

User Manual

Version 1.2



Evercode™ BCR Mega with INTEGRA ASSIST PLUS Barcoding Workflow

For use with

ECIB1500

INTEGRA ASSIST PLUS

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U.S. Pat. No. 10,900,065

U.S. Pat. No. 11,168,355

U.S. Pat. No. 11,427,856

U.S. Pat. No. 11,634,751

U.S. Pat. No. 11,639,519

U.S. Pat. No. 11,680,283

Patents pending in the U.S. and other countries

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Overview

Workflow

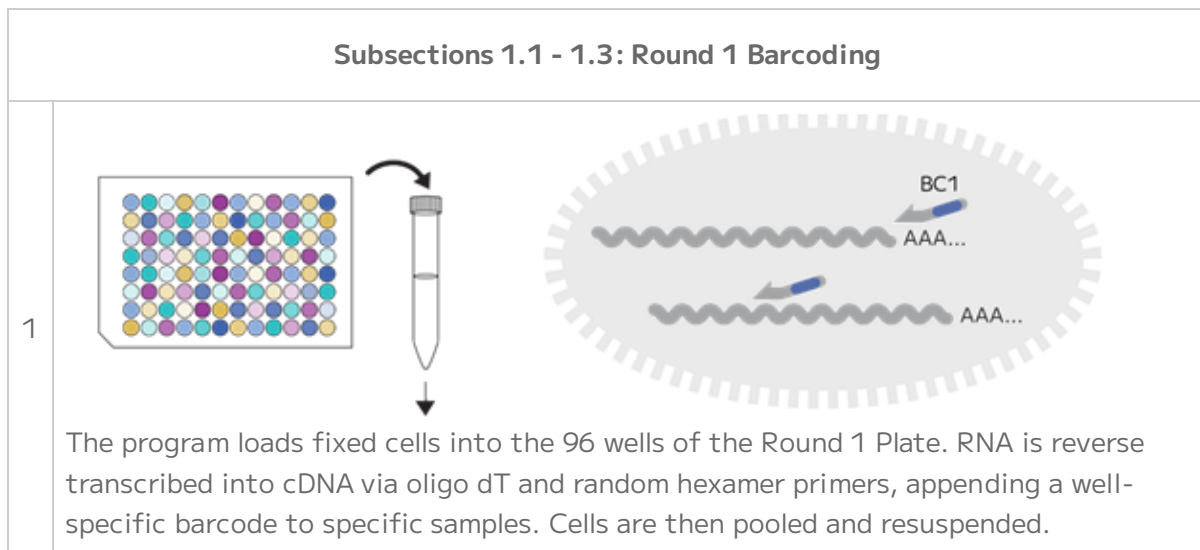
The Evercode combinatorial barcoding workflow is now compatible with the INTEGRA ASSIST PLUS to enable large-scale single cell RNA-Seq experiments through a robust, semi-automated process.

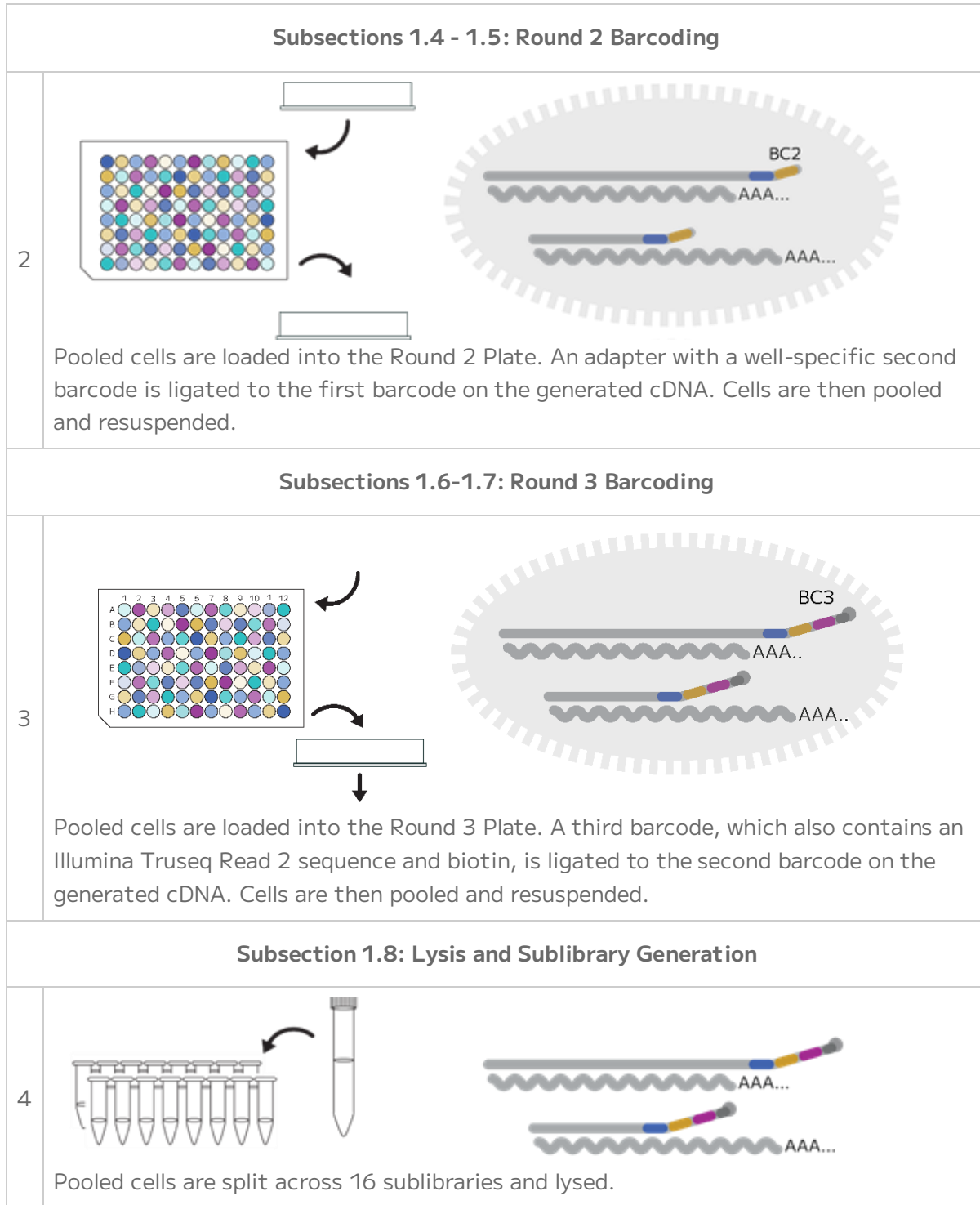
Evercode split-pool combinatorial barcoding brings a simple workflow to large-scale single cell RNA-seq experiments. The Evercode BCR Mega and Whole Transcriptome kit can profile up to 1,000,000 cells across up to 96 different biological samples or experimental conditions. Evercode Fixation kits fix and permeabilize cells so they act as individual reaction compartments. This eliminates the need for dedicated microfluidics instrumentation. Through four rounds of barcoding, the transcriptome of each fixed cell is uniquely labeled. The four rounds of barcoding can yield a vast number of possible barcode combinations, which is more than sufficient to uniquely label up to 1,000,000 cells while avoiding doublets. After sequencing, the Parse Biosciences Analysis Pipeline assigns reads that share the same four barcode combinations to a single cell.

The Evercode BCR and Whole Transcriptome kit is a hybridization-based technology that captures B cells' full length V(D)J sequences.

By integrating the Evercode Mega assay kits with the ASSIST PLUS platform, the semi-automated workflow performs sample normalization and combinatorial barcoding through a series of reverse transcription, ligation, and library preparation steps.

The table below provides a high-level overview of the automated barcoding workflow.





This recommended protocol is intended to be followed when performing the Evercode Mega assays on the INTEGRA ASSIST PLUS liquid handler. The protocol replaces "Section 1. *In Situ* Cell Barcoding" (subsections 1.1 through 1.5) of the standard [Evercode BCR Mega User Guide](#). Upon completing Section 1 of this protocol, proceed to "Section 2. cDNA Capture and Amplification", of the standard Evercode User Guide.

Parse Biosciences and INTEGRA are continuing development and will soon release more semi-automated protocols that will provide comprehensive support for Fixation in addition to Section 2 and Section 3 of the Evercode Whole Transcriptome workflow.

Important Guidelines

The following guidelines provide additional information to obtain optimal performance with the Evercode BCR Mega with INTEGRA ASSIST PLUS barcoding workflow.

Comprehensive guidance on optimizing the complete standard Evercode BCR Mega workflow is provided in the Evercode BCR Mega User Guide. For further information on the experimental workflow, please contact support@parsebiosciences.com.

Please contact support-us@integra-biosciences.com for any questions regarding workflow automation or the INTEGRA ASSIST PLUS instrument.

Sample Input

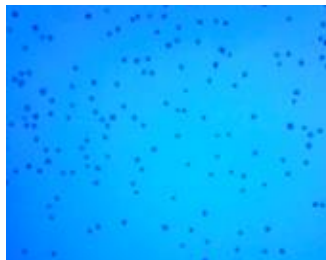
- This protocol begins with cells previously fixed with an Evercode Cell Fixation v3 kit. It is also compatible with samples fixed with Evercode Cell Fixation v2 kits.
- Even if samples were counted before freezing, we strongly recommend counting cells again after thawing to account for any changes in cell concentration during storage and freeze/thaw. Typically, a 5-15% decrease in concentration after thawing should be expected. These counts are used to determine how cells are loaded in the Round 1 Plate, and counting accuracy at this stage is critical to recover the desired number of cells following barcoding.
- When planning on processing many fixed samples, we recommend setting aside a small "counting aliquot" of each sample at the end of fixation. These counting aliquots can be counted the day prior to starting Section 1 of any Evercode assay kit. The Evercode Fixation User Guides outline recommendations for generating aliquots. Because aliquots have undergone a similar storage time and a freeze/thaw, cell counts from these aliquots will be more representative than using counts from immediately after fixation.
- Aliquots should be thawed in a water bath set to 37°C in sets of 2-4 and counted with a hemocytometer or alternative counting device. Cell counts should be recorded in the Sample Loading Table, and any remaining cell material in the thawed counting aliquot should be discarded.
- Once fixed samples have been thawed, they should not be refrozen.

Cell Counting and Quality Assessment

- We recommend a hemocytometer for counting, but alternative counting devices can also be used. If possible, validate counts from alternative devices against a hemocytometer when using Evercode kits for the first time.
- When first using Evercode kits, we suggest saving images at each counting step.

- To assess sample quality, we recommend using viability stains like trypan blue or acridine orange and propidium iodide (AO/PI).
- Examples of trypan blue stained fixed cells are shown below. High quality fixed samples have single distinct cells with <5% cell aggregation and no debris. Higher levels of aggregation will lead to elevated doublets after sequencing. When quantifying fixed samples, it is critical to avoid counting cell debris to avoid overestimating the number of cells.

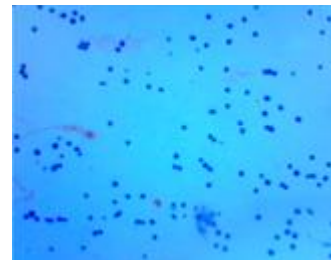
High Quality Sample



Aggregation



Debris



Example trypan blue stained fixed cells.

Avoiding RNase Contamination

- Take standard precautions to avoid introducing RNases into samples or reagents throughout the workflow. Always wear proper laboratory gloves and use aseptic technique.
- Although RNases are not inactivated by ethanol or isopropanol, they are inactivated by products such as RNaseZap RNase Decontamination Solution (Thermo Fisher Scientific). These can be sprayed on benchtops and pipettes.
- Low retention, filtered pipette tips should be used to reduce RNase contamination from pipettes.

Centrifugation

- A range of centrifugation speeds and durations are provided in this workflow in order to optimize and balance high sample retention with resuspension efficiency. Comprehensive information to optimize centrifugation conditions for each sample type is provided in any Evercode assay User Guide.
- Use a swinging bucket rotor for all high-speed centrifugation steps in this workflow. A fixed-angle rotor will lead to substantial cell loss.

Optimizing Cell Recovery

- It is critical to thoroughly resuspend the cells after centrifugation throughout the protocol. Resuspend by repeatedly pipetting until no clumps are visible. Due to cell adherence to tubes, carefully pipette along the bottom and sides of tubes to minimize loss.
- We do not recommend wide bore pipette tips as they make it difficult to resuspend cell pellets adequately.
- Only use recommended polypropylene consumables, as polystyrene tubes will lead to substantial sample loss.
- When using an Evercode assay kit for the first time, we recommend retaining supernatants after each centrifugation step. In the unlikely event of unexpectedly high sample loss, these supernatants can be analyzed to identify points for optimization.

Sample Loading Table

- Ensure that the Parse Evercode WT INTEGRA Mega Sample Loading Table being used is the most up-to-date version. The Sample Loading Table can be downloaded from the Parse Biosciences [Customer Support Suite](#). Customer log-in is required to access the Sample Loading Table.
- The Parse Biosciences Evercode WT INTEGRA Mega Sample Loading Table (Excel spreadsheet) should be completed before starting the experiment.
- If the table isn't working as expected, ensure that Macros are enabled in the Sample Loading Table. Be sure to only edit the colored cells in the table to avoid disturbing any calculations.
- In the unlikely event that samples are not concentrated enough according to the Sample Loading Table (Excel spreadsheet), choose to either:
 - Decrease the "Max number barcoded cells" until the Sample Loading Table no longer gives an error. This will maintain the desired final library proportion between samples but barcode fewer total cells.
 - Proceed as-is. The INTEGRA pipette will dispense the highest possible number of cells based on the existing concentration. This may lead to reduced library yields for samples with particularly low concentrations.

Plate Sealing

- When sealing or unsealing 96 well plates, do not splash liquid onto the PCR plate seal or between wells. Securing plates in PCR tube racks will minimize this occurrence.
- PCR plate seals may be difficult to remove. Carefully peel off the PCR plate seal while applying downward pressure on the edges of the plate to keep it in the PCR plate rack. Avoid touching the top of the open wells.

Sample Concentrations

- The recommended cell concentration is between 3,000 cells per μL . If the cell concentration is too high, dilute the sample with the Pre-Lysis Dilution Buffer to the desired concentration. Ensure you save at least **500 μL** of Pre-Lysis Dilution Buffer for step 1.8.2.

PCR Freezer Block

- The PCR freezer block changes color from dark purple to bright pink (too warm) when the block temperature exceeds 7°C . If 70% of the block is bright pink, replace the PCR freezer block with a fully frozen dark purple block.
- To maintain optimal performance and minimize temperature fluctuations, store the PCR Freezer Blocks in a -20°C freezer when not in use.
- Tip pinching may occur when using a fully frozen PCR freezer block for a plate pooling step. To minimize tip pinching, a fully frozen PCR freezer block should be warmed slightly by a few degrees by leaving it at room temperature for 10 minutes before using it on the INTEGRA ASSIST PLUS Deck.
- To ensure a secure positioning within the freezer block, apply firm pressure on the PCR plates until they are securely seated. Avoid touching the top of the open wells.

INTEGRA ASSIST PLUS Pipetting Programs

- Ensure that the VIALAB program is installed on the same computer that will be used to communicate with the D-ONE Pipetting Module.
- Ensure that Evercode workflow script calibration had been confirmed prior to running the INTEGRA + Parse workflow. This can be done by running the [Evercode WT with INTEGRA ASSIST PLUS Calibration Scripts](#) available on the Customer Support Suite.

- Ensure that the .csv worklists generated via the Parse Biosciences Evercode WT INTEGRA Mega Sample Loading Table (the "DiluentVolumes.csv" worklist and the "SampleVolumes.csv" worklist) are accessible for upload to the VIALAB program.
- Automated pipetting programs are set up and can be selected using the pipette's user interface. In the INTEGRA + Parse workflow, prompts are built into the programs as checkpoints. When the prompt is followed by a double dash, "--", the program will continue. If the prompt does not contain a double dash, "--", it is followed by another prompt.
- When uploading a new worklist to the VIALAB program, all pipetting settings will be automatically reset to standard default settings and must be readjusted to the correct settings specified for that worklist. For images and details of correct pipette settings for each worklist, see Appendix A.



Deck Loading

- To prevent malfunctions during the procedure, ensure that all unnecessary labware is cleared from the deck before initiating a new program on the INTEGRA ASSIST PLUS.







Parse Reagents

The Evercode BCR with ASSIST PLUS includes reagents in the following boxes. Safety Data Sheets for these reagents can be provided upon request.




