tubes/plate on the magnetic rack, air-dry the beads at room temperature for 5 minutes. **Do not over or under dry.**

Note: *Over-drying and under-drying the beads can lead to reduced yield.*

- 4B.8. Remove tubes/wells from the magnetic rack and add 10 µl TE buffer directly onto the pellet for each tube/well. Briefly spin and vortex to resuspend the dried beads completely. The DNA will be immediately released from the beads as long as all beads are in solution. Spin briefly to collect the liquid to the bottom. There is no need to remove the beads. At this point the library is complete and can be stored with beads at –20°C.

Note: *To perform QC and sequencing, use a magnetic rack to separate the beads. Avoid transferring the beads when pipetting the clear supernatant for QC or sequencing.*



Safe Stopping Point. Purified products may be stored with beads at –20°C until ready to sequence. When taking the library out for QC and sequencing, vortex briefly and place the tubes or plate on a magnetic rack to pull the beads to one side. Avoid pipetting the beads, which will affect QC and sequencing.

Quality Control Prior to Sequencing

After library preparation, amplification of viral RNA can be visualized via electrophoresis. This can be accomplished with high sensitivity fragment analyzers such as Agilent® 2100 Bioanalyzer® Instrument and Agilent® High Sensitivity DNA Kit (Agilent, Part. No. 5067-4626). The final library concentration can be obtained via electrophoresis, qPCR method, or Qubit Fluorometer or equivalent. However, qPCR and fluorometric methods will only give you the absolute yield and not differentiate potential background from the actual library. To confirm the quality of the DNA, it is highly recommended that a high sensitivity fragment analyzer is used to visualize the peak shape, size, and potential background concentration.

The presence of a library peak at ~250-350 bp indicates successful amplification of the targeted regions. If no library peak of this size is present, the following reasons can apply:

- The sample can be negative for the targeted regions.
- The viral copy number in the sample is below the limit of detection for this panel.
- The sample contains no SARS-CoV-2, Influenza B, Influenza A H1N1/H1N2/H3N2, or RSV A/B virus.

An in-sample positive control is included in the Respiratory Research Panel v2. A sample with no library peak at the expected range, but with a peak at ~480 bp, can be used to confirm that this protocol was executed correctly.

With sequencing, it can be confirmed that the viral RNA amplified is from the SARS-CoV-2, Influenza B, Influenza A H1N1/H1N2/H3N2, or RSV A/B genome.

Please see troubleshooting guide towards the end of this document if you observe nonspecific peaks or unexpected yield.

After confirmation of library quality, the libraries can be normalized using library peak(s) concentrations only, not including the nonspecific product(s) concentration(s). Then samples with different index combinations can be pooled for sequencing together.

Recommended Sequencing Length and Depth

All CleanPlex Ready-to-Use NGS panels are designed to be compatible with PE 150 bp reads (2x150 bp). Because samples are not likely to contain all for viral targets, the total number of amplified products will vary from vary from one unknown sample to another.

Recommended Sequencing Depth		
Panel	Application	Average Read Depth
CleanPlex Respiratory Research Panel v2	Detection	75-200X
	Subtyping identification	200X-1000X
	co-infection, other in-depth applications	1,000X or more

Terminology and Calculation

Coverage	Also known as depth of coverage, is achieved with one set of paired end reads that cover the entire length of the amplicon
Read	One continuous act of sequencing. For example, 1 million clusters on a flow cell would produce 1 million single reads and 2 million paired-end reads. Paired end reads count as two individual reads, and required for 1x coverage.

When calculating how many samples can be sequenced in one chip, it is Important to refer to the correct total read capacity of the chip.

For example:

For **1000x** coverage of this panel with **493** total amplicons, it requires a total of 493,000 cluster reads or 1 Million paired end reads per sample. With a **Miseq V2 kit** (15 million single reads or 30 million paired end reads) you can sequence about **30** samples per run.

