

USER GUIDE

Chromium Next GEM Single Cell 3' **LT** Reagent Kits v3.1 (Dual Index)



FOR USE WITH

Chromium Next GEM Single Cell 3' LT Kit v3.1, 4 rxns PN-1000325

Chromium Next GEM Chip L Single Cell Kit, 16 rxns PN-1000321

Dual Index Kit TT Set A, 96 rxns PN-1000215

Next GEM reagents are specific to Next GEM products and should not be used interchangeably with non-Next GEM reagents.

Notices

Document Number

CG000399 • Rev B

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Document Revision Summary

| | |
|------------------------|-------------------------------------------------------------------------------|
| Document Number | CG000399 |
| Title | Chromium Next GEM Single Cell 3' LT Reagent Kits v3.1 (Dual Index) User Guide |
| Revision | Rev A to B |
| Revision Date | August 2021 |

Specific Changes:

- Updated step 1.3: Run the Chromium Controller or X/iX.

General Changes:

- Updates for general minor consistency of language and terms throughout.

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Introduction

[Chromium Next GEM Single Cell 3' LT Reagent Kits v3.1 \(Dual Index\)](#)

[10x Genomics Accessories](#)

[Recommended Thermal Cyclers](#)

[Additional Kits, Reagents & Equipment](#)

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Chromium Next GEM Single Cell 3' LT Reagents Kits

Chromium Next GEM Single Cell 3' LT Kit v3.1, 4 rxns PN-1000325

Chromium Next GEM Single Cell 3' GEM LT Kit v3.1 4 rxns PN-1000322 (store at -20°C)

Chromium Next GEM Single Cell 3' LT GEM Kit v3.1

| | # | PN |
|-------------------------|---|---------|
| ● RT Reagent B | 1 | 2000165 |
| ● RT Enzyme C | 1 | 2000102 |
| ● Template Switch Oligo | 1 | 3000228 |
| ○ Reducing Agent B | 1 | 2000087 |
| ● Cleanup Buffer | 1 | 2000088 |
| ● cDNA Primers | 1 | 2000089 |
| ○ Amp Mix | 1 | 2000103 |

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Library Construction Kit 4 rxns PN-1000196 (store at -20°C)

Library Construction Kit

| | # | PN |
|------------------------|---|---------|
| ● Fragmentation Enzyme | 1 | 2000104 |
| ● Fragmentation Buffer | 1 | 2000091 |
| ● Ligation Buffer | 1 | 2000092 |
| ● DNA Ligase | 1 | 220131 |
| ● Adaptor Oligos | 1 | 2000094 |

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Chromium Next GEM LT Single Cell 3' Gel Bead Kit v3.1, 4 rxns PN-1000324 (store at -80°C)



This gel bead kit is specific for the Single Cell 3' LT protocol /assay and should not be used interchangeably with other Single Cell 3' assays.

Chromium Next GEM Single Cell 3' LT v3.1 Gel Beads

| | # | PN |
|-------------------------------------------------|---|---------|
| Single Cell 3' LT v3.1 Gel Beads (4 rxns) | 1 | 2000360 |

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Dynabeads™ MyOne™ SILANE PN-2000048 (store at 4°C)

| | # | PN |
|---------------------------|---|---------|
| Dynabeads MyOne SILANE | 1 | 2000048 |

Dual Index Kit TT Set A, 96 rxns PN-1000215 (store at -20°C)**Dual Index Kit TT Set A**

| | # | PN |
|---------------------------|---|---------|
| Dual Index Plate TT Set A | 1 | 3000431 |

Chromium Next GEM Chip L Single Cell Kit, 16 rxns PN-1000321
(store at ambient temperature)

| Chromium Partitioning Oil | | |
|---------------------------------------------------|---|---------|
| | # | PN |
| <input checked="" type="radio"/> Partitioning Oil | 2 | 2000190 |

| Chromium Recovery Agent | | |
|--------------------------------------|---|--------|
| | # | PN |
| <input type="radio"/> Recovery Agent | 2 | 220016 |

| Chromium Next GEM Chip L & Gaskets | | |
|-----------------------------------------------|---|---------|
| | # | PN |
| Chromium Next GEM Chip L | 2 | 2000414 |
| Chip Gasket, 2-pack | 1 | 3000072 |

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10x Genomics Accessories

| Product | Part Number (Kit) | Part Number (Item) |
|------------------------------------|-------------------|--------------------|
| 10x Vortex Adapter | 120251 | 330002 |
| 10x Magnetic Separator | 120250 | 230003 |
| Chromium Next GEM Secondary Holder | 1000142 | 3000332 |

Recommended Thermal Cyclers

Thermal cyclers used must support uniform heating of 100 μ l emulsion volumes.

| Supplier | Description | Part Number |
|--------------------------|--------------------------------------------------------------|-------------------------------------------------------|
| BioRad | C1000 Touch Thermal Cycler with 96-Deep Well Reaction Module | 1851197 |
| Eppendorf | MasterCycler Pro (discontinued) | North America 950030010 International 6321 000.019 |
| Thermo Fisher Scientific | Veriti 96-Well Thermal Cycler | 4375786 |

Additional Kits, Reagents & Equipment

The items in the table below have been validated by 10x Genomics and are highly recommended for the Single Cell 3' protocols. Substituting materials may adversely affect system performance. This list may not include some standard laboratory equipment.






| Supplier | Description | Part Number (US) |
|----------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------|
| Plastics | | |
| Eppendorf | PCR Tubes 0.2 ml 8-tube strips DNA LoBind Tubes, 1.5 ml DNA LoBind Tubes, 2.0 ml | 951010022 022431021 022431048 |
| USA Scientific | TempAssure PCR 8-tube strip | 1402-4700 |
| Thermo Fisher Scientific | MicroAmp 8-Tube Strip, 0.2 ml MicroAmp 8 -Cap Strip, clear | N8010580 N8010535 |
| Rainin | Tips LTS 200UL Filter RT-L200FLR Tips LTS 1ML Filter RT-L1000FLR Tips LTS 20UL Filter RT-L10FLR | 30389240 30389213 30389226 |
| Kits & Reagents | | |
| Thermo Fisher Scientific | Nuclease-free Water Low TE Buffer (10 mM Tris-HCl pH 8.0, 0.1 mM EDTA) | AM9937 12090-015 |
| Millipore Sigma | Ethanol, Pure (200 Proof, anhydrous) | E7023-500ML |
| Beckman Coulter | SPRIselect Reagent Kit | B23318 |
| Bio-Rad | 10% Tween 20 | 1662404 |
| Ricca Chemical Company | Glycerin (glycerol), 50% (v/v) Aqueous Solution | 3290-32 |
| Qiagen | Qiagen Buffer EB | 19086 |
| Equipment | | |
| VWR | Vortex Mixer Divided Polystyrene Reservoirs VWR Mini Centrifuge (alternatively, use any equivalent mini centrifuge) | 10153-838 41428-958 76269-066 |
| Eppendorf | Eppendorf ThermoMixer C Eppendorf SmartBlock 1.5 ml, Thermoblock for 24 reaction vessel (alternatively, use a temperature-controlled Heat Block) | 5382000023 5360000038 |
| Rainin | Pipet-Lite Multi Pipette L8-50XLS+ Pipet-Lite Multi Pipette L8-200XLS+ Pipet-Lite Multi Pipette L8-10XLS+ Pipet-Lite Multi Pipette L8-20XLS+ Pipet-Lite LTS Pipette L-2XLS+ Pipet-Lite LTS Pipette L-10XLS+ Pipet-Lite LTS Pipette L-20XLS+ Pipet-Lite LTS Pipette L-100XLS+ Pipet-Lite LTS Pipette L-200XLS+ Pipet-Lite LTS Pipette L-1000XLS+ | 17013804 17013805 17013802 17013803 17014393 17014388 17014392 17014384 17014391 17014382 |

Additional Kits, Reagents & Equipment

The items in the table below have been validated by 10x Genomics and are highly recommended for the Single Cell 3' protocols. Substituting materials may adversely affect system performance. This list may not include some standard laboratory equipment.

| Supplier | Description | Part Number (US) |
|---------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Quantification & Quality Control | | |
| Agilent | 2100 Bioanalyzer Laptop Bundle High Sensitivity DNA Kit 4200 TapeStation High Sensitivity D1000 ScreenTape/Reagents High Sensitivity D5000 ScreenTape/Reagents | Choose Bioanalyzer, TapeStation, LabChip, Fragment Analyzer or Qubit based on availability & preference. G2943CA 5067-4626 G2991AA 5067-5584/5067-5585 5067-5592/5067-5593 |
| Thermo Fisher Scientific | Qubit 4.0 Fluorometer Qubit dsDNA HS Assay Kit | Q33226 Q32854 |
| Advanced Analytical | Fragment Analyzer Automated CE System - 12 cap Fragment Analyzer Automated CE System - 48/96 cap High Sensitivity NGS Fragment Analysis Kit | FSv2-CE2F FSv2-CE10F DNF-474 |
| PerkinElmer | LabChip GX Touch HT Nucleic Acid Analyzer DNA High Sensitivity Reagent Kit | CLS137031 CLS760672 |
| KAPA Biosystems | KAPA Library Quantification Kit for Illumina Platforms | KK4824 |

Protocol Steps & Timing

| Day | Steps | Timing | Stop & Store |
|----------------------------------|-----------------------------------------------------------------------------------------|--------|--------------------------------------------------------------------------------------------------------------------|
| 1 h | Cell Preparation | | |
| | Dependent on Cell Type | ~1-2 h | |
| 4h | Step 1 – GEM Generation & Barcoding | | |
| | 1.1 Prepare Reaction Mix | 20 min | |
| | 1.2 Load Chromium Next GEM Chip L | 10 min | |
| | 1.3 Run the Chromium Controller or X/iX | 18 min | |
| | 1.4 Transfer GEMs | 3 min | |
| | 1.5 GEM-RT Incubation | 55 min |  4°C ≤72 h or -20°C ≤1 week |
| 6h | Step 2 – Post GEM-RT Cleanup & cDNA Amplification | | |
| | 2.1 Post GEM RT-Cleanup – Dynabead | 45 min | |
| | 2.2 cDNA Amplification | 40 min |  4°C ≤72 h or -20°C ≤1 week |
| | 2.3 cDNA Cleanup – SPRIselect | 15 min |  4°C ≤72 h or -20°C ≤4 weeks |
| | 2.4 cDNA QC & Quantification | 50 min | |
| 8 h | Step 3 – 3' Gene Expression Library Construction | | |
| | 3.1 Fragmentation, End Repair & A-tailing | 45 min | |
| | 3.2 Post Fragmentation, End Repair & A-tailing Double Sided Size Selection – SPRIselect | 30 min | |
| | 3.3 Adaptor Ligation | 25 min | |
| | 3.4 Post Ligation Cleanup- SPRIselect | 20 min | |
| | 3.5 Sample Index PCR | 40 min |  4°C ≤72 h |
| | 3.6 Post Sample Index PCR Double Sided Size Selection- SPRIselect | 30 min |  4°C ≤72 h or -20°C long term |
| 3.7 Post Library Construction QC | 50 min | | |

Stepwise Objectives



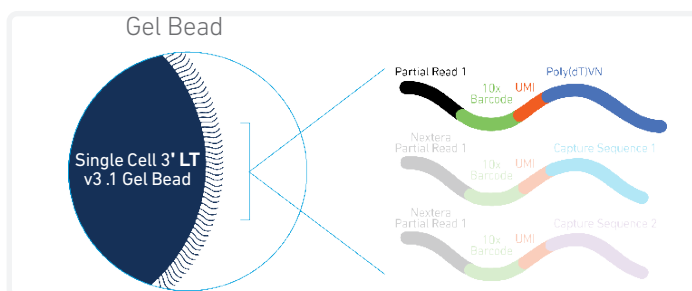
The Chromium Single Cell Gene Expression Solution upgrades short read sequencers to deliver a scalable microfluidic platform for assessing cell surface protein expression combined with 3' digital gene expression of the same single cell by profiling 100-1,000 individual cells per sample. A pool of 9,216 10x Barcodes are sampled separately to index each cell's transcriptome. It is done by partitioning thousands of cells into nanoliter-scale Gel Beads-in-emulsion (GEMs), where all generated DNA molecules share a common 10x Barcode. Libraries are generated and sequenced from the DNA molecules and 10x Barcodes are used to associate individual reads back to the individual partitions.

This document outlines the low throughput (LT) protocol for generating Single Cell 3' Gene Expression.