-20°C Reagents Store -20°C, PN HBG100

| LABEL | ITEM | PN | FORMAT | QTY |
|---|-------------------------|--------|-----------------------------------|-----|
|  | Round 1 Plate | HBG101 | Green semi-skirted 96 well plate | 1 |
|  | Round 2 Plate | MG102 | Blue semi-skirted 96 well plate | 1 |
|  | Round 3 Plate | MG103 | Yellow semi-skirted 96 well plate | 1 |
|  | Resuspension Buffer | MG104 | 5 mL tube | 1 |
|  | Sample Dilution Buffer | MG105 | 2 mL tube | 1 |
|  | Round 2 Ligation Buffer | MG106 | 5 mL tube | 1 |
|  | Round 2 Ligation Enzyme | MG107 | 1.5 mL tube | 1 |
|  | Round 2 Stop Buffer | MG108 | 2 mL tube | 1 |
|  | Round 3 Stop Buffer | MG109 | 5 mL tube | 1 |
|  | Pre-Lysis Wash Buffer | MG110 | 5 mL tube | 1 |








| LABEL | ITEM | PN | FORMAT | QTY |
|---|---------------------------|-------|-------------|-----|
|  | Round 3 Ligation Enzyme | MG111 | 1.5 mL tube | 1 |
|  | Pre-Lysis Dilution Buffer | MG112 | 2 mL tube | 1 |
|  | Lysis Enzyme | MG113 | 1.5 mL tube | 1 |
|  | Bead Wash Buffer | MG114 | 5 mL tube | 1 |
|  | Wash Buffer 1 | MG115 | 5 mL tube | 1 |
|  | Wash Buffer 2 | MG116 | 5 mL tube | 1 |
|  | Capture Enhancer | MG117 | 1.5 mL tube | 1 |
|  | Binding Buffer | MG118 | 1.5 mL tube | 1 |
|  | Wash Buffer 3 | MG119 | 5 mL tube | 1 |
|  | Template Switch Buffer | MG120 | 2 mL tube | 1 |
|  | Template Switch Enzyme | MG121 | 1.5 mL tube | 1 |
|  | Template Switch Primer | MG122 | 1.5 mL tube | 1 |
|  | cDNA Amp Mix | MG123 | 1.5 mL tube | 1 |

| LABEL | ITEM | PN | FORMAT | QTY |
|---|-------------------------|-------|-------------|-----|
|  | cDNA Amp Primers | MG124 | 1.5 mL tube | 1 |
|  | Fragm/End Prep Buffer | MG125 | 1.5 mL tube | 1 |
|  | Fragm/End Prep Enzymes | MG126 | 1.5 mL tube | 1 |
|  | Ligation Adapter | MG127 | 1.5 mL tube | 1 |
|  | Adapter Ligation Buffer | MG128 | 1.5 mL tube | 1 |
|  | Adapter Ligation Enzyme | MG129 | 1.5 mL tube | 1 |
|  | Library Amp Mix | MG130 | 1.5 mL tube | 1 |

4°C Reagents. Store 4°C, PN HBG200

| LABEL | ITEM | PN | FORMAT | QTY |
|---|--------------------|-------|-------------|-----|
|  | Spin Additive | MG201 | 1.5 mL tube | 1 |
|  | Lysis Buffer | MG202 | 1.5 mL tube | 1 |
|  | Streptavidin Beads | MG203 | 1.5 mL tube | 1 |

BCR -20°C Reagents Store at -20°C, PN BGC100

| LABEL | ITEM | PN | FORMAT | QTY |
|---|------------------------------|-------|-------------|-----|
|  | Hybridization Mix | GC101 | 1.5 mL tube | 1 |
|  | Hybridization Enhancer | GC102 | 1.5 mL tube | 1 |
|  | Blocker Solution | GC103 | 1.5 mL tube | 1 |
|  | Evercode Blocker Solution | GC108 | 0.5 mL tube | 1 |
|  | Human BCR Panel | GC109 | 0.5 mL tube | 1 |
|  | Enrichment Primer Mix | GC105 | 1.5 mL tube | 1 |
|  | Enrichment Amplification Mix | GC106 | 0.5 mL tube | 1 |

BCR 4°C Reagents Store at 4°C, PN BGC200

| LABEL | ITEM | PN | FORMAT | QTY |
|---|-----------------------------|-------|-------------|-----|
|  | Bead Wash Buffer A | GC301 | 1.5 mL tube | 1 |
|  | Bead Wash Buffer B | GC302 | 2 mL tube | 1 |
|  | Streptavidin Binding Buffer | GC303 | 5 mL tube | 1 |
|  | Streptavidin Binder Beads | GC304 | 1.5 mL tube | 1 |

Parse-Provided Equipment

The following is a list of equipment provided by Parse Biosciences, required to successfully perform the Evercode workflows on the INTEGRA ASSIST PLUS.

| ITEM | PN | QTY |
|------------------------------------|----------|-----|
| Thermochromic PCR Cold Block | NTAC1102 | 3 |
| Thermochromic PCR Cold Block Riser | NTAC1103 | 3 |
| Parse Cold Block 1 | NTAC1101 | 1 |

INTEGRA Components

The following are required INTEGRA ASSIST PLUS components needed to run Section 1. *In situ* Cell Barcoding (1.1 to 1.5) of the Parse Biosciences assay on the INTEGRA ASSIST PLUS platform.

| ITEM | ITEM TYPE | PN | QTY |
|--|-----------|------|-----|
| Pipette Communication Module for VIAFLO Pipette | Accessory | 4221 | 3 |
| ASSIST PLUS Slanted Plate Holder (0°-30°) | Adapter | 4510 | 1 |
| Tip Deck for D-ONE Pipetting Module | Base | 4535 | 1 |
| Dual Reservoir Adapter (ANSI/SLAS footprint) | Adapter | 4547 | 1 |
| ASSIST PLUS Labware Pedestal (+24 mm) for D-ONE, portrait, for 10 mL, 25 mL, 100 mL, reservoirs and plates/reservoirs in SLAS/ANSI format (24 mm Labware Pedestal) | Adapter | 4551 | 1 |
| D-ONE Pipetting Module 1-Ch, 5-1250 µL | Pipette | 4532 | 1 |
| VIAFLO Pipette 12-Ch, 5-125 µL | Pipette | 4632 | 1 |
| ASSIST PLUS Base Unit | Main | 4505 | 1 |
| Communication/Charging Cable for VIAFLO | Accessory | 4226 | 1 |

INTEGRA-Provided Consumables

The following is a list of consumables provided by INTEGRA, required to successfully perform Parse Evercode workflows on the INTEGRA ASSIST PLUS.

| ITEM | ITEM TYPE | PN | QTY |
|---|------------------|------|-----|
| 8 Row Reagent Reservoirs, Partitioned (32 mL/row) with SUREFLO design | INTEGRA-Provided | 6373 | 1 |
| 25 mL basin reservoir liners | INTEGRA-Provided | 4316 | 1 |
| 1250 μ L pipette tips (Sterile/Filter/Low Retention) | INTEGRA-Provided | 6545 | 1 |
| 125 μ L pipette tips (Sterile/Filter/Low Retention) | INTEGRA-Provided | 6565 | 1 |

Consumables

The following equipment and consumables are required to perform the protocol, but are not provided by INTEGRA or by Parse Biosciences. Note that this list does not include standard laboratory equipment, such as freezers.

Consumables

| ITEM | SUPPLIER | PN | QTY |
|-------------------------------------|---------------------------|------------------|-----|
| Sterilized 40 µm mini cell strainer | DiagnoCine | FNK-HT-AMS-14002 | 2 |
| 10 mL transport tubes | GlobeScientific™ | 6102S | 2 |
| 1.5 mL tubes | GENESEE SCIENTIFIC CORP | 21-257 | 2 |
| PCR strip tubes (bag of 12) | USA SCI | 1402-4700 | 1 |
| Semi skirted plates (clear) | Thermo Fisher Scientific® | E951020362 | 2 |

Equipment

| ITEM | SUPPLIER | PN | NOTES |
|-----------------------|-----------------------|---------|--|
| Microcentrifuge | Various Suppliers | Varies | Compatible with 1.5 mL tubes. |
| Hemocytometer | Sigma-Aldrich® | Z359629 | Or other cell counting device. We recommend validating alternatives relative to a hemocytometer. |
| Plate Seal Applicator | Various Suppliers | Varies | Capable of adhering plate sealing films to 96 well plates. |
| T100 Thermal Cycler | Bio-Rad Laboratories® | 1861096 | Or an equivalent thermocycler compatible with semi-skirted 96 well plates, 0.2mL PCR tubes with up to 100 µL of sample volume, sample heating and cooling from 4-98°C, and a heated lid capable of 30-105°C. |
| Trypan Blue | Various Suppliers | Varies | Or alternative dyes to assess cell viability, such as AO/PI. |

Section 1: Automation Setup

Section 1.1. Sample Normalization

Prior to setting up the Automation workflow, count the cells to assess quality and concentration of the fixed sample(s).

Fixed cells should be diluted to a concentration of 3,000 cells per μL .

After adjusting the sample(s) to the recommended dilution range, download the Sample Loading Table MACRO (Section 1.1.2), which will be used as reference for allocating the fixed cells into the 96-well PCR plate, ready for the protocol to start.

The program uses the sample dilution buffer on Deck A to normalize fixed samples from plate format on Deck C into intermediate dilution plate on Deck B.

1. Gather the following components and reagents:

| ITEM | SOURCE | QTY | HANDLING AND STORAGE |
|---|---|-----------|---|
| D-ONE Pipetting Module 1-Ch, 5-1250 μL | INTEGRA Component | 1 | |
| Tip Deck for D-ONE Pipetting Module | INTEGRA Component | 1 | |
| 24 mm Labware Pedestal | INTEGRA Component | 1 | |
| Thermochromic PCR Cold Block | Parse-Provided | 2 | Pull the Freezer Block with stabilizer from the -20°C freezer and leave them at room temperature for 10 minutes prior to use. |
| Thermochromic PCR Cold Block Riser | Parse-Provided | 2 | |
| Parse Cold Block 1 | Parse-Provided | 1 | Keep on ice when not in use. |
| Semi-Skirted 96 Well PCR Plate | Consumables | 2 | |
| ● Sample Dilution Buffer | -20°C Reagents (Parse Reagents) | 2 mL tube | Thaw at room temperature then store on ice. Mix by inverting 3x. |
| □ Round 1 Plate | -20°C Reagents (Parse Reagents) | 1 | Place directly on ice. |

- Download Biosciences Evercode WT INTEGRA Mega Sample Loading Table. The most current version of the Evercode WT Mega INTEGRA Sample Loading Table can be found on the Parse Biosciences [Customer Support Suite](#). Customer log-in is required to access the Sample Loading Table.
- Start with the Sample Loading Table tab of the worksheet. Per the instructions in the worksheet, input number of samples (Figure 1).



Note: For more information on using the Sample Loading Table, see the "Important Guidelines" section of the User Guide.

This sheet should be filled out prior to starting Section 1.

| Step | Instructions |
|------|--|
| 1 | Ensure Macros are enabled. |
| 2 | Input the number of samples. |
| 3 | Input the target number of barcoded cells. Note: The default is 1,000,000 cells for Evercode WT Mega. |
| 4 | Input your sample names. |
| 5 | Input the target percentage representation of each sample in the final library. CRITICAL: No percentage can be lower than 1.05%. If not already done, count the samples as described in Section 1.1 of the Evercode WT Mega User Manual. |
| 6 | Input stock cell concentration for each sample. |
| 7 | Open the "Integra Loading Table" sheet and load the samples in the appropriate wells and volumes using a semi-skirted plate. |
| 8 | CRITICAL: Ensure that Sample Dilution Buffer is completely thawed before use. |
| 9 | Open the "Diluent Volumes" sheet. Click on the "Generate a Worklist for Import into VIALAB" to generate the worklist file. |
| 10 | Open the "Sample Volumes" sheet. Click on the "Generate a Worklist for Import into VIALAB" to generate the worklist file. |

Number of Samples (Step 2): **CRITICAL:** We do not recommend editing cells highlighted in grey.

Target Number Barcoded Cells (Step 3):

| Sample # | Sample Name (Step 4) | Percent of Library (Step 5) | Stock Concentration (cells/uL) (Step 6) | Number of Wells | Targeted Number of Barcoded Cells | Required Sample Concentration (cells/uL) |
|----------------|----------------------|-----------------------------|---|-----------------|-----------------------------------|--|
| 1 | Sample A | 40.00% | 3,000 | 38 | 400000 | 2148 |
| 2 | Sample B | 35.00% | 2,750 | 34 | 350000 | 2100 |
| 3 | Sample C | 25.00% | 2,500 | 24 | 250000 | 2125 |
| TOTALS: | | 100.00% | | 96 | 1,000,000 | |

Figure 1: Evercode WT Mega Sample Loading Table.

- While minimizing time on ice, count the number of cells in each sample with a hemocytometer or alternative cell counting device. Record the cell count.
- Enter Target Number of Barcoded Cells, Sample Name, Percent of Library and Stock Concentration for corresponding samples (Figure 2).



Note: If any parameter is out of range, the cells will turn pink in color and/or an error message will appear (Figure 2). Be sure to address and adjust worksheet input values appropriately before continuing.

Note: If the cell concentration is too high, we recommend diluting the sample with the Pre-Lysis Dilution Buffer. See the "Important Guidelines" section for details.

This sheet should be filled out prior to starting Section 1.

| Step | Instructions |
|------|---|
| 1 | Ensure Macros are enabled. |
| 2 | Input the number of samples. |
| 3 | Input the target number of barcoded cells. Note: The default is 100,000 cells for Evercode WT. |
| 4 | Input your sample names. |
| 5 | Input the target percentage representation of each sample in the final library. CRITICAL: No percentage can be lower than 2.09%. If not already done, count the samples as described in Section 1.1 of the Evercode WT User Manual. |
| 6 | Input stock cell concentration for each sample. |
| 7 | Prepare the dilutions as described. CRITICAL: Ensure that Sample Dilution Buffer is completely thawed before use. |
| 8 | Open the "Plate Configuration" sheet. With the plate on ice, add 14 μ L of each diluted sample to the appropriate well(s) of the Round 1 Plate as shown in the plate map. CRITICAL: Follow the instructions in the User Guide with respect to sample mixing and changing tips. |

Number of Samples (Step 2): **CRITICAL:** We do not recommend editing cells highlighted in grey.

Target Number Barcoded Cells (Step 3):

| Sample # | Sample Name (Step 4) | Percent of Library (Step 5) | Stock Concentration (cells/ μ L) (Step 6) | Number of Wells | Targeted Number of Barcoded Cells | Required Sample Concentration (cells/ μ L) |
|----------------|----------------------|-----------------------------|---|-----------------|-----------------------------------|--|
| 1 | | 100.00% | 5,000 | 48 | 1000000 | 5203 |
| TOTALS: | | 100.00% | | 48 | 1,000,000 | |

CRITICAL: This cell stock concentration is too low.

Figure 2: Example error message, noting that the sample stock concentration is too low.

- Navigate to the "INTEGRA Loading Table" tab and check that the Minimum Diluent Needed (μ L) does not exceed 1,800 μ L (Figure 3).
- Referring to the "INTEGRA Loading Table" tab, manually load fixed samples into the directed "Sample Location" well into a new Eppendorf semi-skirted plate. Note that any individual sample may require loading into more than one "Sample Location" well. This is the sample stock plate.
- Store the sample stock plate on ice for later use.



Note: Example: Sample 1 is loaded into Sample Location A1 with a minimum volume of 172.4 μ L. More sample volume (up to a maximum of 200 μ L total sample volume) can be loaded to reduce bubbles during mixing.

| Sample Name | Sample Location | Min Sample Stock Needed for Dilution (μ L) | Min Diluent Needed (μ L) |
|-------------|-----------------|---|-------------------------------|
| Sample One | A1 | 172.4 | 1120.0 |
| Sample One | A2 | 172.4 | |
| Sample One | A3 | 172.4 | |
| Sample One | A4 | 172.4 | |
| Sample One | A5 | 172.4 | |
| | A6 | | |
| | A7 | | |
| | A8 | | |
| | A9 | | |
| | A10 | | |
| | A11 | | |
| | A12 | | |
| | B1 | | |
| | B2 | | |
| | B3 | | |
| | B4 | | |
| | B5 | | |
| | B6 | | |
| | B7 | | |
| | B8 | | |
| | B9 | | |
| | B10 | | |
| | B11 | | |
| | B12 | | |
| | C1 | | |
| | C2 | | |
| | C3 | | |
| | C4 | | |
| | C5 | | |
| | C6 | | |
| | C7 | | |

*Note: due to semi-skirted plate volumes, multiple wells might be needed for the same samples.