The calculation above used the most conservative numbers. For assaying samples that may not contain all viral targets of covered in the panel, as in this case with the Respiratory Research Panel v2, the total amplicons in the final library will be less than the number of total amplicons total in the panel. Please refer to the content table under Applications section (pg. 6-7) for more information on amplicon count per virus covered in the panel.

For recommended sample multiplexing on various Illumina NGS instruments, refer to the panel-specific product sheet available for download on the product document page:
https://www.paragongenomics.com/product_documents/

A sample multiplexing calculator also be download from the product document page.

Supporting Information

Dual-Indexed PCR Primers for Illumina

Primer Sequences

Each sample is indexed by a pair of Indexed PCR Primers for sequencing on Illumina platforms. XXXXXXXX denotes the index region of the primer. Index sequences are listed below.

i5 Indexed Primer

5' -AATGATACGGCGACCACCGAGATCTACACXXXXXXXXACACTCTTTCCCTACACGACGCTCTTCCGATCT-3'

i7 Indexed Primer

5' -CAAGCAGAAGACGGCATAACGAGATXXXXXXXXGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT-3'

Set A and Set B have mutually exclusive sequences and allow use together to form 384 combinatorial index pairs for sequencing up to 384 samples on one Illumina flow cell.

CleanPlex Targeted Library Kits and Panels are not compatible with most other commercially available index primer kits. Please use CleanPlex PCR Primers for Illumina for best results.

Index sequences in excel format are available in **Illumina Index sequence and Example Sample Sheets**, which can be downloaded from the Product Documents page:

https://www.paragongenomics.com/customer-support/product_documents/

Index Sequences

CleanPlex Dual-Indexed PCR Primers for Illumina Set T

3 x 3 indexes, 9 reactions (SKU 716021)

A section of three i5 Indexes and three i7 Indexes from Illumina Set A or set B to create 9 unique index combinations. Index selection may vary from kit to kit.

CleanPlex Dual-Indexed PCR Primers for Illumina Set A

12 x 8 indexes, 96 reactions (SKU 716006)

12 x 8 indexes, 384 reactions (SKU 716017)

i7 Index	Index Sequence	17 Bases for Sample Sheet All Illumina Systems	i5 Index	Index Sequence	i5 Bases for Sample Sheet	
					MiSeq, NovaSeq, HiSeq 2000/2500	MiniSeq, NextSeq, HiSeq 3000/4000
A701	GTCGTGAT	ATCACGAC	A501	TGAACCTT	TGAACCTT	AAGGTTCA
A702	ACCACTGT	ACAGTGGT	A502	TGCTAAGT	TGCTAAGT	ACTTAGCA
A703	TGGATCTG	CAGATCCA	A503	TGTTCTCT	TGTTCTCT	AGAGAACA
A704	CCGTTTGT	ACAAACGG	A504	TAAGACAC	TAAGACAC	GTGTCTTA
A705	TGCTGGGT	ACCCAGCA	A505	CTAATCGA	CTAATCGA	TCGATTAG
A706	GAGGGGTT	AACCCCTC	A506	CTAGAACA	CTAGAACA	TGTTCTAG
A707	AGGTTGGG	CCCAACCT	A507	TAAGTTCC	TAAGTTCC	GGAACCTA
A708	GTGTGGTG	CACCACAC	A508	TAGACCTA	TAGACCTA	TAGGTCTA
A709	TGGGTTTC	GAAACCCA				
A710	TGGTCACA	TGTGACCA				
A711	TTGACCCT	AGGGTCAA				
A712	CCACTCCT	AGGAGTGG				

CleanPlex Dual-Indexed PCR Primers for Illumina Set B

12 x 8 indexes, 96 reactions (SKU 716018)