Single Cell 3' LT v3.1 Gel Beads



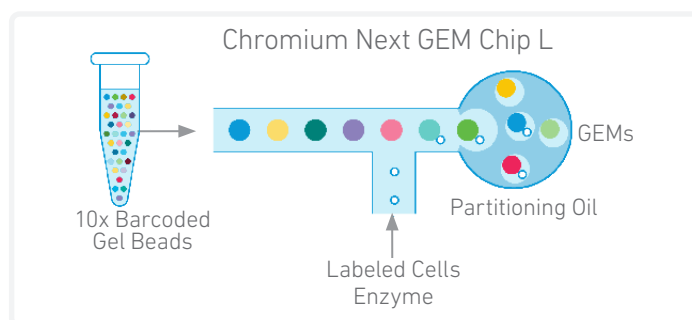
In addition to the poly(dT) primer that enables the production of barcoded, full-length cDNA from poly-adenylated mRNA, the Single Cell 3' LT v3.1 Gel Beads also include two additional primer sequences (Capture Sequence 1 and Capture Sequence 2), that enable capture and priming of Feature Barcode technology compatible targets or analytes of interest. Only the poly(dT) primers are used in this protocol for generating Single Cell 3' Gene Expression libraries.



This gel bead is specific for the Single Cell 3' LT protocol /assay and should not be used interchangeably with other Single Cell 3' assays.

Step 1 GEM Generation & Barcoding

GEMs are generated by combining barcoded Single Cell 3' LT v3.1 Gel Beads, a Master Mix with cell surface protein labeled cells, and Partitioning Oil onto Chromium Chip L. To achieve single cell resolution, cells are delivered at a limiting dilution, such that the majority (~90-99%) of generated GEMs contain no cell, while the remainder largely contain a single cell.



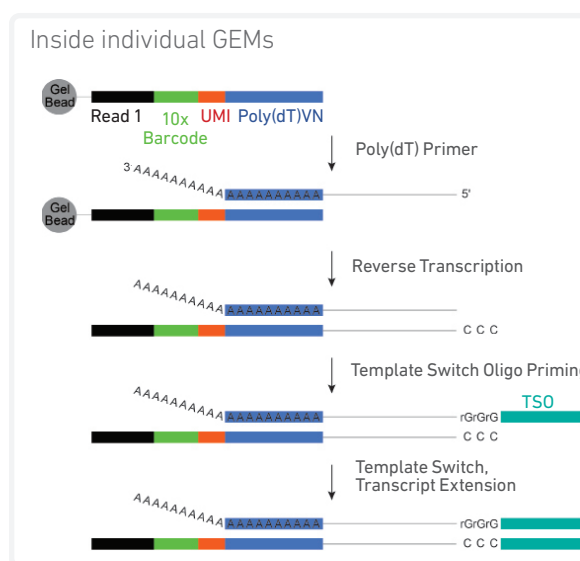
Step 1 GEM Generation & Barcoding

Immediately following GEM generation, the Gel Bead is dissolved, primers are released, and any co-partitioned cell is lysed.

Primers containing:

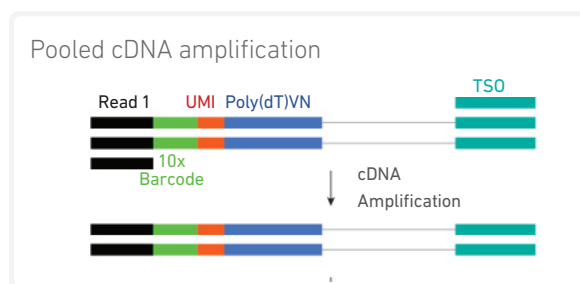
- an Illumina TruSeq Read 1 (read 1 sequencing primer)
- 16 nt 10x Barcode
- 12 nt unique molecular identifier (UMI)
- 30 nt poly(dT) sequence

are mixed with the cell lysate and a Master Mix containing reverse transcription (RT) reagents. Incubation of the GEMs produces barcoded, full-length cDNA from poly-adenylated mRNA.



Step 2 Post GEM-RT Cleanup & cDNA Amplification

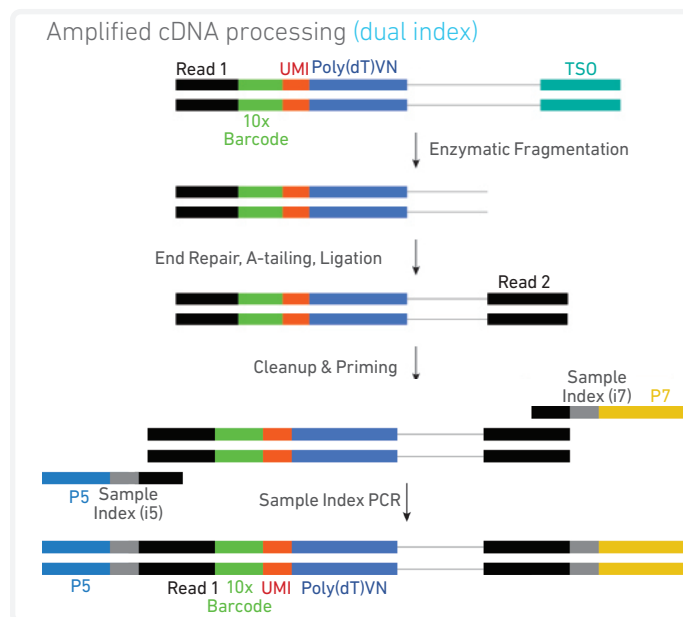
After incubation, GEMs are broken and pooled fractions are recovered. Silane magnetic beads are used to purify the first-strand cDNA from the post GEM-RT reaction mixture, which includes leftover biochemical reagents and primers. Barcoded, full-length cDNA is amplified via PCR to generate sufficient mass for library construction.



Step 3 3' Gene Expression Library Construction



Enzymatic fragmentation and size selection are used to optimize the cDNA amplicon size. P5, P7, i7 and i5 sample indexes, and TruSeq Read 2 (read 2 primer sequence) are added via End Repair, A-tailing, Adaptor Ligation, and PCR. The final libraries contain the P5 and P7 primers used in Illumina amplification.

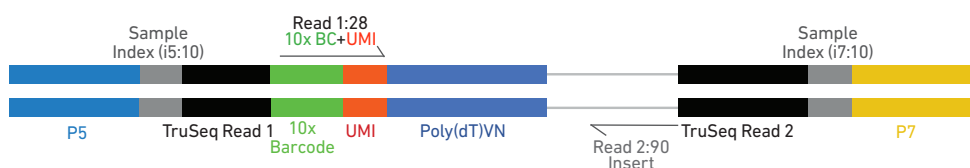


Step 4 Sequencing

A Chromium Single Cell 3' Gene Expression Dual Index library comprises standard Illumina paired-end constructs which begin and end with P5 and P7. The 16 bp 10x Barcode and 12 bp UMI are encoded in Read 1, while Read 2 is used to sequence the cDNA fragment. i7 and i5 index sequences are incorporated as the sample index reads. TruSeq Read 1 and TruSeq Read 2 are standard Illumina sequencing primer sites used in paired-end sequencing.

Illumina sequencer compatibility, sample indices, library loading and pooling for sequencing are summarized in step 4.

Chromium Single Cell 3' Gene Expression Dual Index Library



[See Appendix for Oligonucleotide Sequences](#)

Tips & Best Practices

TIPS

Icons



Tips & Best Practices section includes additional guidance



Signifies critical step requiring accurate execution



Troubleshooting section includes additional guidance



Next GEM Low Throughput (LT) specific protocol step updates



Dual index specific protocol step updates

Emulsion-safe Plastics

- Use validated emulsion-safe plastic consumables when handling GEMs as some plastics can destabilize GEMs. Refer to [Additional Kits, Reagents & Equipments](#) table for validated plastics.

Cell Concentration



- Recommended starting point is to load ~1,667 cells per reaction, resulting in recovery of ~500 cells, and a multiplet rate of ~4%. The optimal input cell concentration is 100-600 cells/ μ l.
- Refer to [Cell Dilution Guidelines](#) for preparing cells.
- The presence of dead cells in the suspension may also reduce the recovery rate. Consult the 10x Genomics Single Cell Protocols Cell Preparation Guide and the Guidelines for Optimal Sample Preparation flowchart (Documents CG00053 and CG000126 respectively) for more information on preparing cells.

| Multiplet Rate (%) | # of Cells Loaded | # of Cells Recovered |
|--------------------|-------------------|----------------------|
| ~0.8% | ~333 | ~100 |
| ~1.5% | ~667 | ~200 |
| ~2.3% | ~1,000 | ~300 |
| ~3.0% | ~1,333 | ~400 |
| ~3.8% | ~1,667 | ~500 |
| ~4.6% | ~2,000 | ~600 |
| ~5.3% | ~2,333 | ~700 |
| ~6.1% | ~2,667 | ~800 |
| ~6.8% | ~3,000 | ~900 |
| ~8.0% | ~3,333 | ~1,000 |

General Reagent Handling

- Fully thaw and thoroughly mix reagents before use.
- Keep all enzymes and Master Mixes on ice during setup and use. Promptly move reagents back to the recommended storage.
- Calculate reagent volumes with 10% excess of 1 reaction values.
- Cover Partitioning Oil tubes and reservoirs to minimize evaporation.
- If using multiple chips, use separate reagent reservoirs for each chip during loading.
- Thoroughly mix samples with the beads during bead-based cleanup steps.

50% Glycerol Solution

- Purchase 50% glycerol solution from Ricca Chemical Company, Glycerin (glycerol), 50% (v/v) Aqueous Solution, PN-3290-32.
- Prepare 50% glycerol solution:
 - i. Mix an equal volume of water and 99% Glycerol, Molecular Biology Grade.
 - ii. Filter through a 0.2 μm filter.
 - iii. Store at -20°C in 1-ml LoBind tubes. 50% glycerol solution should be equilibrated to room temperature before use.

Pipette Calibration

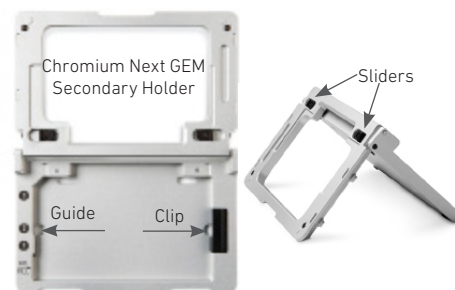
- Follow manufacturer's calibration and maintenance schedules.
- Pipette accuracy is particularly important when using SPRIselect reagents.

Chromium Next GEM Chip Handling

- Minimize exposure of reagents, chips, and gaskets to sources of particles and fibers, laboratory wipes, frequently opened flip-cap tubes, clothing that sheds fibers, and dusty surfaces.
- After removing the chip from the sealed bag, use in ≤ 24 h.
- Execute steps without pause or delay, unless indicated. When multiple chips are to be used, load, run, and collect the content from one chip before loading the next.
- Fill all unused input wells in rows labeled 1, 2, and 3 on a chip with an appropriate volume of 50% glycerol solution before loading the used wells. DO NOT add glycerol to the wells in the bottom NO FILL row.
- Avoid contacting the bottom surface of the chip with gloved hands and other surfaces. Frictional charging can lead to inadequate priming of the channels, potentially leading to either clogs or wetting failures.
- Minimize the distance that a loaded chip is moved to reach the Chromium Controller.
- Keep the chip horizontal to prevent wetting the gasket with oil, which depletes the input volume and may adversely affect the quality of the resulting emulsion.

Chromium Next GEM Secondary Holders

- Chromium Next GEM Secondary Holders encase Chromium Next GEM Chips.
- The holder lid flips over to become a stand, holding the chip at 45 degrees for optimal recovery well content removal.
- Squeeze the black sliders on the back side of the holder together to unlock the lid and return the holder to a flat position.



Chromium Next GEM Chip & Holder Assembly

- Align notch on the chip (upper left corner) and the holder.
- Insert the left-hand side of the chip under the guide. Depress the right-hand side of the chip until the spring-loaded clip engages.
- Close the lid before dispensing reagents into the wells.



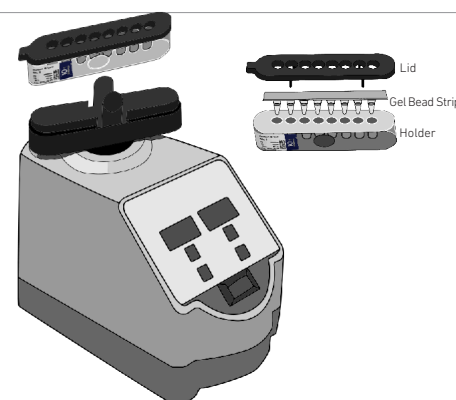
Chromium Next GEM Chip Loading

- Place the assembled chip and holder flat on the bench with the lid closed.
- Dispense at the bottom of the wells without introducing bubbles.
- When dispensing Gel Beads into the chip, wait for the remainder to drain into the bottom of the pipette tips and dispense again to ensure complete transfer.
- Refer to [Load Chromium Next GEM Chip L](#) for specific instructions.