Figure 3: INTEGRA Loading Table tab noting Minimum Diluent Needed and Sample Locations.

- Navigate to the “Diluent Buffer Volumes” tab and click on the purple box labeled “Generate a Worklist for Import into VIALAB”. Save the generated CSV file (called “DiluentVolumes.csv”) for later use (Figure 4).

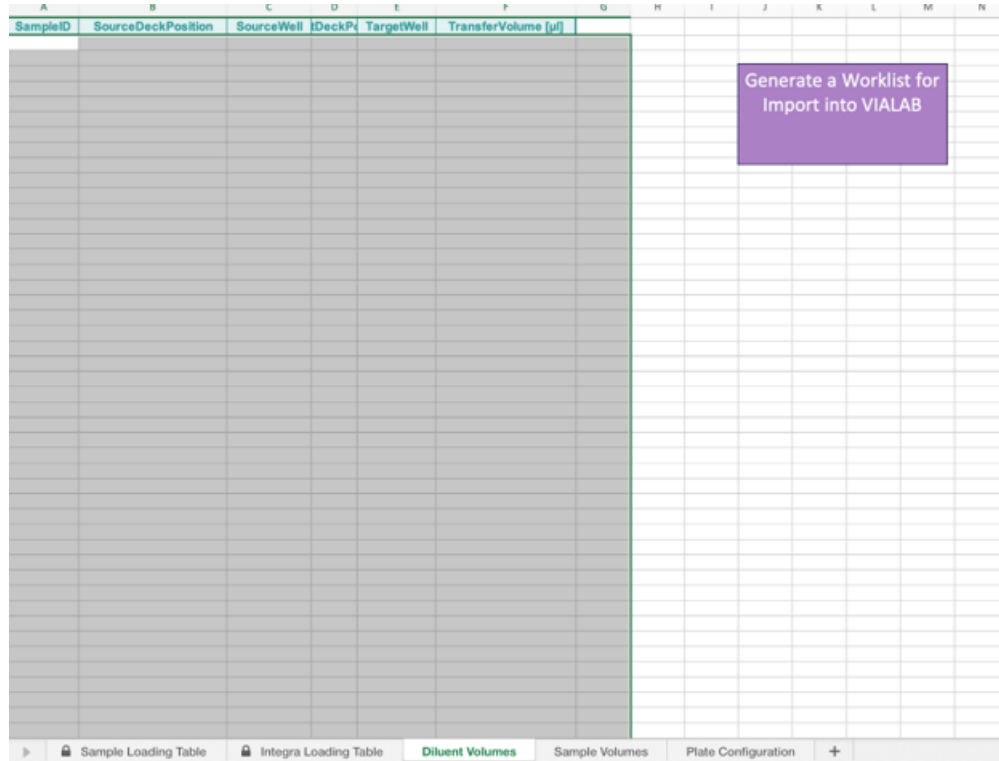
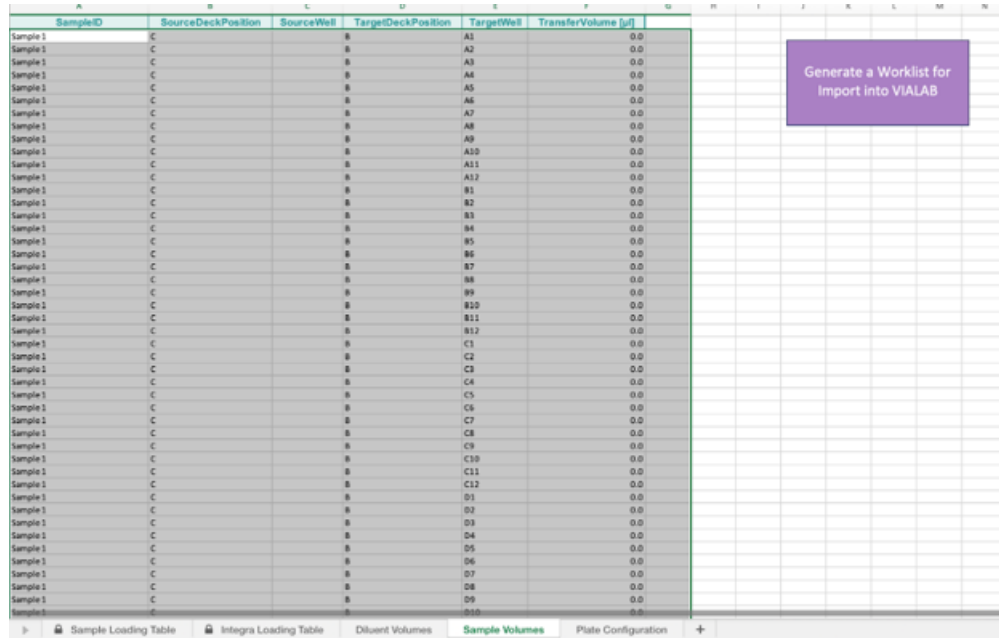


Figure 4: Diluent Buffer Volumes tab for generating a VIALAB worklist.

- Navigate to the “Sample Dilutions Volumes” tab and click on the purple box labeled “Generate a Worklist for Import into VIALAB”. Save the generated CSV file (called “SampleVolumes.csv”) for later use (Figure 5).



| SampleID | SourceDeckPosition | SourceWell | TargetDeckPosition | TargetWell | TransferVolume [µl] |
|----------|--------------------|------------|--------------------|------------|---------------------|
| Sample 1 | C | B | A1 | A1 | 0.0 |
| Sample 1 | C | B | A2 | A2 | 0.0 |
| Sample 1 | C | B | A3 | A3 | 0.0 |
| Sample 1 | C | B | A4 | A4 | 0.0 |
| Sample 1 | C | B | A5 | A5 | 0.0 |
| Sample 1 | C | B | A6 | A6 | 0.0 |
| Sample 1 | C | B | A7 | A7 | 0.0 |
| Sample 1 | C | B | A8 | A8 | 0.0 |
| Sample 1 | C | B | A9 | A9 | 0.0 |
| Sample 1 | C | B | A10 | A10 | 0.0 |
| Sample 1 | C | B | A11 | A11 | 0.0 |
| Sample 1 | C | B | A12 | A12 | 0.0 |
| Sample 1 | C | B | B1 | B1 | 0.0 |
| Sample 1 | C | B | B2 | B2 | 0.0 |
| Sample 1 | C | B | B3 | B3 | 0.0 |
| Sample 1 | C | B | B4 | B4 | 0.0 |
| Sample 1 | C | B | B5 | B5 | 0.0 |
| Sample 1 | C | B | B6 | B6 | 0.0 |
| Sample 1 | C | B | B7 | B7 | 0.0 |
| Sample 1 | C | B | B8 | B8 | 0.0 |
| Sample 1 | C | B | B9 | B9 | 0.0 |
| Sample 1 | C | B | B10 | B10 | 0.0 |
| Sample 1 | C | B | B11 | B11 | 0.0 |
| Sample 1 | C | B | B12 | B12 | 0.0 |
| Sample 1 | C | B | C1 | C1 | 0.0 |
| Sample 1 | C | B | C2 | C2 | 0.0 |
| Sample 1 | C | B | C3 | C3 | 0.0 |
| Sample 1 | C | B | C4 | C4 | 0.0 |
| Sample 1 | C | B | C5 | C5 | 0.0 |
| Sample 1 | C | B | C6 | C6 | 0.0 |
| Sample 1 | C | B | C7 | C7 | 0.0 |
| Sample 1 | C | B | C8 | C8 | 0.0 |
| Sample 1 | C | B | C9 | C9 | 0.0 |
| Sample 1 | C | B | C10 | C10 | 0.0 |
| Sample 1 | C | B | C11 | C11 | 0.0 |
| Sample 1 | C | B | C12 | C12 | 0.0 |
| Sample 1 | C | B | D1 | D1 | 0.0 |
| Sample 1 | C | B | D2 | D2 | 0.0 |
| Sample 1 | C | B | D3 | D3 | 0.0 |
| Sample 1 | C | B | D4 | D4 | 0.0 |
| Sample 1 | C | B | D5 | D5 | 0.0 |
| Sample 1 | C | B | D6 | D6 | 0.0 |
| Sample 1 | C | B | D7 | D7 | 0.0 |
| Sample 1 | C | B | D8 | D8 | 0.0 |
| Sample 1 | C | B | D9 | D9 | 0.0 |
| Sample 1 | C | B | D10 | D10 | 0.0 |

Figure 5: Sample Dilutions Volumes tab for generating a VIALAB worklist.

11. Navigate to the "Plate Configuration" tab to visualize the final sample location and orientation within the 96 well plate format (Figure 6).

Evercode WT Round 1 Barcoding Plate Configuration

- For more details on using this Sample Loading Table, see the Important Guidelines section of the User Manual

Use the following plate layout to load samples into the Round 1 Plate in Section 1.2.

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 |
|---|---|---|---|---|---|---|---|---|---|----|----|----|
| A | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| B | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| C | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 |
| D | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 |
| F | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 |
| F | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 |
| G | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 |
| H | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 |

| Sample Number | Sample Name | Percent Contributing |
|---------------|-------------|----------------------|
| 1 | | 25.00% |
| 2 | | 25.00% |
| 3 | | 25.00% |
| 4 | | 25.00% |

Figure 6: Plate Configuration tab visualizes the sample locations and orientations.

12. Open the VIALAB program **MG S1 St1 DONE V3** and navigate to the "Method" section. In the "02 Worklist", under the "Worklist and Volumes" tab, upload the "DiluentVolume.csv" worklist file generated in Step 9 using the "Import" button (Figure 7).

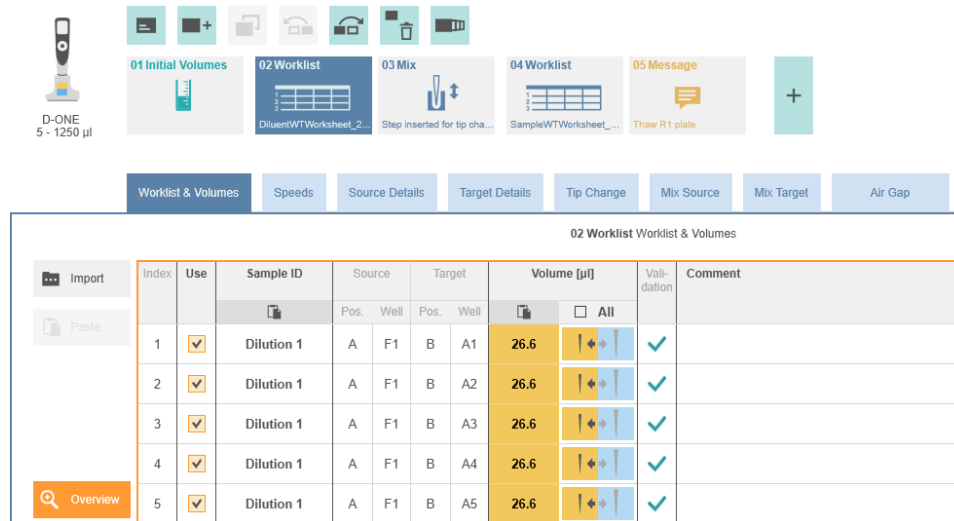


Figure 7: VIALAB worklist generation for diluent volumes using 02 Worklist.



CRITICAL! After uploading the worklist, all pipetting settings will automatically reset to standard default settings. Readjust the pipette settings to the correct worklist parameters. See Appendix A for the complete list of pipette parameters for each worklist.

- In the "04 Worklist", under the "Worklist and Volumes" tab, upload the "SampleVolume.csv" worklist file generated in Step 10 using the "Import" button (Figure 8).

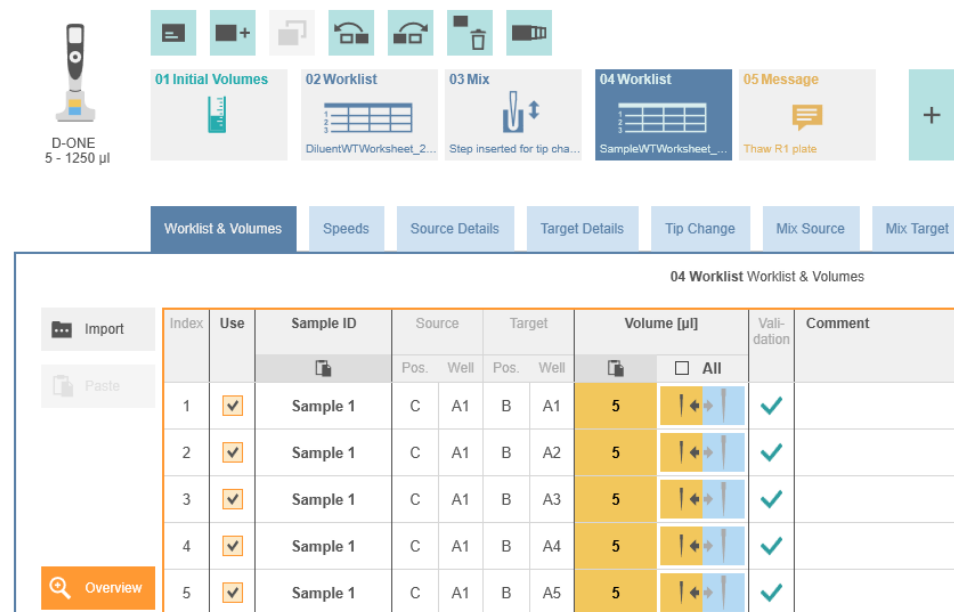


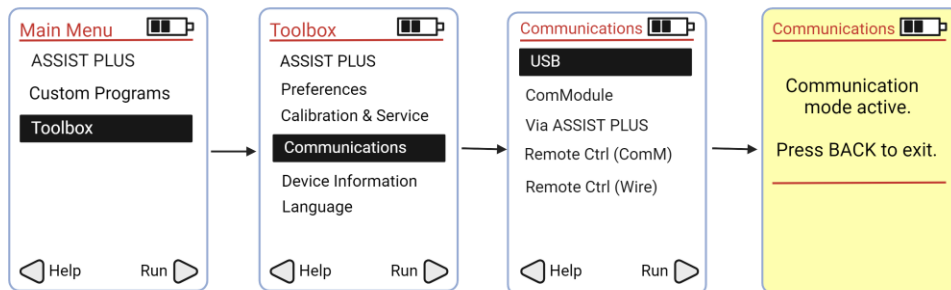
Figure 8: VIALAB worklist generation for sample volumes using 04 Worklist.



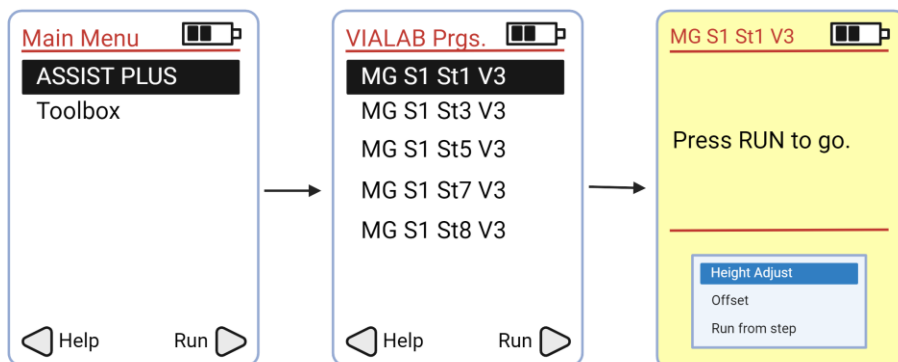
CRITICAL! After uploading the worklist, all pipetting settings will automatically reset to standard default settings. Readjust the pipette settings to the correct worklist parameters. See Appendix A for the complete list of pipette parameters for each worklist.

14. Save and transfer your program to your D-ONE Pipetting Module (1-Ch, 5-1250 μ L) as follows:

- i. Connect your computer with D-ONE Pipette using Communication/Charging Cable for VIAFLO.
- ii. Follow the instructions on the pipette menu, as shown in the diagram below:



- iii. In the VIALAB on your computer, select "Transfer".
- iv. Confirm that the pipette has been recognized by the software. Click "Send to pipette". This will upload the **MG S1 St1 V3** program to the D-ONE Pipette.
- v. Disconnect the cable and proceed with the protocol on the INTEGRA ASSIST PLUS platform.
- vi. If done correctly, a program named **MG S1 St1 V3** will be found on your pipette as shown in the diagram below.