12 x 8 indexes, 384 reactions (SKU 716019)

i7 Index	Index Sequence	I7 Bases for Sample Sheet All Illumina Systems	i5 Index	Index Sequence	i5 Bases for Sample Sheet	
					MiSeq, NovaSeq, HiSeq 2000/2500	MiniSeq, NextSeq, HiSeq 3000/4000
Q7005	ATATTCAC	GTGAATAT	Q5001	AGCGCTAG	AGCGCTAG	CTAGCGCT
Q7006	GCGCCTGT	ACAGGCGC	Q5002	GATATCGA	GATATCGA	TCGATATC
Q7007	ACTCTATG	CATAGAGT	Q5007	ACATAGCG	ACATAGCG	CGCTATGT
Q7008	GTCTCGCA	TGCGAGAC	Q5008	GTGCGATA	GTGCGATA	TATCGCAC
Q7015	AGTAGAGA	TCTCTACT	Q5009	CCAACAGA	CCAACAGA	TCTGTTGG
Q7016	GACGAGAG	CTCTCGTC	Q5010	TTGGTGAG	TTGGTGAG	CTCACCAA
Q7017	AGACTTGG	CCAAGTCT	Q5013	AACCGCGG	AACCGCGG	CCGCGGTT
Q7018	GAGTCCAA	TTGGACTC	Q5014	GGTTATAA	GGTTATAA	TTATAACC
Q7023	AATTCTGC	GCAGAATT				
Q7024	GGCCTCAT	ATGAGGCC				
Q7025	ATCTTAGT	ACTAAGAT				
Q7026	GCTCCGAC	GTCGGAGC				

Plated Unique Dual-Indexed (UDI) PCR Primers for Illumina (Set C, D, E and F)

Primer Sequences

Each sample is indexed by a pair of Unique Dual Indexed PCR Primers (10 nucleotides) for sequencing on Illumina platforms. The indexes are available in sets of 96 for a total of 4 plates of 384 unique UDI for sequencing up to 384 samples in one lane.

Important: These 10 nucleotide plated Unique Dual-Indexed PCR primers **cannot** be sequenced together with the 8-nucleotide CleanPlex Dual-Indexed PCR Primers for Illumina Set T, A and B, or tube formatted UDI sets A and B

Index sequences in excel format are available in **Illumina Index sequence and Example Sample Sheets**, which can be downloaded from the Product Documents page:

https://www.paragongenomics.com/customer-support/product_documents/



For plated indexes, Sets C, D, E, and F, plate map and sequences information can be downloaded from [Product Document Page](#) under Indexes.

Single-Indexed PCR Primers for Ion Torrent

Primer Sequences

Each sample is indexed by uniquely designed Indexed PCR Primers for sequencing on Ion Torrent platforms. Only CleanPlex Single-Indexed PCR Primers for Ion Torrent are compatible with CleanPlex workflow for generating libraries intended for Ion Torrent sequencing.

Index Sequences

CleanPlex Single-Indexed PCR Primers v2 for Ion Torrent Sets C, D, E, and F contain index sequences identical to the sequences of the equivalent IonCode™ barcodes. These indexed PCR primers are provided in sealed 96-well PCR plates and arrange in ascending order in columns.



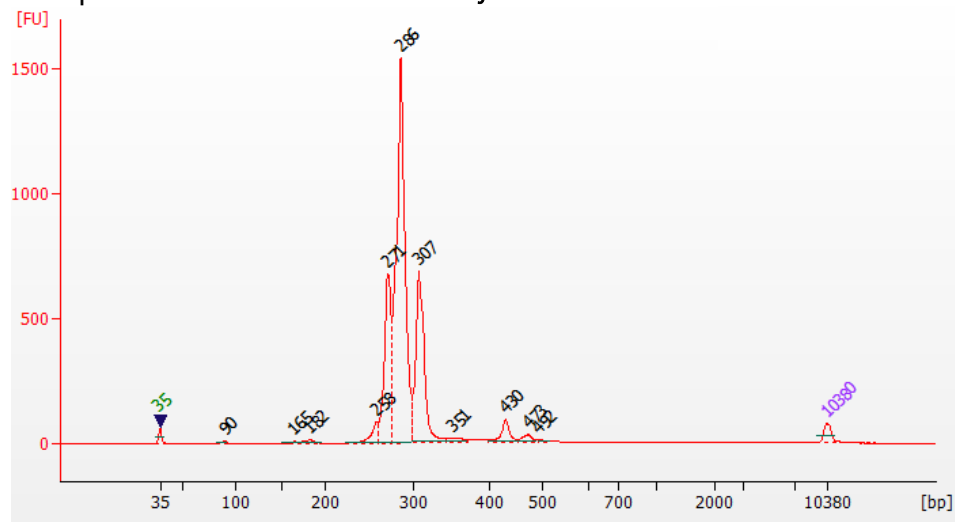
For plated indexes v2 sets C, D, E, and F, plate map and sequences information can be downloaded from [Product Document Page](#) under Indexes.