Gel Bead Handling

- Use one tube of Gel Beads per sample. **DO NOT** puncture the foil seals of tubes not used at the time.
- Equilibrate the Gel Beads strip to room temperature before use.
- Store unused Gel Beads at -80°C and avoid more than 12 freeze-thaw cycles. **DO NOT** store Gel Beads at -20°C .
- Snap the tube strip holder with the Gel Bead strip into a 10x Vortex Adapter. Vortex **30 sec**.
- Centrifuge the Gel Bead strip for **~5 sec** after removing from the holder. Confirm there are no bubbles at the bottom of the tubes and the liquid levels look even. Place the Gel Bead strip back in the holder and secure the holder lid.
- If the required volume of beads cannot be recovered, place the pipette tips against the sidewalls and slowly dispense the Gel Beads back into the tubes. **DO NOT** introduce bubbles into the tubes and verify that the pipette tips contain no leftover Gel Beads. Withdraw the full volume of beads again by pipetting slowly.



10x Gasket Attachment

- After reagents are loaded, attach the gasket by holding the tongue (curved end, to the right) and hook it on the left-hand tabs of the holder. Gently pull the gasket toward the right and hook it on the two right-hand tabs.
- DO NOT touch the smooth side of the gasket. DO NOT press down on the top of the gasket after attachment.
- Keep the assembly horizontal to avoid wetting the gasket with Partitioning Oil.



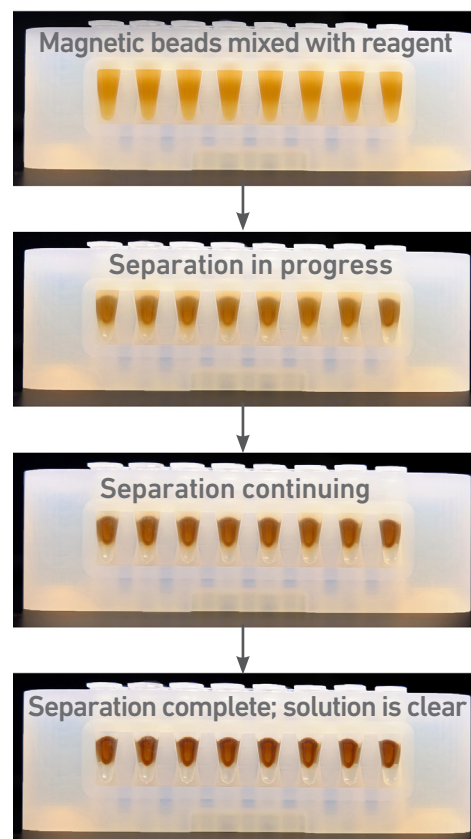
10x Magnetic Separator

- Offers two positions of the magnets (high and low) relative to a tube, depending on its orientation. Flip the magnetic separator over to switch between high (magnet•High) or low (magnet•Low) positions.
- If using MicroAmp 8-Tube Strips, use the high position (magnet•High) only throughout the protocol.



Magnetic Bead Cleanup Steps

- During magnetic bead based cleanup steps that specify waiting “until the solution clears”, visually confirm clearing of solution before proceeding to the next step. See adjacent panel for an example.
- The time needed for the solution to clear may vary based on specific step, reagents, volume of reagents etc.



SPRIselect Cleanup & Size Selection

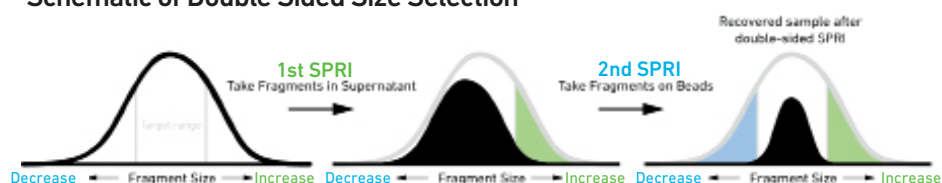
- After aspirating the desired volume of SPRIselect reagent, examine the pipette tips before dispensing to ensure the correct volume is transferred.
- Pipette mix thoroughly as insufficient mixing of sample and SPRIselect reagent will lead to inconsistent results.
- Use fresh preparations of 80% Ethanol.

Tutorial — SPRIselect Reagent:DNA Sample Ratios

SPRI beads selectively bind DNA according to the ratio of SPRIselect reagent (beads).

$$\text{Example: Ratio} = \frac{\text{Volume of SPRIselect reagent added to the sample}}{\text{Volume of DNA sample}} = \frac{50 \mu\text{l}}{100 \mu\text{l}} = 0.5\text{X}$$

Schematic of Double Sided Size Selection



After the first SPRI, supernatant is transferred for a second SPRI while larger fragments are discarded (green). After the second SPRI, fragments on beads are eluted and kept while smaller fragments are discarded (blue). Final sample has a tight fragment size distribution with reduced overall amount (black).

Tutorial — Double Sided Size Selection

Step a – First SPRIselect: Add 50 μl SPRIselect reagent to 100 μl sample (0.5X).

$$\text{Ratio} = \frac{\text{Volume of SPRIselect reagent added to the sample}}{\text{Volume of DNA sample}} = \frac{50 \mu\text{l}}{100 \mu\text{l}} = 0.5\text{X}$$

Step b – Second SPRIselect: Add 30 μl SPRIselect reagent to supernatant from step a (0.8X).

$$\text{Ratio} = \frac{\text{Total Volume of SPRIselect reagent added to the sample (step a + b)}}{\text{Original Volume of DNA sample}} = \frac{50 \mu\text{l} + 30 \mu\text{l}}{100 \mu\text{l}} = 0.8\text{X}$$

Enzymatic Fragmentation

- Ensure enzymatic fragmentation reactions are prepared on ice and then loaded into a thermal cycler pre-cooled to 4°C prior to initiating the Fragmentation, End Repair, and A-tailing incubation steps.

Sample Indices in Sample Index PCR

- Choose the appropriate sample index sets to ensure that no sample indices overlap in a multiplexed sequencing run.
- Verify and use the specified index plate only. DO NOT use the plates interchangeably.
- Each well in the Dual Index Plate contains a unique i7 and a unique i5 oligonucleotide.

Index Hopping Mitigation

Index hopping can impact pooled samples sequenced on Illumina sequencing platforms that utilize patterned flow cells and exclusion amplification chemistry. To minimize index hopping, follow the guidelines listed below.

- Remove adapters during cleanup steps.
- Ensure no leftover primers and/or adapters are present when performing post-Library Construction QC.
- Store each library individually at 4°C for up to 72 h or at -20°C for long-term storage. DO NOT pool libraries during storage.
- Pool libraries prior to sequencing. An additional 1.0X SPRI may be performed for the pooled libraries to remove any free adapters before sequencing.
- Hopped indices can be computationally removed from the data generated from single cell dual index libraries.

Step 1

GEM Generation & Barcoding

- 1.1 Prepare Single Cell Master Mix
- 1.2 Load Chromium Next GEM Chip L
- 1.3 Run the Chromium Controller
- 1.4 Transfer GEMs
- 1.5 GEM-RT Incubation

1

1.0 GEM Generation & Barcoding



| GET STARTED! | | | | |
|----------------------------------------|--------------------------------------------------------|---------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------|
| Action | Item | 10x PN | Preparation & Handling | Storage |
| Equilibrate to Room Temperature | Single Cell 3' LT v3.1 Gel Beads | 2000324 | Equilibrate to room temperature 30 min before loading the chip. | -80°C |
| | <input checked="" type="radio"/> RT Reagent B | 2000165 | Vortex, verify no precipitate, centrifuge briefly. | -20°C |
| | <input checked="" type="radio"/> Template Switch Oligo | 3000228 | Centrifuge briefly, resuspend in 80 µl Low TE Buffer. Vortex 15 sec at maximum speed, centrifuge briefly, leave at room temperature for ≥ 30 min. After resuspension, store at -80°C. | -20°C |
| | <input type="radio"/> Reducing Agent B | 2000087 | Vortex, verify no precipitate, centrifuge briefly. | -20°C |
| Place on Ice | <input checked="" type="radio"/> RT Enzyme C | 2000102 | Centrifuge briefly before adding to the mix. | -20°C |
| Obtain | <input type="radio"/> Partitioning Oil | 2000190 | - | Ambient |
| | Chromium Next GEM Chip L | 2000414 | - | Ambient |
| | 10x Gasket | 3000072 | See Tips & Best Practices. | Ambient |
| | Chromium Next GEM Secondary Holder | 3000332 | See Tips & Best Practices. | Ambient |
| | 10x Vortex Adapter | 330002 | See Tips & Best Practices. | Ambient |
| | 50% glycerol solution | - | See Tips & Best Practices. | - |



Firmware Version 4.0 or higher is required in the Chromium Controller or the Chromium Single Cell Controller used for this protocol.

1.1 Prepare Master Mix

a. Prepare Master Mix on ice. Pipette mix 15x and centrifuge briefly.

| Master Mix <i>Add reagents in the order listed</i> | PN | 1X (μl) | 4X + 10% (μl) |
|-------------------------------------------------------|---------|-------------|------------------|
| ● RT Reagent B | 2000165 | 18.8 | 82.7 |
| ● Template Switch Oligo | 3000228 | 2.4 | 10.6 |
| ○ Reducing Agent B | 2000087 | 2.0 | 8.8 |
| ● RT Enzyme C | 2000102 | 8.7 | 38.3 |
| Total | - | 31.9 | 140.4 |

b. Add 31.9 μl Master Mix into each tube of a PCR 8-tube strip on ice.



Assemble Chromium Next GEM Chip L

After removing the chip from the sealed bag, use the chip in ≤ 24 h.

See Tips & Best Practices for chip handling instructions.

- Align notch on the chip (upper left corner) and the holder.
- Insert the left-hand side of the chip under the guide. Depress the right-hand side of the chip until the spring-loaded clip engages.
- Close the lid before dispensing reagents into the wells.
- The assembled chip is ready for loading the indicated reagents. Refer to step 1.2 for reagent volumes and loading order.



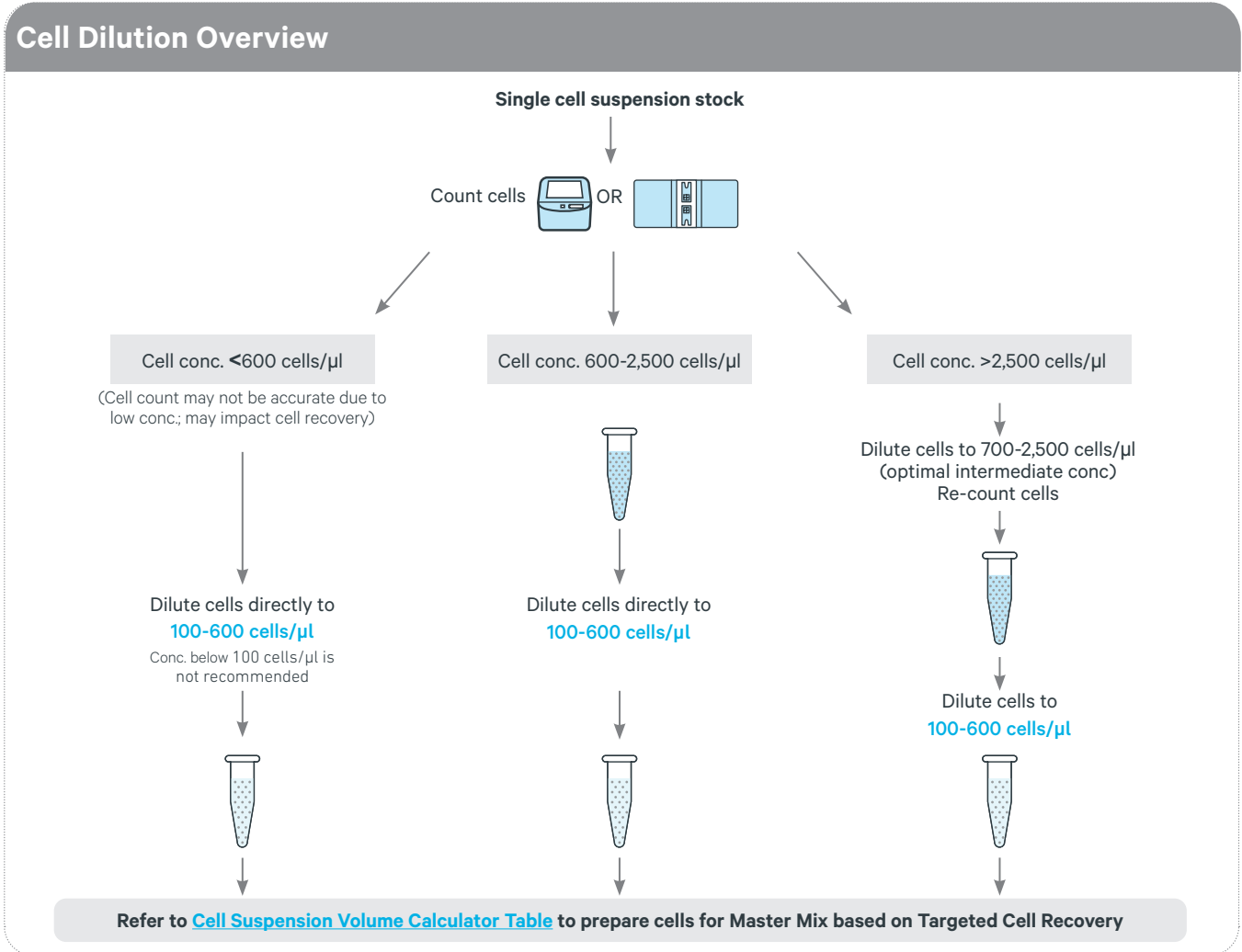
For GEM generation, load the indicated reagents only in the specified rows, starting from row labeled 1, followed by rows labeled 2 and 3. DO NOT load reagents in the bottom row labeled NO FILL. See step 1.2 for details.



