Application Note

Streamlining single-cell sequencing with the Flex Apex workflow using automated liquid handling solutions

Introduction

Single-cell RNA sequencing (scRNA-seq) has become an essential tool for understanding complex biological systems. The Flex Apex workflow from 10x Genomics offers a comprehensive, scalable solution to measure single-cell gene expression. Flex Apex uses probe-based gene expression profiling to maximize discovery power, providing the resolution needed to uncover rare cell states and drivers of disease across hundreds of samples. However, library preparation workflows can be time consuming when using manual pipetting, which is also prone to variability, highlighting the need for automated liquid handling solutions.

This application guide focuses on the implementation of automated liquid handling solutions using the ASSIST PLUS pipetting robot from INTEGRA Biosciences in the Flex Apex workflow. It includes VIALAB programs for optimization of all workflow steps – from sample preparation to sequencing-ready NGS libraries – for efficient lab automation, streamlined sample processing and reduced hands-on time.

Key benefits:

- Automated pipetting simplifies repetitive handling steps – including fixation, washing and probe hybridization – when processing multiple Flex Apex samples in parallel.
- Standardized liquid handling ensures identical processing of fixed samples prior to pooling and GEM generation, supporting reproducible high-plex experiments.
- Automated handling minimizes manual intervention during critical plate-based transfer and pooling steps, lowering the risk of cross contamination.
- Integrated magnetic bead handling enables consistent clean-up performance, supporting robust and reproducible library preparation.

Overview: How to automate the Flex Apex workflow using the ASSIST PLUS pipetting robot

ASSIST PLUS

Application Note

The ASSIST PLUS pipetting robot streamlines the Flex Apex workflow while improving throughput, precision and reliability. This application guide describes pre-programmed VIALAB programs and detailed instructions for each step in the workflow (**Figure 1**), allowing easy set-up of 96 samples. The modular, flexible ASSIST PLUS has the advantage that it can be used with a 300 µl, 12 channel VIAFLO electronic pipette for sample fixation, probe hybridization, barcoding, pooling and washing, and a 1,250 µl D-ONE pipetting module for normalization, pre-amplification PCR set-up, DNA clean-up and indexing PCR set-up (**Figure 1**). This flexibility in pipette selection enables users to combine a multichannel approach – for speed and precision – with a single channel option, for when a broad pipetting range is needed. Furthermore, magnetic bead clean-up steps can be automated with the MAG module, a magnetic separation device that uses vertical magnet array movements to enable automated magnetic bead handling, avoiding unnecessary manual interventions.

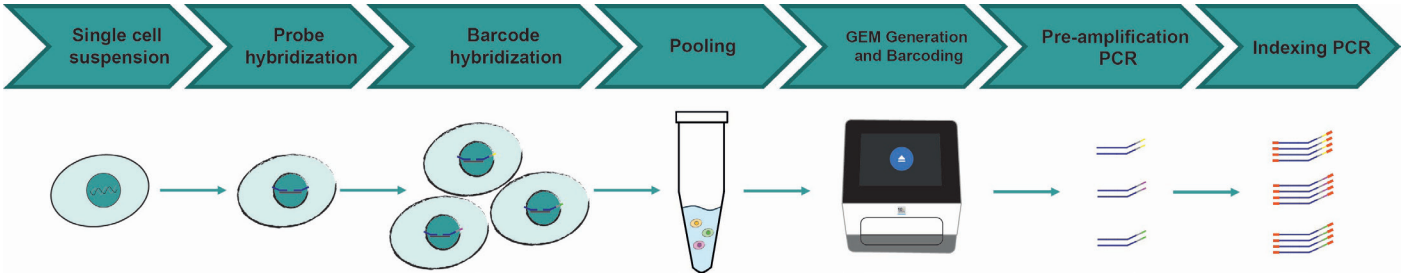

Figure 1: Schematic representation of the Flex Apex workflow.

Step-by-step procedure

Step 1: **Sample fixation and preparation**

How to: Preserve cellular RNA, and prepare samples for storage and downstream processing.

Sample preparation is dependent on the type of starting material, for example, single-cell or nuclei suspensions, tissues, FFPE samples or blood. For each type of sample preparation protocol, please refer to the manufacturer's guidance for more information. This section shows how to automate the Plate-based Sample Preparation for *GEM-X Flex v2* protocol for fresh cell/nuclei suspensions on the ASSIST PLUS.

Sample preparation consists of 4 steps:

- Sample fixation
- Quenching
- Sample storage (optional)
- Post-storage processing (optional)

Two different ASSIST PLUS deck set-ups are needed.

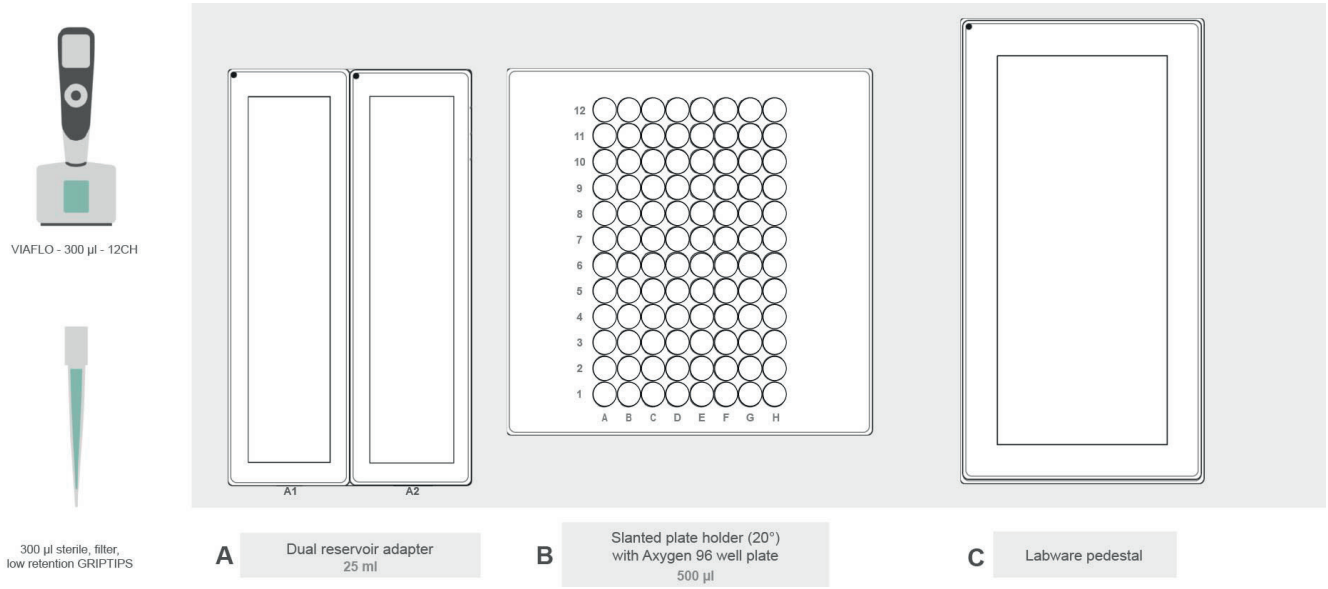

Figure 2: ASSIST PLUS deck set-up 1, for sample preparation. **Position A:** dual reservoir adapter with 25 ml SureFlo™ polystyrene reservoir inserts. **Position B:** slanted plate holder at a 20° angle with an Axygen® 96 well, 500 µl plate. **Position C:** labware pedestal with 100 ml SureFlo polystyrene reservoir for waste collection.