Troubleshooting Guide

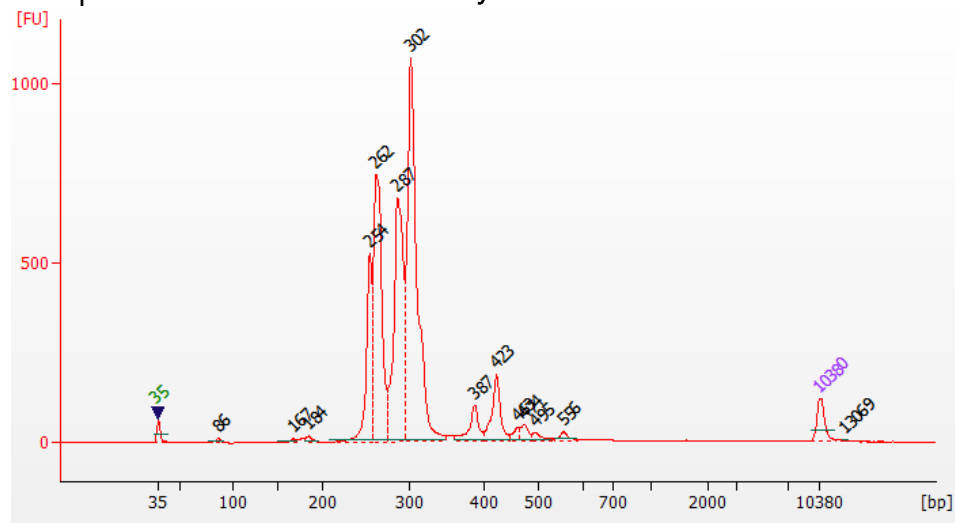
Examples of Libraries Prepared with CleanPlex Respiratory Research Panel v2

Depending on the workflow, the CleanPlex SARS-CoV-2 Panel library peak should be between 250 and 350 bp. Below is a representative Agilent® 2100 Bioanalyzer® trace generated using Pool 1.

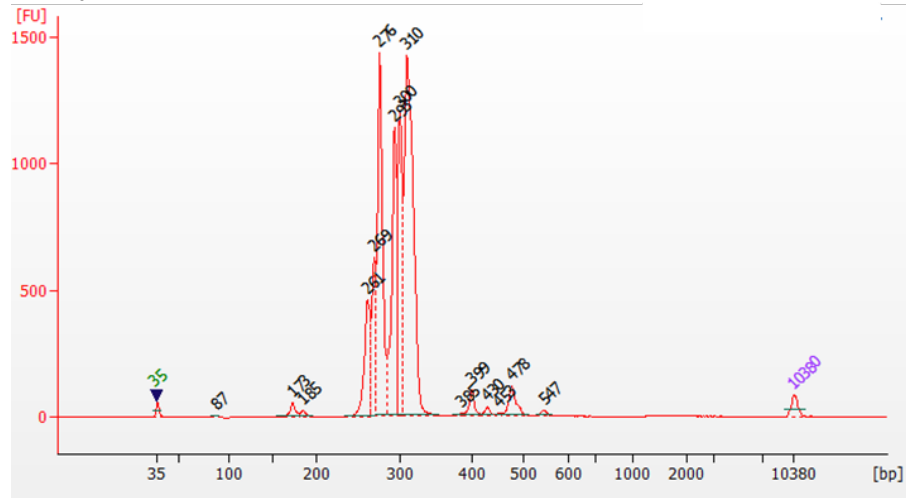
Example of Influenza A H1N1 BioAnalyzer trace