Cell Dilution Guidelines



The optimal cell loading concentration for this protocol is **~100-600 cells/μl**. Dilute cells using only compatible cell media/buffer (minimize carryover of media that can destabilize GEMs & impact GEM-RT reaction). Always mix cells gently and thoroughly before taking an aliquot. See dilution overview and examples below.



| Example Calculations | Example 1 | Example 2 |
|------------------------------------------------------------------------------|------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------|
| Starting Cell Concentration (cells/μl) | 900 cells/μl | 4,000 cells/μl |
| Dilute to 100-600 cells/μl | Dilute (1 part cells + 2 part media) to 300 cells/μl | Dilute (1 part cells + 1 part media) to 2,000 cells/μl; count cells Dilute (1 part cells + 3 part media) to 500 cells/μl |
| Targeted Cell Recovery Loading Cell Concentration | 200 cells 300 cells/μl | 600 cells 500 cells/μl |
| Refer to Cell Suspension Volume Calculator Table for volumes | | |
| Cell susp. stock vol. per rxn (μl) | 2.2 μl | 4.0 μl |
| Nuclease-free water vol. per rxn (μl) | 41.1 μl | 39.3 μl |



Cell Suspension Volume Calculator Table

(for step 1.2 of Chromium Next GEM Single Cell 3' Low Throughput v3.1 protocol)

Volume of Cell Suspension Stock per reaction (µl) | Volume of Nuclease-free Water per reaction (µl)



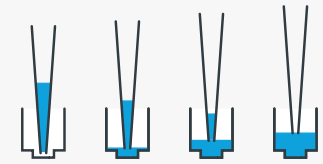
The optimal cell loading concentration for this protocol is ~100-600 cells/µl. Ensure cell counting is conducted in the optimal cell counting concentration and cell stock is diluted to the optimal cell loading concentration prior to adding the single cell suspension volume to the Master Mix for chip loading. DO NOT add nuclease-free water directly to single cell suspension. Add nuclease-free water to the Master Mix. Refer to step 1.2b.

| Cell Stock Concentration (Cells/µl) | Targeted Cell Recovery | | | | | | | | | | |
|--------------------------------------|------------------------|------|------|-----------------------------------|------|------|------|---------------------------|------|------|--|
| | 100 | 200 | 300 | 400 | 500 | 600 | 700 | 800 | 900 | 1000 | |
| 100 | 3.3 | 6.7 | 10.0 | 13.3 | 16.7 | 20.0 | 23.3 | 26.7 | 30.0 | 33.3 | |
| | 40.0 | 36.6 | 33.3 | 30.0 | 26.6 | 23.3 | 20.0 | 16.6 | 13.3 | 10.0 | |
| 200 | 1.7 | 3.3 | 5.0 | 6.7 | 8.3 | 10.0 | 11.7 | 13.3 | 15.0 | 16.7 | |
| | 41.6 | 40.0 | 38.3 | 36.6 | 35.0 | 33.3 | 31.6 | 30.0 | 28.3 | 26.6 | |
| 300 | 1.1 | 2.2 | 3.3 | 4.4 | 5.6 | 6.7 | 7.8 | 8.9 | 10.0 | 11.1 | |
| | 42.2 | 41.1 | 40.0 | 38.9 | 37.7 | 36.6 | 35.5 | 34.4 | 33.3 | 32.2 | |
| 400 | 0.8 | 1.7 | 2.5 | 3.3 | 4.2 | 5.0 | 5.8 | 6.7 | 7.5 | 8.3 | |
| | 42.5 | 41.6 | 40.8 | 40.0 | 39.1 | 38.3 | 37.5 | 36.6 | 35.8 | 35.0 | |
| 500 | 0.7 | 1.3 | 2.0 | 2.7 | 3.3 | 4.0 | 4.7 | 5.3 | 6.0 | 6.7 | |
| | 42.6 | 42.0 | 41.3 | 40.6 | 40.0 | 39.3 | 38.6 | 38.0 | 37.3 | 36.6 | |
| 600 | 0.6 | 1.1 | 1.7 | 2.2 | 2.8 | 3.3 | 3.9 | 4.4 | 5.0 | 5.6 | |
| | 42.7 | 42.2 | 41.6 | 41.1 | 40.5 | 40.0 | 39.4 | 38.9 | 38.3 | 37.7 | |
| 700 | 0.5 | 1.0 | 1.4 | 1.9 | 2.4 | 2.9 | 3.3 | 3.8 | 4.3 | 4.8 | |
| | 42.8 | 42.3 | 41.9 | 41.4 | 40.9 | 40.4 | 40.0 | 39.5 | 39.0 | 38.5 | |
| 800 | N/A | 0.8 | 1.3 | 1.7 | 2.1 | 2.5 | 2.9 | 3.3 | 3.8 | 4.2 | |
| | | 42.5 | 42.1 | 41.6 | 41.2 | 40.8 | 40.4 | 40.0 | 39.6 | 39.1 | |
| 900 | N/A | 0.7 | 1.1 | 1.5 | 1.9 | 2.2 | 2.6 | 3.0 | 3.3 | 3.7 | |
| | | 42.6 | 42.2 | 41.8 | 41.4 | 41.1 | 40.7 | 40.3 | 40.0 | 39.6 | |
| 1000 | N/A | 0.7 | 1.0 | 1.3 | 1.7 | 2.0 | 2.3 | 2.7 | 3.0 | 3.3 | |
| | | 42.6 | 42.3 | 42.0 | 41.6 | 41.3 | 41.0 | 40.6 | 40.3 | 40.0 | |
| Grey boxes: Exceeds allowable volume | | | | Yellow boxes: Low transfer volume | | | | Blue boxes: Optimal range | | | |

1.2 Load Chromium NextGEM Chip L



After removing chip from the sealed bag, use in ≤ 24 h.
When loading the chip, raising and depressing the pipette plunger should each take ~ 5 sec.
When dispensing, raise the pipette tips at the same rate as the liquid is rising, keeping the tips slightly submerged.



a. Add 50% glycerol solution to each unused well (if processing < 8 samples/chip)

- 70 μL in each unused well in row labeled 1
- 50 μL in each unused well in row labeled 2
- 45 μL in each unused well in row labeled 3

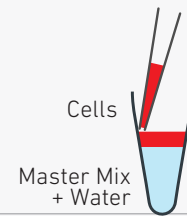
! DO NOT add 50% glycerol solution to the bottom row of NO FILL wells.
DO NOT use any substitute for 50% glycerol solution.

Glycerol



b. Prepare Master Mix + Cell suspension

- Refer to the Cell Suspension Volume Calculator Table.
- Add the appropriate volume of nuclease-free water to Master Mix. Add corresponding volume of single cell suspension to Master Mix. Total of 75 μL in each tube.
- Gently pipette mix the cell suspension before adding to the Master Mix.



c. Load Row Labeled 1

- Gently pipette mix the Master Mix + Cell Suspension
- Using the same pipette tip, dispense 70 μL Master Mix + Cell Suspension into the bottom center of each well in row labeled 1 without introducing bubbles.

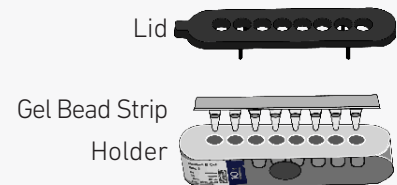
Master Mix + Sample



d. Prepare Gel Beads

- Snap the tube strip holder with the Gel Bead strip into a 10x Vortex Adapter. Vortex 30 sec.
- Centrifuge the Gel Bead strip for ~ 5 sec.
- Confirm there are no bubbles at the bottom of the tubes and the liquid levels are even.
- Place the Gel Bead strip back in the holder. Secure the holder lid.

Prep Gel Beads



e. Load Row Labeled 2

- Puncture the foil seal of the Gel Bead tubes.
- Slowly aspirate 50 μL Gel Beads.
- Dispense into the wells in row labeled 2 without introducing bubbles.
- Wait 30 sec.

Gel Beads



f. Load Row Labeled 3

- Dispense 45 μL Partitioning Oil into the wells in row labeled 3 from a reagent reservoir.


! Failure to add Partitioning Oil to the top row labeled 3 will prevent GEM generation and can damage the Chromium Controller.

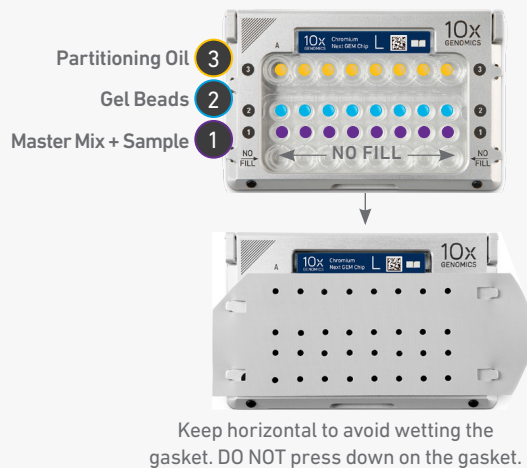
Partitioning Oil



g. Attach GEM Gasket

- Align the notch with the top left-hand corner.
- Ensure the gasket holes are aligned with the wells.
- Avoid touching the smooth surface.

 *Attach the gasket and run the chip in the Chromium Controller immediately after loading the Partitioning Oil.*

GEM Gasket

1.3 Run the Chromium Controller or X/iX

If using Chromium Controller:

- Press the eject button on the Controller to eject the tray.
- Place the assembled chip with the gasket in the tray, ensuring that the chip stays horizontal. Press the button to retract the tray.
- Press the play button.
- At completion of the run (~18 min), the Controller will chime. **Immediately** proceed to the next step.



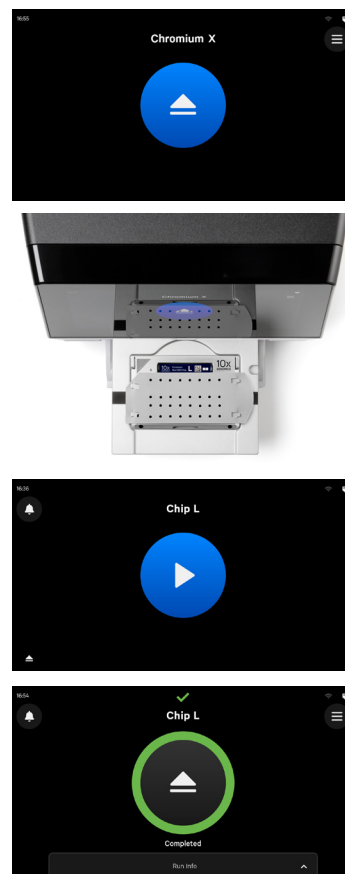
Firmware Version 4.0 or higher is required in the Chromium Controller or the Chromium Single Cell Controller used for this protocol.



If using Chromium X/iX:

Consult the Chromium X series (X/iX) User Guide (CG000396) for detailed instrument operation instructions and follow the instrument touchscreen prompts for execution.

- a. Press the eject button on Chromium X/iX to eject the tray.
If the eject button is not touched within 1 min, tray will close automatically. System requires a few seconds before the tray can be ejected again.
- b. Place the assembled chip with the gasket in the tray, ensuring that the chip stays horizontal. Press the button to retract the tray.
- c. Press the play button.
- d. At completion of the run (~18 min), Chromium X/iX will chime. **Immediately** proceed to the next step.