15. Place the Barcoding Reagents in an ice bucket.

16. Remove both ThermoChromic PCR Cold Blocks with ThermoChromic PCR Cold Block Risers from -20°C and thaw at room temperature for **10 minutes**. Ensure that the corner sizes align between the colored ThermoChromic PCR Cold Block and the gray ThermoChromic PCR Cold Block Riser (Figure 9).

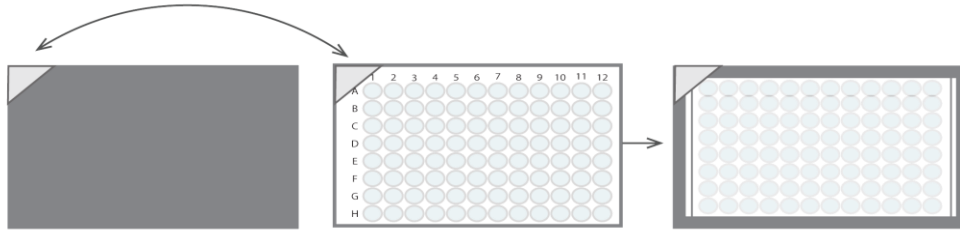
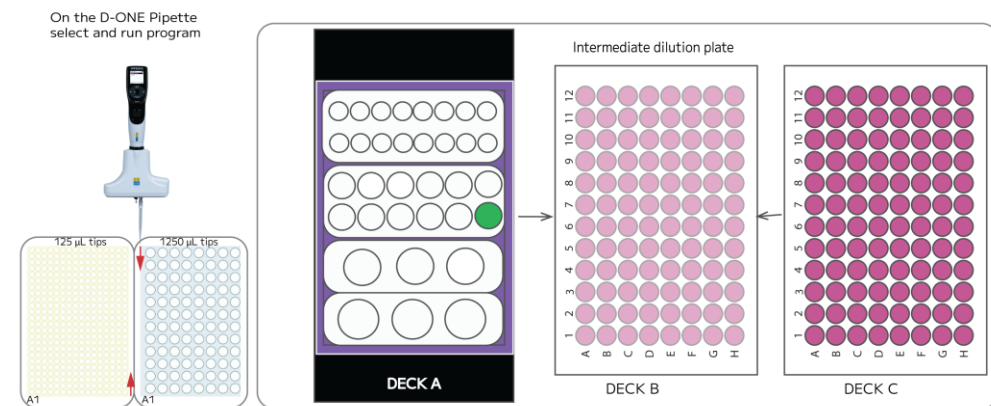


Figure 9: Corners are aligned between the ThermoChromic PCR Cold Block and the ThermoChromic PCR Cold Block Riser.

17. Set up the 3 Position Universal Deck according to the deck configuration below.

Deck Configuration

On the D-ONE Pipette select and run program



| | DECK A | DECK B | DECK C |
|-------------|--|--|--|
| HARDWARE | Parse Cold Block 1 24 mm Labware Pedestal | ThermoChromic PCR Cold Block ThermoChromic PCR Cold Block Riser | ThermoChromic PCR Cold Block ThermoChromic PCR Cold Block Riser |
| CONSUMABLES | | Semi skirted plate (empty) | Semi skirted plate (with sample) |
| REAGENTS | ● S ample Dilution Buffer | | ● Sample Suspension Mix |

18. Attach D-ONE Pipetting Module 1-Ch, 5-1250 μ L and the corresponding Tip Deck.



Note: Ensure the Tip Deck and Tip Boxes are securely positioned by pressing them down firmly until they click into place.

19. Remove the reagent caps, then select and run the program **MG S1 St1 V3**.

Section 1.2. Load and Pool Round 1

The program loads the normalized cells from Section 1.1 on Deck B into the Round 1 Plate on Deck C. After Barcoding Round 1 incubation, move the Round 1 plate onto Deck B.

The program then pools all the samples in the Round 1 Plate into rows A and E.

To load the sample(s):

1. Gather the following components and reagents:

| ITEM | SOURCE | QTY | HANDLING AND STORAGE |
|--|---------------------------------|-----|---|
| VIAFLO Pipette 12-Ch, 5-125 μ L | INTEGRA Component | 1 | |
| Thermochromic PCR Cold Block | Parse-Provided | 2 | Pull the Freezer Block with stabilizer from the -20°C freezer and leave them at room temperature for 10 minutes prior to use. |
| Thermochromic PCR Cold Block Riser | Parse-Provided | 2 | |
| <input type="checkbox"/> Round 1 Plate | -20°C Reagents (Parse Reagents) | 1 | Place directly on ice. |

2. Remove D-ONE Pipetting Module 1-Ch, 5-1250 μ L and corresponding Tip Deck. Replace it with VIAFLO 12-Ch 5-125 μ L Pipette and corresponding Tip Deck.

Note: Before removing the D-ONE Pipetting Module 1-Ch, 5-1250 μ L, ensure it is disconnected by pressing the back button until the main menu is displayed.



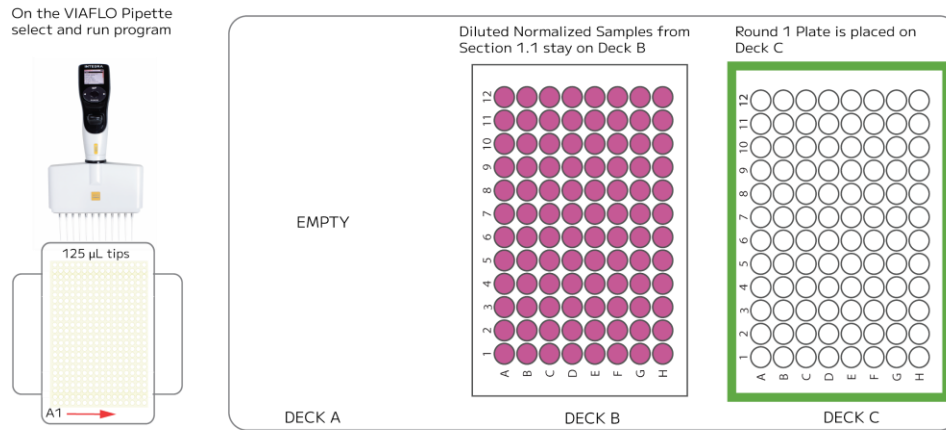
Note: Ensure the Tip Deck and Tip Boxes are securely positioned by pressing them down firmly until they click into place. Remove tip box lid prior to start the program.

3. **When prompted**, thaw the Round 1 Plate using the thermocycling program below.

| THAW ROUND 1 PLATE | | |
|--------------------|-----------------|---------------|
| Run Time | Lid Temperature | Sample Volume |
| 10 min | 70°C | 26 µL |
| Step | Time | Temperature |
| 1 | 10 min | 25°C |
| 2 | Hold | 4°C |

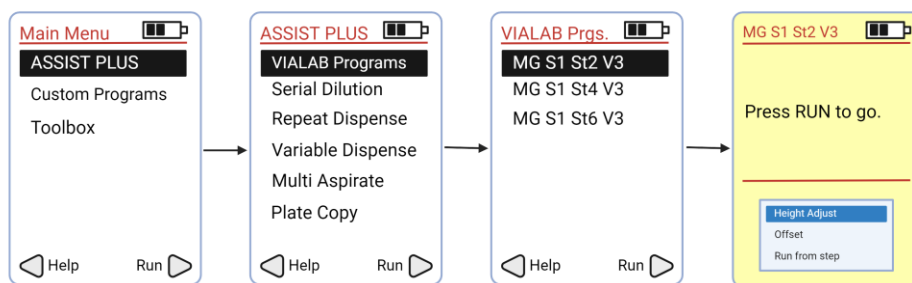
4. Remove the ThermoChromic PCR Cold Block from -20°C freezer and thaw it at room temperature for the duration of the thermocycling program.
5. Gently remove the Round 1 Plate from the thermocycler and centrifuge for **1 minute** at 100 x g at 4°C.
6. Remove the Round 1 Plate from the centrifuge, place in a ThermoChromic PCR Cold Block, remove the plate seal.
7. Replace the ThermoChromic PCR Cold Block on Deck C with the new ThermoChromic PCR Cold Block thawed during step 4. Place this old ThermoChromic PCR Cold Block back in the -20°C freezer for later use.
8. **When prompted**, place the Round 1 Plate in the ThermoChromic PCR Cold Block located on Deck C. Ensure A1 is oriented towards the bottom left corner. Deck should correspond to the diagram below.

Deck Configuration



| | DECK A | DECK B | DECK C |
|-------------|--------|--|--|
| HARDWARE | | Thermochromic PCR Cold Block Thermochromic PCR Cold Block Riser | Thermochromic PCR Cold Block Thermochromic PCR Cold Block Riser |
| CONSUMABLES | | | |
| REAGENTS | | ● Sample Suspension Mix | □ Round 1 Plate |

9. On the VIAFLO Pipette 12-Ch, select and run the program **MG S1 St2 V3** following the diagram below.



10. **When prompted**, seal the □ Round 1 Plate from Deck C using a new plate seal. This is best achieved while the plate is secured in a PCR plate rack and on a flat surface.

11. Place the Round 1 Plate into a thermocycler and run the following program.

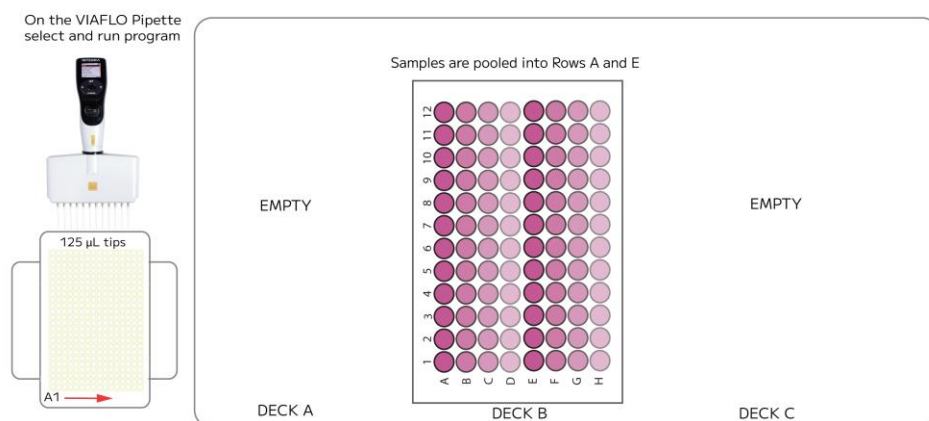
| BARCODING ROUND 1 | | | |
|-------------------|-----------------|---------------|--------|
| Run Time | Lid Temperature | Sample Volume | |
| 40 min | 70°C | 40 µL | |
| Step | Time | Temperature | Cycles |
| 1 | 10 min | 50°C | 1 |
| 2 | 12 s | 8°C | 3 |
| 3 | 45 s | 15°C | |
| 4 | 45 s | 20°C | |
| 5 | 30 s | 30°C | |
| 6 | 2 min | 42°C | |
| 7 | 3 min | 50°C | |
| 8 | 5 min | 50°C | 1 |
| 9 | Hold | 4°C | Hold |

12. Discard the used semi-skirted plate on Deck B. Freeze the Thermochromic PCR Cold Block on Deck B in a -20°C freezer.

13. Ten minutes before Barcoding Round 1 thermocycling program is over, take the Thermochromic PCR Cold Block out of the freezer and place it on Deck B.

14. **When prompted**, once Barcoding Round 1 thermocycling program is over, place Round 1 Plate in Thermochromic PCR Cold Block located on Deck B with A1 oriented towards the bottom left corner. Deck layout should correspond to the configuration below.

Deck Configuration




15. Remove the plate seal.
16. Press "Run" on the pipette to continue the program.
17. At the conclusion of the run, we recommend removing the ThermoChromic PCR Cold Block with the ThermoChromic PCR Cold Block Riser from the deck and storing them in the freezer.

Section 1.3. Round 2 Ligation Preparation

The program pools all the samples from the plate on Deck B into a 10 mL tube on Deck C. After centrifugation, removes supernatant and resuspends the cells in OResuspension Buffer. Mixes ●Round 2 Ligation Enzyme and ORound 2 Ligation Buffer with the resuspended cells. The cells are then put on the left basin (A1) on Deck A.

1. Gather the following components and reagents:

| ITEM | SOURCE | QTY | HANDLING AND STORAGE |
|--|--------------------|-----|---|
| D-ONE Pipetting Module 1-Ch, 5-1250 µL | INTEGRA Components | N/A | |
| ThermoChromic PCR Cold Block | Parse-Provided | 1 | Pull the freezer block with stabilizer from the -20°C freezer and leave them at room temperature for 10 minutes prior to use. |
| ThermoChromic PCR Cold Block Riser | Parse-Provided | 1 | |

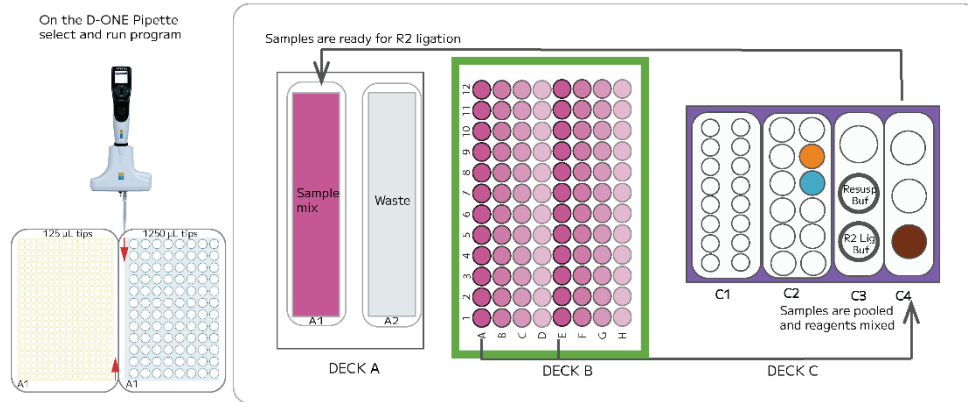
| ITEM | SOURCE | QTY | HANDLING AND STORAGE |
|---|---------------------------------|-------------|--|
| Parse Cold Block 1 | Parse-Provided | 1 | Keep on ice when not in use. |
| Tip Deck for D-ONE Pipetting Module | INTEGRA Components | N/A | |
| 10 mL transport tube | Consumables | 1 | |
| Dual Reservoir Adapter (ANSI/SLAS footprint) | INTEGRA Components | N/A | |
| 25 mL basin reservoir liners | INTEGRA-Provided | 2 | |
|  Round 2 Plate | -20°C Reagents (Parse Reagents) | 1 | Place directly on ice. |
|  Round 2 Ligation Enzyme | -20°C Reagents (Parse Reagents) | 1.5 mL tube | Place directly on ice. Briefly centrifuge before use. |
|  Round 2 Ligation Buffer | -20°C Reagents (Parse Reagents) | 5 mL tube | Thaw at room temperature then store on ice. Mix by inverting 3x. |
|  Resuspension Buffer | -20°C Reagents (Parse Reagents) | 5 mL tube | |
|  Spin Additive | 4°C Reagents (Parse Reagents) | 1.5 mL tube | Briefly centrifuge. Keep at room temperature. |

- Place the Tube Block 1 on Deck C.
- Place the Dual Reservoir Adapter (INTEGRA logo oriented to the front) on Deck A lined with two new 25 mL basin reservoir liners.
- Configure the deck layout as follows:



Note: Centrifuge reagents before loading on Deck C.