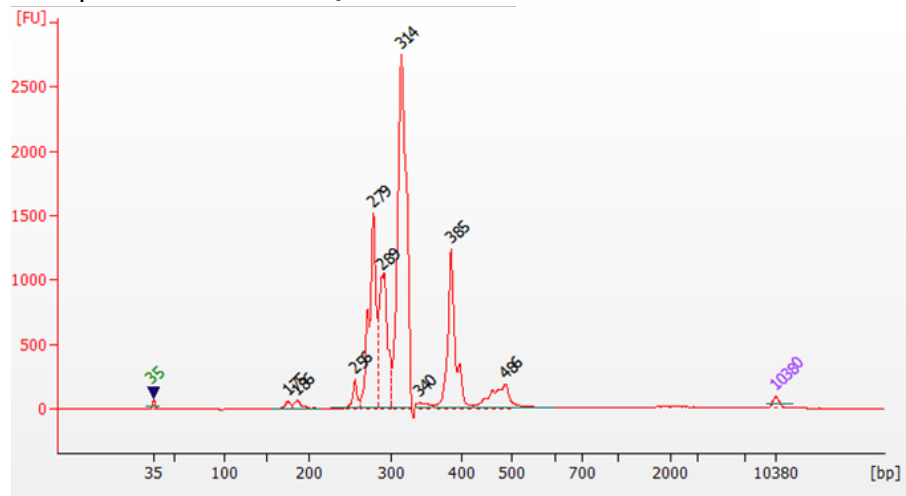
Example of Influenza A H3N2 BioAnalyzer trace



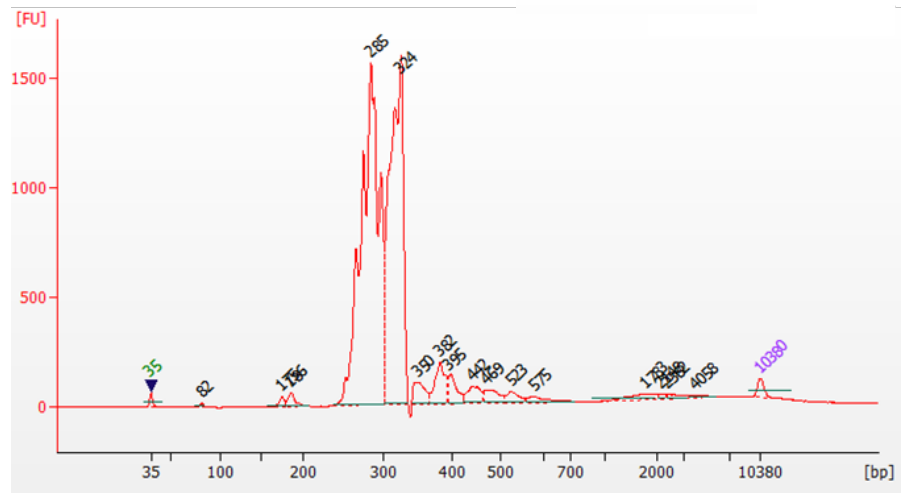
Example of Influenza B BioAnalyzer trace



Example of RSV A BioAnalyzer trace



Example of RSV B BioAnalyzer trace



Potential Causes for Extra Peaks and Suggested Solutions

Peaks around 70–90 bp are index primer dimers from the Second PCR Reaction and result from incomplete removal of low molecular weight DNA fragments during the final magnetic bead purification (Post-Second PCR Purification). When these peaks are high, it usually indicates one or more of the following:

- Inaccurate pipetting of magnetic beads when making a large number of libraries in a short period of time.
- Insufficient removal of supernatant and/or ethanol washes during the last purification.
- Adding more than specified amount of indexed primers to Second PCR Reaction Primer.