1.4 Transfer GEMs

- a. Place a tube strip on ice.
- b. Press the eject button of the Controller and remove the chip.
- c. Discard the gasket. Open the chip holder. Fold the lid back until it clicks to expose the wells at 45 degrees.



- d. Check the volume in rows labeled 1-2. Abnormally high volume in any well indicates a clog.
- e. Slowly aspirate **100 µl** GEMs from the lowest points of the recovery wells in the top row labeled 3 without creating a seal between the tips and the bottom of the wells.



- f. Withdraw pipette tips from the wells. GEMs should appear opaque and uniform across all channels. Excess Partitioning Oil (clear) in the pipette tips indicates a potential clog.
- g. Over the course of **~20 sec**, dispense GEMs into the tube strip on ice with the pipette tips against the sidewalls of the tubes.
- h. If multiple chips are run back-to-back, cap/cover the GEM-containing tube strip and place on ice for no more than 1 h.

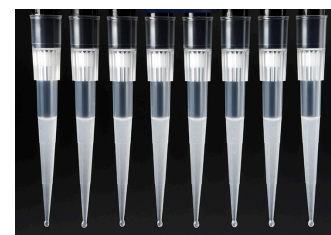
Expose Wells at 45 Degrees



Transfer GEMs



GEMs



1.5 GEM-RT Incubation

Use a thermal cycler that can accommodate at least 100 µl volume. A volume of 125 µl is the preferred setting on Bio-Rad C1000 Touch. In alternate thermal cyclers, use highest reaction volume setting.

- a. Incubate in a thermal cycler with the following protocol.

| Lid Temperature | Reaction Volume | Run Time |
|-----------------|-----------------|----------|
| 53°C | 125 µl | ~55 min |
| Step | Temperature | Time |
| 1 | 53°C | 00:45:00 |
| 2 | 85°C | 00:05:00 |
| 3 | 4°C | Hold |



- b. Store at **4°C** for up to **72 h** or at **-20°C** for up to a **week**, or proceed to the next step.

Step 2


Post GEM-RT Cleanup & cDNA Amplification

- 2.1 Post GEM-RT Cleanup – Dynabeads
- 2.2 cDNA Amplification
- 2.3 cDNA Cleanup – SPRIselect
- 2.4 cDNA QC & Quantification



2.0 Post GEM-RT Cleanup & cDNA Amplification



| GET STARTED! | | | | |
|----------------------------------------|-----------------------------------------------------------------------------------------------------------------------------|---------|--------------------------------------------------------------------------------------------------------------|---------|
| Action | Item | 10x PN | Preparation & Handling | Storage |
| Equilibrate to Room Temperature | Reducing Agent B | 2000087 | Thaw, vortex, verify no precipitate, centrifuge. | -20°C |
| |  cDNA Primers 1 Verify name & PN | 2000089 | Vortex, centrifuge briefly. | -20°C |
| | Dynabeads MyOne SILANE | 2000048 | Vortex thoroughly (≥30 sec) immediately before adding to the mix. | 4°C |
| | Beckman Coulter SPRIselect Reagent | - | Manufacturer's recommendations. | - |
| | Agilent Bioanalyzer High Sensitivity Kit If used for QC and quantification | - | Manufacturer's recommendations. | - |
| | Agilent TapeStation ScreenTape and Reagents If used for QC and quantification | - | Manufacturer's recommendations. | - |
| | Qubit dsDNA HS Assay Kit If used for QC and quantification | - | Manufacturer's recommendations. | - |
| Place on ice | <input type="radio"/> Amp Mix | 2000103 | Vortex, centrifuge briefly. | -20°C |
| Thaw at 65°C | <input checked="" type="radio"/> Cleanup Buffer | 2000088 | Thaw for 10 min at 65°C at max speed on a thermomixer. Verify no visible crystals. Cool to room temperature. | -20°C |
| Obtain | <input type="radio"/> Recovery Agent | 220016 | - | Ambient |
| | Qiagen Buffer EB | - | Manufacturer's recommendations. | - |
| | Bio-Rad 10% Tween 20 | - | Manufacturer's recommendations. | - |
| | 10x Magnetic Separator | 230003 | - | Ambient |
| | Prepare 80% Ethanol Prepare 8 ml for 4 reactions | - | Prepare fresh. | Ambient |

2.1 Post GEM-RT Cleanup – Dynabeads

- a. Add **125 μ l** Recovery Agent to each sample at room temperature. **DO NOT** pipette mix or vortex the biphasic mixture. Wait **2 min**.

The resulting biphasic mixture contains Recovery Agent/Partitioning Oil (pink) and aqueous phase (clear), with no persisting emulsion (opaque).



If biphasic separation is incomplete:

Firmly secure the cap on the tube strip, ensuring that no liquid is trapped between the cap and the tube rim. Mix by inverting the capped tube strip 5x, centrifuge briefly, and proceed to step b. **DO NOT** invert without firmly securing the caps.




A smaller aqueous phase volume indicates a clog during GEM generation.



- b. Slowly remove and discard **125 μ l** Recovery Agent/Partitioning Oil (pink) from the bottom of the tube. **DO NOT** aspirate any aqueous sample.



- c. Prepare Dynabeads Cleanup Mix.

| Dynabeads Cleanup Mix <i>Add reagents in the order listed</i> | PN | 1X (μ l) | 4X + 10% (μ l) | 8X + 10% (μ l) |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------|---------------|------------------------|------------------------|
| Cleanup Buffer | 2000088 | 182 | 801 | 1602 |
| Dynabeads MyOne SILANE Vortex thoroughly (≥ 30 sec) immediately before adding to the mix. | | | | |
|  Aspirate the full liquid volume with a pipette tip to verify that the beads have not settled in the bottom of the tube. If clumps are present, pipette mix to resuspend completely. DO NOT centrifuge before use. | 2000048 | 8 | 35 | 70 |
| Reducing Agent B | 2000087 | 5 | 22 | 44 |
| Nuclease-free Water | | 5 | 22 | 44 |
| Total | - | 200 | 880 | 1760 |



- d. Vortex and add **200 μ l** to each sample. Pipette mix 10x (pipette set to 200 μ l).
- e. Incubate **10 min** at room temperature (keep caps open). Pipette mix again at **~5 min** after start of incubation to resuspend settled beads.



f. Prepare Elution Solution I. Vortex and centrifuge briefly.

| Elution Solution I <i>Add reagents in the order listed</i> | PN | 1X (μl) | 10X (μl) |
|---------------------------------------------------------------|---------|------------|-------------|
| Buffer EB | - | 98 | 980 |
| 10% Tween 20 | - | 1 | 10 |
| <input type="radio"/> Reducing Agent B | 2000087 | 1 | 10 |
| Total | - | 100 | 1000 |

g. At the end of **10 min** incubation, place on a 10x Magnetic Separator • **High** position (magnet • **High**) until the solution clears.

A white interface between the aqueous phase and Recovery Agent is normal.

h. Remove the supernatant (aqueous phase and Recovery Agent).

i. Add **300 μl** 80% ethanol to the pellet while on the magnet. Wait **30 sec**.

j. Remove the ethanol.

k. Add **200 μl** 80% ethanol to pellet. Wait **30 sec**.

l. Remove the ethanol.

m. Centrifuge briefly. Place on the magnet • **Low**.n. Remove remaining ethanol. Air dry for **1 min**.o. Remove from the magnet. Immediately add **35.5 μl** Elution Solution I.

p. Pipette mix (pipette set to 30 μl) without introducing bubbles.

q. Incubate **2 min** at **room temperature**.r. Place on the magnet • **Low** until the solution clears.s. Transfer **35 μl** sample to a new tube strip.

2.2 cDNA Amplification



a. Prepare cDNA Amplification Mix on ice. Vortex and centrifuge briefly.

| cDNA Amplification Reaction Mix <i>Add reagents in the order listed</i> | PN | 1X (μl) | 4X + 10% (μl) | 8X + 10% (μl) |
|----------------------------------------------------------------------------|---------------------|-----------|------------------|------------------|
| ○ Amp Mix | 2000047/ 2000103 | 50 | 220 | 440 |
| ● cDNA Primers | 2000089 | 15 | 66 | 132 |
| Total | - | 65 | 286 | 572 |

b. Add 65 μl cDNA Amplification Reaction Mix to 35 μl sample.

c. Pipette mix 15x (pipette set to 90 μl). Centrifuge briefly.

d. Incubate in a thermal cycler with the following protocol.

| Lid Temperature | Reaction Volume | Run Time |
|-----------------|-----------------------------------------------------|------------|
| 105°C | 100 μl | ~30-45 min |
| Step | Temperature | Time |
| 1 | 98°C | 00:03:00 |
| 2 | 98°C | 00:00:15 |
| 3 | 63°C | 00:00:20 |
| 4 | 72°C | 00:01:00 |
| 5 | Go to Step 2, see table below for total # of cycles | |
| 6 | 72°C | 00:01:00 |
| 7 | 4°C | Hold |

Recommended starting point for cycle number optimization.

| Targeted Cell Recovery | Total Cycles |
|------------------------|--------------|
| <500 | 13 |
| 500-1,000 | 12 |

The optimal number of cycles is a trade-off between generating sufficient final mass for library construction and minimizing PCR amplification artifacts. The number of cDNA cycles should also be reduced if large numbers of cells are sampled.



e. Store at 4°C for up to 72 h or -20°C for ≤1 week, or proceed to the next step.

2.3 cDNA Cleanup – SPRIselect

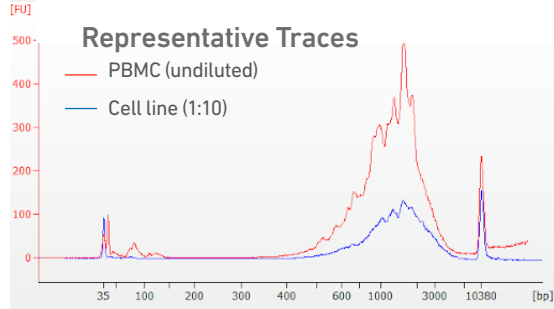
- a. Vortex to resuspend the SPRIselect reagent. Add **60 µl** SPRIselect reagent (**0.6X**) to each sample and pipette mix 15x (pipette set to 150 µl).
- b. Incubate **5 min** at **room temperature**.
- c. Place on the magnet•**High** until the solution clears.
- d. Remove the supernatant.
- e. Add **200 µl** 80% ethanol to the pellet. Wait **30 sec**.
- f. Remove the ethanol.
- g. **Repeat** steps e and f for a total of 2 washes.
- h. Centrifuge briefly and place on the magnet•**Low**.
- i. Remove any remaining ethanol. Air dry for **2 min**. **DO NOT** exceed **2 min** as this will decrease elution efficiency.
- j. Remove from the magnet. Add **40.5 µl** Buffer EB. Pipette mix 15x (pipette set to 35 µl).
- k. Incubate **2 min** at **room temperature**.
- l. Place the tube strip on the magnet•**High** until the solution clears.
- m. Transfer **40 µl** sample to a new tube strip.
- n. Store at **4°C** for up to **72 h** or at **-20°C** for up to **4 weeks**, or proceed to the next step.



2.4
Post cDNA
Amplification QC &
Quantification

a. Run 1 µl sample, diluted 1:10 on an Agilent Bioanalyzer High Sensitivity chip.

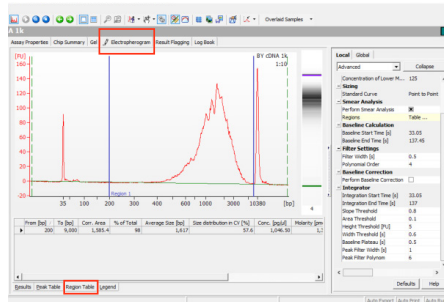
For input cells with low RNA content (<1pg total RNA/cell), 1 µl undiluted product may be run. Lower molecular weight product (35 – 150 bp) may be present. This is normal and does not affect sequencing or application performance.



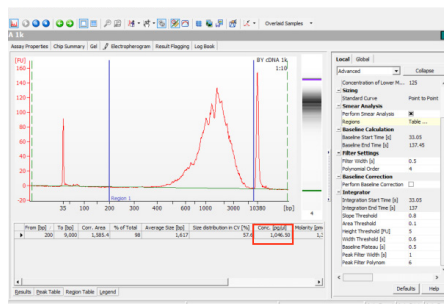
EXAMPLE CALCULATION

i. Select Region

Under the “Electropherogram” view choose the “Region Table”. Manually select the region of ~200 – ~9000 bp.



ii. Note Concentration [pg/µl]



iii. Calculate

Multiply the cDNA concentration [pg/µl] reported via the Agilent 2100 Expert Software by the elution volume (40 µl) of the Post cDNA Amplification Reaction Clean Up sample (taking any dilution factors into account) and then divide by 1000 to obtain the total cDNA yield in ng.