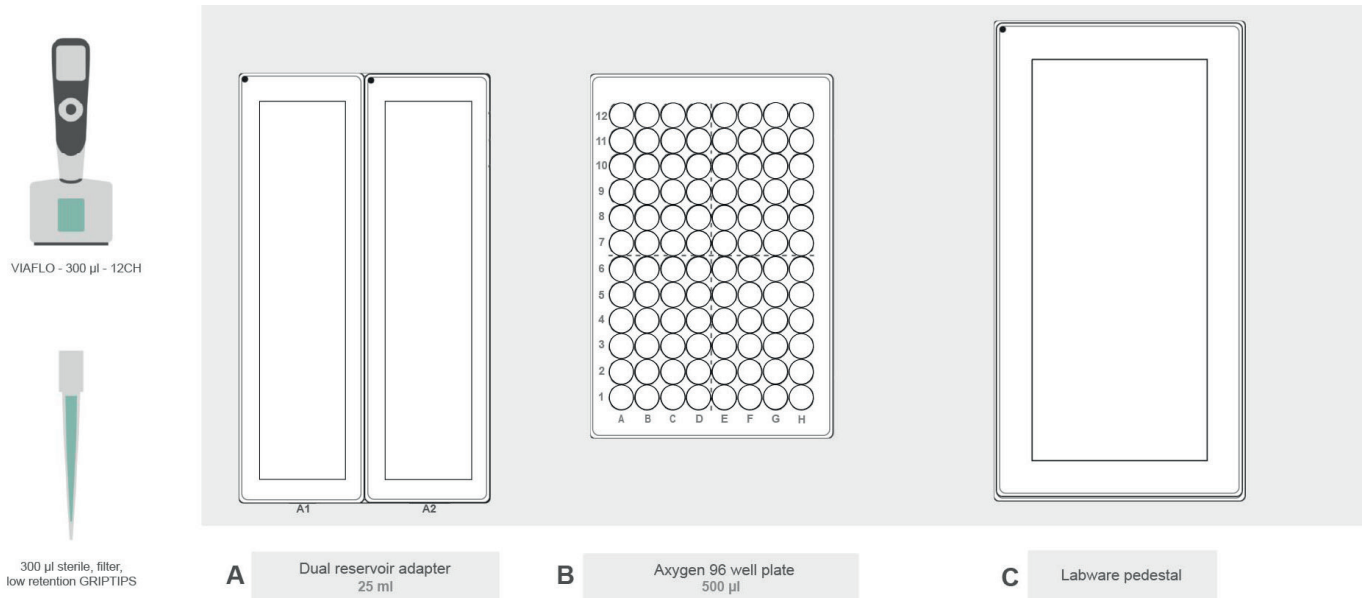

Figure 3: ASSIST PLUS deck set-up 2, for sample preparation. **Position A:** dual reservoir adapter with 25 ml SureFlo polystyrene reservoir inserts. **Position B:** Axygen 96 well, 500 µl plate. **Position C:** labware pedestal with 100 ml SureFlo polystyrene reservoir for waste collection.

Sample fixation

Following the set-up shown in **Figure 2**, fill reservoir A2 with 10.56 ml of room temperature fixation buffer B, centrifuge the sample plate at 300-400 rcf for 5 min (PBMCs/cell lines) at 4°C and place it onto the slanted plate holder (20° tilt) in position B. Place an empty 100 ml reservoir in position C. Run program '0-1_Fixation_SPH'. After aspiration of the supernatant, remove the slanted plate holder and place the sample plate directly onto deck position B (**Figure 3**), then resuspend the samples in fixation buffer B. Seal the plate and incubate the samples at 20 °C for 1 h in a thermal cycler.

Quenching

After fixation, the reaction needs to be quenched. For this step, fill reservoir A1 with 21.12 ml of additive C and reservoir A2 with 22 ml of quenching buffer B at 4 °C, keeping the samples from the previous step in position B and the waste reservoir in position C (**Figure 3**). Keep samples on ice until ready to run program '0-2_Additive C_Quench_SPH'. In this program, additive C is added to the samples and mixed, then the plate needs to be sealed for centrifugation. After centrifugation at 850 rcf for 5 min at 4 °C, place the slanted plate holder (20° tilt) back on position B and place the centrifuged sample plate on it (**Figure 2**). Next, the ASSIST PLUS removes the supernatant and resuspends the samples in the chilled quenching buffer B.

Long-term storage (optional)
After quenching, the samples can either be stored for up to 12 months or used immediately for probe hybridization. Please refer to the manufacturer's protocol *Fixation of Cells & Nuclei for GEM-X Flex Gene Expression* for more information about long-term storage.

For long-term storage, fill reservoir A1 with 3 ml of thawed, pre-warmed enhancer (10x Genomics, #2000482) and reservoir A2 with 6 ml of 50 % glycerol, then place the samples from the previous step directly onto position B without the slanted plate holder. position C is not required in this program; the waste reservoir from the previous step can be left in place or removed. (**Figure 3**). Run program '0-3_Storage'. This program adds enhancer and glycerol to the samples, with gentle mixing. After sealing the plate, the samples are now ready for storage at -80 °C.

Post-storage processing (optional)
Samples that have been stored frozen need to be thawed, processed and optionally normalized prior to use in the Flex Apex workflow. Please refer to the manufacturer's protocol *Fixation of Cells & Nuclei for GEM-X Flex Gene Expression* for more information processing samples after long-term storage.

Fill reservoir A1 with 22 ml of quenching buffer B, place samples that have been thawed at room temperature and centrifuged onto position B and a 100 ml reservoir for waste collection onto position C (**Figure 3**). Keep samples on ice until ready to run program '0-4_Post Storage Processing SPH'. This program removes supernatant from the centrifuged samples and resuspends them in quenching buffer B, restoring the samples to a post-quenching, pre-storage state. It is recommended that normalized samples are used for hybridization, to ensure equal representation of each sample in the final pool. This can be achieved using the ASSIST PLUS set-up shown in **Figure 3**, exchanging the 12 channel VIAFLO pipette for a D-ONE pipetting module. Run the program '0-5_Residual Sample Normalization_SPH', described in detail in the *ASSIST PLUS Flex Apex user guide*.

Step 2: **Sample normalization and probe hybridization**

How to: Tag the transcriptome using whole transcriptome probe pairs.

During hybridization, whole transcriptome probe pairs – each consisting of a left-hand side (LHS) and a right-hand side (RHS) targeting a specific gene – are added to the fixed and normalized samples. The probe pairs hybridize to their complementary target RNA during an overnight incubation.

This step consists of two stages:

- Normalization
- Probe hybridization

Normalization

It is recommended that normalized samples are used for hybridization, to ensure equal representation of each sample in the final pool. Normalization can be performed at this stage using the ASSIST PLUS and the D-ONE pipetting module with the program '1-1_Normalization' (**Figure 4**), described in detail in the ASSIST PLUS Flex Apex user guide, if it was not done during sample preparation.