Deck Configuration



| | DECK A | DECK B | DECK C |
|-------------|------------------------------|--|--|
| HARDWARE | Dual Reservoir Adapter | Thermochromic PCR Cold Block Thermochromic PCR Cold Block Riser | Parse Cold Block 1 |
| CONSUMABLES | 25 mL basin reservoir liners | | ● 10 mL transport tube |
| REAGENTS | ● Sample Suspension Mix | □ Round 1 Plate | ● Spin Additive ● Round 2 Ligation Enzyme ○ Resuspension Buffer ○ Round 2 Ligation Buffer |

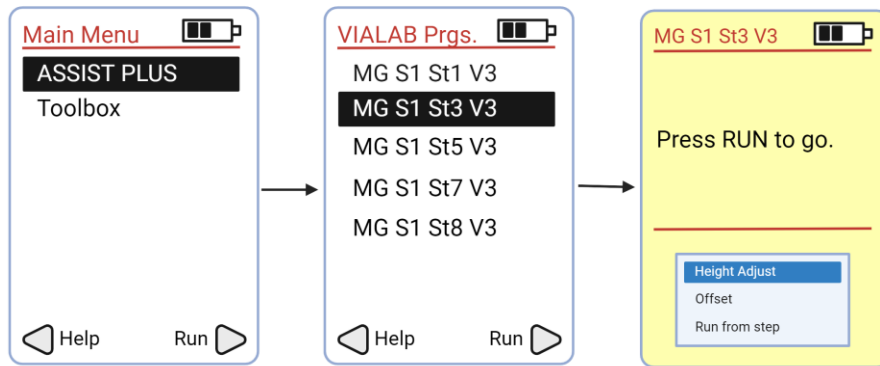
- Remove VIAFLO Pipette 12-Ch, 5-125 μ L and corresponding Tip Deck. Replace it with the D-ONE Pipetting Module 1-Ch, 5-1250 μ L and corresponding Tip Deck.



Note: Before removing the VIAFLO Pipette 12-Ch, 5-125 μ L, ensure it is disconnected by pressing the back button until the main menu is displayed.

Note: Ensure the Tip Deck and Tip Boxes are securely positioned by pressing them down firmly until they click into place. Remove tip box lid prior to start the program.

- Remove the reagent caps, then run the program **MG S1 St3 V3** following the diagram below.



7. **When prompted**, cap and invert the 10 mL transport tube containing the pooled cells. Centrifuge the sample in a swinging bucket centrifuge cooled to 4°C for **10 minutes** at 250 x g.
8. During the 10 minutes spin, **when prompted**, thaw the Round 2 Plate using the program below for later use. Proceed to the next step while the program is still running.

| THAW ROUND 2 PLATE | | |
|--------------------|-----------------|---------------|
| Run Time | Lid Temperature | Sample Volume |
| 10 min | 70°C | 10 µL |
| Step | Time | Temperature |
| 1 | 10 min | 25°C |
| 2 | Hold | 4°C |

9. Remove a new Thermochromic PCR Cold Block with Thermochromic PCR Cold Block Riser from -20°C freezer and thaw for **10 minutes** during centrifugation for later use.
10. Once centrifugation is complete, **when prompted**, remove the cap from the 10 mL transport tube and place it back in its original position within the Parse Cold Block 1 located on Deck C4. Immediately proceed to the next step.
11. Press “Run” to continue.
12. Clear the deck from the Thermochromic PCR Cold Block, the Thermochromic PCR Cold Block Riser and store them in the freezer. Remove the Parse Cold Block 1 and place it on ice.

Section 1.4. Round 2 Ligation

The program transfers Cell Suspension Mix from the left reservoir (A1) on Deck A to Round 2 Plate on Deck B. Following Round 2 Incubation, the program will load Round 2 Stop Buffer in the right reservoir (A2) into each well. After Round 2 Stop incubation, it pools all samples together in the left reservoir (A1) on Deck A.

1. Gather the following items and handle as indicated below:

| ITEM | SOURCE | QTY | HANDLING AND STORAGE |
|---|---------------------------------|-----------|--|
| VIAFLO Pipette 12-Ch, 5-125 µL | INTEGRA Components | N/A | |
| Tip Deck for VIAFLO Pipette 12-Ch, 5-125 µL | INTEGRA Components | N/A | |
| Thermochromic PCR Cold Block | Parse-Provided | 1 | Pull the Freezer Block with riser from the -20°C freezer and leave them at room temperature for 10 minutes prior to use. |
| Thermochromic PCR Cold Block Riser | Parse-Provided | 1 | |
| INTEGRA Dual 25mL Basin Reservoir Adapter | INTEGRA-Provided | N/A | |
| 25 mL basin reservoir liners | INTEGRA-Provided | 2 | |
| ● Round 2 Stop Buffer | -20°C Reagents (Parse Reagents) | 2 mL tube | Thaw at room temperature then store on ice. Mix by vortexing. |



2. Remove D-ONE Pipetting Module 1-Ch, 5-1250 µL and corresponding Tip Deck. Replace it with VIAFLO 12-Ch 5-125 µL and corresponding 125 µL Tip Deck.

Note: Before removing the D-ONE Pipetting Module 1-Ch, 5-1250 µL, ensure it is disconnected by pressing the back button until the main menu is displayed.

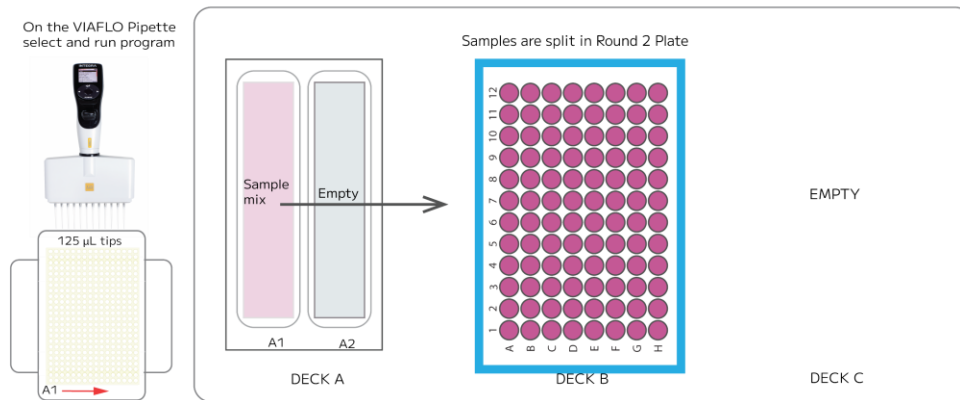



Note: Ensure the Tip Deck and Tip Boxes are securely positioned by pressing them down firmly until they click into place. Remove tip box lid prior to start the program.

3. Remove the Round 2 Plate from the thermocycler and centrifuge for **1 minute** at 100 x g at 4°C.

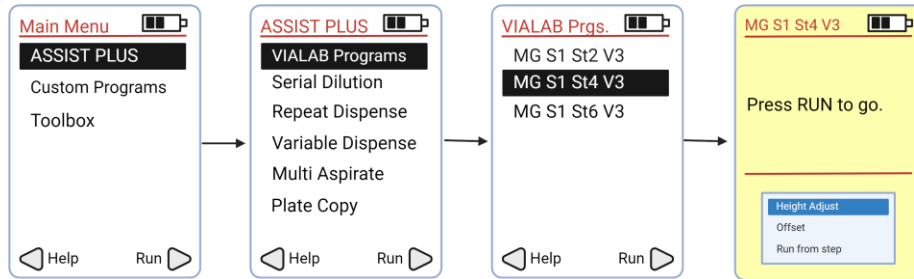
- While secured in a PCR plate rack on a flat surface, remove the plate seal from the  Round 2 Plate and store on ice.
- Place the ThermoChromic PCR Cold Block thawed during Section 1.3 step 5 on Deck B.
- Place the  Round 2 Plate on Deck B in the ThermoChromic PCR Cold Block with ThermoChromic PCR Cold Block Riser with A1 oriented towards the bottom left corner and remove the seal. The deck should correspond to the configuration below.

Deck Configuration



| | DECK A | DECK B | DECK C |
|-------------|-------------------------|---|--------|
| HARDWARE | Dual Reservoir Adapter | ThermoChromic PCR Cold Block ThermoChromic PCR Cold Block Riser | |
| CONSUMABLES | 25 mL Reservoir liners | | |
| REAGENTS | ● Sample Suspension Mix |  Round 2 Plate | |

- Select and run the program **MG S1 St4 V3** following the diagram below.



8. **When prompted**, reseal the Round 2 Plate with an adhesive seal, place it into a thermocycler, and run the following program. Upon completion, proceed immediately to the next step.

| BARCODING ROUND 2 | | |
|-------------------|-----------------|---------------|
| Run Time | Lid Temperature | Sample Volume |
| 15 min | 50°C | 50 µL |
| Step | Time | Temperature |
| 1 | 15 min | 16°C |
| 2 | Hold | 4°C |

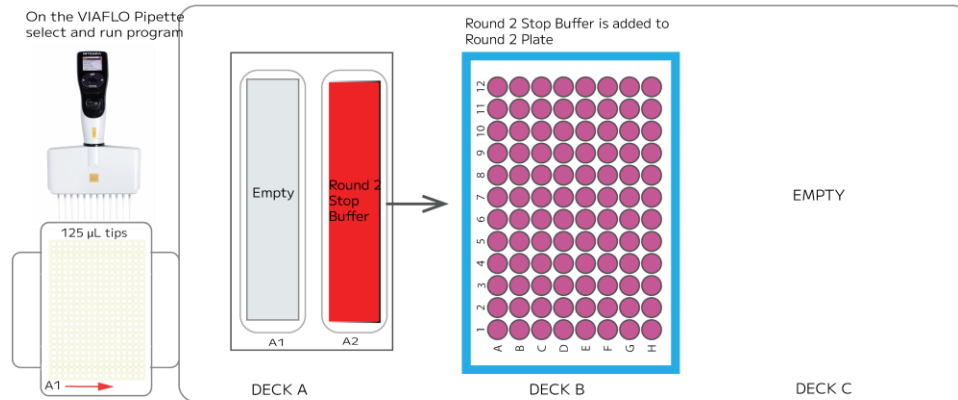
9. Remove the Round 2 Plate from the thermocycler and place in a PCR plate rack.
10. Remove the plate seal and place the Round 2 Plate back on Deck B with A1 oriented towards the lower left corner.
11. **When prompted**, replace the 25 mL basin reservoir liners with a new 25 mL basin reservoir liner.



Note: The right basin liner contains general waste and can be flushed down the sink. Dispose basin liners in biohazard waste.

12. Briefly vortex (2-3 seconds) and centrifuge the Parse ● Round 2 Stop Buffer. **When prompted**, using a P1000 pipette, add the total volume (~1.4 mL) to the right basin (A2) on Deck A.

Deck Configuration



| | DECK A | DECK B | DECK C |
|-------------|------------------------|--|--------|
| HARDWARE | Dual Reservoir Adapter | Thermochromic PCR Cold Block Thermochromic PCR Cold Block Riser | |
| CONSUMABLES | 25 mL reservoir liners | | |
| REAGENTS | ● Round 2 Stop Buffer | □ Round 2 Plate | |



CRITICAL! When adding the ● Round 2 Stop Buffer to the reservoir ensure the volume is evenly distributed for optimal pipetting.

13. Remove the reagent caps, then press "Run" to continue.

14. **When prompted**, reseal the Round 2 Plate with an adhesive seal, and incubate the Round 2 Plate in a thermocycler using the following protocol. Upon completion, proceed immediately to the next step.

| ROUND 2 STOP | | |
|--------------|-----------------|---------------|
| Run Time | Lid Temperature | Sample Volume |
| 5 min | 50°C | 60 µL |
| Step | Time | Temperature |
| 1 | 5 min | 16°C |
| 2 | Hold | 4°C |



15. Place the Round 2 Plate within the Thermochromic PCR Cold Block with Thermochromic PCR Cold Block Riser located on Deck B with A1 oriented towards the bottom left.
16. Remove the seal and press "Run".
17. At the conclusion of the run, we recommend removing the Thermochromic PCR Cold Block with the Thermochromic PCR Cold Block Riser from the deck and storing them in the freezer.

Section 1.5. Round 3 Ligation Preparation

The pooled cell suspension in the left reservoir (A1) on Deck A is strained into the 10 mL transport tube on Deck C4. The program adds Round 3 Ligation Enzyme into the cells and mixes. It then transfers the cell suspension mix to the top reservoir (A1) within the slanted plate holder on Deck B.

1. Gather the following components and reagents:


| ITEM | SOURCE | QTY | HANDLING AND STORAGE |
|--|-------------------|-----|------------------------------|
| D-ONE Pipetting Module 1-Ch, 5-1250 µL | INTEGRA Component | N/A | |
| Tip Deck for D-ONE Pipetting Module | INTEGRA Component | N/A | |
| Parse Cold Block 1 | Parse-Provided | 1 | Keep on ice when not in use. |

| ITEM | SOURCE | QTY | HANDLING AND STORAGE |
|---|---------------------------------|-------------|---|
| Dual Reservoir Adapter (ANSI/SLAS footprint) | INTEGRA Component | N/A | |
| ASSIST PLUS Slanted Plate Holder | INTEGRA Component | N/A | |
| 10 mL transport tube | Consumables | 1 | |
| 25 mL basin reservoir liners | INTEGRA-Provided | 2 | |
| 40 µm cell strainer | Consumables | 1 | |
| 125 µL Tip Rack | INTEGRA-Provided | 1 | |
| 1250 µL Tip Rack | INTEGRA-Provided | 1 | |
|  Round 3 Plate | -20°C Reagents (Parse Reagents) | 1 | Place directly on ice. |
|  Round 3 Ligation Enzyme | -20°C Reagents (Parse Reagents) | 1.5 mL tube | Place directly on ice. Briefly centrifuge before use. |

2. Add the ASSIST PLUS Slanted Plate Holder on Deck B, incorporating a 10° tilt.



Note: Ensure that the lowest side is positioned adjacent to Deck A.

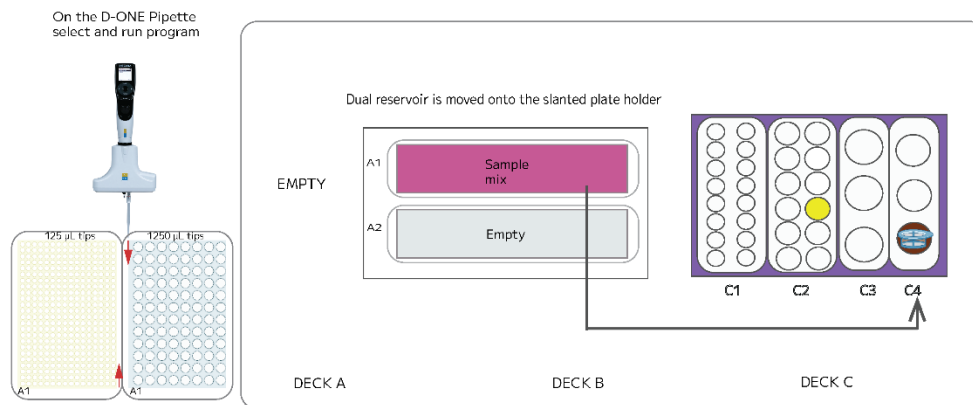
3. Place the Parse Cold Block 1 on Deck C.
4. Briefly centrifuge and insert the  Round 3 Ligation Enzyme tube in the appropriate location in the Parse Cold Block 1.
5. Place a 10 mL transport tube with the 40 µm cell strainer within its respective location in the Parse Cold Block 1 located in the Reagent Block in C4 position. Deck layout should correspond to the Deck Configuration below.

Deck Configuration

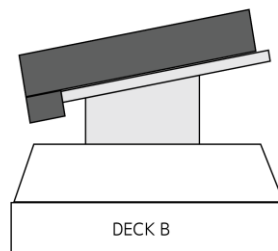


Note: When moving the dual reservoir adapter onto the slanted plate holder on Deck B, ensure the INTEGRA logo is oriented towards the front left.

Note: Use extra care when moving the cell suspension to avoid spills.



Slanted Plate Holder (10°) front view



| | DECK A | DECK B | DECK C |
|-------------|--------|--|---|
| HARDWARE | | Slanted Plate Holder (10°) Dual Reservoir Adapter | Parse Cold Block 1 |
| CONSUMABLES | | 25 mL reservoir liners | ● 10 mL transport tube with cell strainer |
| REAGENTS | | ● Sample Suspension Mix | ● Round 3 Ligation Enzyme |

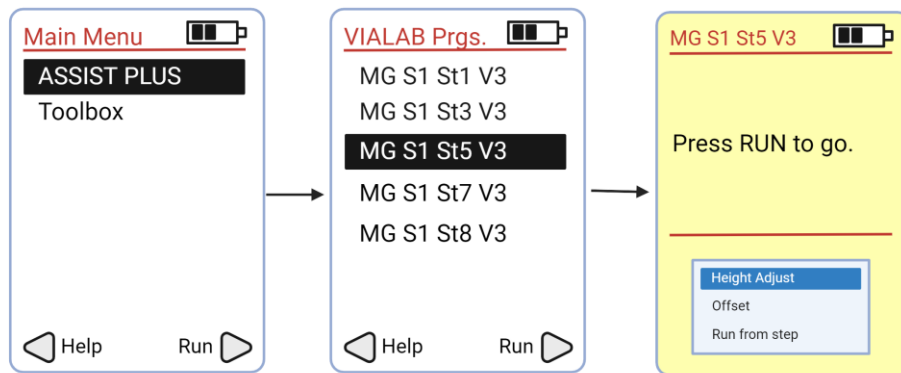
- Remove VIAFLO Pipette 12-Ch, 5-125 μL and corresponding tip deck. Replace it with D-ONE Pipetting Module 1-Ch, 5-1250 μL and corresponding Tip Deck.