Example Calculation of cDNA Total Yield

Concentration: 1046.5 pg/µl
 Elution Volume: 40
 Dilution Factor: 10

Total cDNA Yield

$$= \text{Conc'n (pg/µl)} \times \text{Elution Volume} \times \text{Dilution Factor} / 1000 \text{ (pg/ng)}$$

$$= 1046.5 \text{ (pg/µl)} \times 40 \times 10 = 418.6 \text{ ng} / 1000 \text{ (pg/ng)}$$



Carry forward **ONLY 25%** of total cDNA yield into 3' Gene Expression Library Construction (step 3)

$$= 0.25 \times \text{Total cDNA yield}$$

$$= 0.25 \times 418.6 = 104.65 \text{ ng}$$

Refer to step 3.5 for appropriate number of Sample Index PCR cycles based on carry forward cDNA yield/input cDNA.

Alternate Quantification Methods [See Appendix for representative traces](#)

- Agilent TapeStation
- LabChip

Agilent Bioanalyzer, Agilent TapeStation, LabChip are the recommended methods for accurate quantification.

(If using Qubit Fluorometer and Qubit dsDNA HS Assay Kit, [see Appendix](#))

Step 3

3' Gene Expression Library Construction

- 3.1 Fragmentation, End Repair & A-tailing
- 3.2 Post Fragmentation End Repair & A-tailing Double Sided Size Selection – SPRIselect
- 3.3 Adaptor Ligation
- 3.4 Post Ligation Cleanup – SPRIselect
- 3.5 Sample Index PCR
- 3.6 Post Sample Index PCR Double Sided Size Selection – SPRIselect
- 3.7 Post Library Construction QC

3.0 3' Gene Expression Library Construction

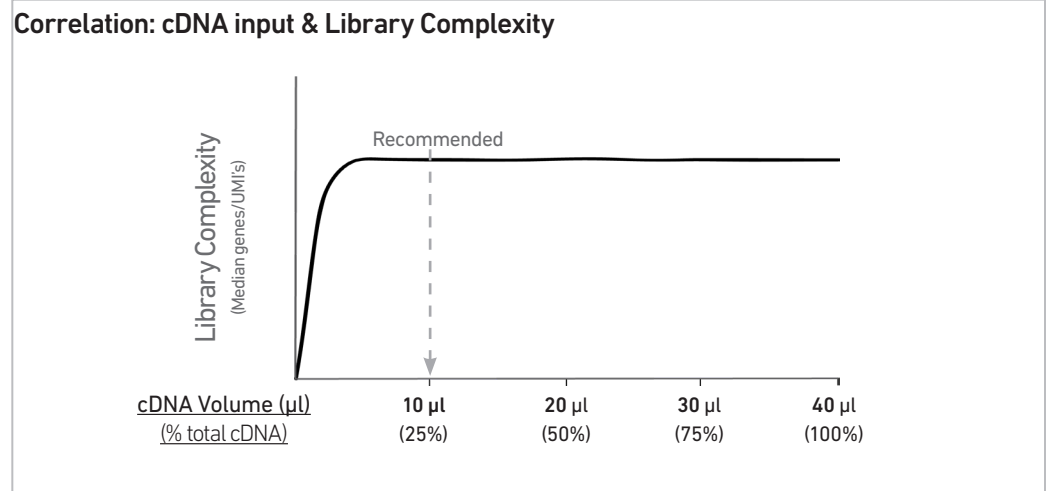


| GET STARTED! | | | | |
|----------------------------------------|----------------------------------------------------------------------------------------------|---------------------|----------------------------------------------------|---------|
| Action | Item | 10x PN | Preparation & Handling | Storage |
| Equilibrate to Room Temperature | Fragmentation Buffer | 2000091 | Vortex, verify no precipitate, centrifuge briefly. | -20°C |
| | Adaptor Oligos | 2000094 | Vortex, centrifuge briefly. | -20°C |
| | Ligation Buffer | 2000092 | Vortex, verify no precipitate, centrifuge briefly. | -20°C |
| DUAL INDEX | Dual Index Plate TT Set A <i>Verify name & PN Use indicated plate only</i> | 3000431 | - | -20°C |
| | Beckman Coulter SPRiselect Reagent | - | Manufacturer's recommendations. | - |
| | Agilent TapeStation Screen Tape and Reagents If used for QC | - | Manufacturer's recommendations. | - |
| | Agilent Bioanalyzer High Sensitivity kit If used for QC | - | Manufacturer's recommendations. | - |
| | DNA High Sensitivity Reagent Kit If LabChip used for QC | - | Manufacturer's recommendations. | - |
| | Place on Ice Fragmentation Enzyme | 2000104 | Centrifuge briefly. | -20°C |
| | DNA Ligase | 220131 | Centrifuge briefly. | -20°C |
| Amp Mix | 2000103 | Centrifuge briefly. | -20°C | |
| | KAPA Library Quantification Kit for Illumina Platforms | - | Manufacturer's recommendations. | - |
| Obtain | Qiagen Buffer EB | - | - | Ambient |
| | 10x Magnetic Separator | 230003 | See Tips & Best Practices. | Ambient |
| | Prepare 80% Ethanol Prepare 10 ml for 4 reactions | - | Prepare fresh. | Ambient |

Step Overview (Step 3.1d)


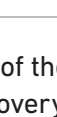

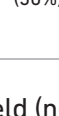
Correlation between input & library complexity

A Single Cell 3' Gene Expression library is generated using a fixed proportion (10 μ l, 25%) of the total cDNA (40 μ l) obtained at step 2.3m. The complexity of this library will be comparable to one generated using a higher proportion (>25%) of the cDNA. The remaining proportion (30 μ l, 75%) of the cDNA may be stored at 4°C for up to 72 h or at -20°C for longer-term storage (up to 4 weeks).



Note that irrespective of the total cDNA yield (ng), which may vary based on cell type, targeted cell recovery etc., this protocol has been optimized for a broad range of input mass (ng), as shown in the example below. The total number of SI PCR cycles (step 3.5e) should be optimized based on carrying forward a fixed proportion (10 μ l, 25%) of the total cDNA yield calculated during Post cDNA Amplification QC & Quantification (step 2.4).

Example: Library Construction Input Mass & SI PCR Cycles

| Cell Type | Targeted Cell Recovery | Total cDNA Yield (ng) | cDNA Input into Fragmentation | | SI PCR Cycle Number |
|------------------|------------------------------------------------------------------------------------------|-----------------------|-------------------------------|-----------|---------------------|
| | | | Volume (μ l) | Mass (ng) | |
| High RNA Content | Low  | 250 ng | 10 μ l | 62.5 ng | 13 |
| | High  | 1900 ng | 10 μ l | 475 ng | 10 |
| Low RNA Content | Low  | 1 ng | 10 μ l | 0.25 ng | 16 |
| | High  | 200 ng | 10 μ l | 50 ng | 12 |

3.1 Fragmentation, End Repair & A-tailing

- a. Prepare a thermal cycler with the following incubation protocol.

| Lid Temperature | Reaction Volume | Run Time |
|----------------------------------------------------------------------------------|-----------------|----------|
| 65°C | 50 µl | ~35 min |
| Step | Temperature | Time |
| Pre-cool block <i>Pre-cool block prior to preparing the Fragmentation Mix</i> | 4°C | Hold |
| Fragmentation | 32°C | 00:05:00 |
| End Repair & A-tailing | 65°C | 00:30:00 |
| Hold | 4°C | Hold |



- b. Vortex Fragmentation Buffer. Verify there is no precipitate.
c. Prepare Fragmentation Mix on ice. Pipette mix and centrifuge briefly.

| Fragmentation Mix <i>Add reagents in the order listed</i> | PN | 1X (µl) | 4X + 10% (µl) | 8X + 10% (µl) |
|--------------------------------------------------------------|---------|-----------|------------------|------------------|
| ● Fragmentation Buffer | 2000091 | 5 | 22 | 44 |
| ● Fragmentation Enzyme | 2000104 | 10 | 44 | 88 |
| Total | - | 15 | 66 | 132 |

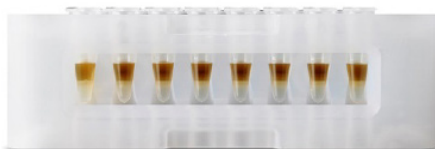
- d. Transfer **ONLY 10 µl** purified cDNA sample from Pellet Cleanup (step 2.3m) to a tube strip.
Note that only **10 µl** (25%) cDNA sample transfer is sufficient for generating 3' Gene Expression library.
The remaining **30 µl** (75%) cDNA sample can be stored at **4°C** for up to **72 h** or at **-20°C** for up to **4 weeks** for generating additional 3' Gene Expression libraries.
- e. Add **25 µl** Buffer EB to each sample.
f. Add **15 µl** Fragmentation Mix to each sample.
g. Pipette mix 15x (pipette set to 35 µl) on ice. Centrifuge briefly.
h. Transfer into the pre-cooled thermal cycler (**4°C**) and press "SKIP" to initiate the protocol.

3.2 Post Fragmentation, End Repair & A-tailing Double Sided Size Selection – SPRIselect

- a. Vortex to resuspend SPRIselect reagent. Add **30 μ l** SPRIselect (**0.6X**) reagent to each sample. Pipette mix 15x (pipette set to 75 μ l).
- b. Incubate **5 min** at **room temperature**.
- c. Place on the magnet•**High** until the solution clears. **DO NOT** discard supernatant.



- d. Transfer **75 μ l** supernatant to a new tube strip.
- e. Vortex to resuspend SPRIselect reagent. Add **10 μ l** SPRIselect reagent (**0.8X**) to each sample. Pipette mix 15x (pipette set to 80 μ l).
- f. Incubate **5 min** at **room temperature**.
- g. Place on the magnet•**High** until the solution clears.



- h. Remove **80 μ l** supernatant. **DO NOT** discard any beads.
- i. Add **125 μ l** 80% ethanol to the pellet. Wait **30 sec**.
- j. Remove the ethanol.
- k. **Repeat** steps i and j for a total of 2 washes.
- l. Centrifuge briefly. Place on the magnet•**Low** until the solution clears. Remove remaining ethanol. **DO NOT** over dry to ensure maximum elution efficiency.
- m. Remove from the magnet. Add **50.5 μ l** Buffer EB to each sample. Pipette mix 15x (pipette set to 45 μ l).
- n. Incubate **2 min** at **room temperature**.
- o. Place on the magnet•**High** until the solution clears.
- p. Transfer **50 μ l** sample to a new tube strip.

3.3 Adaptor Ligation

a. Prepare Adaptor Ligation Mix. Pipette mix and centrifuge briefly.

| Adaptor Ligation Mix <i>Add reagents in the order listed</i> | PN | 1X (μl) | 4X + 10% (μl) | 8X + 10% (μl) |
|-----------------------------------------------------------------|---------|-----------|------------------|------------------|
| ● Ligation Buffer | 2000092 | 20 | 88 | 176 |
| ● DNA Ligase | 220131 | 10 | 44 | 88 |
| ● Adaptor Oligos | 2000094 | 20 | 88 | 176 |
| Total | - | 50 | 220 | 440 |

b. Add 50 μl Adaptor Ligation Mix to 50 μl sample. Pipette mix 15x (pipette set to 90 μl). Centrifuge briefly.

c. Incubate in a thermal cycler with the following protocol.

| Lid Temperature | Reaction Volume | Run Time |
|-----------------|-----------------|----------|
| 30°C | 100 μl | 15 min |
| Step | Temperature | Time |
| 1 | 20°C | 00:15:00 |
| 2 | 4°C | Hold |

3.4 Post Ligation Cleanup – SPRIselect

- a. Vortex to resuspend SPRIselect Reagent. Add **80 μ l** SPRIselect Reagent (**0.8X**) to each sample. Pipette mix 15x (pipette set to 150 μ l).
- b. Incubate **5 min** at **room temperature**.
- c. Place on the magnet•**High** until the solution clears.
- d. Remove the supernatant.
- e. Add **200 μ l** 80% ethanol to the pellet. Wait **30 sec**.
- f. Remove the ethanol.
- g. **Repeat** steps e and f for a total of 2 washes.
- h. Centrifuge briefly. Place on the magnet•**Low**.
- i. Remove any remaining ethanol. Air dry for **2 min**.
DO NOT exceed **2 min** as this will decrease elution efficiency.
- j. Remove from the magnet. Add **30.5 μ l** Buffer EB. Pipette mix 15x.
- k. Incubate **2 min** at **room temperature**.
- l. Place on the magnet•**Low** until the solution clears.
- m. Transfer **30 μ l** sample to a new tube strip.