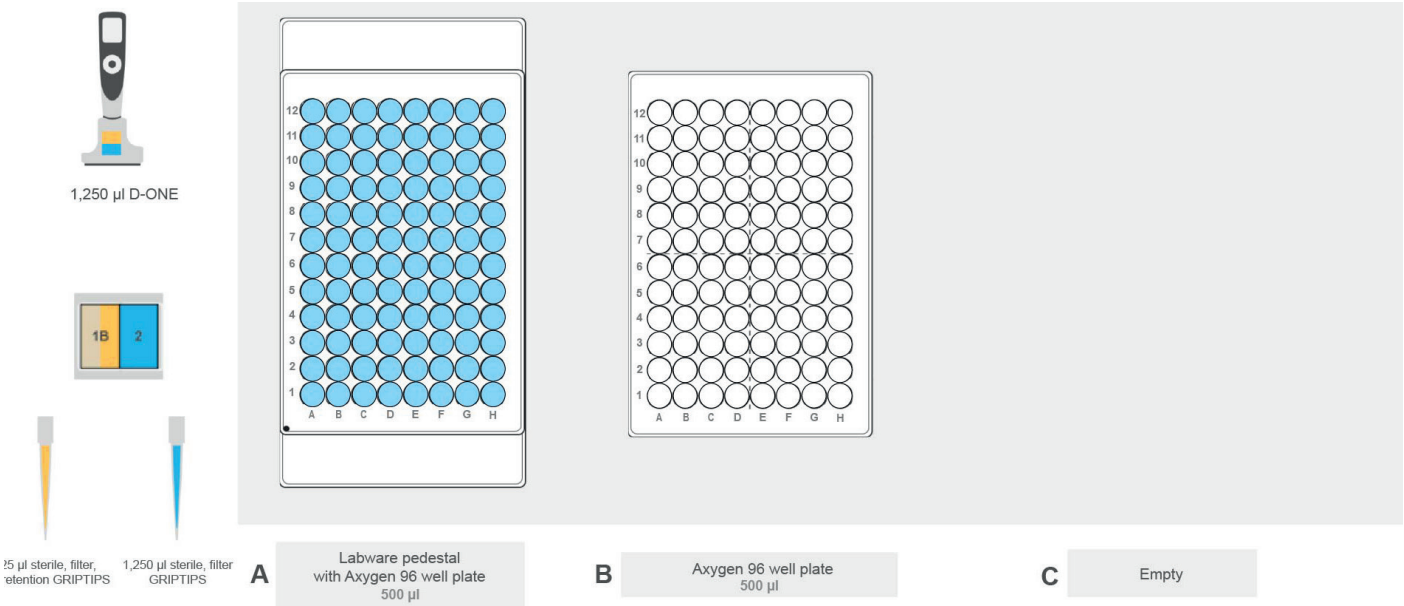

Figure 4: ASSIST PLUS deck set-up for sample normalization. **Position A:** labware pedestal with Axygen 96 well, 500 µl plate containing fixed samples (blue). **Position B:** Axygen 96 well, 500 µl plate.

Probe hybridization

The normalized samples are centrifuged at 850 rcf for 5 min at 4 °C, ready to be used for probe hybridization. Exchange the D-ONE pipetting module with the 12 channel VIAFLO pipette. Fill reservoir B1 with 5.28 ml of manually prepared hybridization mix, pre-warmed to 42 °C, and place the sample plate on position A. Reservoir B2 will be used for waste collection (**Figure 5**). Run program '1-2_Probe Hybridization' to remove supernatant from the samples and resuspend them in the hybridization mix. Seal the plate and incubate at 42 °C for 16-24 h.

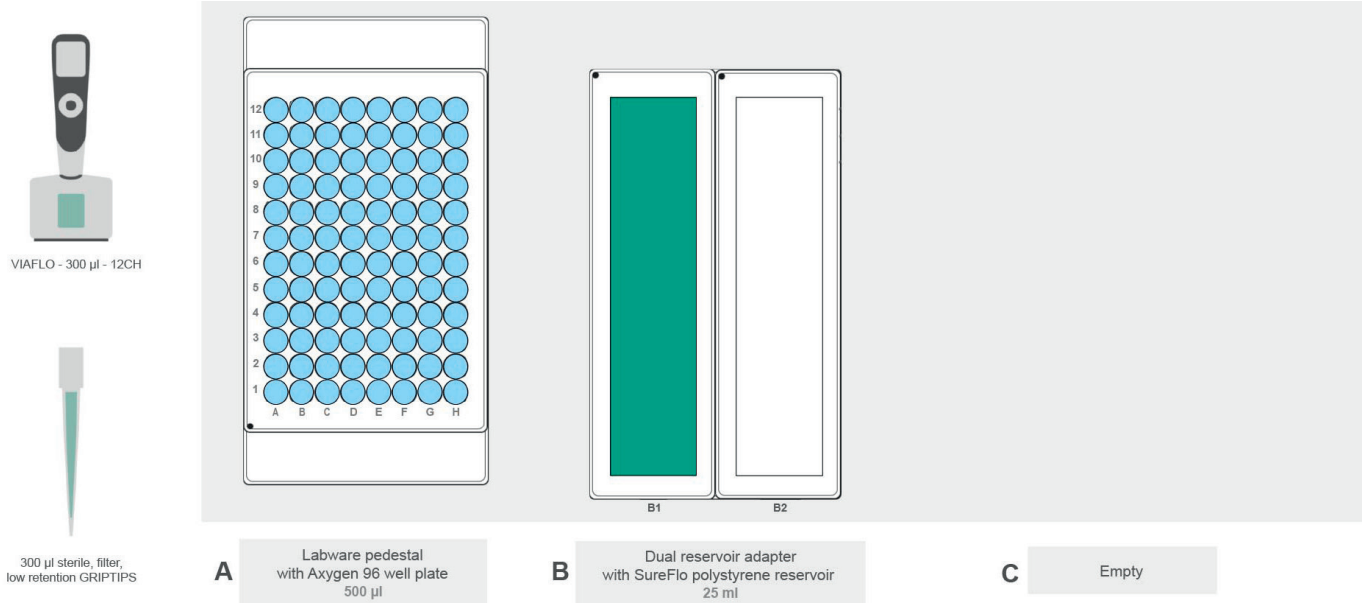

Figure 5: ASSIST PLUS deck set-up for probe hybridization. **Position A:** labware pedestal with Axygen 96 well, 500 µl plate containing normalized, fixed samples (blue). **Position B:** dual reservoir adapter with a 25 ml SureFlo polystyrene reservoir containing hybridization mix (green) in position B1 and 25 ml polypropylene reservoir insert for waste collection in position B2.

Step 3: **Post-hybridization washing and barcoding**

How to: Wash samples after probe hybridization and hybridize barcode oligos.

A post-hybridization washing step is performed after overnight probe hybridization to remove excess unbound probes. This ensures that subsequently introduced barcoding oligos – comprising a partial capture sequence, a sample barcode and a partial constant sequence – hybridize specifically to probe-target complexes, enabling accurate sample multiplexing while minimizing off-target interactions.

This step consists of two stages:
- Post-hybridization washing
- Barcode oligo hybridization

The ASSIST PLUS labware set-up for these stages is shown in **Figure 6**.