Note: Before removing the VIAFLO Pipette 12-Ch, 5-125 μL , ensure it is disconnected by pressing the back button until the main menu is displayed.

Note: Ensure the Tip Deck and Tip Boxes are securely positioned by pressing them down firmly until they click into place.

- Remove the reagent caps, then select and run the program **MG S1 St5 V3** following the diagram below.



- Proceed to the next step while the program is still running.
- Place the  Round 3 Plate into a second thermocycler and run the program below. Proceed to the next step while the program is still running.

| THAW ROUND 3 PLATE | | |
|--------------------|-----------------|------------------|
| Run Time | Lid Temperature | Sample Volume |
| 10 min | 70°C | 10 μL |
| Step | Time | Temperature |
| 1 | 10 min | 25°C |
| 2 | Hold | 4°C |

- Take a new Thermochromic PCR Cold Block with Thermochromic PCR Cold Block Riser from -20°C freezer and thaw for **10 minutes** during Round 3 Plate Thaw.

11. **When prompted**, remove the 40 µm cell strainer.



Note: There may be bubbles left on the strainer. This will not affect the results.

12. **When prompted**, replace the basin reservoirs containing the supernatant with new 25 mL basin reservoirs and press “Run” to continue the protocol.

13. At the conclusion of the run, remove Parse Cold Block 1 from the Deck C and place it on ice.

Section 1.6. Round 3 Ligation

The program loads the Cell Suspension Mix on Deck A into the Round 3 plate on Deck B. Following the prompts for Round 3 incubation, the program will then load Round 3 Ligation Stop Buffer into all the wells and pool all the samples together on Deck A.

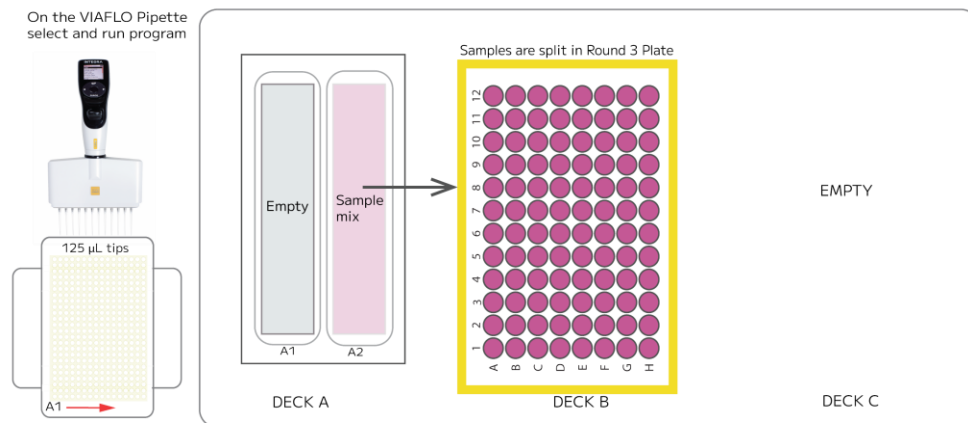
1. Gather the following components and reagents:

| ITEM | SOURCE | QTY | HANDLING AND STORAGE |
|---|-------------------|-----|--|
| VIAFLO Pipette 12-Ch, 5-125 µL | INTEGRA Component | N/A | |
| Tip Deck for D-ONE Pipetting Module | INTEGRA Component | N/A | |
| Thermochromic PCR Cold Block | Parse-Provided | 1 | Pull the freezer block with riser from the -20°C freezer and leave them at room temperature for 10 minutes prior to use. |
| Thermochromic PCR Cold Block Riser | Parse-Provided | 1 | |
| INTEGRA Dual 25mL Basin Reservoir Adapter | INTEGRA Component | 1 | |
| 10 mL transport tube | Consumables | 1 | |
| 25 mL basin reservoir liners | INTEGRA-Provided | 2 | |
| 40 µm cell strainer | Consumables | 1 | |
| 125 µL Tip Rack | INTEGRA-Provided | 1 | |

| ITEM | SOURCE | QTY | HANDLING AND STORAGE |
|-----------------------|---------------------------------|-----------|---|
| 1250 µL Tip Rack | INTEGRA-Provided | 1 | |
| ○ Round 3 Stop Buffer | -20°C Reagents (Parse Reagents) | 5 mL tube | Thaw at room temperature then store on ice. Mix by vortexing. |

- Place Thermochromic PCR Cold Block with Thermochromic PCR Cold Block Riser on Deck B.
- Remove the Round 3 Plate from the thermocycler and centrifuge for **1 minute** at 100 x g at 4°C.
- When prompted**, place the Round 3 Plate within the Thermochromic PCR Cold Block with Thermochromic PCR Cold Block Riser located on Deck B with A1 oriented towards the bottom left corner, and remove the seal. Deck layout should correspond to the configuration below.

Deck Configuration



| | DECK A | DECK B | DECK C |
|-------------|-----------------------------|--|--------|
| HARDWARE | Dual Reservoir Adapter | Thermochromic PCR Cold Block Thermochromic PCR Cold Block Riser | |
| CONSUMABLES | 25 mL basin reservoir liner | | |

| | DECK A | DECK B | DECK C |
|----------|-------------------------|-----------------|--------|
| REAGENTS | ● Sample Suspension Mix | □ Round 3 Plate | |

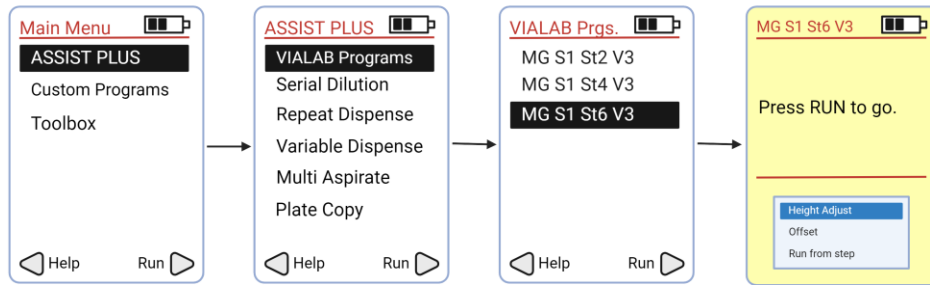
- Remove D-ONE Pipetting Module 1-Ch, 5-1250 μL and corresponding tip deck. Replace it with VIAFLO Pipette 12-Ch, 5-125 μL and corresponding Tip Deck.



Note: Before removing the D-ONE Pipetting Module 1-Ch, 5-1250 μL , ensure it is disconnected by pressing the back button until the main menu is displayed.

Note: Ensure the Tip Deck and Tip Boxes are securely positioned by pressing them down firmly until they click into place.

- Once the pipette and tip deck with tips are loaded on deck, select and run the program **MG S1 St6 V3** following the diagram below.



- When prompted**, reseal the □ Round 3 Plate with an adhesive seal and incubate the □ Round 3 Plate in a thermocycler with the following protocol.

| BARCODING ROUND 3 | | |
|-------------------|-----------------|------------------|
| Run Time | Lid Temperature | Sample Volume |
| 15 min | 50°C | 60 μL |
| Step | Time | Temperature |
| 1 | 15 min | 16°C |
| 2 | Hold | 4°C |

- When prompted**, place the □ Round 3 Plate on Deck B.

9. **When prompted**, replace the 25 mL basin reservoir liners with new 25 mL basin reservoir liners. Dispose used basin liners in biohazard waste.
10. Press “Run” on Pipette.
11. **When prompted**, follow the prompts to add all the **ORound 3 Stop Buffer** to the A2 basin ensuring that the volume added into the reservoir basin is evenly distributed.
12. Press “Run” to continue.
13. At the conclusion of the run, we recommend removing the Thermochromic PCR Cold Block with the Thermochromic PCR Cold Block Riser from the deck and storing them in the freezer.

Section 1.7. Pre-Lysis

The pooled cell suspension on Deck B is strained into the 10 mL transport tube on Deck C4. The **Spin Additive** is then added into the cells and centrifuged. Supernatant is removed, the cells are resuspended in **OPre Lyse Wash Buffer**. and centrifuged again. The supernatant is then removed.

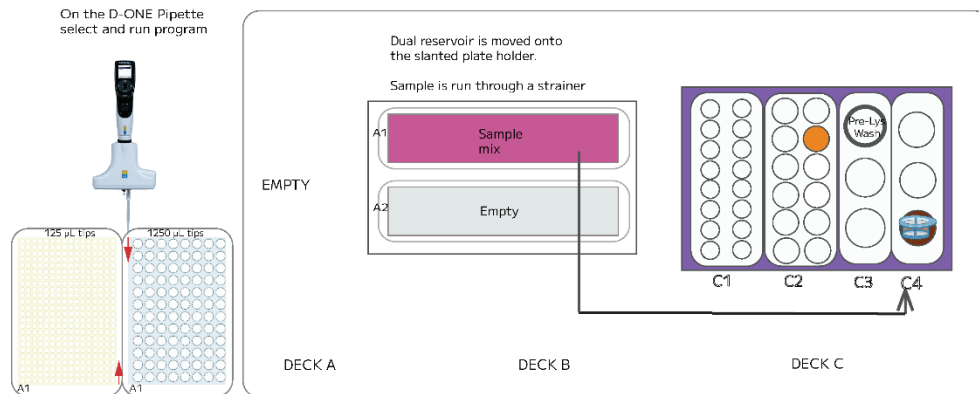
1. Gather the following components and reagents:

| ITEM | SOURCE | QTY | HANDLING AND STORAGE |
|--|--------------------|-----|------------------------------|
| D-ONE Pipetting Module 1-Ch, 5-1250 µL | INTEGRA Components | N/A | |
| Tip Deck for D-ONE Pipetting Module | INTEGRA Components | N/A | |
| Parse Cold Block 1 | Parse-Provided | 1 | Keep on ice when not in use. |
| Dual 25mL Basin Reservoir Adapter | INTEGRA Components | N/A | |
| 10 mL transport tube | Consumables | 1 | |
| 25 mL basin reservoir liners | INTEGRA-Provided | 2 | |
| 40 µm cell strainer | Consumables | 1 | |
| 125 µL Tip Rack | INTEGRA-Provided | 1 | |

| ITEM | SOURCE | QTY | HANDLING AND STORAGE |
|-------------------------|---------------------------------|-------------|--|
| 1250 µL Tip Rack | INTEGRA-Provided | 1 | |
| ● Spin Additive | 4°C Reagents (Parse Reagents) | 1.5 mL tube | Keep at room temperature. |
| ○ Pre-Lysis Wash Buffer | -20°C Reagents (Parse Reagents) | 5 mL tube | Thaw at room temperature then store on ice. Mix by pipetting 3x. |

2. Add slanted plate holder on Deck B and incorporate a 10 degree tilt (lowest side adjacent to Deck A).
3. Place the Parse Cold Block 1 on Deck C.
4. Place the reagent tubes in their respective orientation found in the deck configuration.
5. Put the 10 mL transport tube with the cell strainer in the C4 position of the Parse Cold Block 1.
6. Put the new 1.5 mL tube in the C2 position of the Parse Cold Block 1. Deck layout should correspond to the configuration below.

Deck Configuration



| | DECK A | DECK B | DECK C |
|------------|--------|---|---|
| HARDWARE | | Slanted Plate Holder (10 °) Dual Reservoir Adapter | Parse Cold Block 1 |
| CONSUMABLE | | 25 mL reservoir liner | ● 10 mL transport tube and cell strainer |
| REAGENTS | | ● Sample Suspension Mix | ● Spin Additive ○ Pre Lyse Wash Buffer |

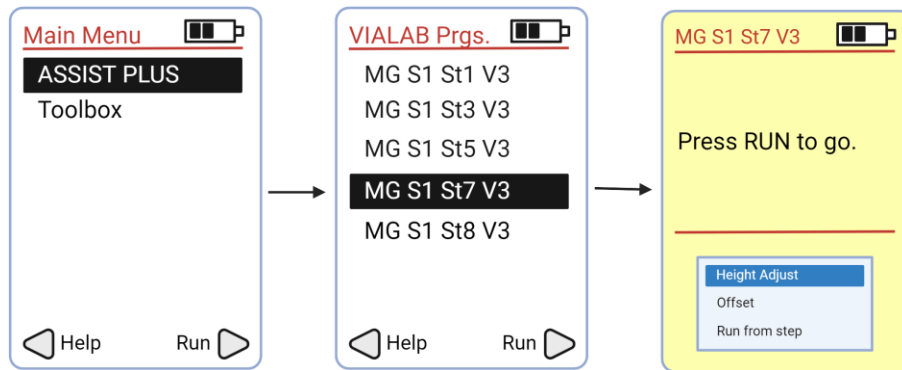
- Remove the VIAFLO Pipette 12-Ch, 5-125 µL Pipette and corresponding Tip Deck. Attach the D-ONE Pipetting Module 1-Ch, 5-1250 µL and corresponding Tip Deck.

Note: Before removing the VIAFLO Pipette 12-Ch, 5-125 µL, ensure it is disconnected by pressing the back button until the main menu is displayed.



Note: Ensure the Tip Deck and Tip Boxes are securely positioned by pressing them down firmly until they click into place.

- Remove reagent caps, select and run the program **MG S1 St7 V3** following the diagram below.



9. **When prompted**, remove the cell strainer.
10. **When prompted**, cap and invert the 10 mL transport tube, and centrifuge the pooled cells in a swinging bucket centrifuge cooled to 4°C for **10 minutes** at 250 x g.
11. **When prompted** after the centrifugation is complete, remove the cap from the 10 mL transport tube and place it back in its original position within the Parse Cold Block 1 located on Deck C4.
12. Press "Run" to continue.
13. **When prompted**, centrifuge the 10 mL transport tube in a swinging bucket centrifuge cooled to 4°C for **10 minutes** at 250 x g for a second spin.
14. Press "Run" to continue.
15. **When prompted** after the centrifugation is complete, remove the cap from the 10 mL transport tube and place it back in its original position within the Parse Cold Block 1 located on Deck C4.
16. Press "Run" to continue.
17. While minimizing time on ice, count the number of cells in the sample from the 10 mL transport tube on Deck C4 with a hemocytometer or alternative cell counting device. Record the cell count.
18. Clear the deck from the Dual 25 mL Basin Reservoir Adapter.

Section 1.8. Lysis and Sublibrary Generation

The program requires a dilution of the sample to 2500 cells per μL with a volume of 420 μL . The program will create sixteen lysates with 62,500 cells each. It then mixes the Lysis Master Mix and aliquots the master mix into the generated lysates.