3.5 Sample Index PCR

DUAL
INDEX



- Choose the appropriate sample index sets to ensure that no sample indices overlap in a multiplexed sequencing run. Record the 10x Sample Index name (PN-3000431 Dual Index Plate TT Set A well ID) used.
- Add **50 µl** Amp Mix (2000103) to **30 µl** sample.
- Add **20 µl** of an individual Dual Index TT Set A to each sample and record the well ID used. Pipette mix 5x (pipette set to 90 µl). Centrifuge briefly.
- Incubate in a thermal cycler with the following protocol.

| Lid Temperature | Reaction Volume | Run Time |
|-----------------|-----------------------------------------|------------|
| 105°C | 100 µl | ~25-40 min |
| Step | Temperature | Time |
| 1 | 98°C | 00:00:45 |
| 2 | 98°C | 00:00:20 |
| 3 | 54°C | 00:00:30 |
| 4 | 72°C | 00:00:20 |
| 5 | Go to step 2, see below for # of cycles | |
| 6 | 72°C | 00:01:00 |
| 7 | 4°C | Hold |



The total cycles should be optimized based on 25% carry forward cDNA yield/input calculated during cDNA QC & Quantification (step 2.4)

| cDNA Input | Total Cycles |
|----------------|--------------|
| 0.25-25 ng | 14-16 |
| 25-150 ng | 12-14 |
| 150-500 ng | 10-12 |
| 500-1,000 ng | 8-10 |
| 1,000-1,500 ng | 6-8 |
| >1500 ng | 5 |



- Store at **4°C** for up to **72 h** or proceed to the next step.

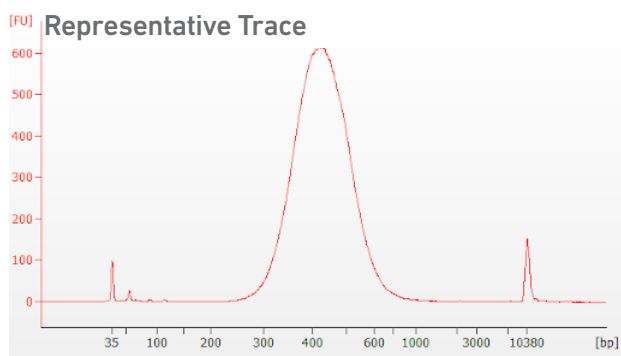
3.6 Post Sample Index PCR Double Sided Size Selection – SPRIselect

- a. Vortex to resuspend the SPRIselect reagent. Add **60 μ l** SPRIselect Reagent (**0.6X**) to each sample. Pipette mix 15x (pipette set to 150 μ l).
- b. Incubate **5 min** at **room temperature**.
- c. Place the magnet•**High** until the solution clears. **DO NOT** discard supernatant.
- d. Transfer **150 μ l** supernatant to a new tube strip.
- e. Vortex to resuspend the SPRIselect reagent. Add **20 μ l** SPRIselect Reagent (**0.8X**) to each sample. Pipette mix 15x (pipette set to 150 μ l).
- f. Incubate **5 min** at **room temperature**.
- g. Place the magnet•**High** until the solution clears.
- h. Remove **165 μ l** supernatant. **DO NOT** discard any beads.
- i. With the tube still in the magnet, add **200 μ l** 80% ethanol to the pellet. Wait **30 sec**.
- j. Remove the ethanol.
- k. **Repeat** steps i and j for a total of 2 washes.
- l. Centrifuge briefly. Place on the magnet•**Low**. Remove remaining ethanol.
- m. Remove from the magnet. Add **35.5 μ l** Buffer EB. Pipette mix 15x.
- n. Incubate **2 min** at **room temperature**.
- o. Place on the magnet•**Low** until the solution clears.
- p. Transfer **35 μ l** to a new tube strip.
- q. Store at **4°C** for up to **72 h** or at **-20°C** for **long-term** storage.



3.7 Post Library Construction QC

Run 1 μl sample at 1:10 dilution on an Agilent Bioanalyzer High Sensitivity chip.



Determine the average fragment size from the Bioanalyzer trace. This will be used as the insert size for library quantification.

Alternate QC Method:

- Agilent TapeStation
- LabChip

[See Appendix for representative traces](#)

[See Appendix for Post Library Construction Quantification](#)

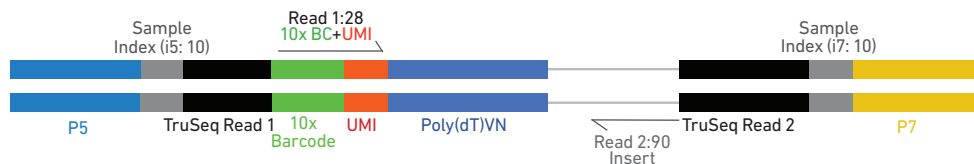
Sequencing

4

Sequencing Libraries

Single Cell 3' Gene Expression libraries comprise standard Illumina paired-end constructs which begin with P5 and end with P7. 16 bp 10x Barcodes are encoded at the start of TruSeq Read 1, while 10 bp i5 and i7 sample index sequences are incorporated as sample index reads. TruSeq Read 1 and Read 2 are standard Illumina sequencing primer sites used in paired-end sequencing. TruSeq Read 1 is used to sequence 16 bp 10x Barcodes and 12 bp UMI. Sequencing these libraries produces a standard Illumina BCL data output folder.

Chromium Single Cell 3' Gene Expression Dual Index Library



Illumina Sequencer Compatibility

The compatibility of the listed sequencers has been verified by 10x Genomics. Some variation in assay performance is expected based on sequencer choice. For more information about performance variation, visit the 10x Genomics Support website.

- MiSeq
- NextSeq 500/550
- NextSeq 1000/2000
- HiSeq 2500 (Rapid Run)
- HiSeq 3000/4000
- NovaSeq

Sample Indices

Each sample index in the Dual Index Kit TT Set A (PN-1000215) is a mix of one unique i7 and one unique i5 sample index. If multiple samples are pooled in a sequence lane, the sample index name (i.e. the Dual Index TT Set A plate well ID, SI-TT-) is needed in the sample sheet used for generating FASTQs with "cellranger mkfastq". Samples utilizing the same sample index should not be pooled together, or run on the same flow cell lane, as this would not enable correct sample demultiplexing.

3' Gene Expression Library Sequencing Depth & Run Parameters

| | |
|-------------------------|------------------------------------|
| Sequencing Depth | Minimum 20,000 read pairs per cell |
| Sequencing Type | Paired-end, dual indexing |
| Sequencing Read | Recommended Number of Cycles |
| Read 1 | 28 cycles |
| i7 Index | 10 cycles |
| i5 Index | 10 cycles |
| Read 2 | 90 cycles |

Library Loading

Once quantified and normalized, the 3' Gene Expression libraries should be denatured and diluted as recommended for Illumina sequencing platforms. Refer to Illumina documentation for denaturing and diluting libraries. Refer to the 10x Genomics Support website, for more information.

| Instrument | Loading Concentration (pM) | PhiX (%) |
|-------------------|----------------------------|----------|
| MiSeq | 11 | 1 |
| NextSeq 500/550 | 1.8 | 1 |
| NextSeq 1000/2000 | 650 | 1 |
| HiSeq 2500 (RR) | 11 | 1 |
| HiSeq 4000 | 240 | 1 |
| NovaSeq | 150*/300 | 1 |

* Use 150 pM loading concentration for Illumina XP workflow.

Library Pooling

The 3' Gene Expression libraries may be pooled for sequencing, taking into account the differences in cell number and per-cell read depth requirements between each library. Samples utilizing the same sample index should not be pooled together, or run on the same flow cell lane, as this would not enable correct sample demultiplexing.

Data Analysis and Visualization

Sequencing data may be analyzed using Cell Ranger or 10x Genomics Cloud Analysis and visualized using Loupe Browser. Key features for these tools are listed below. For detailed product-specific information, visit the 10x Genomics Support website.

Cell Ranger

Cell Ranger is a set of analysis pipelines that processes Chromium Single Gene Expression data to align reads, generate Feature Barcode matrices and perform clustering and gene expression analysis.

- Input: Base call (BCL) and FASTQ
- Output: BAM, MEX, CSV, HDF5, Web Summary, .cloupe/.loupe
- Operating System: Linux



Cloud Analysis

Cloud Analysis is currently only available for US customers.

Cloud Analysis allows users to run Cell Ranger analysis pipelines from a web browser while computation is handled in the cloud.

- Key features: scalable, highly secure, simple to set up and run
- Input: FASTQ
- Output: BAM, MEX, CSV, HDF5, Web Summary, .cloupe/.loupe.



Loupe Browser

Loupe Browser is an interactive data visualization tool that requires no prior programming knowledge.

- Input: .cloupe
- Output: Data visualization, including t-SNE and UMAP projections, custom clusters, differentially expressed genes
- Operating System: MacOS, Windows



Troubleshooting



5

GEMs

STEP NORMAL REAGENT CLOGS & WETTING FAILURES

1.4 d
After Chip L is removed from the Controller and the wells are exposed

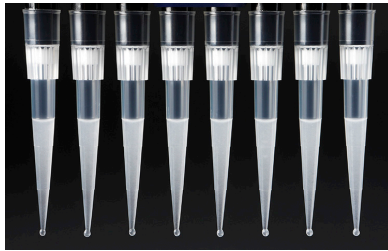


All 8 recovery wells are similar in volume and opacity.

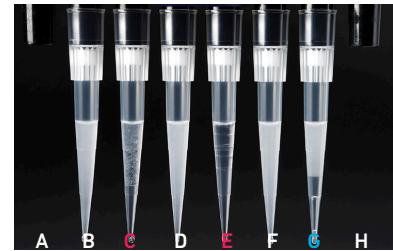


Recovery well G indicates a reagent clog. Recovery well C and E indicate a wetting failure. Recovery wells B, D, and F are normal. Wells A and H contain 50% Glycerol Solution.

1.4 f
Transfer GEMs from Chip L Row Labeled 3



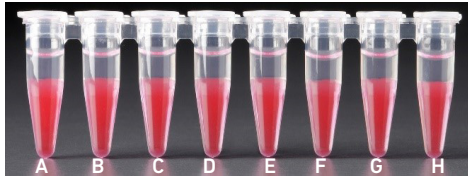
All liquid levels are similar in volume and opacity without air trapped in the pipette tips.



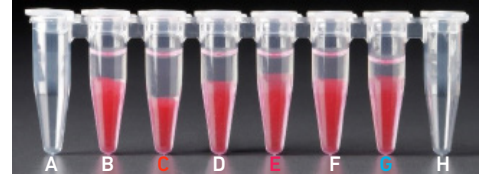
Pipette tips C and E indicate a wetting failure. Pipette tip C contains partially emulsified GEMs. Emulsion is absent in pipette tip E. Pipette tip G indicates a reagent clog.

| STEP | NORMAL | REAGENT CLOGS & WETTING FAILURES |
|------|--------|----------------------------------|
|------|--------|----------------------------------|

2.1 a
After transfer of the
GEMs +
Recovery Agent

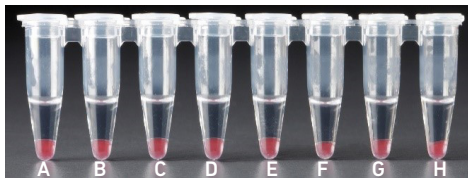


All liquid levels are similar in the aqueous sample volume (clear) and Recovery Agent/Partitioning Oil (pink).

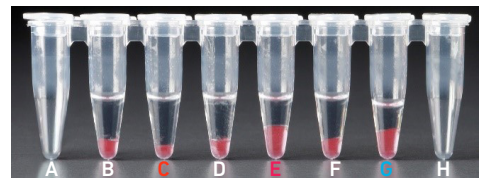


Tube **G** indicates a reagent clog has occurred. There is a decreased volume of aqueous layer (clear).
Tube **C** and **E** indicate a wetting failure has occurred. There is an abnormal volume of Recovery Agent/Partitioning Oil (pink).

2.1 b
After aspiration of
Recovery Agent/
Partitioning Oil



All liquid volumes are similar in the aqueous sample volume (clear) and residual Recovery Agent/Partitioning Oil (pink).



Tube **G** indicates a reagent clog has occurred. There is a decreased volume of aqueous layer (clear). There is also a greater residual volume of Recovery Agent/Partitioning Oil (pink).
Tube **C** and **E** indicate a wetting failure has occurred. There is an abnormal residual volume of Recovery Agent/Partitioning Oil (pink).