Peaks around 150–190 bp are residues of digested non-specific amplification products and adapter dimers. They come from incomplete removal of low molecular weight DNA fragments during the Post-Digestion Purification or nonspecific products formed during or after the Multiplex PCR (mPCR) Reaction due to deviation from protocol or high concentration of panel. The digestion reagent degrades non-specific amplification products into small pieces, which are then removed during magnetic bead purification. These peaks are usually caused by one or more of the following:

- Inaccurate pipetting of magnetic bead volume.
- Insufficient mixing of reaction solutions or bead and sample mixture.
- Insufficient removal of supernatant and ethanol washes during purification.
- Allowing mPCR products to sit for too long (and form nonspecific products) before purification.
- CleanPlex Custom NGS Panels may require panel titration for optimal performance. Often dimers will decrease by reducing the panel concentration in the mPCR Reaction Mixture.
- Incorrect annealing time, specifically unnecessarily longer annealing time.
- Cross contamination of Pool 1 and Pool 2 primers in mPCR reactions.
- Low viral loads

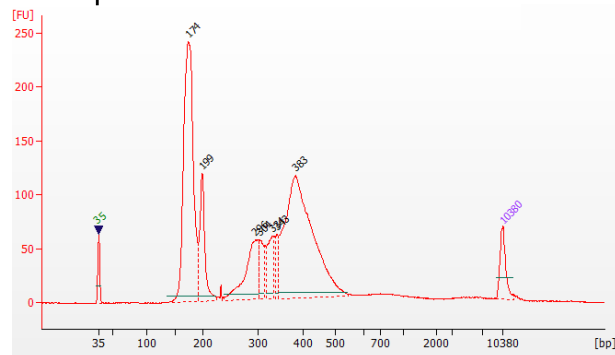
Broad peaks spread across 500 – 10,000 bp range are nonspecific products due to overamplification. Double check that the correct mPCR and Second PCR cycle numbers were used. PCR cycles are determined based on the amplicon count per pool of your panel, RNA input amount, and RNA quality. Try reducing the Second PCR cycles by 2-3 cycles if issue persists. If you're working with a custom panel for organisms with a much smaller genome than human's, consider reducing the RNA input and Second PCR cycles accordingly.

Removing nonspecific products from final libraries

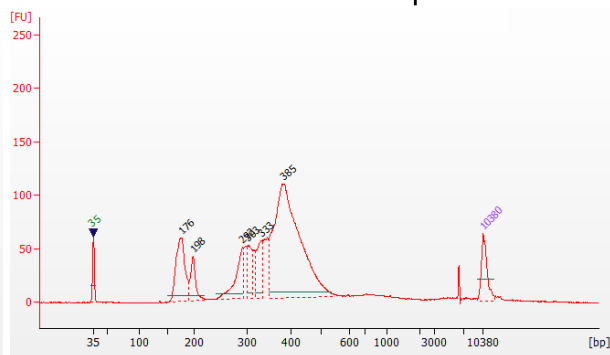
If short nonspecific products described above are present in significant amounts, they can be reduced by pooling indexed libraries (that will be sequenced in the same lane) and performing one additional round of 1X magnetic bead-based purification if the pooled library **concentrations is >3,000 pM** and the **total volume is >20 µL**. Low volume and low concentration libraries should not be bead purified again as it will lead to significant loss of the library of interest. In the figures below, the Agilent Bioanalyzer trace on the left shows a CleanPlex Hereditary Cancer NGS library that contains significant adapter dimers due to poor library preparation. The Bioanalyzer trace on the right shows the same library after an additional 1X magnetic bead-based purification. The bead purification can be repeated once more if volume and concentration still meet the criteria above. We recommend keeping short adapter dimer peaks to less

than 5% for best results. When possible, it's always better to repeat the library preparation with the corrected steps so nonspecific products do not form in the first place.