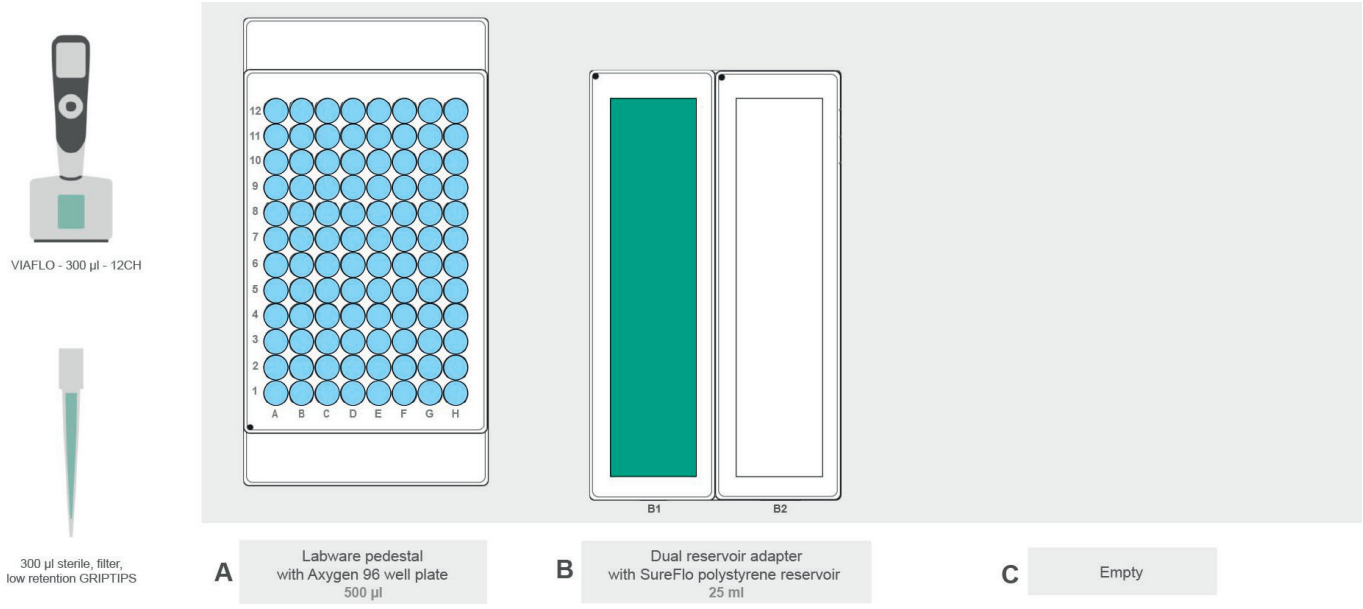

Figure 6: ASSIST PLUS deck set-up for post hybridization washing and barcoding. **Position A:** labware pedestal with Axygen 96 well, 500 µl plate containing samples after hybridization (blue). **Position B:** dual reservoir adapter with a 25 ml SureFlo polystyrene reservoir containing post-hybridization wash buffer B (green) in position B1 and 25 ml polypropylene reservoir insert for waste collection in position B2.

Post-hybridization washing

Place the sample plate in position A and fill reservoir B1 with 21 ml manually prepared post-hybridization wash buffer B at room temperature. Reservoir B2 will be used for waste collection (**Figure 6**). Run program '2-1_Post Hyb Wash'. This program adds the post-hybridization wash buffer B and mixes the samples. Seal the plate and centrifuge.

Barcode oligo hybridization

The barcode oligo hybridization mix is added after centrifugation of the samples. For this step, place the sample plate in position A, 4.25 ml of manually prepared oligo hybridization mix in reservoir B1 and a 96 well plate containing the barcode oligos in position C. Reservoir B2 is used for waste collection (**Figure 7**). Run program '2-2_Barcoding' to remove the supernatant from the samples and resuspend them in oligo hybridization mix to transfer the barcode oligos to the samples. Seal the plate and incubate for 2 h at 42 °C.

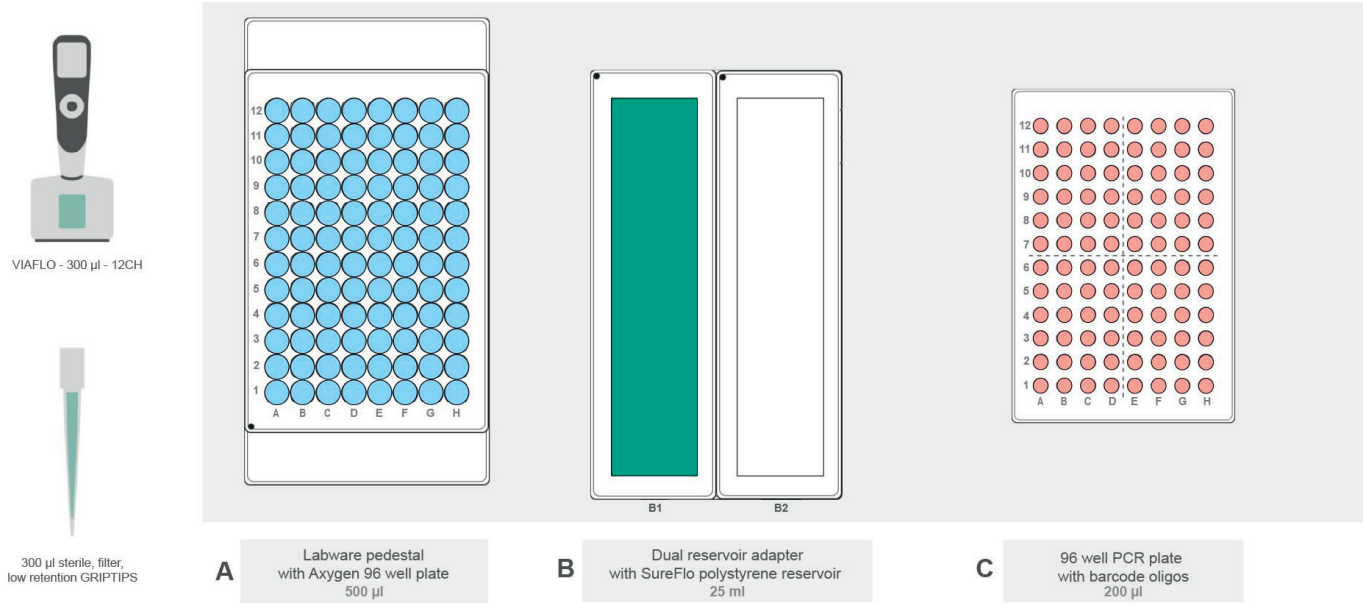

Figure 7: ASSIST PLUS deck set-up for barcode oligo hybridization. **Position A:** labware pedestal with Axygen 96 well, 500 µl plate containing samples after hybridization (blue). **Position B:** dual reservoir adapter with a 25 ml SureFlo polystyrene reservoir containing oligo hybridization mix (green) in position B1 and 25 ml polypropylene reservoir insert for waste collection in position B2. **Position C:** 96 well plate containing barcode oligos (salmon).

Step 4 **Pooled washing**

How to: Wash and pool samples after barcode hybridization.

Samples hybridized with unique sample barcodes can be cleaned up following the Individual Wash workflow, where samples are washed individually and pooled once washing is complete. Alternatively, the samples can be pooled immediately after hybridization, and washed as a pool. The Pooled Wash workflow is combined into one program and described below.

The ASSIST PLUS labware set-up for this step is shown in **Figure 8**.