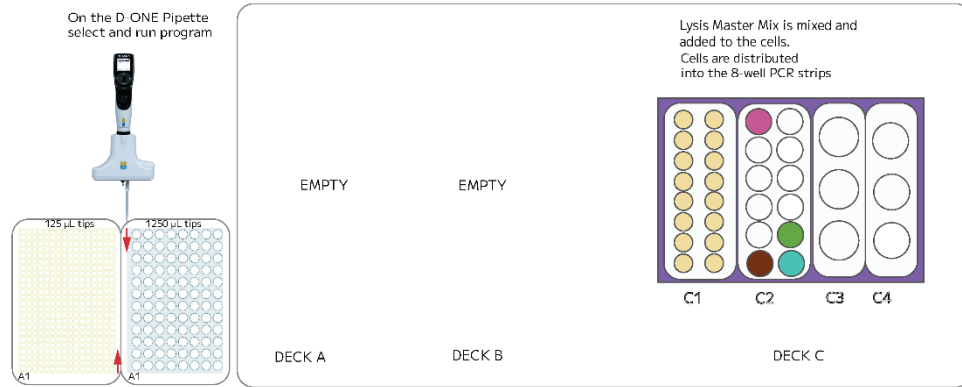
To generate and lyse sublibraries:

1. Gather the following components and reagents:

| ITEM | SOURCE | QTY | HANDLING AND STORAGE |
|---|---------------------------------|-------------|--|
| D-ONE Pipetting Module 1-Ch, 5-1250 μL | INTEGRA Component | N/A | |
| Tip Deck for D-ONE Pipetting Module | INTEGRA Component | N/A | |
| Parse Cold Block 1 | Parse-Provided | 1 | Keep on ice when not in use. |
| 8 PCR strip tubes | Consumables | 2 | |
| 1.5 mL tube | Consumables | 2 | |
| 125 μL Tip Rack | INTEGRA-Provided | 1 | |
| 1250 μL Tip Rack | INTEGRA-Provided | 1 | |
| ● Pre-Lysis Dilution Buffer | -20°C Reagents (Parse Reagents) | 2 mL tube | Thaw at room temperature then store on ice. Mix by pipetting 3x. |
| ● Lysis Buffer | 4°C Reagents (Parse Reagents) | 1.5 mL tube | Place directly on ice. Briefly centrifuge before use. |
| ● Lysis Enzyme | -20°C Reagents (Parse Reagents) | 1.5 mL tube | Place in a 37°C water bath until use. |

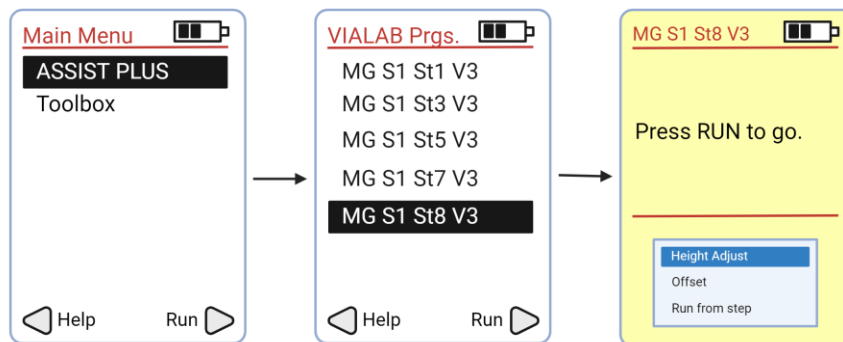
2. Dilute the cells to a concentration of 2500 cells per μL for a total volume of **420 μL** using the ●Pre-Lysis Dilution Buffer in a 1.5 mL transport tube. Store this dilution on ice until ready to use.
3. Place the PCR strip tubes on Deck C1.
4. Place the Lysis Buffer, Lysis Enzyme, empty 1.5 mL transport tube, and diluted sample from Step 2 on Deck C2. Deck should correspond to the Deck Configuration below.

Deck Configuration



| | DECK A | DECK B | DECK C |
|-------------|--------|--------|---|
| HARDWARE | | | Parse Cold Block 1 |
| CONSUMABLES | | | <ul style="list-style-type: none"> ● 16-count PCR Tube ● 1.5 mL Transport Tube |
| REAGENTS | | | <ul style="list-style-type: none"> ● 250 µL Sample Suspension Mix suspension ● Lysis Buffer ● Lysis Enzyme |

- Remove the reagent caps, ensure that all strip tubes are open, select and run the program **MG S1 St8 V3** following the diagram below.



- Vortex the 0.2 mL tube(s) for **10 seconds**. Briefly centrifuge.
- Place the tube(s) into a thermocycler and run the following program.

CELL LYSIS

| Run Time | Lid Temperature | Sample Volume |
|----------|-----------------|---------------|
| 15 min | 80°C | 55 µL |
| Step | Time | Temperature |
| 1 | 15 min | 65°C |
| 2 | Hold | 4°C |

- If continuing to Section 2 without freezing the sample, proceed to **Section 2: cDNA Capture and Amplification** in the [Evercode BCR Mega User Guide](#) while the program is still running.



Safe stopping point: Sublibrary lysates can be stored at -80°C for up to 6 months.

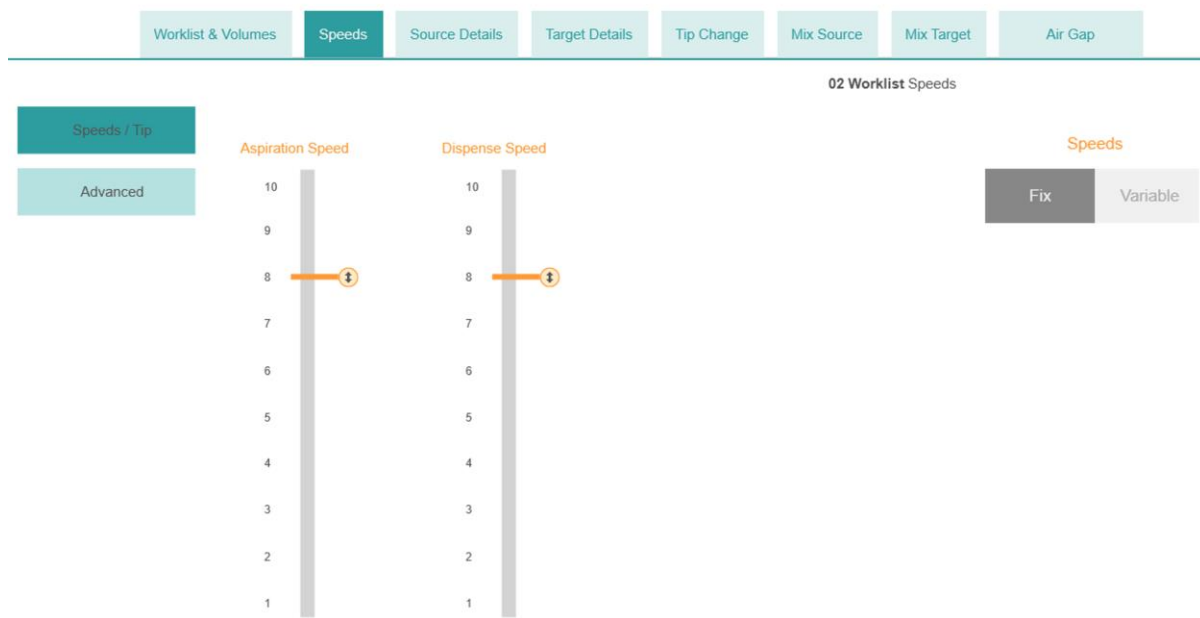
Appendices

Appendix A: Worklist Settings

The worklist settings are shown below. Ensure that the settings in both the diluent addition and sample addition worklist steps match the settings shown below. Anything not shown can be left at its default settings.

Diluent Addition

Dilution 1



The screenshot displays the '02 Worklist Speeds' configuration interface. At the top, a navigation bar includes tabs for 'Worklist & Volumes', 'Speeds', 'Source Details', 'Target Details', 'Tip Change', 'Mix Source', 'Mix Target', and 'Air Gap'. The 'Speeds' tab is selected. Below the navigation bar, there are two vertical sliders: 'Aspiration Speed' and 'Dispense Speed'. Both sliders have a scale from 1 to 10, and the current value for each is 8. To the right of the sliders, there is a 'Speeds' dropdown menu with 'Fix' and 'Variable' options; 'Variable' is selected. On the left side, there are two buttons: 'Speeds / Tip' and 'Advanced'.

Dilution 2

Worklist & Volumes | Speeds | **Source Details** | Target Details | Tip Change | Mix Source | Mix Target | Air Gap

Source Labware Pedestal (+24m... | 02 Worklist Source Details

A

Heights Variable

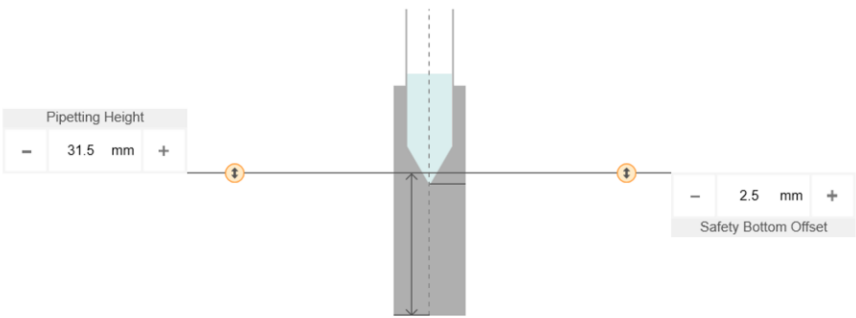
Offsets

Pipetting Height: - 31.5 mm +

Safety Bottom Offset: - 2.5 mm +

Liquid Level Detection: Yes No

Tip Travel: Yes No



Dilution 3

Worklist & Volumes | Speeds | Source Details | **Target Details** | Tip Change | Mix Source | Mix Target | Air Gap

Target PCR Freezer Block with... | 02 Worklist Target Details

B

Heights Variable

Tip Touch

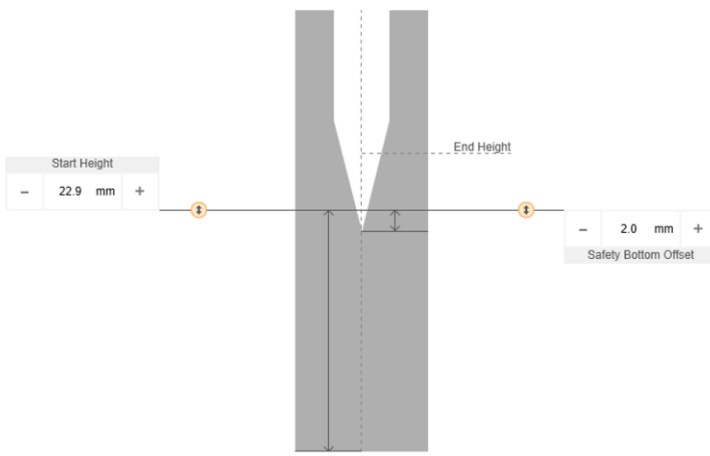
Offsets

Start Height: - 22.9 mm +

End Height

Safety Bottom Offset: - 2.0 mm +

Tip Travel: Yes No



Dilution 4

Worklist & Volumes | Speeds | Source Details | Target Details | **Tip Change** | Mix Source | Mix Target | Air Gap

02 Worklist Tip Change

| Index | Source | | Target | | <input type="checkbox"/> | Eject Tip | <input type="checkbox"/> | After each dispense |
|-------|--------|------|--------|------|-------------------------------------|-----------|--------------------------|---------------------|
| | Pos. | Well | Pos. | Well | | | | |
| 39 | A | F1 | B | D3 | <input type="checkbox"/> | | | |
| 40 | A | F1 | B | D4 | <input type="checkbox"/> | | | |
| 41 | A | F1 | B | D5 | <input type="checkbox"/> | | | |
| 42 | A | F1 | B | D6 | <input type="checkbox"/> | | | |
| 43 | A | F1 | B | D7 | <input type="checkbox"/> | | | |
| 44 | A | F1 | B | D8 | <input type="checkbox"/> | | | |
| 45 | A | F1 | B | D9 | <input type="checkbox"/> | | | |
| 46 | A | F1 | B | D10 | <input type="checkbox"/> | | | |
| 47 | A | F1 | B | D11 | <input type="checkbox"/> | | | |
| 48 | A | F1 | B | D12 | <input checked="" type="checkbox"/> | | | |

Dilution 5

Worklist & Volumes | Speeds | Source Details | Target Details | Tip Change | **Mix Source** | Mix Target | Air Gap

Source Labware Pedestal (+24m...

02 Worklist Mix Source

A

Mixing

Yes No

Dilution 6

Worklist & Volumes | Speeds | Source Details | Target Details | Tip Change | Mix Source | **Mix Target** | Air Gap

Target PCR Freezer Block with...

02 Worklist Mix Target

B

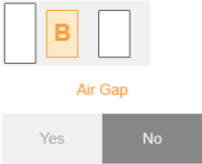
Mixing

Yes No

Dilution 7

Worklist & Volumes | Speeds | Source Details | Target Details | Tip Change | Mix Source | Mix Target | **Air Gap**

Target PCR Freezer Block with... 02 Worklist Volumes



Air Gap

Yes No

Volume

Fix Variable

Sample Addition

Sample 1


Worklist & Volumes | **Speeds** | Source Details | Target Details | Tip Change | Mix Source | Mix Target | Air Gap

04 Worklist Speeds


Speeds / Tip

Advanced

Aspiration Speed



Dispense Speed



Speeds

Fix Variable

Sample 2

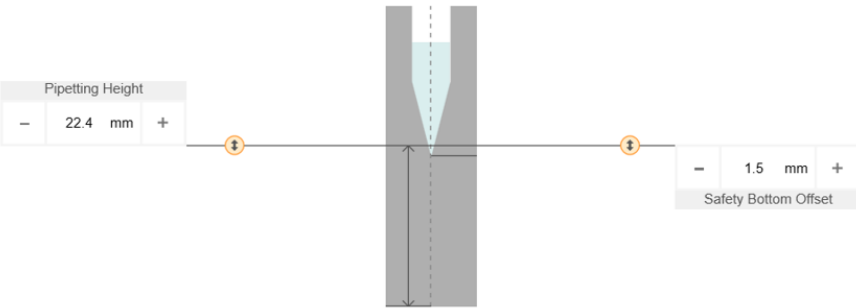
Worklist & Volumes | Speeds | **Source Details** | Target Details | Tip Change | Mix Source | Mix Target | Air Gap

Source PCR Freezer Block with... 04 Worklist Source Details

C

Heights

Offsets



Pipetting Height: - 22.4 mm +

Safety Bottom Offset: - 1.5 mm +

Liquid Level Detection: Yes No

Tip Travel: Yes No

Sample 3

Worklist & Volumes | Speeds | Source Details | **Target Details** | Tip Change | Mix Source | Mix Target | Air Gap

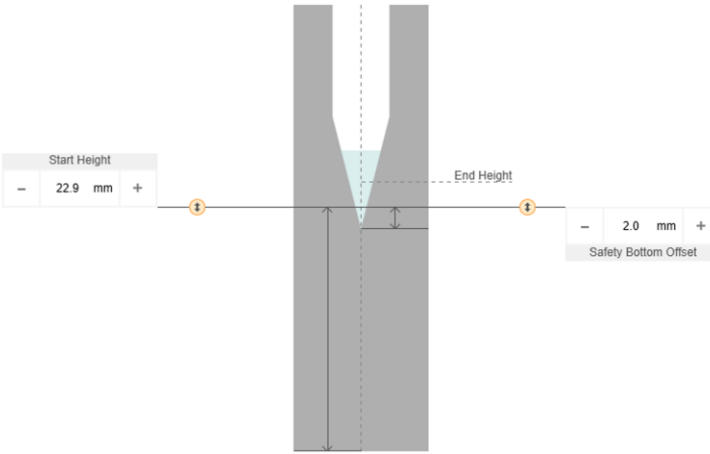
Target PCR Freezer Block with... 04 Worklist Target Details

B

Heights

Tip Touch

Offsets



Start Height: - 22.9 mm +

End Height

Safety Bottom Offset: - 2.0 mm +

Heights

Fix Variable

Tip Travel: Yes No

Sample 4

Worklist & Volumes Speeds Source Details Target Details **Tip Change** Mix Source Mix Target Air Gap

04 Worklist Tip Change

| Index | Source Pos. | Source Well | Target Pos. | Target Well | <input checked="" type="checkbox"/> Eject Tip | <input type="checkbox"/> After each dispense |
|-------|-------------|-------------|-------------|-------------|---|--|
| 1 | C | A1 | B | A1 | <input checked="" type="checkbox"/> | |
| 2 | C | A1 | B | A2 | <input checked="" type="checkbox"/> | |
| 3 | C | A1 | B | A3 | <input checked="" type="checkbox"/> | |
| 4 | C | A1 | B | A4 | <input checked="" type="checkbox"/> | |
| 5 | C | A1 | B | A5 | <input checked="" type="checkbox"/> | |
| 6 | C | A1 | B | A6 | <input checked="" type="checkbox"/> | |
| 7 | C | A1 | B | A7 | <input checked="" type="checkbox"/> | |
| 8 | C | A1 | B | A8 | <input checked="" type="checkbox"/> | |
| 9 | C | A1 | B | A9 | <input checked="" type="checkbox"/> | |
| 10 | C | A1 | B | A10 | <input checked="" type="checkbox"/> | |

Sample 5

Worklist & Volumes Speeds Source Details Target Details Tip Change **Mix Source** Mix Target Air Gap

Source PCR Freezer Block with...