Before purification



After additional 1X bead-based purification



Potential Reasons for No Library Peak and No In-Sample Positive Control Peak

- 30% ethanol instead of 70% ethanol was used in DNA or cDNA purification with magnetic beads.
- Magnetic beads were not added for one or more of the purification steps.
- Stop Buffer was not added or was added too late after Digestion Reaction, resulting in over-digestion of the samples. This may happen when handling a large number of samples.
- RNA quantification was inaccurate, especially if using spectrophotometric methods, such as the NanoDrop instrument. Try using more input RNA.
- RNA quality is extremely degraded. Try using more input RNA.
- Incompatible indexed PCR primers were using in the Second PCR Reaction.
- A weak or incompatible magnetic rack was used to perform magnetic bead purification, resulting in significant bead loss. Do **not** use magnetic racks designed for 1.5 ml tubes.

Additional Resources

Please visit www.paragongenomics.com/product/faq/ for additional troubleshooting resources.

Data Analysis Recommendations for Illumina

This panel contains a total of 493 amplicons. Of those, 343 amplicons cover 99.7% of the SARS-CoV-2 genome (MN908947/NC_045512.2) with 92 bases uncovered at the ends of the genome. These 343 amplicons are evenly distributed into Pool1 and Pool2 of the Respiratory Research Panel v2. Additional 149 amplicons allow detection of Influenza A (H1N1, H1N2, H3N2), Influenza B, and RSV A/B. These are present in Pool 1 of the panel. Lastly, 1 amplicon covering the TATA Binding protein (TBP) housekeeping gene of the human (host) serves as the control is also in Pool 1. The panel can be used for Illumina 2X150. Below are some notes on data processing.

We recommend the Broad Institute's GATK Best Practice (<https://software.broadinstitute.org/gatk/best-practices/>) as general guiding principles for sequencing data analysis. Analysis can also be performed using Illumina's DNA Amplicon Module, following Illumina's user guide.

1. BED Files.

Visit <https://www.paragongenomics.com/my-account/downloads/> to download panel-specific amplicon insert BED file.

2. Adapter Trimming.

For panels with amplicons of lengths <150 bp, it is recommended to trim leftover adapter sequences for 2X150 sequencing before read mapping.

Following is an example command with open source software cutadapt (<https://cutadapt.readthedocs.io/en/stable/>).

```
cutadapt -g CCTACACGACGCTCTTCCGATCT \
-a AGATCGGAAGAGCACACGTCTGAA \
-A AGATCGGAAGAGCGTCGTGTAGG \
-G TTCAGACGTGTGCTCTTCCGATCT \
-e 0.1 -O 9 -m 20 -n 2 \
-o R1_out.fq.gz -p R2_out.fq.gz R1_in.fq.gz R2_in.fq.gz \
> cutadapt_report.output.txt
```

3. Map reads to reference genome.

The table below lists the isolates used for design and it is recommended to perform read mapping against each viral pathogen reference individually to prevent ambiguous mapped reads. Please note that since the Influenza genomes are segmented, each subtype reference contains multiple sequences.

Pathogen	Reference Sequence Identifier (8 references total for each flu)	Isolate Name
SARS-CoV-2	MN908947/NC_045512.2	Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1
Influenza A H1N1	NC_026431.1 to NC_026438.1	Influenza A virus (A/California/07/2009(H1N1))

Influenza A H1N2	CY017115.1 to CY017122.1	Influenza A virus (A/New York/C1/2003(H1N2))
Influenza A H3N2	NC_007366.1 to NC_007373.1	Influenza A virus (A/New York/392/2004(H3N2))
Influenza B	NC_002204.1 to NC_002211.1	Influenza B virus (B/Lee/1940)
RSV A	AY911262.1	Human respiratory syncytial virus strain ATCC VR-26
RSV B	AY353550.1	Human Respiratory syncytial virus 9320

Bwa mem is recommended for read mapping and de-duplication procedure shall be skipped for amplicon-based analysis.

3. Trim primer sequences.

Before construction of a consensus genome sequence, it is recommended to remove primer sequences. The trimming should be based primarily on reads' mapping starts/ends positions and primers 3' ends' coordinates in ampInser.bed files. We recommend using the DNA amplicon workflow on Illumina instruments for trimming primers and calling variants. An alternative approach for primer trimming is using the software package fgbio. It requires primer genomic coordinates in a tab delimited file which can be provided by Paragon Genomics to customers.