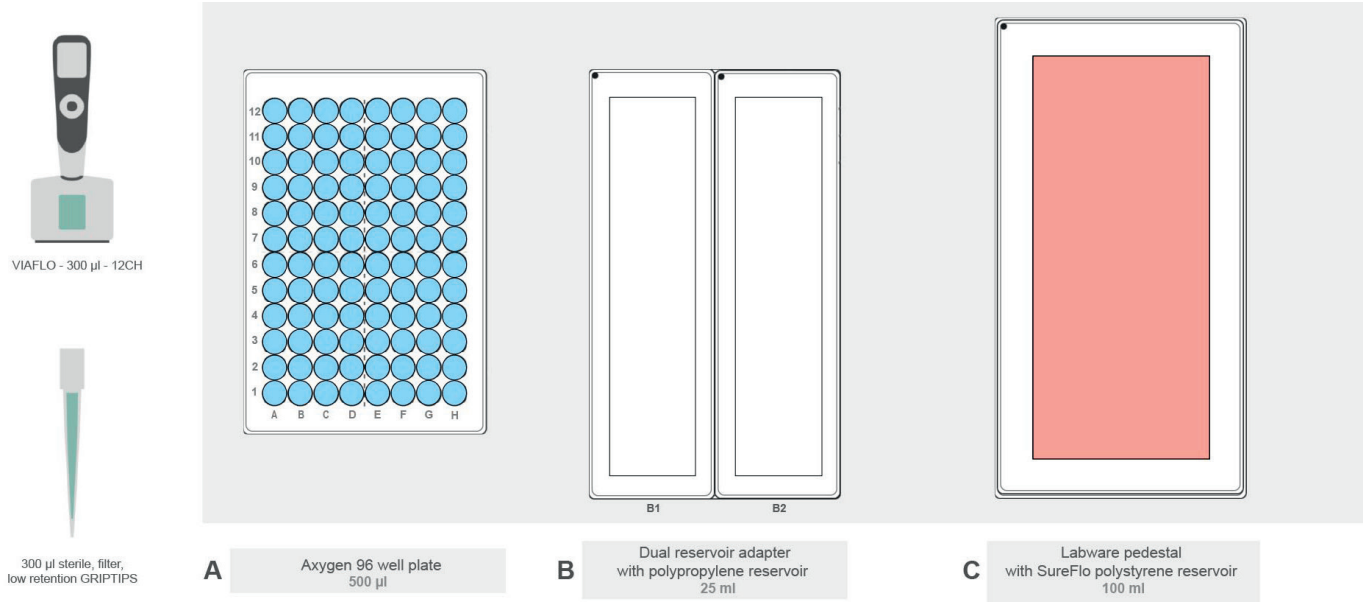

Figure 8: ASSIST PLUS deck set-up for pooled washing. **Position A:** labware pedestal with Axygen 96 well, 500 µl plate containing samples after barcode hybridization (blue). **Position B:** dual reservoir adapter with a 25 ml polypropylene reservoir insert for pool collection in position B2. **Position C:** labware pedestal with a 100 ml SureFlo polystyrene reservoir containing post-hybridization wash buffer B (salmon).

Place the sample plate in position A. Reservoir B2 will be used for collection of the pooled libraries. Fill reservoir C1 with 35 ml manually prepared post-hybridization wash buffer B at room temperature. Off deck, prepare a 50 ml centrifuge tube with 9.6 ml (100 µl per sample) post-hybridization wash buffer B (**Figure 8**). Run program '3-0_Pre-Wash Cooling'. This program pools samples and subsequently performs an additional wash of the sample wells to ensure complete collection of each sample. 150 µl of post-hybridization wash buffer B is added to each sample and pooled in reservoir B2. Manually transfer the samples to a 50 ml centrifuge tube after mixing. The sample plate is washed again with 200 µl of post-hybridization wash buffer B, pooled in reservoir B2, mixed and manually transferred to the pooled samples in the 50 ml centrifuge tube. The pooled samples are then centrifuged, and the supernatant is removed manually according to the manufacturer's protocol, *GEM-X Flex Apex v2 user guide*, provided in the downloads.

Step 5 **Gel bead-in-emulsion (GEM) generation**

How to: Generate GEMs.

This step is performed off deck using a Chromium X/iX instrument (10x Genomics) according to the manufacturer's protocol, *GEM-X Flex Apex v2 user guide*, provided in the downloads.

After pooling and washing, samples are diluted according to the protocol, and combined with barcoded gel beads, enzymes and oil on a GEM-X Chip. These components are partitioned into oil-emulsified droplets – ideally containing a single gel bead and a single cell or nucleus – within the Chromium X/iX (**Figure 9**). Following GEM generation, the gel beads are dissolved, cells are lysed and barcoded primers are released into the droplets. Subsequent enzymatic reactions, including ligation, hybridization, PCR and heat inactivation, result in a non-amplified library ready for downstream processing.

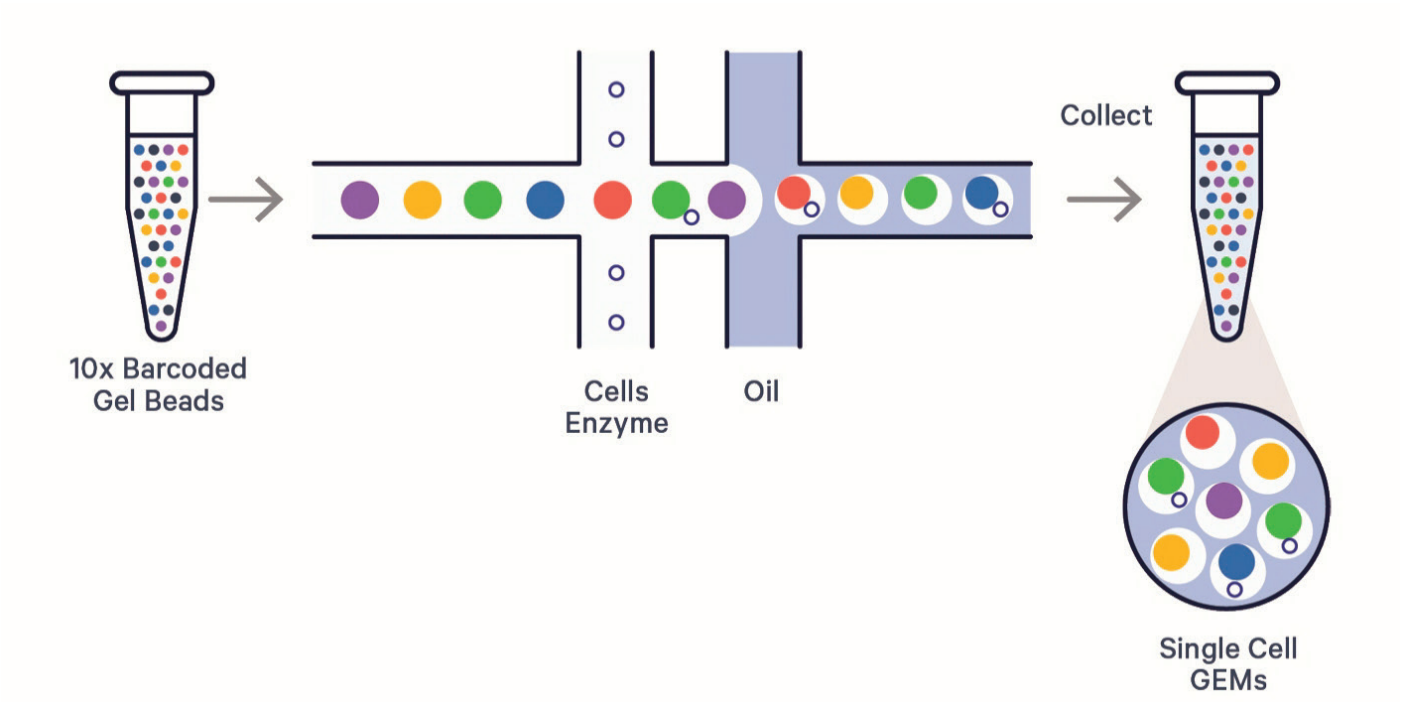

Figure 9: A schematic representation of the GEM-X Chip workflow. Barcoded gel beads (left), sample and enzyme mix (left intersection) and oil (right intersection) are combined in a GEM-X 3' or 5' Chip. The barcoded beads flow from left to right and intersect orthogonally with streams of enzyme/sample mix and oil to form GEMs (right).

Step 6 **GEM recovery and pre-amplification PCR**

How to: Recover GEMs and prepare the libraries for pre-amplification PCR.