2.1 d
After addition of
Dynabeads
Cleanup Mix



All liquid volumes are similar after addition of the Dynabeads Cleanup Mix.



Tube **G** indicates a reagent clog has occurred. There is an abnormal ratio of Dynabeads Cleanup Mix (brown) to Recovery Agent/Partitioning Oil (appears white).
Tube **C** and **E** indicate a wetting failure has occurred. There is an abnormal ratio of Dynabeads Cleanup Mix (brown) to Recovery Agent/Partitioning Oil (appears white).

If a channel clogs or wetting failure occurs during GEM generation, it is recommended that the sample be remade. If any of the listed issues occur, take a picture and send it to support@10xgenomics.com for further assistance.

Chromium Controller Errors

If the Chromium Controller or the Chromium Single Cell Controller fails to start, an error tone will sound and one of the following error messages will be displayed:

- a. **Chip not read – Try again:** Eject the tray, remove and/or reposition the Chromium Next GEM Secondary Holder assembly and try again. If the error message is still received after trying this more than twice, contact support@10xgenomics.com for further assistance.
- b. **Check gasket:** Eject the tray by pressing the eject button to check that the 10x Gasket is correctly installed on the Chromium Next GEM Chip. If the error message persists, contact support@10xgenomics.com for further assistance.
- c. **Error Detected: Row _ Pressure:**
 - i. If this message is received within a few seconds of starting a run, eject the tray by pressing the eject button and check for dirt or deposits on the 10x Gasket. If dirt is observed, replace with a new 10x Gasket and try again. If the error message is still received after trying this more than twice, contact support@10xgenomics.com for further assistance.
 - ii. If this message is received after a few minutes into the run, the Chromium Next GEM Chip must be discarded. **Do not try running this Chromium Next GEM Chip again as this may damage the Chromium Controller.**
- d. **Invalid Chip CRC Value:** This indicates that a Chromium Next GEM Chip has been used with an older firmware version. The chip must be discarded. Contact support@10xgenomics.com for further assistance.
- e. **Chip Holder Not Present:** Open the controller drawer and check if chip holder is present. Insert chip properly into chip holder and retry.
- f. **Unauthorized Chip:** This indicates that an incompatible non-Next GEM chip has been used with an instrument that only can run Next GEM assays. Use only Chromium Controller (PN-120223;120246) or Chromium Single Cell Controller (PN-120263;120212) to run that chip or chip must be discarded. Contact support@10xgenomics.com for further assistance.
- g. **Endpoint Reached Early:** If this message is received, contact support@10xgenomics.com for further assistance.

Chromium X Series Errors

The Chromium X touchscreen will guide the user through recoverable errors. If the error continues, or if the instrument has seen critical or intermediate errors, email support@10xgenomics.com with the displayed error code. Support will request a troubleshooting package. Upload pertinent logs to 10x Genomics by navigating to the Logs menu option on screen.

There are two types of errors:

Critical Errors — When the instrument has seen a critical error, the run will immediately abort. Do not proceed with any further runs. Contact support@10xgenomics.com with the error code.

- a. System Error
- b. Pressure Error
- c. Chip Error
- d. Run Error
- e. Temperature Error
- f. Software Error

User Recoverable Errors — Follow error handling instructions through the touchscreen and continue the run.

- a. Gasket Error
- b. Tray Error
- c. Chip Error
- d. Unsupported Chip Error
- e. Update Error



Consult the Chromium X Series (X/iX) User Guide (CG000396) for additional information and follow the Chromium X touchscreen prompts for execution.

Appendix

Post Library Construction Quantification

Agilent TapeStation Traces

LabChip Traces

Oligonucleotide Sequences




Post Library Construction Quantification

- Thaw KAPA Library Quantification Kit for Illumina Platforms.
- Dilute 2 μl sample with deionized water to appropriate dilutions that fall within the linear detection range of the KAPA Library Quantification Kit for Illumina Platforms. (For more accurate quantification, make the dilution(s) in duplicate).
- Make enough Quantification Master Mix for the DNA dilutions per sample and the DNA Standards (plus 10% excess) using the guidance for 1 reaction volume below.

| Quantification Master Mix | 1X (μl) |
|-------------------------------|----------------------|
| SYBR Fast Master Mix + Primer | 12 |
| Water | 4 |
| Total | 16 |

- Dispense 16 μl Quantification Master Mix for sample dilutions and DNA Standards into a 96 well PCR plate.
- Add 4 μl sample dilutions and 4 μl DNA Standards to appropriate wells. Centrifuge briefly.
- Prepare a qPCR system with the following protocol. Insert the plate and start the program.

| Step | Temperature | Run Time |
|------|----------------------------------------------------------------------------------------------------------|----------|
| 1 | 95°C | 00:03:00 |
| 2 | 95°C | 00:00:05 |
| 3 | 67°C  Read signal | 00:00:30 |
| 4 | Go to Step 2, 29X (Total 30 cycles) | |

- Follow the manufacturer's recommendations for qPCR-based quantification. For library quantification for sequencer clustering, determine the concentration based on insert size derived from the Bioanalyzer/TapeStation trace.

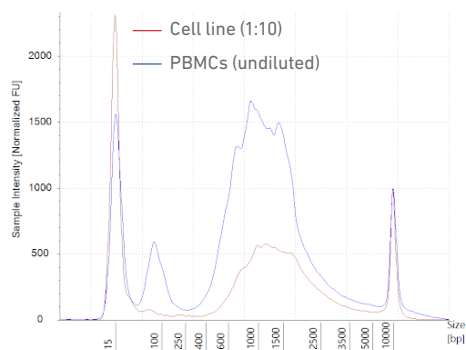
Agilent TapeStation Traces

Agilent TapeStation Traces

Agilent TapeStation High Sensitivity D5000 ScreenTape was used. Protocol steps correspond to the Chromium Next GEM Single Cell 3' LT (Dual Index) v3.1 User Guide (CG000399)

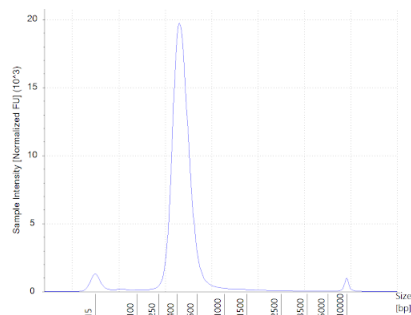
Protocol Step 2.4 – cDNA QC & Quantification

Run 2 μ l sample mixed with 2 μ l loading buffer. Ensure dilution factor is factored in when calculating cDNA yield/ μ l.



Protocol Step 3.7 – Post Library Construction QC

Run 2 μ l diluted sample (1:10 dilution) mixed with 2 μ l loading buffer.



All traces are representative.

LabChip Traces

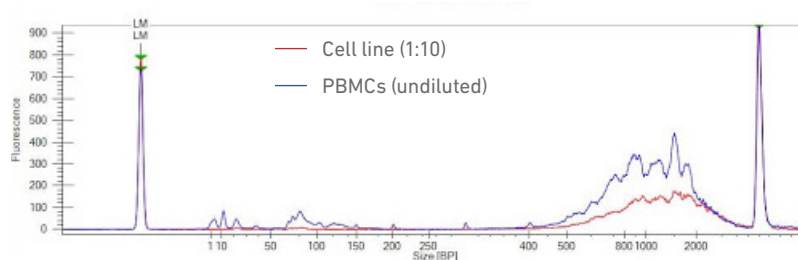
LabChip Traces

DNA High Sensitivity Reagent Kit was used.

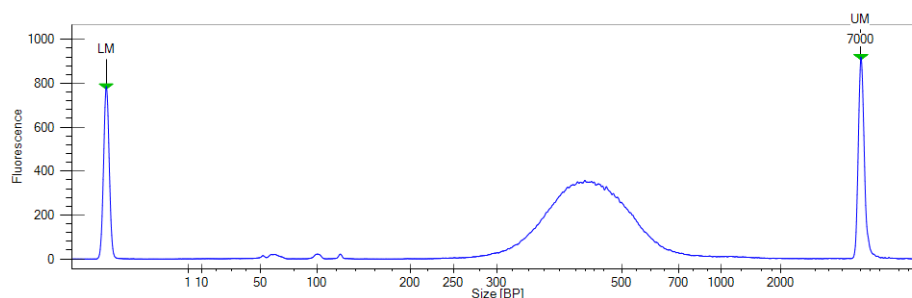
Protocol steps correspond to the Chromium Next GEM Single Cell 3' LT Reagent Kits v3.1 (Dual Index) User Guide (CG000399)

Protocol Step 2.4 – cDNA QC & Quantification

Run 10 μ l sample. cDNA yield calculation is same as Agilent Bioanalyzer traces.



Protocol Step 3.7 – Post Library Construction QC



Run 10 μ l diluted sample (1:10 dilution).

All traces are representative.

Alternate QC Method:

[Qubit Fluorometer and Qubit dsDNA HS Assay Kit](#)

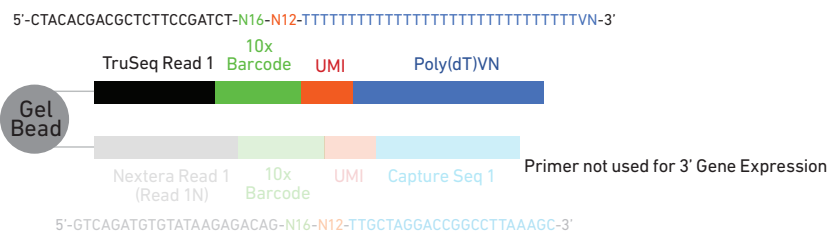
Multiply the cDNA concentration reported via the Qubit Fluorometer by the elution volume (40 μ l) to obtain the total cDNA yield in ng. To determine the equivalent range using the Agilent 2100 Expert Software, select the region encompassing 35-10,000 bp.

Oligonucleotide Sequences

Protocol steps correspond to the Chromium Next GEM Single Cell 3' LT Reagent Kits v3.1 (Dual Index) User Guide (CG000399)

Protocol Step 1.5 – GEM-RT Incubation

Gel Bead
Primers



● Template Switch
Oligo
PN-3000228



PCR Product



Protocol Step 2.2 – cDNA Amplification

● cDNA Primers
PN-2000089

Forward Primer: Partial Read 1
5'-CTACACGACGCTCTCCGATCT-3'

Reverse Primer: Partial TSO
5'-AAGCAGTGGTATCAACGCAGAG-3'

Amplification
Products



Protocol Step 3.3 – Adaptor Ligation

● Adaptor Oligos
PN-2000094

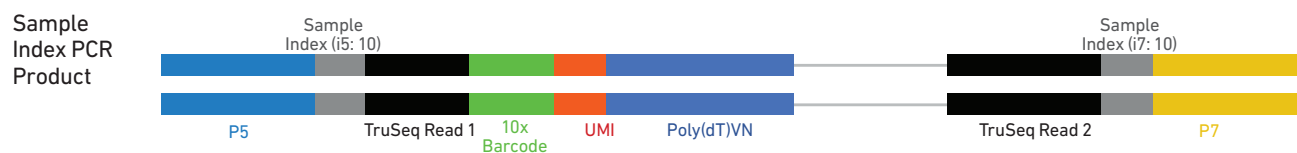
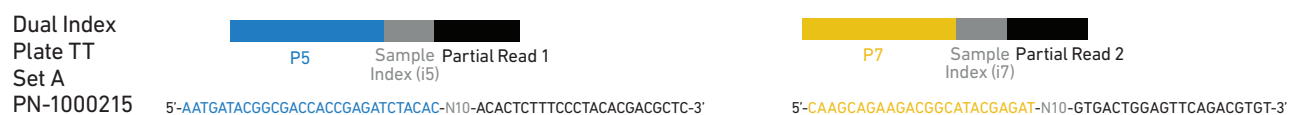
Partial Read 2
5'-GATCGGAAGAGCACAGTCTGAACTCCAGTCAC-3'
3'-TCTAGCCTTCTCG-5'

Ligation
Product



Oligonucleotide Sequences

Protocol Step 3.5 – Sample Index PCR



5-AATGATACGGCGACCCAGATCTACAC-N10-ACACTCTTCCCTACACGACGCTCTCCGATCT-N16-N12-TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT-VN-cDNA_Insert-AGATCGGAAGACACACGCTGAACCTCAGTCAC-N10-ATCTCGTATGCCGCTCTCTGCTTC-3'
 3-TTACTATGCCGCTGGTGGCTTAGATGTG-N10-TGTGAGAAAGGGATGTGCTGCGAGAAGGCTAGA-N16-N12-AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAABN-cDNA_Insert-TCTAGCCTTCTCGTGTGCGAGACTTGAGGTCAGTG-N10-TAGAGCATACGGCAGAGACGAAC-5'