Following is an example command.

```
java -jar fgbio-1.2.0-e7ac607-SNAPSHOT.jar TrimPrimers -i input.bam -o
output.primerTrim.bam -p primer_info.tab -H true
```

4. Calculate QC metrics.

In order to assess the quality of the sequencing results, it is recommended to assign mapped reads to amplicons based on mapping position. Subsequently, the following metrics can be used to measure general performance of the panel.

- **Mapping Rate:** Percentage of reads mapped to reference genome. It assesses primer-dimers and other PCR artifacts.
- **On-Target Rate:** Percentage of mapped reads that aligned to the targeted regions. It assesses binding/amplification specificity of designed primers.
- **Coverage Uniformity:** Percentage of amplicons with read depth equal to or greater than 20% of mean read depth of all amplicons in the panel. It measures performance uniformity of amplicons in the panel. The uniformity of viral panels is not a good indicator of performance as different target regions often have variable expressions.

5. Downstream analysis.

Paragon Genomics could provide required design files to be used in virus detection or strain identification. The suggestions on analysis solutions, please contact sales@paragongenomics or techsupport@paragongenomics.com

Data Analysis Recommendations for Ion Torrent

We recommend customers to use analysis software provided by Ion Torrent. A few suggestions specific to Paragon Genomics panels are given below.

1. **BED Files.** Visit <https://www.paragongenomics.com/my-account/downloads/> to download respiratory panel-specific amplicon insert BED files, which should be used for variant calling on Torrent Suite (TS) and Ion Reporter (IR). Reference genomes can be found in the previous section for Illumina analysis recommendations.
2. **Extra Trimming settings.** When working in the Ion environment, such as the Torrent Suite, Ion Reporter, or VariantCaller Plugin, discard any custom argument and revert to default arguments for your chip type and application combination, then try adding to both Pre-BaseCaller Args and BaseCaller Args : `--extra-trim-left 24 --extra-trim-right 24` , to avoid misassignment of read quality.

Setting	Description
Pre Basecaller args for calibration	<code>--extra-trim-left 24 --extra-trim-right 24</code>
Basecaller args	<code>--extra-trim-left 24 --extra-trim-right 24</code>

3. **Trim tag sequences.** If working with FASTQ directly without BaseCaller trimming setting above, tag sequences can be trimmed with the following instructions. If you're working with already trimmed BAM files, additional trimming with cutadapt is not necessary.

As shown in the diagram of library structure below, a short tag sequence (TAG-1 and TAG-2 respectively) is attached to both ends of an amplicon. The tag sequences are added during primer synthesis and they serve as priming site in second PCR reaction where Ion Torrent adapters are added. It is the best to trim those sequences from sequencing read before read mapping.



It is recommended to trim the tag sequences with open-source software cutadapt using the following options:

```
cutadapt -g CCTACACGACGCTCTTCCGATCT \  
-g TTCAGACGTGTGCTCTTCCGATCT \  
-a AGATCGGAAGAGCGTCGTGTAGG \  
-a AGATCGGAAGAGCACACGTCTGAA \  
-e 0.1 -O 9 -m 20 -n 2 \  
-o out.fq.gz in.fq.gz \  
> cutadapt_report.output.txt
```

The above command would trim left-over adapter sequences as well.

4. **Trim primer sequences.** For a single-pool panel, we don't recommend to trim primer sequences from sequencing reads. For a two-pool panel, however, trimming primer sequences with a software is recommended to avoid false positive calls from primer binding sites. The trimming should be based primarily on reads' mapping starts/ends positions and primers 3' ends' coordinates in amplInsert bed files. We recommend using the Torrent Variant Caller plugin for trimming primers and calling variants. For other applications that require actual primer sequences, please contact Paragon Genomics to acquire them.

Technical Support

For technical assistance, please contact Paragon Genomics Technical Support.

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