04 Worklist Mix Source

Mixing

Yes No

Mix Volume

Mix Height

Mix Cycles

- 6 +

Mix Pause


- 0 s +

Volume

Fix Variable

Volume

- 75.0 µl +



Sample 6

Worklist & Volumes | Speeds | Source Details | Target Details | Tip Change | **Mix Source** | Mix Target | Air Gap

Source PCR Freezer Block with... 04 Worklist Mix Source

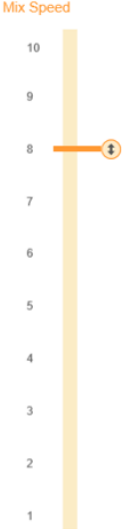
Mixing

Yes No

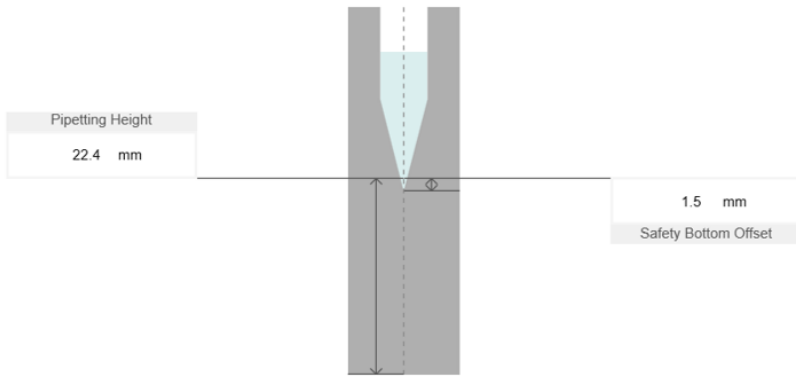
Mix Volume

Mix Height

Mix Speed



LLD: No / Tip Travel : No



Pipetting Height: 22.4 mm

Safety Bottom Offset: 1.5 mm

Sample 7

Worklist & Volumes | Speeds | Source Details | Target Details | Tip Change | Mix Source | **Mix Target** | Air Gap

Target PCR Freezer Block with... 04 Worklist Mix Target

Mixing

Yes No

Sample 8

Worklist & Volumes | Speeds | Source Details | Target Details | Tip Change | Mix Source | Mix Target | **Air Gap**

Target PCR Freezer Block with... 04 Worklist Volumes

Air Gap

Yes No

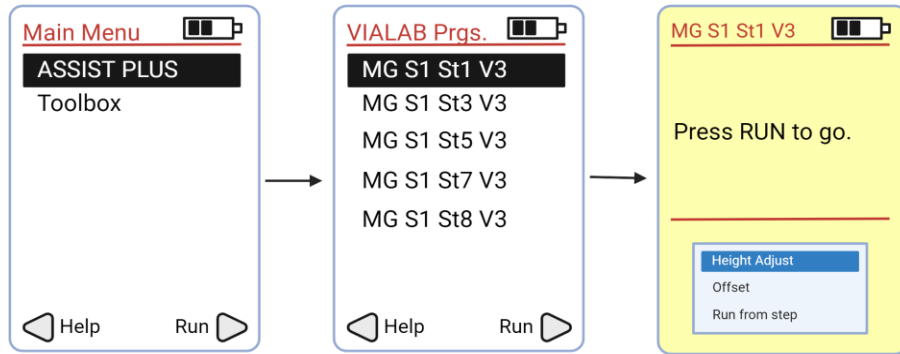
Volume

Fix Variable

Appendix B: Pipetting Programs

Section 1.1. Sample Normalization

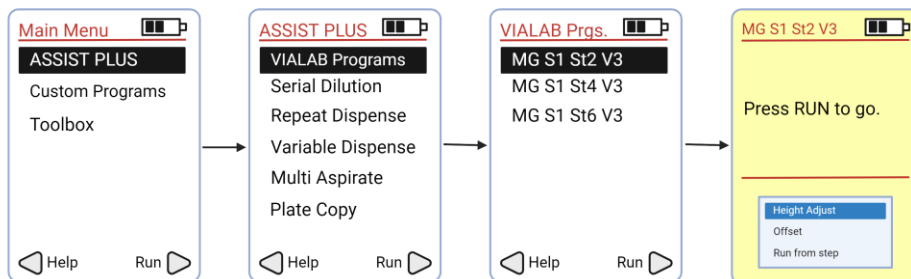
MG S1 St1 V3



| STEPS | ACTION |
|-------|-------------------------|
| 1 | Initial Volumes |
| 2 | Diluent Worklist |
| 3 | Discard Tip |
| 4 | Sample Worklist |
| 5 | "Thaw R1 Plate" message |

Section 1.2. Round 1 Plate Loading and Pooling

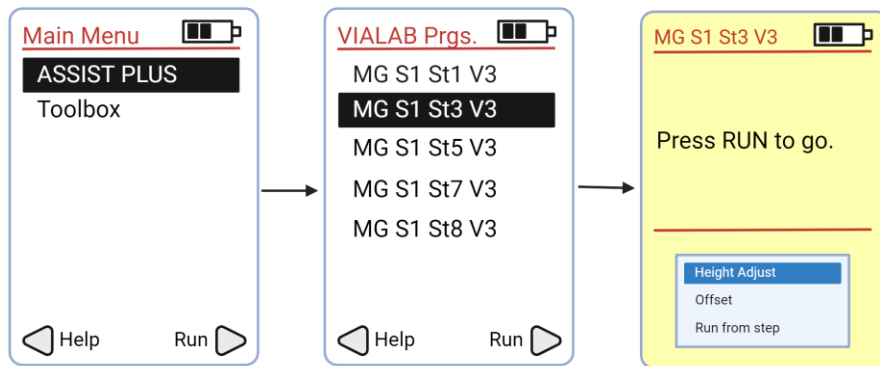
MG S1 St2 V3



| STEPS | ACTION |
|-------|--|
| 1 | Initial Volumes |
| 2 | “Change Plate on Deck C to R1 plate” message |
| 3 | Transfer Diluted Fixed Sample to Round 1 Barcoding Plate |
| 4 | “Seal and incubate for Round 1 RT” message |
| 5 | “Plate R1 on Deck B” message |
| 6 | Volume Change |
| 7-8 | Pool Cells to Intermediate Wells |

Section 1.3. Round 2 Ligation Preparation

MG S1 St3 V3

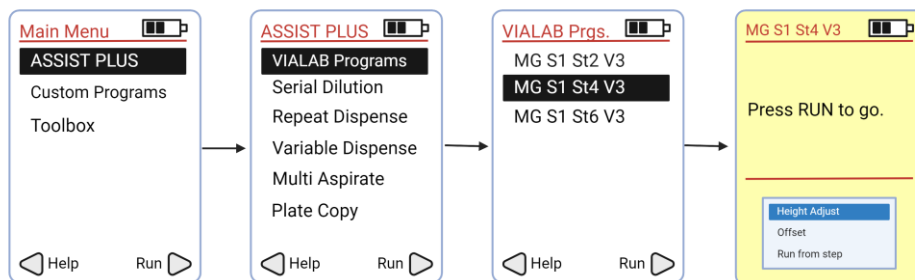


| STEPS | ACTION |
|-------|--|
| 1 | Initial Volumes |
| 2 | Pool row A into 10 mL Tube with 1000 µL tips |
| 3 | Pool row E into 10 mL Tube with 1000 µL tips |
| 4 | Pool rows into 10 mL Tube with 125 µL tips |
| 5 | Add Spin Additive |
| 6 | “Invert Tube and Spin for 10 min” message |
| 7 | “Thaw R2 Plate” message |

| STEPS | ACTION |
|-------|--|
| 8 | "Return tube to Deck C" message |
| 9 | Volume Change |
| 10-16 | Remove Supernatant |
| 17-18 | Resuspend Cell Pellet with Resuspension Buffer |
| 19 | Add R2 Ligation Enzyme to Buffer |
| 20 | Mix Cells in Ligation Mix |
| 21 | Volume Change |
| 22 | Transfer Cells to Ligation Mix |
| 23 | Mix Cells in Ligation Mix |
| 24-27 | Transfer Ligation Mix to Basin |
| 28-30 | Mix Sample in Basin |

Section 1.4. Round 2 Ligation

MG S1 St4 V3

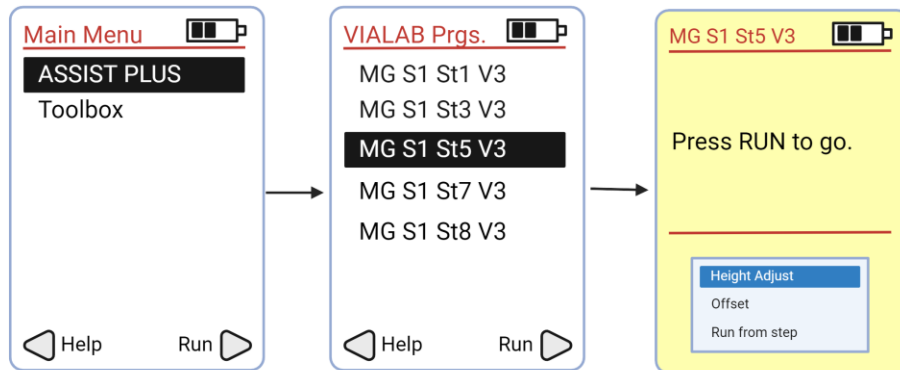


| STEPS | ACTION |
|-------|---|
| 1 | Initial Volumes |
| 2-4 | Mix samples in basins |
| 5-12 | Load Sample into Round 2 Plate |
| 13 | "Seal and incubate for R2 Ligation" message |

| STEPS | ACTION |
|-------|--|
| 14 | "Replace both basin liners" message |
| 15 | "Reload R2 plate on Deck B" message |
| 16 | "Add R2 Stop to right basin" message |
| 17 | Volume Change |
| 18 | Add Stop |
| 19 | "Seal and incubate for Round 2 Stop" message |
| 20 | "Thaw R3 plate" message |
| 21 | "Replace right basin liner" message |
| 22 | "Reload R2 Plate on Deck B" message |
| 23 | Pool R2 Plate to basin |

Section 1.5. Round 3 Ligation Preparation

MG S1 St5 V3

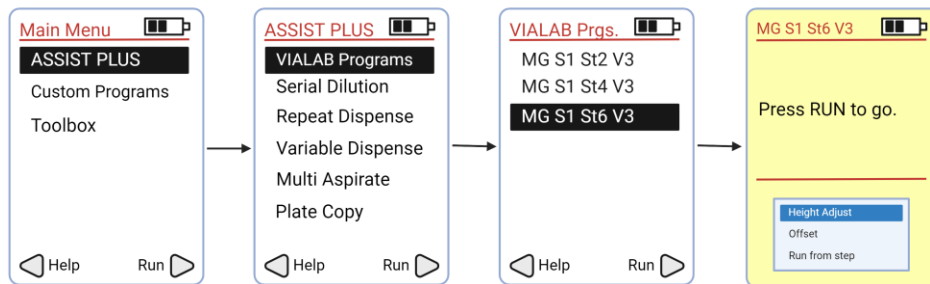


| STEPS | ACTION |
|-------|--|
| 1 | Initial Volumes |
| 2 | "Move basin to slanted holder" message |
| 3 | "Insert cell strainer in 10 mL tube" message |
| 4 | Wash basin mix |

| STEPS | ACTION |
|-------|---------------------------------------|
| 5 | Volume change |
| 6-10 | Strain cells |
| 11 | "Move Basin Holder to Deck A" message |
| 12 | "Remove cell strainer" message |
| 13 | Volume change |
| 14 | Add R3 Ligation Enzyme |
| 15 | Mix Ligation Enzyme with sample |
| 16 | Volume change |
| 17-21 | Transfer cells to right basin |

Section 1.6. Round 3 Ligation

MG S1 St6 V3

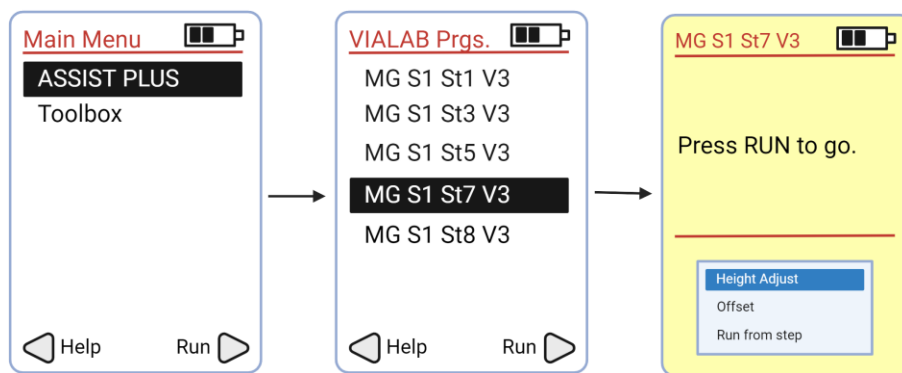


| STEPS | ACTION |
|-------|---|
| 1 | Initial Volumes |
| 2-4 | Mix sample in basin |
| 5-12 | Add sample to Round 3 Plate |
| 13 | "Seal and incubate for R3 Ligation" message |
| 14 | "Change both basin liners" message |
| 15 | "Reload R3 Plate on Deck B" message |
| 16 | "Add R3 Stop to right basin" message |

| STEPS | ACTION |
|-------|----------------------|
| 17 | Volume change |
| 18 | Add R3 Stop to plate |
| 19 | Pool R3 Plate |

Section 1.7. Pre-Lysis

MG S1 St7 V3

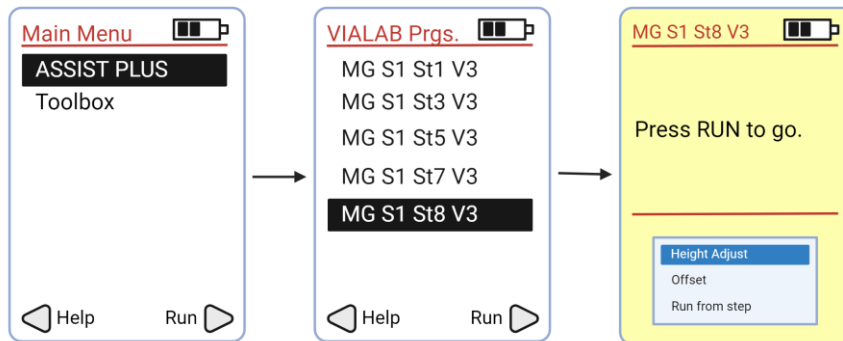


| STEPS | ACTION |
|-------|--|
| 1 | Initial Volumes |
| 2 | "Move Basin Holder to Deck B" message |
| 3 | "Insert cell strainer in 10 mL tube" message |
| 4 | Wash basin |
| 5 | Volume change |
| 6-12 | Strain cells |
| 13 | "Move Basin Holder to Deck A" message |
| 14 | "Remove cell strainer" message |
| 15 | Add Spin Additive |
| 16 | "Invert and spin for 10 min" message |
| 17 | "Return 10 mL tube to Deck C" message |

| STEPS | ACTION |
|-------|---------------------------------------|
| 18 | Volume change |
| 19-23 | Remove supernatant |
| 24-25 | Resuspend Pre-Lyse |
| 26 | "Spin for 10 min" message |
| 27 | "Return 10 mL Tube to Deck C" message |
| 28 | Volume change |
| 29-33 | Remove supernatant |
| 34 | "Count cells/nuclei" message |

Section 1.8. Lysis and Sublibrary Generation

MG S1 St8 V3



| STEPS | ACTION |
|-------|---|
| 1 | Initial Volumes |
| 2-5 | Aliquot 25 µL of sample |
| 6 | Lysis Mastermix |
| 7 | Mix Lysis Mastermix |
| 8 | Add Lysis Mastermix to sample |
| 9 | "Vortex and centrifuge samples" message |

Appendix C: Troubleshooting

Error warning during the execution of a program

- In case of an error warning, abort the program. Do not press "RUN". Scroll down "Run from step". You can then continue from the error location. This allows to resume directly from the point of error.

Tip Pinching

- Tip pinching may occur when using a newly frozen PCR freezer block for a plate pooling step. Ensure that your PCR Freezer Block has been thawed at room temperature for at least 10 minutes.
- Ensure to apply sufficient pressure when placing the plate onto the frozen PCR freezer block.

Incorrect tip location inputted

- The D-ONE Pipette will check the pipette tips before the step starts. The ASSIST PLUS will display an error warning if a pipette tip is incorrectly detected. Abort and restart the program with the correct tip location input.
- The VIAFLO will check the pipette tip after the step is finished. The ASSIST PLUS will display an error warning if a pipette tip is incorrectly detected. Abort and restart the program with the correct tip location input.

Appendix D: Revision History

| Version | Description | Date |
|---------|--------------------------------------|-------------|
| 1.0 | Initial release | June 2024 |
| 1.1 | Updated Sample Loading Table version | July 2024 |
| 1.2 | Updated box configurations | August 2024 |



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