GEM recovery is performed manually according to the manufacturer's protocol. After GEM recovery, the libraries are pre-amplified using PCR. Set up the ASSIST PLUS deck according to **Figure 10**. Add one strip of 8 PCR tubes in row 12 of the PCR cooling block on deck position A with samples (split pools) in wells E12-H12. Load the manually prepared pre-amplification mix into a 1.5 ml microcentrifuge tube in position A1 of the 1.5 ml tube rack on deck position B. Deck position C is not used in this step, but a MAG module with a 96 well PCR plate adapter can be placed in this position in preparation for the steps that follow **(Figure 10**). Run program '5-2_Pre-Amplification' on the D-ONE pipetting module. This program distributes the pre-amplification mix to the samples. After the program is finished, close the tubes and mix the samples again by inverting the strip eight times followed by a quick centrifugation. Transfer the sample tubes to a thermal cycler and run the appropriate 8-cycle PCR program according to the manufacturer's protocol, *GEM-X Flex Apex v2 user guide*, provided in the downloads.

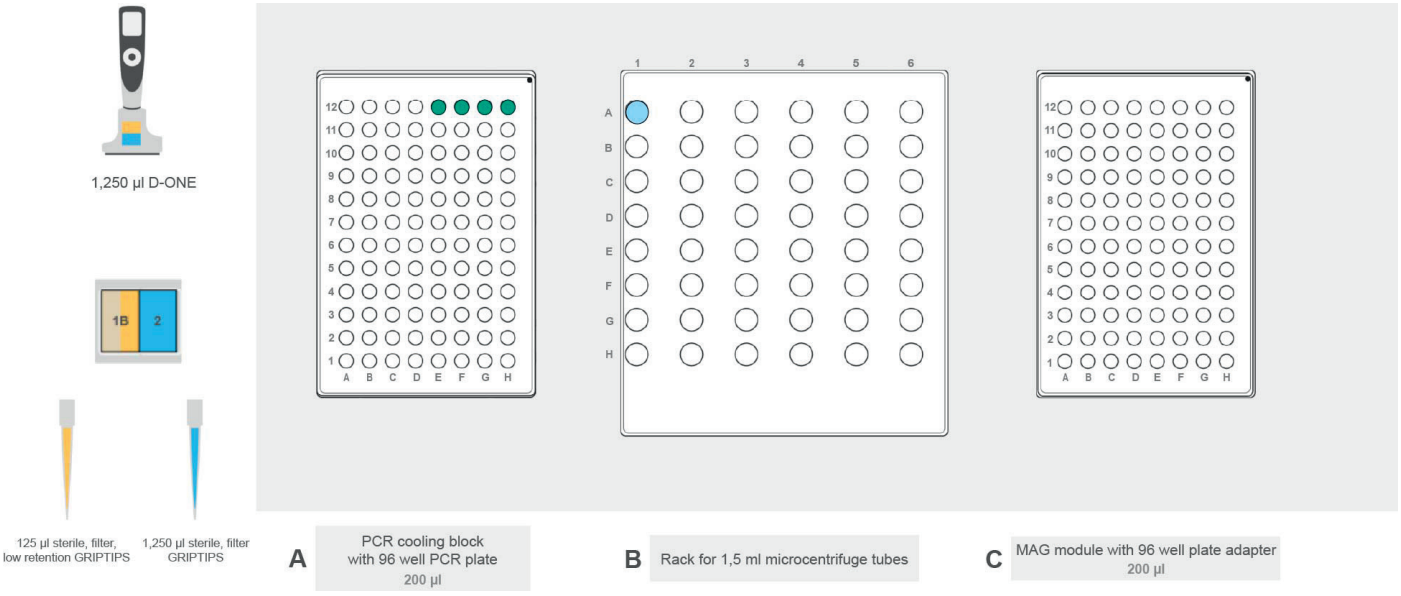

Figure 10: ASSIST PLUS deck set-up for pre-amplification PCR. **Position A:** PCR cooling block with a strip of 8 PCR tubes containing samples after GEM recovery (green) in row 12, wells E12-H12. **Position B:** Rack for 1.5 ml microcentrifuge tubes with a tube containing pre-amplification mix (blue) in position A1. **Position C:** MAG module with 96 well plate adapter.

Step 7 **DNA clean-up**

How to: Clean up your library after pre-amplification.

A magnetic bead-based clean-up is performed after pre-amplification PCR to remove excess primers, nucleotides, enzymes and other reaction components. This ensures efficient and specific downstream library preparation.

Centrifuge the sample PCR strip for 30 seconds in a microcentrifuge to separate the samples from the recovery agent. Manually transfer 70 µl into fresh tubes and place them in row 12 of the PCR cooling block on deck position A, with the samples in wells E12-H12. Place a fresh strip of PCR tubes in row 10, for post clean-up collection. On deck position B, place a 1.5 ml microcentrifuge tube with 560 µl of SPRIselect magnetic beads in position A2, ensuring that the magnetic beads are well homogenized by vortexing prior to transfer to the tube. Place two fresh 1.5 ml microcentrifuge tubes filled with 1 ml of 80 % ethanol in positions B2 and C2, and two empty tubes for waste collection in positions D2 and E2. Finally, manually prepare 600 µl elution buffer according to the manufacturer's protocol, *GEM-X Flex Apex v2 user guide*, provided in the downloads, and place it in a 1.5 ml microcentrifuge tube in position A3. Place a fresh Eppendorf twin.tec® PCR Plate LoBind® on the MAG module with a 96 well PCR plate adapter in position C (**Figure 11**). Follow the instructions given in the *ASSIST PLUS Flex Apex user guide* to set up the DNA Clean-up Worklist.csv file, available in the downloads. Run program '5-3_DNA Cleanup' on the D-ONE pipetting module. This program transfers the libraries to the plate on the MAG module, adds magnetic beads to the samples and washes them with 80 % ethanol, then elutes the libraries from the beads and transfers them to clean tubes in row 10 of deck position A.

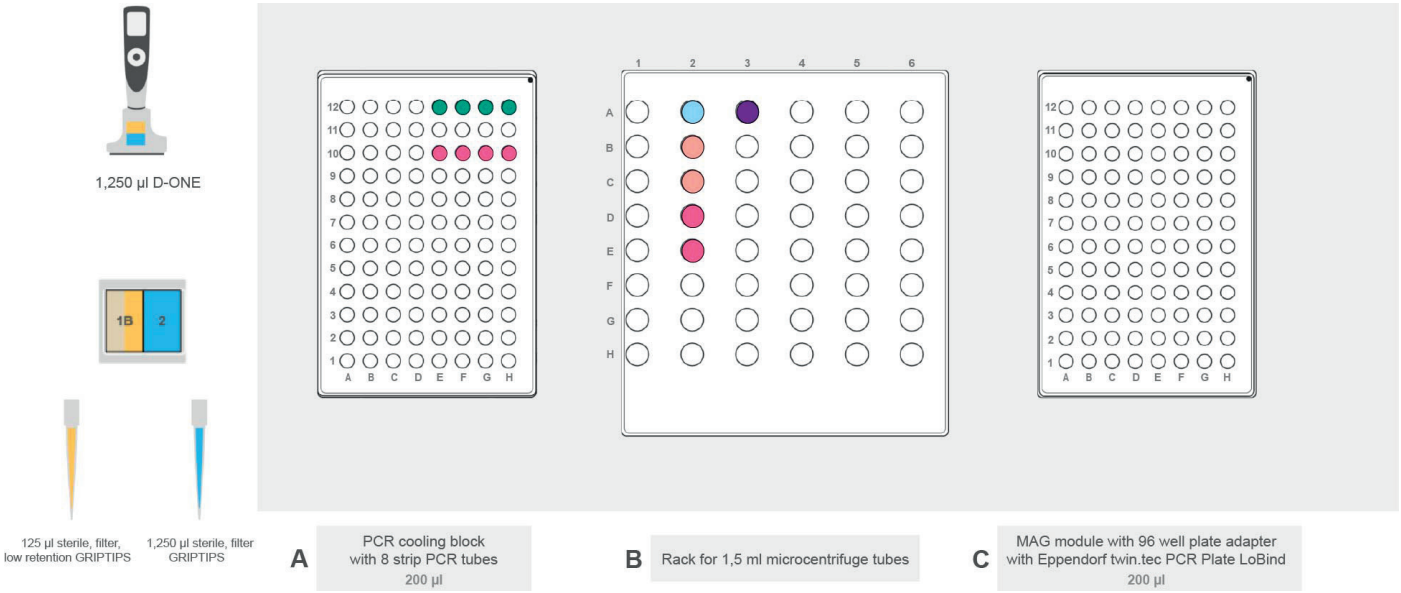

Figure 11: Deck set-up of the ASSIST PLUS for DNA clean-up. **Position A:** PCR cooling block with a strip of 8 200 µl PCR tubes containing samples after pre-amplification (green) in row 12, and a fresh strip in row 10 (pink) for sample collection. **Position B:** Rack for 1.5 ml microcentrifuge tubes with tubes containing SPRIselect magnetic beads (A2, blue), 80 % ethanol (B2 and C2, salmon), fresh tubes for waste collection (D2 and E2), and elution buffer in position A3. **Position C:** MAG module with 96 well plate adapter with a clean Eppendorf twin.tec PCR Plate LoBind.

Step 8 **Indexing PCR and final size selection**

How to: Prepare the libraries for indexing PCR and final size selection.

Indexing PCR introduces sequencing adapters and sample-specific indices to the library fragments, enabling downstream multiplexed sequencing. Subsequent magnetic bead-based size selection removes excess primers, adapter dimers, enzymes and nucleotides, while enriching for correctly constructed library molecules.

This step consists of two stages:
- Sample indexing PCR
- Library size selection

Sample indexing PCR

Place the sample PCR strip tubes in row 12 of the PCR cooling block on deck position A. Place a fresh strip of PCR tubes in row 10 of deck position A. These tubes will contain the final mix for indexing PCR. On deck position B, place a 1.5 ml microcentrifuge tube with manually prepared sample index PCR mix in position A2. Place the 96 well plate containing indexing primers on the MAG module in position C (**Figure 12**). Follow the instructions given in the *ASSIST PLUS Flex Apex user guide* to set up the Indexing PCR Worklist.csv file, available in the downloads. Run program '6-1_Sample Index PCR' on the D-ONE pipetting module. This program distributes the sample indexing mix and the indexing primers to the fresh tubes provided in deck position A, row 10. Finally, a portion of the sample is added to the reaction. The remaining sample can be stored at -80 °C. The strip tubes containing the reactions are transferred to a thermal cycler and the appropriate PCR cycle program run.

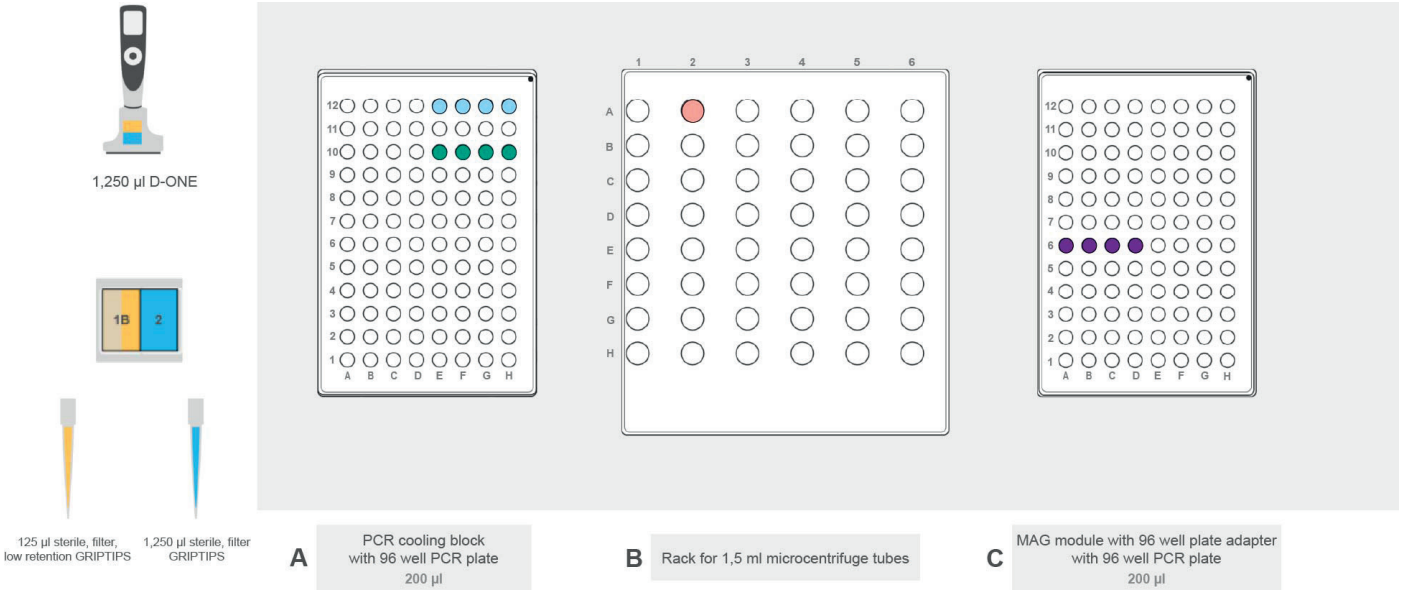

Figure 12: ASSIST PLUS deck set-up for indexing PCR. **Position A:** PCR cooling block with a strip of 8 200 µl PCR tubes containing samples in row 12 (blue) and a fresh strip in row 10 (green). **Position B:** Rack for 1.5 ml microcentrifuge tubes with tubes in position A2 containing indexing PCR mix (salmon). **Position C:** MAG module with 96 well plate adapter with a 96 well plate containing indexing primers (lilac).

Library size selection

Place the indexed libraries in row 12 of the PCR cooling block on deck position A. Place a fresh strip of PCR tubes in row 10 on position A, for post size selection collection. On deck position B, place a 1.5 ml microcentrifuge tube with 450 µl of SPRIselect magnetic beads in position A2, 1 ml of 80 % ethanol in positions B2 and C2, empty tubes for waste collection in positions D2 and E2, and 450 µl of elution buffer in position A3. Place a fresh 96 well PCR plate on the MAG module with a 96 well PCR plate adapter in position C (**Figure 13**). Follow the instructions given in the *ASSIST PLUS Flex Apex user guide* to set up the Library Size Selection Worklist.csv file, available in the downloads. Run program '6-2_Library size selection' on the D-ONE pipetting module. This program transfers the libraries onto the MAG module, adds magnetic beads to the samples and washes them with 80 % ethanol, then elutes the libraries from the beads and transfers them to clean tubes in row 10 on deck position A. Your libraries are now ready for sequencing.

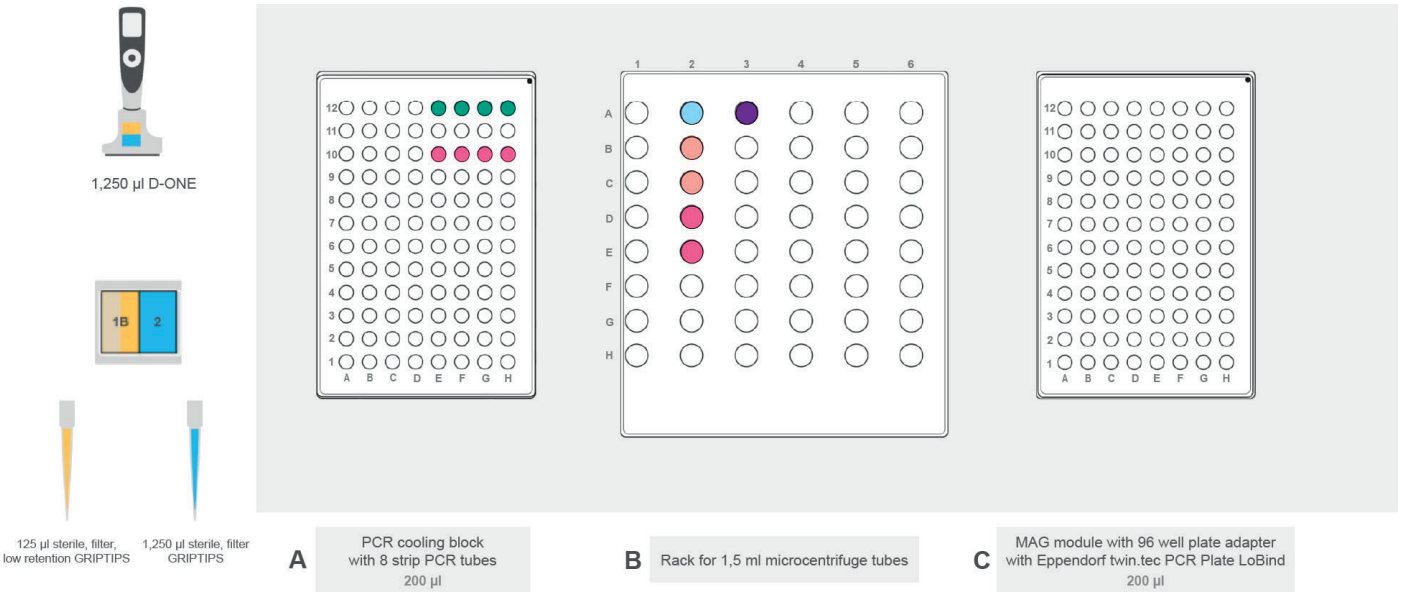

Figure 13: ASSIST PLUS deck set-up for library size selection. **Position A:** PCR cooling block with a strip of 8 200 µl PCR tubes containing indexed samples in row 12 (green) and a fresh strip in row 10 (pink) for sample collection. **Position B:** Rack for 1.5 ml microcentrifuge tubes with tubes containing SPRIselect magnetic beads (A2, blue), 80 % ethanol (B2 and C2, salmon), fresh tubes for waste collection (D2 and E2), and elution buffer in position A3. **Position C:** MAG module with 96 well plate adapter with a clean Eppendorf twin.tec PCR Plate LoBind.

Remarks

- **VIALAB software:** The 96 sample Flex Apex workflow detailed above is supported by ready-to-use VIALAB programs that can be adapted to specific pipettes, labware and protocols. Template programs for 48 samples are also provided, enabling flexible adjustment of sample numbers.
- **Program validation:** All 96 sample programs have been user validated, except for '5-3_DNA Cleanup', '6-1_Sample Index PCR' and '6-2_Library size selection'. These programs are intended as skeleton programs to provide a base for user optimization.
- Flex Apex and GEM-X Flex V2 refer to the same product, namely the plate-based Flex kit.

Conclusion

- This comprehensive guide discusses free-of-charge VIALAB templates for the Flex Apex workflow from 10x Genomics, providing a backbone for automated protocol development.
- Combining the ASSIST PLUS with the MAG module enables efficient magnetic bead separation, supporting critical steps in library preparation.
- The detailed ASSIST PLUS deck layouts and the user guide provided here minimize set-up errors and ensure reproducibility across multiple runs, supporting robust method standardization in diverse lab environments.
- The modular structure of the automated ASSIST PLUS workflow offers easy customization and scalability, making it adaptable to future protocol updates or changing sample input requirements.

Materials

Manufacturer	Part Number	Description	Link
INTEGRA Biosciences	4505	ASSIST PLUS Base Unit	https://www.integra-biosciences.com/en/pipetting-robots/assist-plus
INTEGRA Biosciences	4633	12 channel, 300 µl VIAFLO electronic pipette	https://www.integra-biosciences.com/en/electronic-pipettes/viaflo
INTEGRA Biosciences	4510	Slanted plate holder (0°-30°)	https://www.integra-biosciences.com/en/pipetting-robots/assist-plus
INTEGRA Biosciences	4547	Dual reservoir adapter	https://www.integra-biosciences.com/en/pipetting-robots/assist-plus
INTEGRA Biosciences	4551	Portrait labware pedestal (+24 mm)	https://www.integra-biosciences.com/en/pipetting-robots/assist-plus
INTEGRA Biosciences	4540	Rack for 1.5 / 2 ml microcentrifuge tubes	https://www.integra-biosciences.com/en/pipetting-robots/assist-plus
INTEGRA Biosciences	6250	PCR 96 well cooling block	https://www.integra-biosciences.com/en/pipetting-robots/assist-plus
INTEGRA Biosciences	4900	MAG module for magnetic separation	https://www.integra-biosciences.com/en/modules/mag-and-heatmag
INTEGRA Biosciences	4906	Adapter for 96 well PCR plate (MAG /HEATMAG)	https://www.integra-biosciences.com/en/modules/mag-and-heatmag
INTEGRA Biosciences	4532	D-ONE single channel pipetting module, 5-1250 µl	https://www.integra-biosciences.com/en/pipetting-robots/d-one-for-assist-plus
INTEGRA Biosciences	4535	Tip deck for D-ONE on ASSIST PLUS	https://www.integra-biosciences.com/en/pipetting-robots/d-one-for-assist-plus
INTEGRA Biosciences	6565	125 µl sterile, filter, low retention GRIPTIPS	https://www.integra-biosciences.com /en/griptips/griptips-selector-guide

Manufacturer	Part Number	Description	Link
INTEGRA Biosciences	6535	300 µl sterile, filter, low retention GRIPTIPS	https://www.integra-biosciences.com /en/griptips/griptips-selector-guide
INTEGRA Biosciences	6545	1250 µl sterile, filter, low retention GRIPTIPS	https://www.integra-biosciences.com /en/griptips/griptips-selector-guide
INTEGRA Biosciences	4391, 4392, 4393	100 ml disposable reservoirs, sterile, polystyrene, SureFlo	https://www.integra-biosciences.com/en/reagent-reservoirs/automation-friendly-reagent-reservoirs
INTEGRA Biosciences	4381, 4382, 4383	25 ml disposable reservoirs, sterile, polystyrene, SureFlo	https://www.integra-biosciences.com/en/reagent-reservoirs/multichannel-reagent-reservoirs
INTEGRA Biosciences	4316, 4317	25 ml disposable reservoirs, polypropylene	https://www.integra-biosciences.com/en/reagent-reservoirs/multichannel-reagent-reservoirs
Corning	P-96-450V-C	Axygen 96-well, clear, V-bottom, 500 µl, polypropylene, deep well plate, nonsterile	https://www.corning.com/
10x Genomics	1000781	GEM-X Flex Sample Preparation v2 Kit	https://www.10xgenomics.com/
10x Genomics	1000928, 1000929	GEM-X Flex v2 Human, 96 / 384 samples	https://www.10xgenomics.com/
10x Genomics	1000932, 1000933	GEM-X Flex v2 Mouse, 96 / 384 samples	https://www.10xgenomics.com/

Contact us: