CG000330 Rev B

USER GUIDE

Chromium Next GEM Single Cell 5' Reagent Kits v2 (Dual Index)

with Feature Barcode technology for Cell Surface Protein & Immune Receptor Mapping

FOR USE WITH

Chromium Next GEM Single Cell 5' Kit v2, 16 rxns PN-1000263
Chromium Next GEM Single Cell 5' Kit v2, 4 rxns PN-1000265
Library Construction Kit, 16 rxns PN-1000190
5' Feature Barcode Kit, 16 rxns PN-1000256
Chromium Single Cell Human TCR Amplification Kit, 16 rxns PN-1000252
Chromium Single Cell Human BCR Amplification Kit, 16 rxns PN-1000253
Chromium Single Cell Mouse TCR Amplification Kit, 16 rxns PN-1000254
Chromium Single Cell Mouse BCR Amplification Kit, 16 rxns PN-1000255
Chromium Next GEM Chip K Single Cell Kit, 48 rxns PN-1000286
Chromium Next GEM Chip K Single Cell Kit, 16 rxns PN-1000287
Dual Index Kit TT Set A, 96 rxns PN-1000215
Dual Index Kit TN Set A, 96 rxns PN-1000250

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

10x GENOMICS

Notices

Document Number

CG000330• Rev B

Legal Notices

Instrument & Licensed Software Updates Warranties

Updates to existing Instruments and Licensed Software may be required to enable customers to use new or existing products. In the event of an Instrument failure resulting from an update, such failed Instrument will be replaced or repaired in accordance with the 10x Limited Warranty, Assurance Plan or service agreement, only if such Instrument is covered by any of the foregoing at the time of such failure. Instruments not covered under a current 10x Limited Warranty, Assurance Plan or service agreement will not be replaced or repaired.

Support

Email: support@10xgenomics.com

10x Genomics

6230 Stoneridge Mall Road

Pleasanton, CA 94588 USA

Document Revision Summary

Document Number	CG000330
Title	Chromium Next GEM Single Cell 5' Reagent Kits v2 (Dual Index) User Guide with Feature Barcode technology for Cell Surface Protein & Immune Receptor Mapping
Revision	Rev B
Revision Date	May 2021

Specific Changes:

Updated loading concentration for NovaSeq.

General Changes:

Updates for general minor consistency of language and terms throughout.

Table of Contents

Introduction

Chromium Next GEM Single Cell 5' Reagent Kits v2 (Dual Index)
10x Genomics Accessories
Recommended Thermal Cyclers
Additional Kits, Reagents & Equipment
Protocol Steps & Timing
Stepwise Objectives
Cell Labeling Guidelines

Chromium Next GEM Single Cell 5' Reagent Kits v2 (Dual Index)

Chromium Next GEM Single Cell 5' Kit v2, 16 rxns PN-1000263

Chromium Next GEM Single Cell 5' GEM Kit v2, 16 rxns PN-1000244 (store at –20°C)

Chromium Next GEM Single Cell 5' GEM Kit v2

	#	PN
RT Reagent B	1	2000165
RT Enzyme C	1	2000085
Reducing Agent B	1	2000087
Poly-dT RT Primer	1	2000007
Cleanup Buffer	2	2000088
Amp Mix	1	2000047
cDNA Primers	1	2000089

10xGenomics.com

Library Construction Kit, 16 rxns PN-1000190 (store at –20°C)

Library Construction Kit

	#	PN
Fragmentation Buffer	1	2000091
Fragmentation Enzyme	1	2000090
Ligation Buffer	1	2000092
DNA Ligase	1	220110
Adaptor Oligos	1	2000094
Amp Mix	1	2000047

10xGenomics.com

Chromium Next GEM Single Cell 5' Gel Bead Kit v2, 16 rxns PN-1000264 (store at –80°C)

Chromium Next GEM Single Cell 5' Gel Beads v2

	#	PN
Single Cell VDJ 5' Gel Bead	2	1000264

10xGenomics.com

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

	#	PN
Dynabeads MyOne SILANE	1	2000048

Chromium Next GEM Single Cell 5' Kit v2, 4 rxns PN-1000265

Chromium Next GEM Single Cell 5' GEM Kit v2, 4 rxns PN-1000266 (store at –20°C)

Chromium
Next GEM
Single Cell 5'
GEM Kit v2

	#	PN
RT Reagent B	1	2000165
RT Enzyme C	1	2000102
Reducing Agent B	1	2000087
Poly-dT RT Primer	1	2000007
Cleanup Buffer	1	2000088
Amp Mix	1	2000103
cDNA Primers	1	2000089

10xGenomics.com 10x GENOMICS

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

Library Construction Kit

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

10xGenomics.com 10x GENOMICS

Chromium Next GEM Single Cell 5' Gel Bead Kit v2, 4 rxns PN-1000267 (store at –80°C)

Chromium
Next GEM
Single Cell 5'
Gel Beads v2

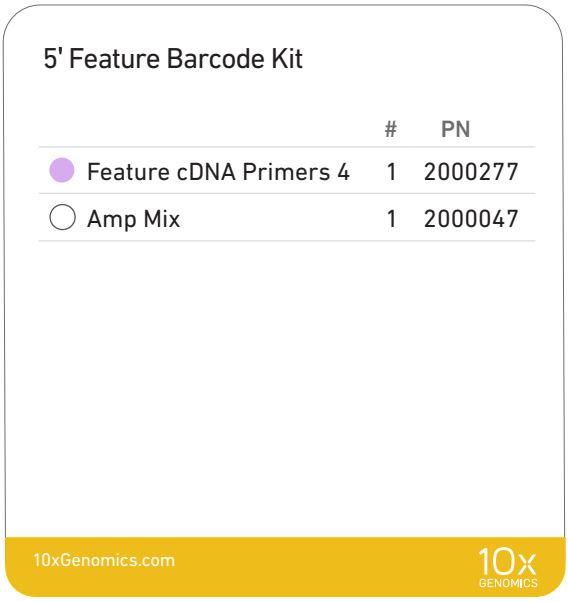
	#	PN
Single Cell VDJ 5' Gel Bead	1	1000267

10xGenomics.com 10x GENOMICS

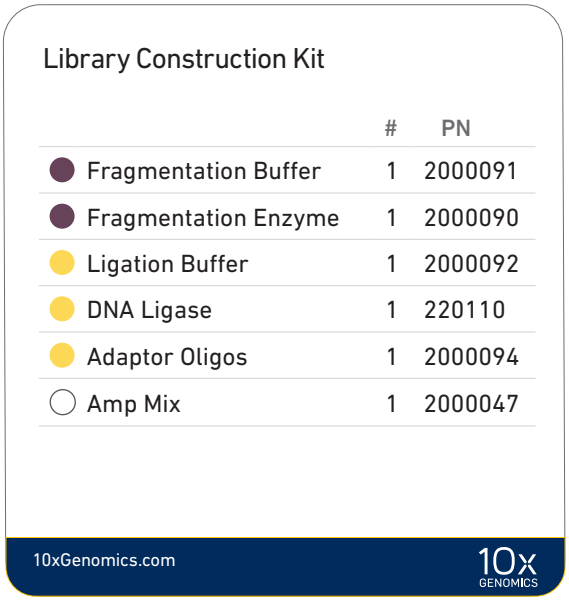
Dynabeads™ MyOne™ SILANE PN-2000048 (store at 4°C)

	#	PN
Dynabeads MyOne SILANE	1	2000048

5' Feature Barcode Kit, 16 rxns PN-1000256 (store at -20°C)



Library Construction Kit, 16 rxns PN-1000190 (store at -20°C)*



* Depending on the experimental goals, additional Library Construction Kits (PN-1000190) may be required. Refer to 10x Genomics support website for further guidance.

Chromium Single Cell V(D)J Amplification Kits, Human (store at –20°C)

TCR Amplification Kit, 16 rxns PN-1000252

Chromium
Single Cell
Human TCR
Amplification Kit

	#	PN
Human T Cell Mix 1 v2	1	2000242
Human T Cell Mix 2 v2	1	2000246
Amp Mix	2	2000047

10xGenomics.com 10x GENOMICS

BCR Amplification Kit, 16 rxns PN-1000253

Chromium
Single Cell
Human BCR
Amplification Kit

	#	PN
Human B Cell Mix 1 v2	1	2000254
Human B Cell Mix 2 v2	1	2000255
Amp Mix	2	2000047

10xGenomics.com 10x GENOMICS

Chromium Single Cell V(D)J Amplification Kits, Mouse (store at –20°C)

TCR Amplification Kit, 16 rxns PN-1000254

Chromium
Single Cell
Mouse TCR
Amplification Kit

	#	PN
Mouse T Cell Mix 1 v2	1	2000256
Mouse T Cell Mix 2 v2	1	2000257
Amp Mix	2	2000047

10xGenomics.com 10x GENOMICS

BCR Amplification Kit, 16 rxns PN-1000255

Chromium
Single Cell
Mouse BCR
Amplification Kit

	#	PN
Mouse B Cell Mix 1 v2	1	2000258
Mouse B Cell Mix 2 v2	1	2000259
Amp Mix	2	2000047

10xGenomics.com 10x GENOMICS

Chromium Next GEM Chip K Single Cell Kit, 48 rxns PN-1000286 (store at ambient temperature)

Chromium
Partitioning Oil

	#	PN
Partitioning Oil	6	2000190

Chromium
Recovery Agent

	#	PN
Recovery Agent	6	220016

Chromium
Next GEM
Chip K & Gaskets

	#	PN
Chromium Next GEM Chip K	6	2000182
Gasket, 6-pack	1	370017

10xGenomics.com

10x GENOMICS

Chromium Next GEM Chip K Single Cell Kit, 16 rxns PN-1000287 (store at ambient temperature)

Chromium
Partitioning Oil

	#	PN
Partitioning Oil	2	2000190

Chromium
Recovery Agent

	#	PN
Recovery Agent	2	220016

Chromium
Next GEM
Chip K & Gaskets

	#	PN
Chromium Next GEM Chip K	2	2000182
Gasket, 2-pack	1	3000072

10xGenomics.com

10x GENOMICS

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

Dual Index Kit TN Set A, 96 rxns PN-1000250 (store at –20°C)

Dual Index Kit TN Set A

	#	PN
Dual Index Plate TN Set A	1	3000510

10x Genomics Accessories

Product	PN (Kit)	PN (Item)
10x Vortex Adapter	120251	330002
Chromium Next GEM Secondary Holder	1000195	3000332
10x Magnetic Separator	120250	230003

Recommended Thermal Cyclers

Thermal cyclers used must support uniform heating of 100 µl 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 5' 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	AM9937
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 Mini Centrifuge (alternatively, use any equivalent mini centrifuge)	10153-838 41428-958 76269-064
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

Choose either Eppendorf, USA Scientific or Thermo Fisher Scientific PCR 8-tube strips.

Additional Kits, Reagents & Equipment

The items in the table below have been validated by 10x Genomics and are highly recommended for the Single Cell 5' 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 D5000 ScreenTape High Sensitivity D5000 Reagents Choose Bioanalyzer, TapeStation or Qubit based on availability & preference.	G2943CA 5067-4626 G2991AA 5067-5592 5067-5593
Thermo Fisher Scientific	Qubit 4.0 Fluorometer Qubit dsDNA HS Assay Kit	Q33238 Q32854
KAPA Biosystems	KAPA Library Quantification Kit for Illumina Platforms	KK4824

Protocol Steps & Timing

	Steps		Timing	Stop & Store
3 h	**Cell Preparation and Labeling** Dependent on cell type and labeling protocol used		~1-2 h	
	Step 1 – GEM Generation & Barcoding			
	1.1	Prepare Reaction Mix	20 min	
	1.2	Load Chromium Next GEM Chip K	10 min	
	1.3	Run the Chromium Controller	18 min	
	1.4	Transfer GEMs	3 min	
	1.5	GEM-RT Incubation	55 min STOP	4°C ≤72 h or –20°C ≤1 week
6 h	**Step 2 – Post GEM RT Cleanup, cDNA Amplification & QC**			
	2.1	Post GEM-RT Cleanup – Dynabead	45 min	
	2.2	cDNA Amplification	50 min STOP	4°C ≤72 h or –20°C ≤1 week
	2.3	cDNA Cleanup		
		2.3A Pellet Cleanup	15 min STOP	4°C ≤72 h or –20°C ≤4 weeks
		2.3B Supernatant Cleanup	20 min STOP	4°C ≤72 h or –20°C ≤4 weeks
	2.4	cDNA Quantification & QC	50 min	
	Step 3 – V(D)J Amplification from cDNA			
	3.1	V(D)J Amplification 1	40 min STOP	4°C ≤72 h
	3.2	Post V(D)J Amplification 1 Double Sided Size Selection – SPRIselect	20 min STOP	4°C ≤72 h or –20°C ≤1 week
	3.3	V(D)J Amplification 2	40 min STOP	4°C ≤72 h
	3.4	Post V(D)J Amplification 2 Double Sided Size Selection – SPRIselect	30 min STOP	4°C ≤72 h or –20°C ≤1 week
	3.5	Post V(D)J Amplification QC & Quantification	50 min	
10 h plus* *Time dependent on Stop options used.	**Step 4 – V(D)J Library Construction**			
	4.1	Fragmentation, End Repair & A-tailing	45 min	
	4.2	Adaptor Ligation	25 min	
	4.3	Post Ligation Cleanup – SPRIselect	20 min	
	4.4	Sample Index PCR	40 min STOP	4°C ≤72 h
	4.5	Post Sample Index PCR Cleanup – SPRIselect	20 min STOP	4°C ≤72 h or –20°C long-term
	4.6	Post Library Construction QC	50 min	
	Step 5 – 5' Gene Expression (GEX) Library Construction			
	5.1	GEX Fragmentation, End Repair & A-tailing	45 min	
	5.2	GEX Post Fragmentation, End Repair & A-tailing Double Sided Size Selection – SPRIselect	30 min	
	5.3	GEX Adaptor Ligation	25 min	
	5.4	GEX Post Ligation Cleanup – SPRIselect	20 min	
	5.5	GEX Sample Index PCR	40 min STOP	4°C ≤72 h
	5.6	GEX Post Sample Index PCR Double Sided Cleanup – SPRIselect	30 min STOP	4°C ≤72 h or –20°C long-term
	5.7	GEX Post Library Construction QC	50 min	
	Step 6 – Cell Surface Protein/Immune Receptor Mapping Library Construction			
	6.1	Sample Index PCR	30 min	
	6.2	Post Sample Index PCR Size Selection – SPRIselect	20 min STOP	4°C ≤72 h or –20°C long-term
	6.3	Post Library Construction QC	50 min	

Stepwise Objectives

The Chromium Single Cell 5' v2 workflow with Feature Barcode technology offers a comprehensive, scalable approach to detect cell surface proteins and analyze antigen specificity along with the gene expression and immune repertoire information from the same single cell. This is accomplished by labeling cell surface proteins with antibodies or multimeric MHC peptide complexes, such as Dextramer reagents conjugated to a Feature Barcode oligonucleotide, followed by direct capture of the Feature Barcode by the Gel Bead primer. To profile the immune repertoire of cells, full-length (5' UTR to constant region), paired T-cell receptor (TCR) and/or B-cell receptor (BCR) transcripts from 500-10,000 individual cells per sample can be assessed.

A pool of ~750,000 barcodes are sampled separately to index each cell's transcriptome and antigen specificity. It is done by partitioning thousands of cells into nanoliter-scale Gel Beads-in-emulsion (GEMs), where all generated cDNA share a common 10x Barcode. Libraries are generated and sequenced and 10x Barcodes are used to associate individual reads back to the individual partitions.

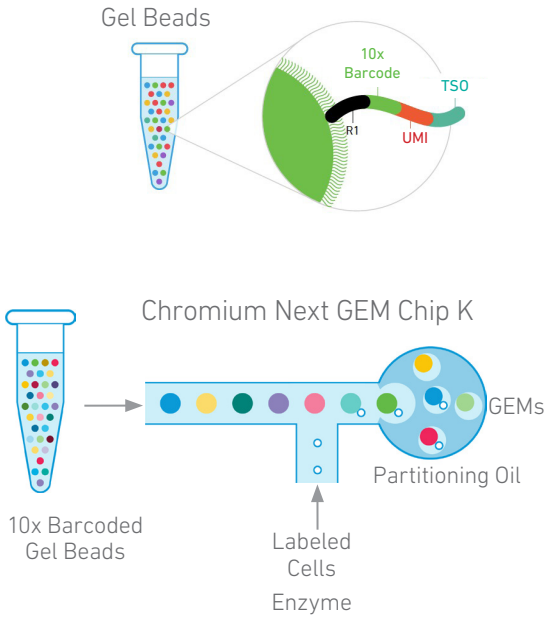
This document outlines the protocols to generate the following libraries:

- Single Cell V(D)J libraries from V(D)J-amplified cDNA derived from poly-adenylated mRNA
- Single Cell 5' Gene Expression libraries from amplified cDNA derived from poly-adenylated mRNA
- Single Cell 5' Cell Surface Protein libraries (include immune receptor mapping when cells are also labeled with multimeric MHC peptide complexes, such as Dextramer reagents) from amplified DNA derived from Feature Barcode

Step 1 GEM Generation & Barcoding

GEMs are generated by combining barcoded Single Cell VDJ 5' Gel Beads, a Master Mix with cell surface protein labeled cells, and Partitioning Oil onto Chromium Next GEM Chip K.

To achieve single cell resolution, cells are delivered at a limiting dilution, such that the majority (~90 – 99%) of generated GEMs contains no cell, while the remainder largely contain a single cell.



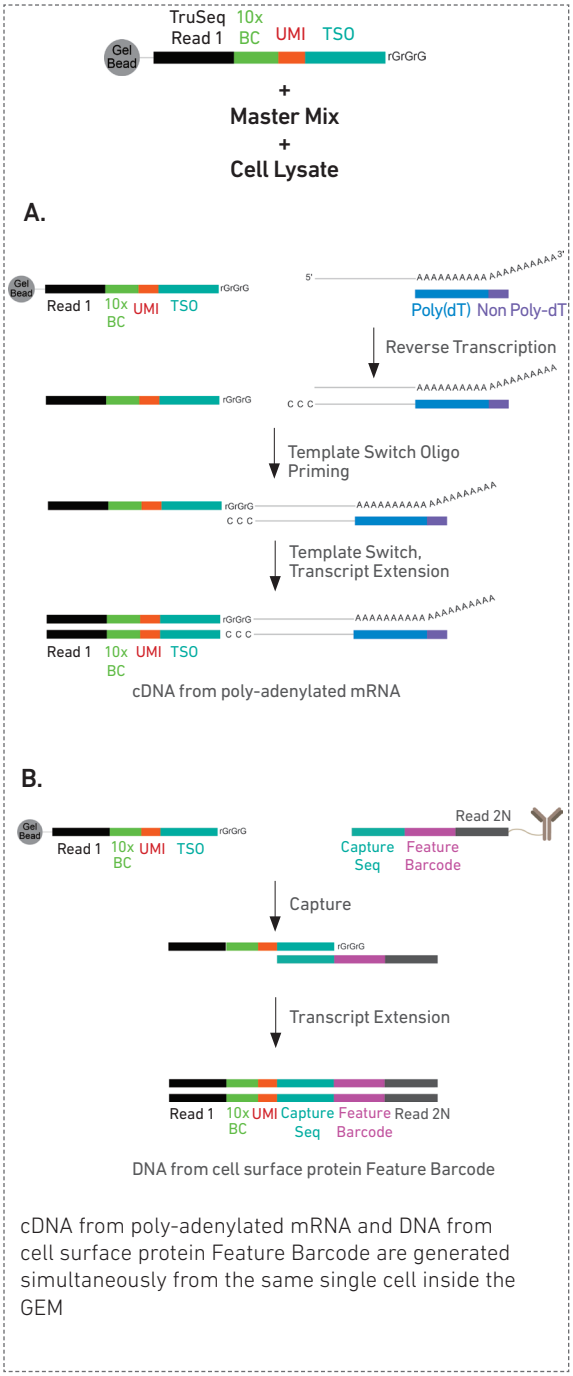
Step 1 GEM Generation & Barcoding

Immediately following GEM generation, the Gel Bead is dissolved and any co-partitioned cell is lysed. Gel Bead primers containing (i) an Illumina TruSeq Read 1 sequence (read 1 sequencing primer), (ii) a 16 nt 10x Barcode, (iii) a 10 nt unique molecular identifier (UMI), and (iv) 13 nt template switch oligo (TSO) are released and mixed with the cell lysate and a Master Mix containing reverse transcription (RT) reagents and poly(dT) primers.

A. The cell lysate and the released Gel Bead primer incubated with the Master Mix containing RT reagents, produce 10x Barcoded, full-length cDNA from poly-adenylated mRNA.

B. Simultaneously in the same partition, the Gel Bead primer captures the cell surface protein Feature Barcode conjugated to the antibody or to antibody and antigen containing (i) a Nextera Read 2 (Read 2N), (ii) a 15 nt Feature Barcode, and (iii) Capture Sequence. Incubation of the GEMs with the Master Mix containing RT reagents, produces 10x Barcoded, DNA from the cell surface protein Feature Barcode.

Inside individual GEMs



cDNA from poly-adenylated mRNA and DNA from cell surface protein Feature Barcode are generated simultaneously from the same single cell inside the GEM

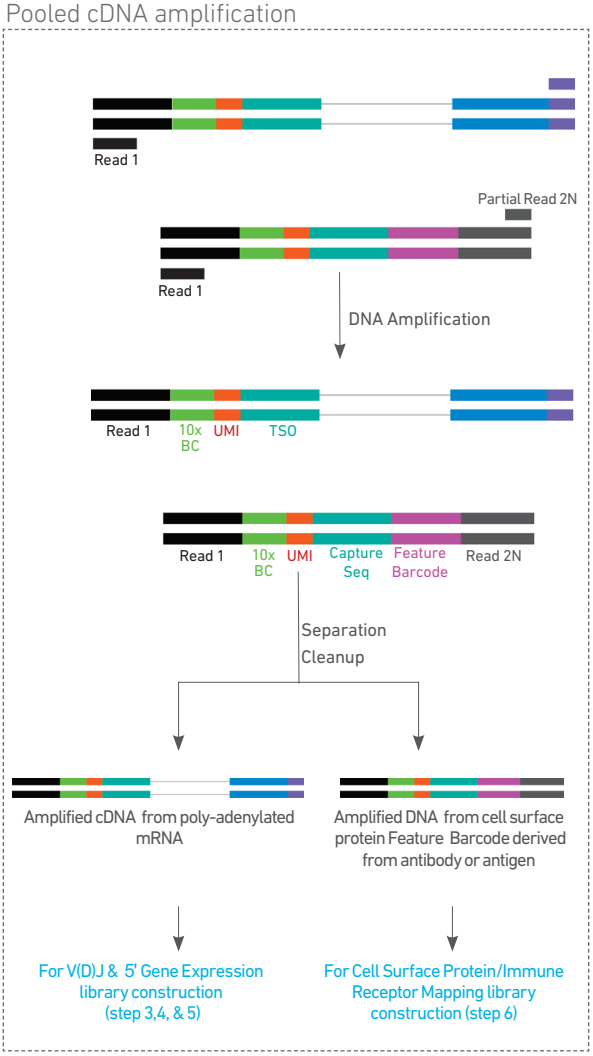
Step 2
Post GEM-RT Cleanup & cDNA Amplification

GEMs are broken and pooled after GEM-RT reaction mixtures are recovered. Silane magnetic beads are used to purify the 10x Barcoded first-strand cDNA from poly-adenylated mRNA and DNA from cell surface protein/antigen specificity Feature Barcode from the post GEM-RT reaction mixture, which includes leftover biochemical reagents and primers.

10x Barcoded, full-length cDNA from poly-adenylated mRNA and DNA from protein Feature Barcode are amplified. Amplification generates sufficient material to construct multiple libraries from the same cells, e.g. both T and/or B cell libraries (steps 3 and 4), 5' Gene Expression libraries (step 5), and Cell Surface Protein libraries (step 6).

The amplified cDNA from poly-adenylated mRNA and the amplified DNA from cell surface protein Feature Barcode are separated by size selection for generating V(D)J and/or 5' Gene Expression libraries and Cell Surface Protein libraries, respectively.

Pooled cDNA amplification



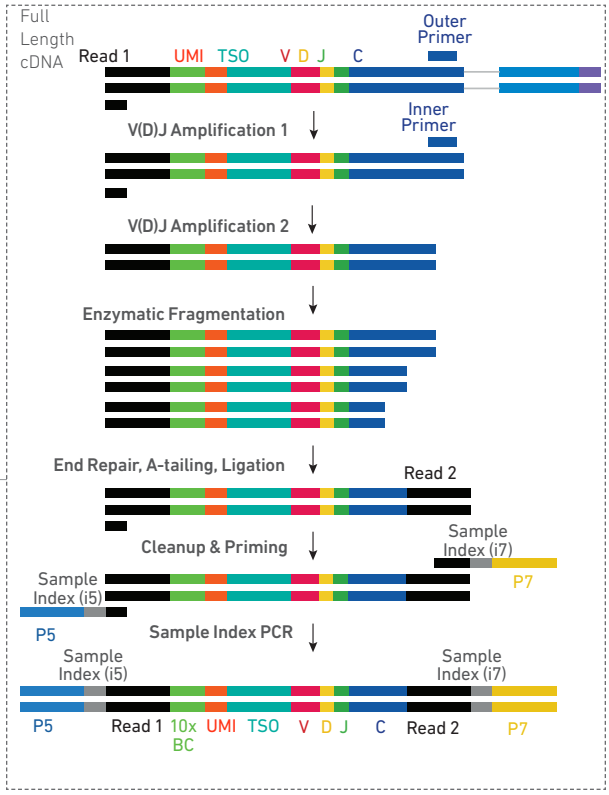
Step 3 V(D)J Amplification from cDNA

Amplified full-length cDNA from poly-adenylated mRNA is used to enrich full-length V(D)J segments (10x Barcoded) via PCR amplification with primers specific to either the TCR or BCR constant regions. If both T and B cells are expected to be present in the partitioned cell population, TCR and BCR transcripts can be amplified in separate reactions from the same amplified cDNA material.

Step 4 V(D)J Library Construction

Enzymatic fragmentation and size selection are used to generate variable length fragments that collectively span the V(D)J segments of the amplified TCR or BCR transcripts prior to library construction.

Pooled amplified cDNA processed in bulk

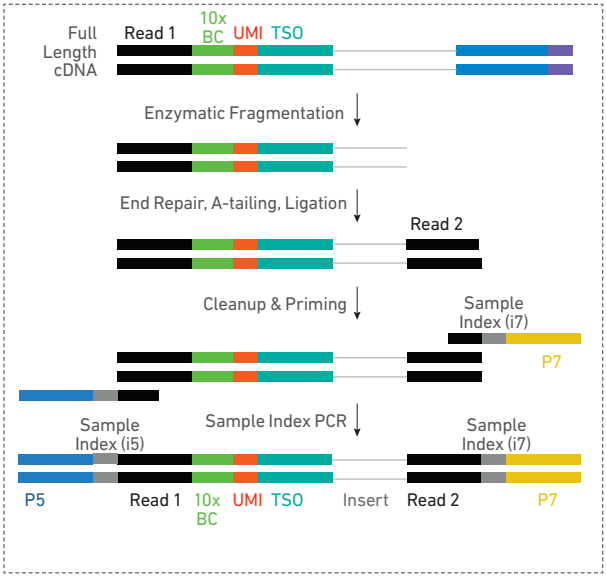


P5, P7, i5 and i7 sample indexes, and an Illumina R2 sequence (read 2 primer sequence) are added via End Repair, A-tailing, Adaptor Ligation, and Sample Index PCR. The final libraries contain the P5 and P7 priming sites used in Illumina sequencing.

Step 5 5' Gene Expression (GEX) Library Construction

Amplified full-length cDNA from poly-adenylated mRNA is used to generate 5' Gene Expression library. Enzymatic fragmentation and size selection are used to optimize the cDNA amplicon size prior to 5' gene expression library construction. P5, P7, i5 and i7 sample indexes, and Illumina R2 sequence (read 2 primer sequence) are added via End Repair, A-tailing, Adaptor Ligation, and Sample Index PCR. The final libraries contain the P5 and P7 priming sites used in Illumina sequencers.

Pooled amplified cDNA processed in bulk

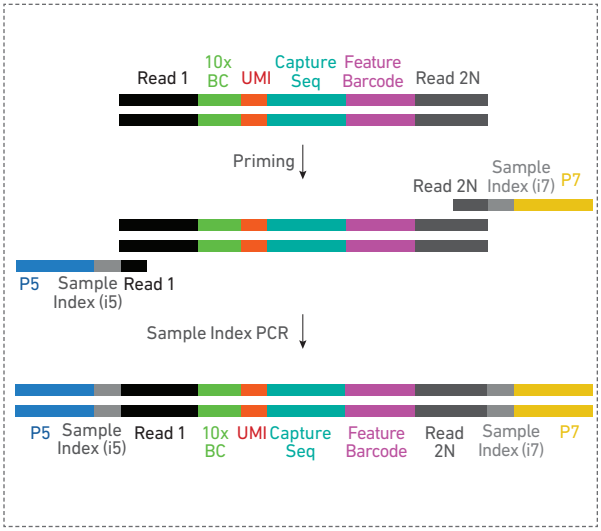


Step 6 Cell Surface Protein/ Immune Receptor Mapping Library Construction

Amplified DNA from the cell surface protein Feature Barcodes derived from the antibody or antibody and multimeric MHC peptide complexes, such as Dextramer reagents is used to construct the Cell Surface Protein library. A Cell Surface Protein library also detects antigen specificity if cells were labeled with both antibody and antigen.

P5, P7, i5 and i7 sample indexes, and Nextera Read 2 (Read 2N primer sequence) are added via Sample Index PCR.

Pooled amplified DNA processed in bulk

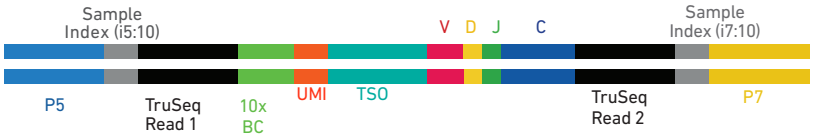


The final libraries contain the P5 and P7 priming sites used in Illumina sequencers.

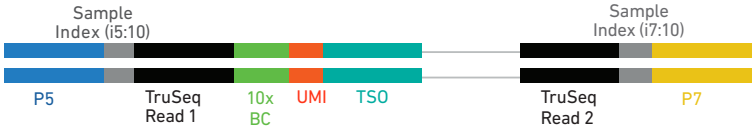
Step 7 Sequencing

Illumina-ready dual index libraries can be sequenced at the recommended depth & run parameters. Illumina sequencer compatibility, sample indices, library loading and pooling for sequencing are summarized in step 7.

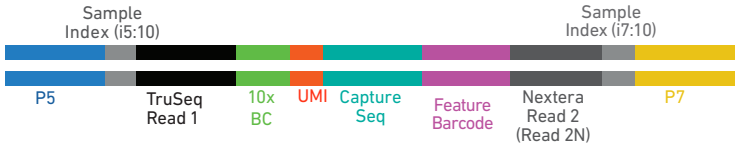
Chromium Single Cell V(D)J Dual Index Library



Chromium Single Cell 5' Gene Expression Dual Index Library



Chromium Single Cell 5' Cell Surface Protein Dual Index Library*



*Detects antigen specificity in cells labeled with antibodies and antigen

See Appendix for Oligonucleotide Sequences

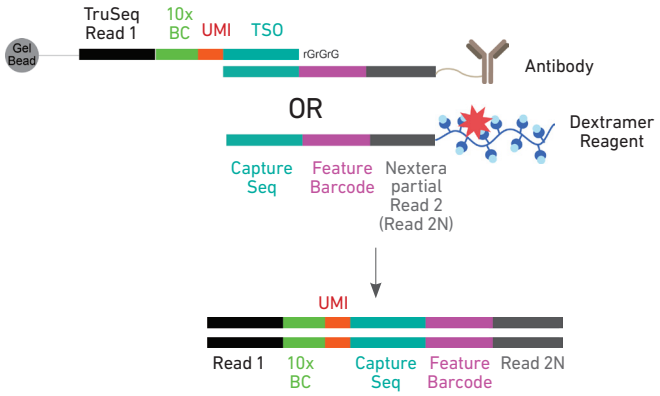
Cell Labeling Guidelines

Overview

Protein/s on the surface of a cell can be labeled with:

- a Feature Barcode oligonucleotide conjugated to a specific protein binding molecule, such as an antibody for detecting cell surface protein expression
- a Feature Barcode oligonucleotide conjugated to an MHC peptide, such as a dCODE Dextramer along with the Feature Barcode oligonucleotide conjugated antibody for mapping immune receptors

The Feature Barcode conjugated molecule bound to the cell surface protein can be directly captured by the Gel Bead inside a GEM during GEM generation and amplified (see Stepwise Objectives for assay scheme specifics). The amplified DNA generated from the Feature Barcode can be used for Cell Surface Protein/Immune Receptor Mapping Library Construction.



DNA from cell surface protein Feature Barcode

Demonstrated Protocols for cell labeling

- Demonstrated Protocol Cell Surface Protein Labeling for Single Cell RNA Sequencing Protocols with Feature Barcode technology (Document CG000149).
- Demonstrated Protocol Cell Labeling with Dextramer Reagents for Single Cell RNA Sequencing Protocols with Feature Barcode technology (Document CG000203).

Cell Surface Protein Library:

Amplified DNA from the cell surface protein Feature Barcode derived from the antibody or antibody and antigen is used to construct the Cell Surface Protein library. If cells were labeled with both antibody and antigen, the cell surface protein library will also map immune receptor.

Failure to label cell surface proteins with a Feature Barcode conjugated to a specific protein binding molecule prior to using the cells for GEM Generation & Barcoding will preclude generation of Cell Surface Protein library.

Tips & Best Practices

Icons

Tips & Best Practices section includes additional guidance

Signifies critical step requiring accurate execution

Troubleshooting section includes additional guidance

Version Specific Update

Indicates version specific updates in a particular protocol step to inform users who have used a previous version of the product. The updates may be in volume, temperature, calculation instructions etc.

Emulsion-safe Plastics

- Use validated emulsion-safe plastic consumables when handling GEMs as some plastics can destabilize GEMs.

Cell Concentration

- Recommended starting point is to load ~1700 cells per reaction, resulting in recovery of ~1000 cells, and a multiplet rate of ~0.8%. The optimal input cell concentration is 700-1,200 cells/µl.
- 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.
- Refer to the 10x Genomics Support website for more information regarding cell type specific sample preparation, for example, the Demonstrated Protocol for Enrichment of CD3+ T Cells from Dissociated Tissues for Single Cell RNA Sequencing and Immune Repertoire Profiling (Document CG000123).

Multiplet Rate (%)	# of Cells Loaded	# of Cells Recovered
~0.4%	~870	~500
~0.8%	~1,700	~1,000
~1.6%	~3,500	~2,000
~2.3%	~5,300	~3,000
~3.1%	~7,000	~4,000
~3.9%	~8,700	~5,000
~4.6%	~10,500	~6,000
~5.4%	~12,200	~7,000
~6.1%	~14,000	~8,000
~6.9%	~15,700	~9,000
~7.6%	~17,400	~10,000

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 after use.
- 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

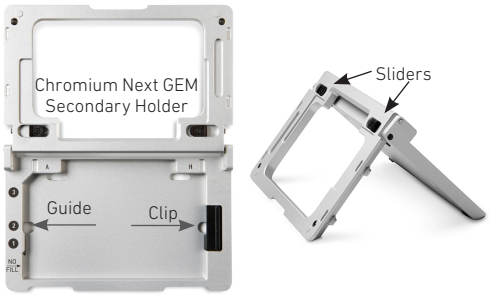
- Follow manufacturer's calibration and maintenance schedules.
- Pipette accuracy is particularly important when using SPRIselect reagents.

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

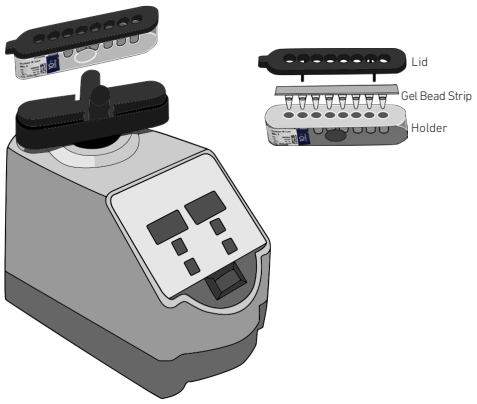
- Align notch on the chip (upper left corner) and the holder.
- Insert the left-hand side of the chip under the guide. Depress the right-hand side of the chip until the spring-loaded clip engages.
- Close the lid before dispensing reagents into the wells.

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 K 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.



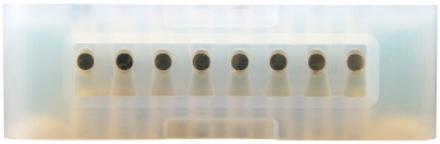
- Snap the tube strip holder with the Gel Bead strip into a 10x Vortex Adapter. Vortex **30 sec**.
- Centrifuge the Gel Bead strip for ~**5 sec** after removing from the holder. Confirm there are no bubbles at the bottom of the tubes and the liquid levels look even. Place the Gel Bead strip back in the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

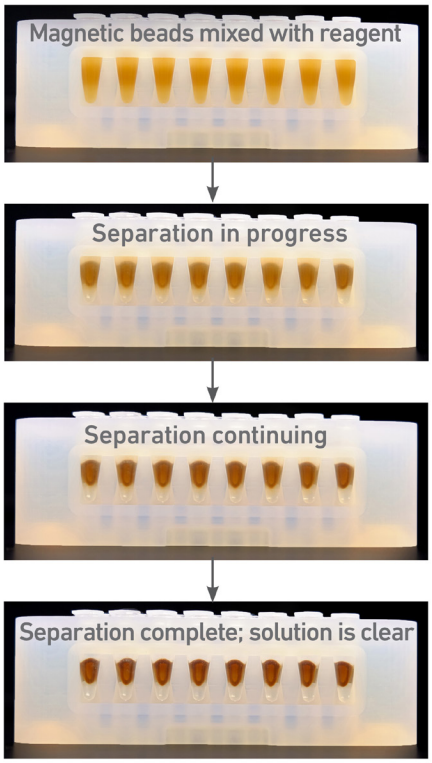
10x Magnetic Separator

- 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 need for the solution to clear may vary based on specific step, reagents, volume of reagents used etc.



SPRIselect Cleanup & Size Selection

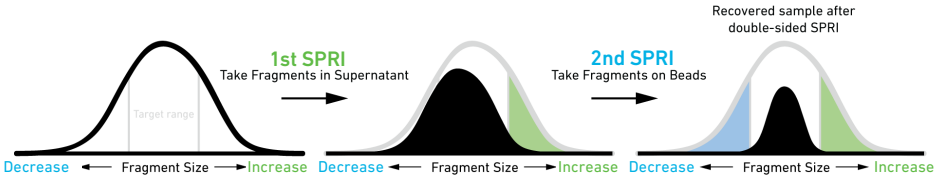
- After aspirating the desired volume of SPRIselect reagent, examine the pipette tips before dispensing to ensure the correct volume is transferred.
- Pipette mix thoroughly as insufficient mixing of sample and SPRIselect reagent will lead to inconsistent results.
- Use fresh preparations of 80% Ethanol.

Tutorial — SPRIselect Reagent : DNA Sample Ratios

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

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

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**).

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

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

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

cDNA Amplification PCR Cycle Numbers

- Follow cycle number recommendations for high and low RNA content cells based on Targeted Cell Recovery and cell sample.

Recommended starting point for cycle number optimization.

Targeted Cell Recovery	Low RNA Content Cells e.g., Primary Cells Total Cycles	High RNA Content Cells e.g., Cell Lines Total Cycles
500-2,000	16	14
2,001-6,000	14	12
6,001-10,000	13	11

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.
- Each well in the Dual Index Plate contains a unique i7 and a unique i5 oligonucleotide.
- Use **ONLY** Dual Index Plate TT, Set A for V(D)J and 5' Gene Expression libraries. Use **ONLY** Dual Index Plate TN, Set A for Cell Surface Protein library.
- Consider sample index compatibility when pooling different libraries; a unique sample index for each of the pooled libraries is required.
- The sample indices of Dual Index Plate TT, Set A are unique from those of Dual Index Plate TN, Set A. Therefore, respective libraries from the two plates may be pooled.

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 Master Mix

1.2 Load Chromium Next GEM Chip K

1.3 Run the Chromium Controller

1.4 Transfer GEMs

1.5 GEM-RT Incubation

1.0 GEM Generation & Barcoding

VERSION SPECIFIC

GET STARTED!				
	Item	10x PN	Preparation & Handling	Storage
Equilibrate to Room Temperature				
☐	**Single Cell VDJ 5' Gel Bead**	1000264/ 1000267	Equilibrate to room temperature 30 min before loading the chip.	–80°C
☐	**RT Reagent B**	2000165	Vortex, verify no precipitate, centrifuge briefly.	–20°C
☐	**Poly-dT RT Primer**	2000007	Vortex, verify no precipitate, centrifuge briefly.	–20°C
☐	**Reducing Agent B**	2000087	Vortex, verify no precipitate, centrifuge briefly.	–20°C
Place on ice				
☐	**RT Enzyme C**	2000085/ 2000102	Centrifuge briefly before adding to the mix.	–20°C
☐	**Labeled Cells** Refer to Demonstrated Protocols for Cell Surface Protein Labeling (CG000149, CG000203).			
Obtain				
☐	**Partitioning Oil**	2000190	-	Ambient
☐	**Chromium Next GEM Chip K** Verify name & PN	2000182	-	Ambient
☐	**10x Gasket**	370017/ 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** If using <8 reactions	-	See Tips & Best Practices.	-

Firmware Version 4.0 or higher is required in the Chromium Controller or the Chromium Single Cell Controller used for the Single Cell 5' v2 protocol.

1.1 Prepare Reaction Mix

VERSION SPECIFIC

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

Master Mix *Add reagents in the order listed*	PN	1X (µl)	4X + 10% (µl)	8X + 10% (µl)
● **RT Reagent B**	2000165	18.8	82.7	165.4
● **Poly-dT RT Primer**	2000007	7.3	32.1	64.2
○ **Reducing Agent B**	2000087	1.9	8.4	16.7
● **RT Enzyme C**	2000085/ 2000102	8.3	36.5	73.0
Total	-	**36.3**	**159.7**	**319.3**

b. Add **36.3 µl** Master Mix into each tube of a PCR 8-tube strip on ice.

Assemble Chromium Next GEM Chip

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

TIPS 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 Suspension Volume Calculator Table

(for step 1.2 of Chromium Next GEM Single Cell 5' v2 (Dual Index) protocol)

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

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										
	500	1000	2000	3000	4000	5000	6000	7000	8000	9000	10000
100	8.3 30.4	16.5 22.2	33.0 5.7	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
200	4.1 34.6	8.3 30.4	16.5 22.2	24.8 13.9	33.0 5.7	n/a	n/a	n/a	n/a	n/a	n/a
300	2.8 35.9	5.5 33.2	11.0 27.7	16.5 22.2	22.0 16.7	27.5 11.2	33.0 5.7	n/a	n/a	n/a	n/a
400	2.1 36.6	4.1 34.6	8.3 30.5	12.4 26.3	16.5 22.2	20.6 18.1	24.8 13.9	28.9 9.8	33.0 5.7	n/a	n/a
500	1.7 37.0	3.3 35.4	6.6 32.1	9.9 28.8	13.2 25.5	16.5 22.2	19.8 18.9	23.1 15.6	26.4 12.3	29.7 9.0	33.0 5.7
600	1.4 37.3	2.8 35.9	5.5 33.2	8.3 30.5	11.0 27.7	13.8 24.9	16.5 22.2	19.3 19.4	22.0 16.7	24.8 13.9	27.5 11.2
700	1.2 37.5	2.4 36.3	4.7 34.0	7.1 31.6	9.4 29.3	11.8 26.9	14.1 24.6	16.5 22.2	18.9 19.8	21.2 17.5	23.6 15.1
800	1.0 37.7	2.1 36.6	4.1 34.6	6.2 32.5	8.3 30.4	10.3 28.4	12.4 26.3	14.4 24.3	16.5 22.2	18.6 20.1	20.6 18.1
900	0.9 37.8	1.8 36.9	3.7 35.0	5.5 33.2	7.3 31.4	9.2 29.5	11.0 27.7	12.8 25.9	14.7 24.0	16.5 22.2	18.3 20.4
1000	0.8 37.9	1.7 37.0	3.3 35.4	5.0 33.7	6.6 32.1	8.3 30.4	9.9 28.8	11.6 27.1	13.2 25.5	14.9 23.8	16.5 22.2
1100	0.8 37.9	1.5 37.2	3.0 35.7	4.5 34.2	6.0 32.7	7.5 31.2	9.0 29.7	10.5 28.2	12.0 26.7	13.5 25.2	15.0 23.7
1200	0.7 38.0	1.4 37.3	2.8 35.9	4.1 34.6	5.5 33.2	6.9 31.8	8.3 30.4	9.6 29.1	11.0 27.7	12.4 26.3	13.8 24.9
1300	0.6 38.1	1.3 37.4	2.5 36.2	3.8 34.9	5.1 33.6	6.3 32.4	7.6 31.1	8.9 29.8	10.2 28.5	11.4 27.3	12.7 26.0
1400	0.6 38.1	1.2 37.5	2.4 36.3	3.5 35.2	4.7 34.0	5.9 32.8	7.1 31.6	8.3 30.4	9.4 29.3	10.6 28.1	11.8 26.9
1500	0.6 38.1	1.1 37.6	2.2 36.5	3.3 35.4	4.4 34.3	5.5 33.2	6.6 32.1	7.7 31.0	8.8 29.9	9.9 28.8	11.0 27.7
1600	0.5 38.2	1.0 37.7	2.1 36.6	3.1 35.6	4.1 34.6	5.2 33.5	6.2 32.5	7.2 31.5	8.3 30.4	9.3 29.4	10.3 28.4
1700	0.5 38.2	1.0 37.7	1.9 36.8	2.9 35.8	3.9 34.8	4.9 33.8	5.8 32.9	6.8 31.9	7.8 30.9	8.7 30.0	9.7 29.0
1800	0.5 38.2	0.9 37.8	1.8 36.9	2.8 35.9	3.7 35.0	4.6 34.1	5.5 33.2	6.4 32.3	7.3 31.4	8.3 30.5	9.2 29.5
1900	0.4 38.3	0.9 37.8	1.7 37.0	2.6 36.1	3.5 35.2	4.3 34.4	5.2 33.5	6.1 32.6	6.9 31.8	7.8 30.9	8.7 30.0
2000	0.4 38.3	0.8 37.9	1.7 37.0	2.5 36.2	3.3 35.4	4.1 34.6	5.0 33.7	5.8 32.9	6.6 32.1	7.4 31.3	8.3 30.4

Grey boxes: Volumes that would exceed the allowable water volume in each reaction

Yellow boxes: Indicate a low transfer volume that may result in higher cell load variability

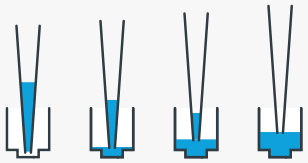
Blue boxes: Optimal range of cell stock concentration to maximize the likelihood of achieving the desired cell recovery target

1.2 Load Chromium Next GEM Chip K

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)

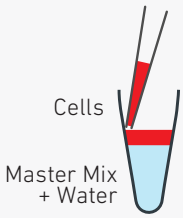
- **45 µl** in each unused well in row labeled **3**
- **50 µl** in each unused well in row labeled **2**
- **70 µl** in each unused well in row labeled **1**

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

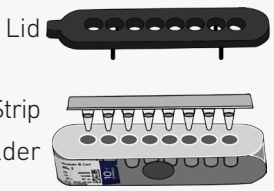
- Gently pipette mix the Master Mix + Cell Suspension
- Using the same pipette tip, dispense **70 µl** Master Mix + Cell Suspension into the bottom center of each well in **row labeled 1** without introducing bubbles.

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.

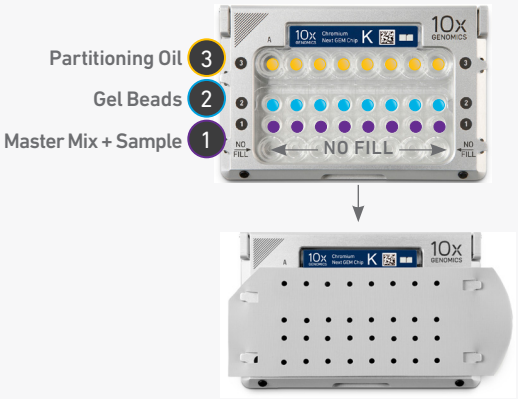
Partitioning Oil

g. Attach 10x 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.

10x Gasket



Keep horizontal to avoid wetting the gasket. DO NOT press down on the gasket.

1.3 Run the Chromium Controller

Next GEM

a. Press the eject button on the Controller to eject the tray.

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. Confirm the Chromium Chip K program on screen. Press the play button.

d. 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 the Single Cell 5' v2 protocol.

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 pipette 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.

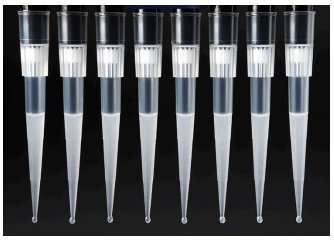
g. Over the course of **~20 sec**, dispense GEMs into the tube strip on ice with the pipette tips against the sidewalls of the tubes.

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

STOP

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

2.1 cDNA QC & Amplification

2.0 Post GEM-RT Cleanup & cDNA Amplification

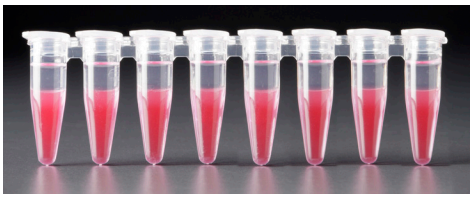
VERSION SPECIFIC

GET STARTED!			
Item	**10x PN**	**Preparation & Handling**	**Storage**
Equilibrate to Room Temperature			
☐ ◯ **Reducing Agent B**	2000087	Thaw, vortex, verify no precipitate, centrifuge briefly.	–20°C
☐ **Feature cDNA Primers 4**	2000277	Thaw, vortex, centrifuge briefly.	–20°C
☐ **Dynabeads MyOne SILANE**	2000048	Vortex thoroughly (≥30 sec) **immediately** before adding to the mix. If still clumpy, pipette mix to resuspend completely. DO NOT centrifuge before use.	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 quantification	-	Manufacturer's recommendations.	-
Place on ice			
☐ ◯ **Amp Mix**	2000047/ 2000103	Vortex, centrifuge briefly.	–20°C
Thaw at 65°C			
☐ **Cleanup Buffer**	2000088	Thaw for 10 min at 65°C at max speed on a thermomixer. Verify there are no visible crystals. Cool to room temperature.	–20°C
Obtain			
☐ ◯ **Recovery Agent**	220016	-	Ambient
☐ **Qiagen Buffer EB**	-	Manufacturer's recommendations.	Ambient
☐ **Bio-Rad 10% Tween 20**	-	Manufacturer's recommendations.	-
☐ **10x Magnetic Separator**	230003	-	Ambient
☐ **Prepare 80% Ethanol** Prepare 15 ml for 8 reactions	-	Prepare fresh.	Ambient

2.1 Post GEM-RT Cleanup – Dynabeads

a. Add **125 µl** Recovery Agent to each sample (post GEM-RT incubation) at room temperature. DO NOT pipette mix or vortex the biphasic mixture. Wait **2 min**.

Biphasic Mixture

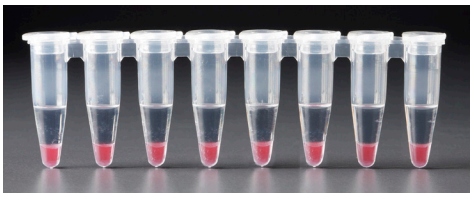


The resulting biphasic mixture contains Recovery Agent/Partitioning Oil (pink) and aqueous phase (clear), with no persisting emulsion (opaque).

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.

Remove Recovery Agent



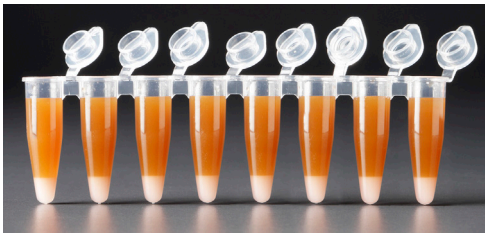
b. Slowly remove and discard **125 µl** Recovery Agent/Partitioning Oil (pink) from the bottom of the tube. DO NOT aspirate any aqueous sample.

c. Prepare Dynabeads Cleanup Mix.

Dynabeads Cleanup Mix *Add reagents in the order listed*	PN	1X (µl)	4X + 10% (µl)	8X + 10% (µl)
Nuclease-free Water		5	22	44
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
Total	-	**200**	**880**	**1760**

Resuspend clump

Add Dynabeads Cleanup Mix



d. Vortex and add **200 µl** to each sample. Pipette mix 5x (pipette set to 200 µl).

e. Incubate **10 min** at **room temperature** (keep caps open).

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

	Elution Solution I *Add reagents in the order listed*	PN	1X (µl)	10X (µl)
	Buffer EB	-	98	980
	10% Tween 20	-	1	10
◯	**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.

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 10x Magnetic Separator•**Low position** (magnet•**Low)**.

n. Remove remaining ethanol. Air dry for **2 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. Pipette mix 15x. If beads still appear clumpy, continue pipette mixing until fully resuspended.

q. Incubate **1 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

VERSION SPECIFIC

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

cDNA Amplification Mix *Add reagents in the order listed*	PN	1X (µl)	4X + 10% (µl)	8X + 10% (µl)
◯ **Amp Mix**	2000047/ 2000103	50	220	440
● **Feature cDNA Primers 4** Verify name & PN	2000277	15	66	132
Total	-	**65**	**286**	**572**

b. Add **65 µl** cDNA Amplification Mix to **35 µl** sample (Post GEM-RT Cleanup, step 2.1s).

c. Pipette mix 5x (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	~25-50 min
Step	**Temperature**	**Time**
1	98°C	00:00:45
2	98°C	00:00:20
3	63°C	00:00:30
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	Low RNA Content Cells e.g., Primary Cells Total Cycles	High RNA Content Cells e.g., Cell Lines Total Cycles
500-2,000	16	14
2,001-6,000	14	12
6,001-10,000	13	11

TIPS

The optimal number of cycles is a trade-off between generating sufficient final mass for library construction and minimizing PCR amplification artifacts.

STOP

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

Step Overview (steps 2.2 & 2.3)

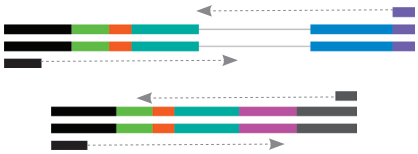
VERSION SPECIFIC

Amplification Products generated in Step 2.2 – cDNA Amplification

Post GEM-RT Cleanup Products

+

Feature cDNA Primers 4
PN-2000277



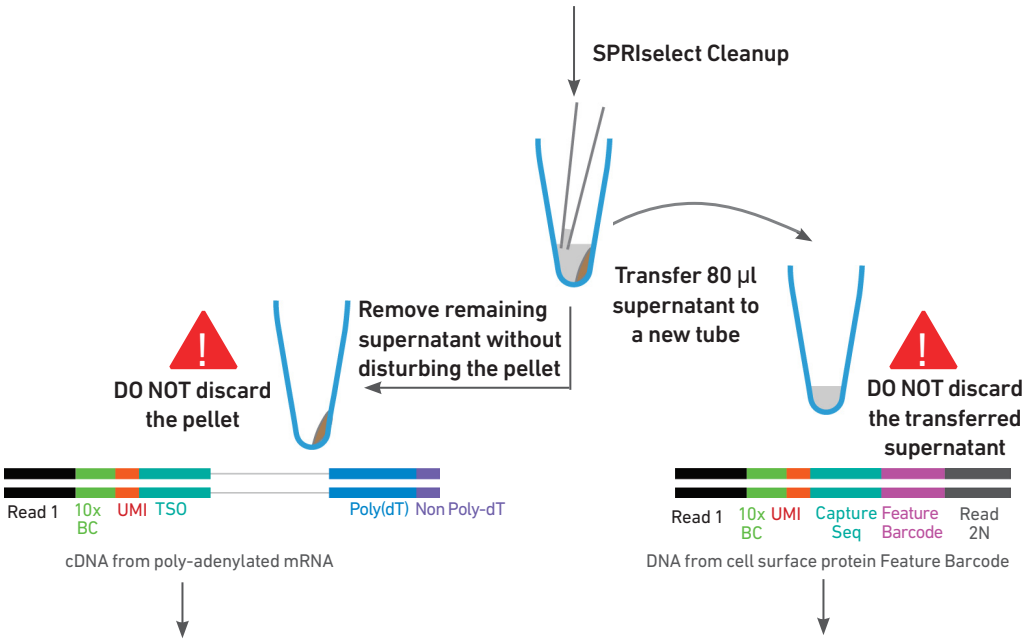
DNA Amplification

Amplification Products

cDNA from poly-adenylated mRNA

DNA from cell surface protein Feature Barcode

Step 2.3 – cDNA Cleanup – SPRIselect Overview



2.3A – Pellet Cleanup

(for V(D)J & 5' Gene Expression library)

2.3B – Supernatant Cleanup

(for Cell Surface Protein/Immune Receptor Mapping Library)

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 140 µl).

b. Incubate **5 min** at **room temperature**.

c. Place on the magnet•**High** until the solution clears.

d. Transfer and save **80 µl** supernatant in a new tube strip without disturbing the pellet. Maintain at **room temperature**. DO NOT discard the transferred supernatant (cleanup for Cell Surface Protein library construction).

e. Remove the remaining supernatant from the pellet without disturbing the pellet. DO NOT discard the pellet (cleanup for V(D)J and 5' Gene Expression library construction). **Immediately** proceed to Pellet Cleanup (step 2.3A).

2.3A Pellet Cleanup
(for V(D)J & 5' Gene Expression library)

i. Add **200 µl** 80% ethanol to the pellet while still on magnet•**High**. Wait **30 sec**.

ii. Remove the ethanol.

iii. **Repeat** steps i and ii for a total of 2 washes.

iv. Centrifuge briefly and place on the magnet•**Low**.

v. Remove any remaining ethanol. Air dry for **2 min**. DO NOT exceed **2 min** as this will decrease elution efficiency.

vi. Remove from the magnet. Add **45.5 µl** Buffer EB. Pipette mix 15x.

vii. Incubate **2 min** at **room temperature**.

viii. Place the tube strip on the magnet•**High** until the solution clears.

ix. Transfer **45 µl** sample to a new tube strip.

x. STOP Store at **4°C** for up to **72 h** or at **–20°C** for up to **4 weeks**, or proceed to **step 2.4** for cDNA QC & Quantification.

2.3B Transferred Supernatant Cleanup
(for Cell Surface Protein/Immune Receptor Mapping library)

i. Vortex to resuspend the SPRIselect reagent. Add **70 µl** SPRIselect reagent **(2.0X)** to **80 µl** of the transferred supernatant and pipette mix 15x (pipette set to 150 µl).

ii. Incubate for **5 min** at **room temperature**.

iii. Place on the magnet•**High** until the solution clears.

iv. Remove the supernatant.

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

vi. Remove the ethanol.

vii. **Repeat** steps v and vi for a total of 2 washes.

viii. Centrifuge briefly and place on the magnet•**Low**.

ix. Remove any remaining ethanol. Air dry for **2 min**. DO NOT exceed **2 min** as this will decrease elution efficiency.

x. Remove from the magnet. Add **45.5 µl** Buffer EB. Pipette mix 15x.

xi. Incubate **2 min** at **room temperature**.

xii. Place the tube strip on the magnet•**High** until the solution clears.

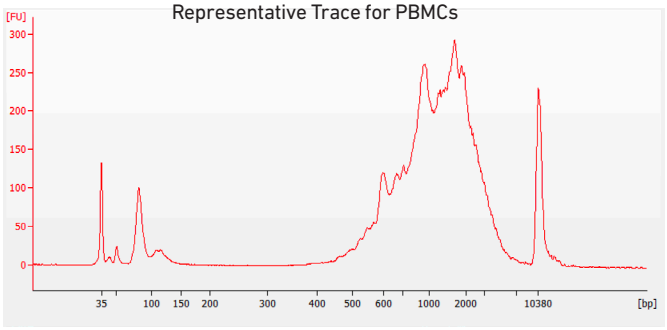
xiii. Transfer **45 µl** sample to a new tube strip.

xiv STOP Store at **4°C** for up to **72 h** or at **–20°C** for up to **4 weeks**, or proceed directly to **step 6** for Cell Surface Protein/Immune Receptor Mapping Library.

2.4 cDNA QC & Quantification

a. Run **1 µl** undiluted sample from the Pellet Cleanup step 2.3A-x (Dilution Factor 1) on an Agilent Bioanalyzer High Sensitivity chip.

Run 1 µl undiluted product for input cells with low RNA content (<1pg total RNA/cell), and 1 µl of 1:10 diluted product for input cells with high RNA content.



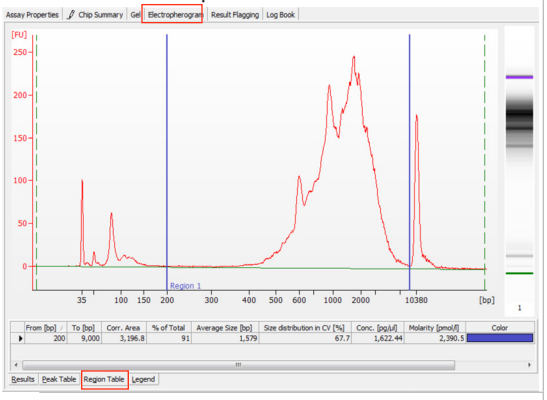
For 5' Gene Expression Library Construction proceed directly to step 5 after step 2.4.

b. If proceeding to 5' GEX Library Construction (step 5), determine cDNA yield for each sample. Example calculation below.

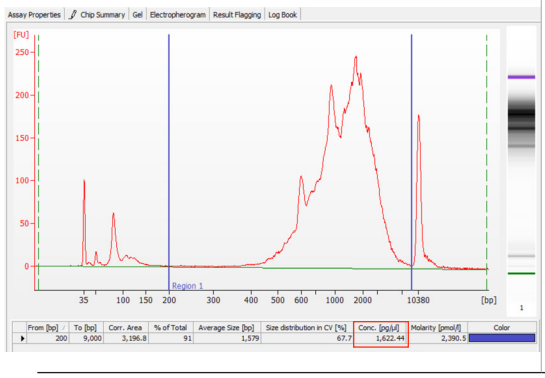
EXAMPLE CALCULATION

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

Concentration: 1622.44 pg/µl
Dilution Factor: 1

cDNA Conc. =

$$\frac{\text{Conc. (pg/µl)} \times \text{Dilution Factor}}{1000\ \text{(pg/ng)}} = \frac{1622.44 \times 1}{1000} = \textbf{1.6 ng/µl}$$

Example Calculation for Carrying Forward 50 ng Sample for 5' GEX Library Construction

Volume for 50 ng = $\frac{50\ \text{ng}}{1.6\ \text{(ng/µl)}} =$ **31.25 µl**

- If the volume required for 50 ng is less than 20 µl, adjust the total volume of each sample to 20 µl with nuclease-free water.
- If the volume for 50 ng exceeds 20 µl (as in above example), carry ONLY 20 µl sample into library construction.

Sample volume for library construction = **20 µl**

If <50 ng available, carry forward 20 µl sample (2-50 ng) into 5' GEX Library Construction.

DO NOT exceed a mass of 50 ng in the 20 µl carry forward volume.

Alternate Quantification Methods (See Appendix for representative traces)

- Agilent TapeStation.
- LabChip
- Qubit Fluorometer and Qubit dsDNA HS Assay Kit.

Step 3

V(D)J Amplification from cDNA

3.1 V(D)J Amplification 1

3.2 Post V(D)J Amplification 1 Cleanup – Double Sided Size Selection – SPRIselect

3.3 V(D)J Amplification 2

3.4 Post V(D)J Amplification 2 Cleanup – Double Sided Size Selection – SPRIselect

3.5 Post V(D)J Amplification QC & Quantification

3.0 V(D)J Amplification from cDNA

VERSION SPECIFIC

GET STARTED!			
Item	**10x PN**	**Preparation & Handling**	**Storage**
Equilibrate to Room Temperature			
For Human Samples (Choose B or T-cell primers based on desired amplification products)			
☐ **Human T Cell Mix 1 v2**	2000242	Thaw, vortex, centrifuge briefly.	–20°C
☐ **Human T Cell Mix 2 v2**	2000246	Thaw, vortex, centrifuge briefly	–20°C
☐ **Human B Cell Mix 1 v2**	2000254	Thaw, vortex, centrifuge briefly	–20°C
☐ **Human B Cell Mix 2 v2**	2000255	Thaw, vortex, centrifuge briefly	–20°C
For Mouse Samples (Choose B or T-cell primers based on desired amplification products)			
☐ **Mouse T Cell Mix 1 v2**	2000256	Thaw, vortex, centrifuge briefly	–20°C
☐ **Mouse T Cell Mix 2 v2**	2000257	Thaw, vortex, centrifuge briefly	–20°C
☐ **Mouse B Cell Mix 1 v2**	2000258	Thaw, vortex, centrifuge briefly	–20°C
☐ **Mouse B Cell Mix 2 v2**	2000259	Thaw, vortex, centrifuge briefly	–20°C
For all Samples			
☐ **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 quantification	-	Manufacturer's recommendations.	-
Place on ice			
☐ **Amp Mix**	2000047/ 2000103	Vortex, centrifuge briefly.	–20°C
Obtain			
☐ **Qiagen Buffer EB**	-	Manufacturer's recommendations.	Ambient
☐ **10x Magnetic Separator**	230003	-	Ambient
☐ **Prepare 80% Ethanol** Prepare 15 ml for 8 reactions	-	Prepare fresh.	Ambient

3.1 V(D)J Amplification 1

VERSION SPECIFIC

a. Place a tube strip on ice and transfer **2 µl** sample (post cDNA Amplification & QC, step 2.3A) to the same tube.

b. Prepare V(D)J Amplification 1 Reaction Mix on ice. Vortex and centrifuge briefly.

V(D)J Amplification 1 Reaction Mix *Add reagents in the order listed*	PN	1X (µl)	4X + 10% (µl)	8X + 10% (µl)
◯ **Amp Mix**	2000047/ 2000103	50	220	440
● **T Cell Mix 1 v2** **or** ● **B Cell Mix 1 v2**	Human 2000242/ Mouse 2000256 or Human 2000254/ Mouse 2000258	48	211.2	422.4
Total	-	**98**	**431.2**	**862.4**

c. Add **98 µl** V(D)J Amplification 1 Reaction Mix to each tube containing **2 µl** sample.

d. Pipette mix 5x (pipette set to 90 µl). Centrifuge briefly.

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

Lid Temperature	Reaction Volume	Run Time
105°C	100 µl	~20-30 min
Step	**Temperature**	**Time**
1	98°C	00:00:45
2	98°C	00:00:20
3	62°C	00:00:30
4	72°C	00:01:00
5 Different cycle numbers for T & B cells	T Cell: Go to Step 2, 11x (total 12 cycles) B Cell Go to Step 2, 7x (total 8 cycles)	
6	72°C	00:01:00
7	4°C	Hold

STOP

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

3.2 Post V(D)J Amplification 1 Cleanup Double Sided Size Selection – SPRIselect

VERSION SPECIFIC

a. Vortex to resuspend the SPRIselect reagent. Add **50 µl** SPRIselect reagent **(0.5X)** to each sample. Pipette mix 15x (pipette set to 140 µl).

b. Incubate **5 min** at **room temperature**.

c. Place tube strip on the magnet•**High** until the solution clears.

DO NOT discard supernatant.

d. Transfer **145 µl** supernatant to a new tube strip.

e. Vortex to resuspend SPRIselect reagent. Add **30 µl** SPRIselect reagent **(0.8X)** to each sample. Pipette mix 15x (pipette set to 150 µl).

f. Incubate **5 min** at **room temperature**.

g. Place on the magnet•**High** until the solution clears.

h. Remove **170 µl** supernatant. DO NOT discard any beads.

i. Add **200 µl** 80% ethanol. 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**.

m. Remove remaining ethanol wash. DO NOT over-dry beads to ensure maximum elution efficiency.

n. Remove from the magnet. Add **35.5 µl** Buffer EB. Pipette mix 15x.

o. Incubate **2 min** at **room temperature**.

p. Place on the magnet•**Low** until the solution clears.

q. Transfer **35 µl** sample to a new tube strip.

r. Store at **4°C** for up to **72 h** or at **–20°C** for up to **1 week**, or proceed to the next step.

3.3 V(D)J Amplification 2

VERSION SPECIFIC

a. Prepare V(D)J Amplification 2 Reaction Mix on ice. Vortex and centrifuge briefly.

V(D)J Amplification 2 Reaction Mix *Add reagents in the order listed*	PN	1X (µl)	4X + 10% (µl)	8X + 10% (µl)
○ **Amp Mix**	2000047/ 2000103	50	220	440
● **T Cell Mix 2 v2** **or** ● **B Cell Mix 2 v2**	Human 2000246/ Mouse 2000257 or Human 2000255/ Mouse 2000259	15	66	132
Total	-	**65**	**286**	**572**

b. Add **65 µl** V(D)J Amplification 2 Reaction Mix to each tube containing **35 µl** sample.

c. Pipette mix 5x (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	~25-30 min
Step	**Temperature**	**Time**
1	98°C	00:00:45
2	98°C	00:00:20
3	62°C	00:00:30
4	72°C	00:01:00
5 Different cycle numbers for T & B cells	T Cell: Go to Step 2, 9x (total 10 cycles) B Cell: Go to Step 2, 7x (total 8 cycles)	
6	72°C	00:01:00
7	4°C	Hold

STOP

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

3.4 Post V(D)J Amplification 2 Cleanup Double Sided Size Selection – SPRIselect

a. Vortex to resuspend SPRIselect reagent. Add **50 µl** SPRIselect reagent **(0.5X)** to each sample. Pipette mix 15x (pipette set to 145 µl).

b. Incubate **5 min** at **room temperature**.

c. Place on the magnet•**High** until the solution clears. DO NOT discard supernatant.

d. Transfer **145 µl** supernatant to a new tube strip.

e. Vortex to resuspend SPRIselect reagent. Add **30 µl** SPRIselect reagent **(0.8X)** to each sample. Pipette mix 15x (pipette set to 150 µl).

f. Incubate **5 min** at **room temperature**.

g. Place on the magnet•**High** until the solution clears.

h. Remove **170 µl** supernatant. DO NOT discard any beads.

i. Add **200 µl** 80% ethanol. 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**.

m. Remove remaining ethanol wash. DO NOT over-dry beads to ensure maximum elution efficiency.

n. Remove from the magnet. Add **45.5 µl** Buffer EB. Pipette mix 15x.

o. Incubate **2 min** at **room temperature**.

p. Place on the magnet•**Low** until the solution clears.

q. Transfer **45 µl** sample to a new tube strip.

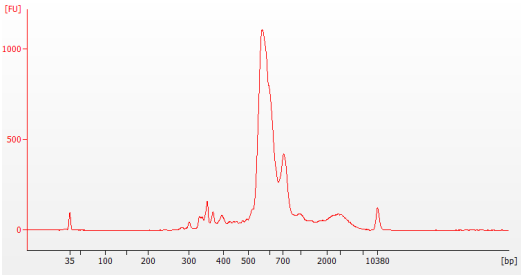
r. Store at **4°C** for up to **72 h** or at **–20°C** for up to **1 week**, or proceed to the next step.

3.5 Post V(D)J Amplification QC & Quantification

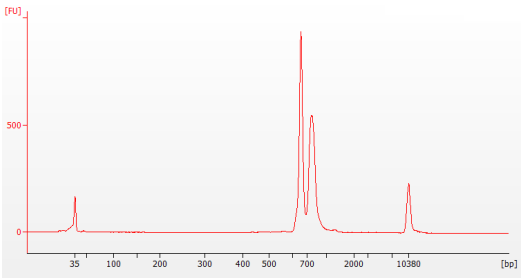
a. Run **1 µl** sample at **1:5 dilution** (Dilution Factor 5) on an Agilent Bioanalyzer High Sensitivity chip.

Samples of RNA-rich cells may require additional dilution in nuclease-free water. The number of distinct peaks may vary. Higher molecular weight product (2,000- 9,000 bp) may be present. This does not affect sequencing.

Representative Trace - PBMCs amplified for TCR



Representative Trace - PBMCs amplified for BCR

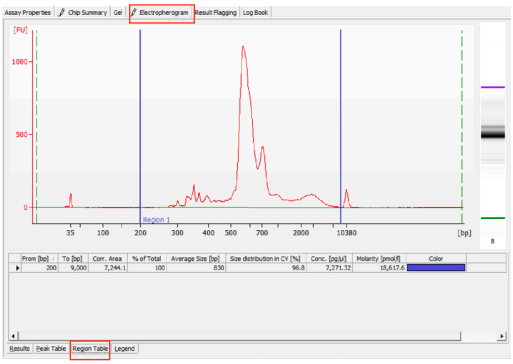


b. Determine yield for each sample. Example calculation below.

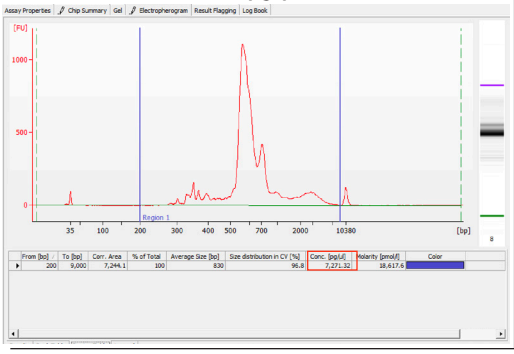
EXAMPLE CALCULATION

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

Concentration: 7271.32 pg/µl
Dilution Factor: 5

Amplified Product Conc.

$$\frac{\text{Conc. (pg/µl)} \times \text{Dilution Factor}}{1000\ \text{(pg/ng)}} = \frac{7271.32 \times 5}{1000}$$

$$= \mathbf{36.35\ ng/µl}$$

Example Calculation for Carrying Forward 50 ng Sample for V(D)J Library Construction

Volume for 50 ng = $\frac{50\ \text{ng}}{36.35\ \text{(ng/µl)}} = \mathbf{1.37\ µl}$

V(D)J Library Construction Sample
=1.37 µl + 18.63 µl nuclease-free water
=20 µl total

If <50 ng available, carry forward 20 µl sample (2-50 ng) into V(D)J Library Construction.

DO NOT exceed a mass of 50 ng in the 20 µl carry forward volume.

Alternate Quantification Methods (See Appendix for representative traces)

- Agilent TapeStation
- LabChip
- Qubit Fluorometer and Qubit dsDNA HS Assay Kit

Step 4

V(D)J Dual Index Library Construction

4.0 V(D)J Library Construction

VERSION SPECIFIC

GET STARTED!				
	Item	10x PN	Preparation & Handling	Storage
	Equilibrate to Room Temperature			
☐	**Fragmentation Buffer**	2000091	Thaw, vortex, verify no precipitate, centrifuge briefly.	–20°C
☐	**Adaptor Oligos**	2000094	Thaw, vortex, centrifuge briefly.	–20°C
☐	**Ligation Buffer**	2000092	Thaw, vortex, verify no precipitate, centrifuge briefly.	–20°C
☐	**Dual Index Plate TT Set A** Verify name & PN	3000431	-	–20°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 quantification	-	Manufacturer's recommendations.	-
	Place on ice			
☐	**Fragmentation Enzyme**	2000090/ 2000104	Centrifuge briefly.	–20°C
☐	**DNA Ligase**	220110/ 220131	Centrifuge briefly.	–20°C
☐	**Amp Mix**	2000047/ 2000103	Vortex, centrifuge briefly.	–20°C
	Obtain			
☐	**Qiagen Buffer EB**	-	-	Ambient
☐	**10x Magnetic Separator**	230003	See Tips & Best Practices.	Ambient
☐	**Prepare 80% Ethanol** Prepare 15 ml for 8 reactions	-	Prepare fresh.	Ambient

4.1 Fragmentation, End Repair & A-tailing

VERSION SPECIFIC

a. Determine the volume for **50 ng** mass of sample (see example calculation at step 3.5). Dispense the sample volume in a tube strip **on ice**. If the volume required for **50 ng** is less than **20 µl**, adjust the total volume of each sample to **20 µl** with nuclease-free water. If the volume for **50 ng** exceeds **20 µl**, carry only **20 µl** sample into library construction.

b. 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 Pre-cool block prior to preparing the Fragmentation Mix	4°C	Hold
Fragmentation	32°C	00:02:00
End Repair & A-tailing	65°C	00:30:00
Hold	4°C	Hold

c. Vortex Fragmentation Buffer. Verify there is no precipitate.

d. Prepare Fragmentation Mix on ice. Pipette mix and centrifuge briefly.

Fragmentation Mix *Add reagents in the order listed*	PN	1X (µl)	4X + 10% (µl)	8X + 10% (µl)
Nuclease-free Water	-	15	66	132
● **Fragmentation Buffer**	2000091	5	22	44
● **Fragmentation Enzyme**	2000090/ 2000104	10	44	88
Total	-	**30**	**132**	**264**

e. Add **30 µl** Fragmentation Mix into each tube containing **20 µl** sample.

f. Pipette mix 15x (pipette set to 30 µl) on ice. Centrifuge briefly.

g. Transfer into the pre-cooled thermal cycler **(4°C)** and press "SKIP" to initiate the protocol.

4.2 Adaptor Ligation

VERSION SPECIFIC

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

Adaptor Ligation Mix *Add reagents in the order listed*	PN	1X (µl)	4X + 10% (µl)	8X + 10% (µl)
Ligation Buffer	2000092	20	88	176
DNA Ligase	220110/ 220131	10	44	88
Adaptor Oligos	2000094	20	88	176
Total	-	**50**	**220**	**440**

b. Remove the sample from the thermal cycler.

c. Add **50 µl** Adaptor Ligation Mix to **50 µl** sample. 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
30°C	100 µl	15 min
Step	**Temperature**	**Time**
1	20°C	00:15:00
2	4°C	Hold

4.3 Post Ligation Cleanup – SPRIselect

a. Vortex to resuspend SPRIselect Reagent. Add **80 µl** SPRIselect Reagent **(0.8X)** to each sample. 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. Place on the magnet•**Low**.

i. Remove any remaining ethanol. Air dry for **2 min**.

j. Remove from the magnet. Add **30.5 µl** Buffer EB. Pipette mix 15x. If beads still appear clumpy, continue pipette mixing until fully resuspended.

k. Incubate **2 min** at **room temperature**.

l. Place on the magnet•**Low** until the solution clears.

m. Transfer **30 µl** sample to a new tube strip.

4.4 Sample Index PCR

VERSION SPECIFIC

a. 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.

b. Add **50 µl** Amp Mix (PN-2000047/2000103) to **30 µl** sample.

c. Add **20 µl** of an individual Dual Index TT Set A to each well and record the well ID used. Pipette mix 5x (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 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, 7x (total 8 cycles)	
6	72°C	00:01:00
7	4°C	Hold

STOP

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

4.5 Post Sample Index PCR Cleanup – SPRIselect

a. Vortex to resuspend the SPRIselect reagent. Add **80 µl** SPRIselect Reagent **(0.8X)** to each sample. Pipette mix 15x (pipette set to 150 µl).

b. Incubate **5 min** at **room temperature**.

c. Place 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. Place on the magnet•**Low**.

i. Remove remaining ethanol. Air dry for **2 min**.

j. Remove from the magnet. Add **35.5 µl** Buffer EB. Pipette mix 15x.

k. Incubate **2 min** at **room temperature**.

l. Place on the magnet•**Low** until the solution clears.

m. Transfer **35 µl** to a new tube strip.

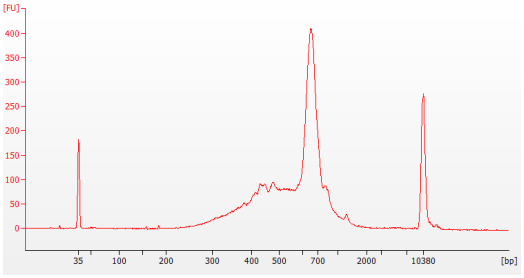
STOP

n. Store at **4°C** for up to **72 h** or at **–20°C** for **long-term** storage.

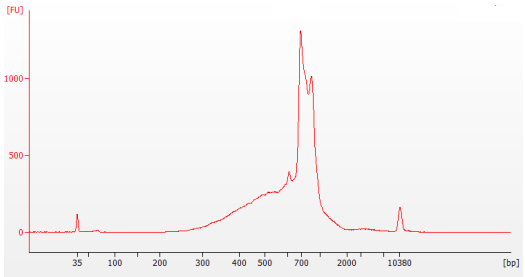
4.6 Post Library Construction QC

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

Representative Trace - PBMCs amplified for TCR



Representative Trace - PBMCs amplified for BCR



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

Alternate QC Method (See Appendix for representative traces)

- Agilent TapeStation
- LabChip

See Appendix for Post Library Construction Quantification

Step 5

5' Gene Expression (GEX) Library Construction

5.1 GEX Fragmentation, End Repair & A-tailing

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

5.3 GEX Adaptor Ligation

5.4 GEX Post Ligation Cleanup – SPRIselect

5.5 GEX Sample Index PCR

5.6 GEX Post Sample Index Double Sided Size Selection – SPRIselect

5.7 GEX Post Library Construction QC

5.0 5' Gene Expression (GEX) Library Construction

VERSION SPECIFIC

GET STARTED!			
Item	**10x PN**	**Preparation & Handling**	**Storage**
Equilibrate to Room Temperature			
☐ **Fragmentation Buffer**	2000091	Thaw, vortex, verify no precipitate, centrifuge briefly.	–20°C
☐ **Adaptor Oligos**	2000094	Thaw, vortex, centrifuge briefly.	–20°C
☐ **Ligation Buffer**	2000092	Thaw, vortex, verify no precipitate, centrifuge briefly.	–20°C
☐ **Dual Index Plate TT Set A** Verify name & PN	3000431	-	–20°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 quantification	-	Manufacturer's recommendations.	-
Place on ice			
☐ **Fragmentation Enzyme**	2000090/ 2000104	Centrifuge briefly.	–20°C
☐ **DNA Ligase**	220110/ 220131	Centrifuge briefly.	–20°C
☐ **Amp Mix**	2000047/ 2000103	Vortex, centrifuge briefly.	–20°C
☐ **KAPA Library Quantification Kit for Illumina Platforms**	-	Manufacturer's recommendations.	–20°C
Obtain			
☐ **Qiagen Buffer EB**	-	-	Ambient
☐ **10x Magnetic Separator**	230003	See Tips & Best Practices.	Ambient
☐ **Prepare 80% Ethanol** Prepare 15 ml for 8 reactions	-	Prepare fresh.	Ambient

5.1 GEX Fragmentation, End Repair & A-tailing

VERSION SPECIFIC

a. Determine the volume for **50 ng** mass of sample (see example calculation at step 2.4). Dispense the sample volume in a tube strip **on ice**. If the volume required for **50 ng** is less than **20 µl**, adjust the total volume of each sample to **20 µl** with nuclease-free water. If the volume for **50 ng** exceeds **20 µl**, carry ONLY **20 µl** sample into library construction.

b. 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 Pre-cool block prior to preparing the Fragmentation Mix	4°C	Hold
Fragmentation	32°C	00:05:00
End Repair & A-tailing	65°C	00:30:00
Hold	4°C	Hold

c. Vortex Fragmentation Buffer. Verify there is no precipitate.

d. Prepare Fragmentation Mix on ice. Pipette mix and centrifuge briefly.

Fragmentation Mix *Add reagents in the order listed*	PN	1X (µl)	4X + 10% (µl)	8X + 10% (µl)
Nuclease-free Water	-	15	66	132
● **Fragmentation Buffer**	2000091	5	22	44
● **Fragmentation Enzyme**	2000090/ 2000104	10	44	88
Total	-	**30**	**132**	**264**

e. Add **30 µl** Fragmentation Mix into each tube containing **20 µl** sample.

f. Pipette mix 15x (pipette set to 30 µl) on ice. Centrifuge briefly.

g. Transfer into the pre-cooled thermal cycler **(4°C)** and press "SKIP" to initiate the protocol.

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

a. Vortex to resuspend SPRIselect Reagent. Add 3**0 µl** SPRIselect Reagent **(0.6X)** to each sample. Pipette mix 15x (pipette set to 75 µl).

b. Incubate **5 min** at **room temperature**.

c. Place on the magnet•**High** until the solution clears. DO NOT discard supernatant.

d. Transfer **75 µl** supernatant to a new tube strip.

e. Add **10 µl** SPRIselect reagent **(0.8X)** to each sample. Pipette mix 15x (pipette set to 75 µl).

f. Incubate **5 min** at **room temperature**.

g. Place on the magnet•**High** until the solution clears.

h. Remove **80 µl** supernatant. DO NOT discard any beads.

i. With the tube strip still on the magnet, add **125 µl** 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**.

m. Remove the ethanol. DO NOT over-dry beads to ensure maximum elution efficiency.

n. Remove from the magnet. Add **50.5 µl** Buffer EB. Pipette mix 15x.

o. Incubate **2 min** at **room temperature**.

p. Place on the magnet•**High** until the solution clears.

q. Transfer **50 µl** sample to a new tube strip.

5.3 GEX Adaptor Ligation

VERSION SPECIFIC

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

Adaptor Ligation Mix *Add reagents in the order listed*	PN	1X (µl)	4X + 10% (µl)	8X + 10% (µl)
Ligation Buffer	2000092	20	88	176
DNA Ligase	220110/ 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

5.4 GEX Post Ligation Cleanup – SPRIselect

a. Vortex to resuspend SPRIselect Reagent. Add **80 µl** SPRIselect Reagent **(0.8X)** to each sample. 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. Place on the magnet•**Low**.

i. Remove any remaining ethanol. Air dry for **2 min**.

j. Remove from the magnet. Add **30.5 µl** 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 µl** sample to a new tube strip.

5.5 GEX Sample Index PCR

VERSION SPECIFIC

a. 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.

b. Add **50 µl** Amp Mix (PN-2000047/2000103) to **30 µl** sample.

c. Add **20 µl** of an individual Dual Index TT Set A to each well and record the well ID used. Pipette mix 5x (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 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 table recommends starting point for optimization. If less than 50 ng was carried into 5' Gene Expression Library Construction, refer to the product yield calculation example in step 2.4 to determine the mass input into Library Construction.

Recommended cycle numbers

cDNA Input	Total Cycles
1-25 ng	16
26-50 ng	14

STOP

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

5.6 GEX Post Sample Index PCR Double Sided Size Selection – SPRIselect

a. Vortex to resuspend SPRIselect reagent. Add **60 µl** SPRIselect reagent **(0.6X)** to each sample. 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. DO NOT discard supernatant.

d. Transfer **150 µl** supernatant to a new tube strip.

e. Vortex to resuspend SPRIselect reagent. Add **20 µl** SPRIselect reagent **(0.8X)** to each sample. Pipette mix 15x (pipette set to 150 µl).

f. Incubate **5 min** at **room temperature.**

g. Place on the magnet•**High** until the solution clears.

h. Remove **165 µl** supernatant. DO NOT discard any beads.

i. With the tube strip still on the magnet, add **200 µl** 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**.

m. Remove the remaining ethanol. DO NOT over-dry beads to ensure maximum elution efficiency.

n. Remove the tube strip from the magnet. Add **35.5 µl** Buffer EB. Pipette mix 15x.

o. Incubate **2 min** at **room temperature**.

p. Place on the magnet•**Low** until the solution clears.

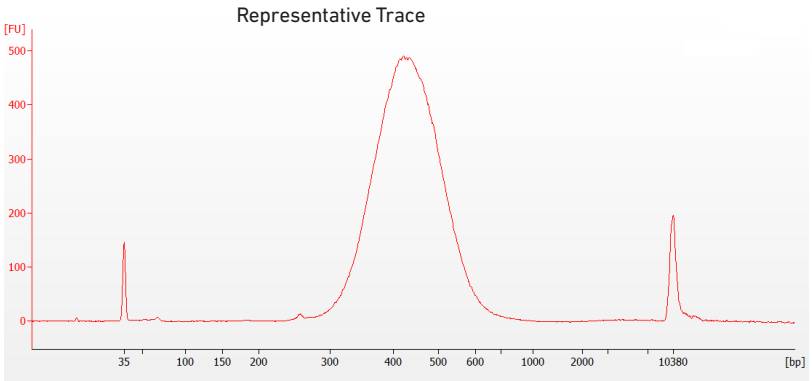
q. Transfer **35 µl** sample to a new tube strip.

STOP

r. Store at **4°C** for up to **72 h** or at **–20°C** for **long-term** storage.

5.7 GEX Post Library Construction QC

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



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

Alternate QC Method (See Appendix for representative traces)

- Agilent TapeStation
- LabChip

See Appendix for Post Library Construction Quantification

Step 6

Cell Surface Protein/Immune Receptor Mapping Library Construction

6.0 Cell Surface Protein/ Immune Receptor Mapping Library Construction

VERSION SPECIFIC

GET STARTED!				
	Item	10x PN	Preparation & Handling	Storage
	Equilibrate to Room Temperature			
☐	**Dual Index Plate TN Set A** Verify name & PN	3000510	-	–20°C
☐	**Beckman Coulter SPRIselect Reagent**	-	Manufacturer's recommendations.	-
☐	**Agilent Bioanalyzer High Sensitivity Kit** If used for QC	-	Manufacturer's recommendations.	-
☐	**Agilent TapeStation ScreenTape and Reagents** If used for QC and quantification	-	Manufacturer's recommendations.	-
	Place on ice			
☐ ◯	**Amp Mix**	2000047	Vortex, centrifuge briefly.	–20°C
☐	**KAPA Library Quantification Kit for Illumina Platforms**	-	Manufacturer's recommendations.	–20°C
	Obtain			
☐	**Qiagen Buffer EB**	-	Manufacturer's recommendations.	Ambient
☐	**10x Magnetic Separator**	230003	-	Ambient
☐	**Prepare 80% Ethanol** Prepare 20 ml for 8 reactions	-	Prepare fresh.	Ambient

6.1 Sample Index PCR

VERSION SPECIFIC

a. 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-3000510 Dual Index Plate TN Set A well ID; verify name and part number) used.

b. Prepare Sample Index PCR Mix.

Sample Index PCR Mix *Add reagents in the order listed*	PN	1X (µl)	4X + 10% (µl)	8X + 10% (µl)
Nuclease-free Water		25	110	220
◯ **Amp Mix**	2000047	50	220	440
Total	-	**75**	**330**	**660**

c. Transfer **ONLY 5 µl** sample from the Transferred Supernatant Cleanup (step 2.3B-xiv) to a new tube strip.
Note that only **5 µl** of the DNA sample is adequate for generating Cell Surface Protein library. The remaining DNA sample can be stored at **4°C** for up to **72 h** or at **–20°C** for up to **4 weeks** for generating additional Cell Surface Protein libraries.

d. Add **75 µl** Sample Index PCR Mix to the **5 µl** Transferred Supernatant Cleanup sample.

e. Add **20 µl** of an individual sample index (Dual Index Plate TN Set A) to each well and record the well ID. Pipette mix 5x (pipette set to 90 µl). Centrifuge briefly.

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

Lid Temperature	Reaction Volume	Run Time
105°C	100 µl	~30 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, repeat 7X (total 8 cycles)*	
6	72°C	00:01:00
7	4°C	Hold

*Optimization of cycle number may be needed based on target protein expression levels and number of antibodies used for labeling.

6.2 Post Sample Index PCR Size Selection – SPRIselect

a. Vortex to resuspend the SPRIselect reagent. Add **120 µl** SPRIselect Reagent **(1.2X)** to each sample. Pipette mix 15x (pipette set to 150 µl).

b. Incubate **5 min** at **room temperature**.

c. Place the magnet•**High** until the solution clears. Remove the supernatant.

d. Add **300 µl** 80% ethanol to the pellet. Wait **30 sec**.

e. Remove the ethanol.

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

g. Remove the ethanol.

h. Centrifuge briefly. Place on the magnet•**Low**. Remove remaining ethanol.

i. Remove from the magnet. Add **35.5 µl** Buffer EB. Pipette mix 15x.

j. Incubate **2 min** at **room temperature**.

k. Place on the magnet•**Low** until the solution clears.

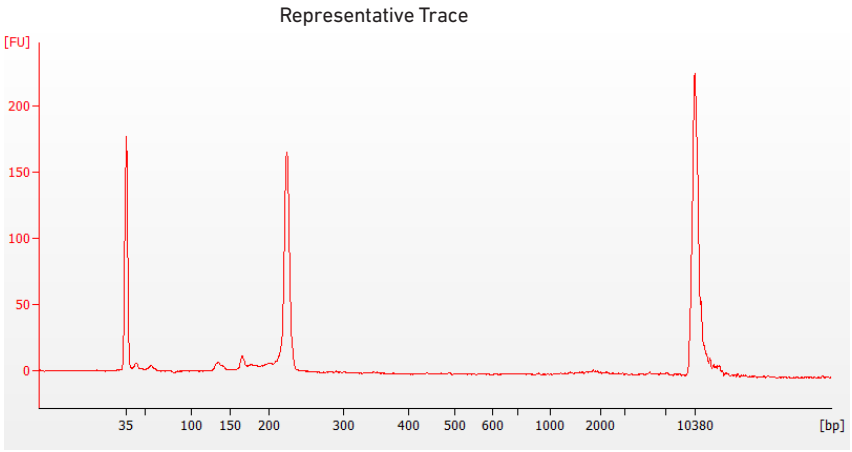
l. Transfer **35 µl** to a new tube strip.

STOP

m. Store at **4°C** for up to **72 h** or at **–20°C** for **long-term** storage.

6.3 Post Library Construction QC

Run **1 µl s**ample 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 (See Appendix for representative traces)

- Agilent TapeStation
- LabChip

See Appendix for Post Library Construction Quantification

Sequencing

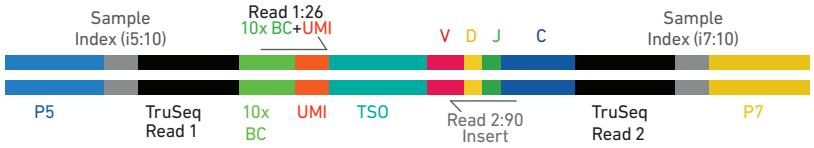
7

Sequencing Libraries

Chromium Single Cell V(D)J, 5' Gene Expression, and Cell Surface Protein Dual Index libraries comprise standard Illumina paired-end constructs which begin with P5 and end with P7. These libraries include 16 bp 10x Barcodes encoded at the start of TruSeq Read 1. Sample index sequences are incorporated as the i5 and i7 index read for V(D)J and 5' Gene Expression libraries; as i5 and i7 index read N for Cell Surface Protein library.

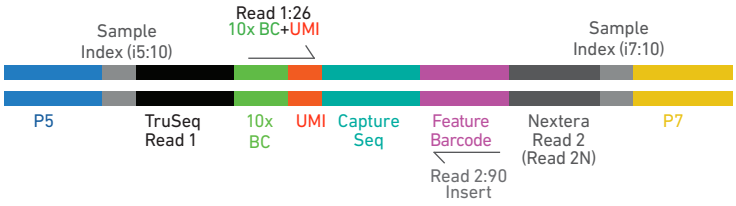
TruSeq Read 1, TruSeq Read 2, and Nextera Read 2 (Read 2N) are all standard Illumina sequencing primer sites. TruSeq Read 1 and TruSeq Read 2 are used in paired-end sequencing of V(D)J and 5' Gene Expression libraries. TruSeq Read 1 and Nextera Read 2 (Read 2N) are used for paired-end sequencing of Cell Surface Protein library. Sequencing these libraries produce a standard Illumina BCL data output folder.

Chromium Single Cell V(D)J Dual Index Library



Chromium Single Cell 5' Gene Expression Dual Index Library

Chromium Single Cell 5' Cell Surface Protein 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 500/550/2000
- HiSeq 2500 (Rapid Run)
- HiSeq 3000/4000
- NovaSeq

Sample Indices

Each well of the Dual Index Kit TT Set A (PN-1000215) and Dual Index Kit TN Set A (PN-1000250) contains 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 plate well ID) is needed in the sample sheet used for generating FASTQs with "cellranger mkfastq". If multiple libraries are pooled in a sequence lane, a separate sample index is needed with each library (see Tips & Best Practices).

Library Sequencing Depth & Run Parameters

Sequencing Depth	Minimum 5,000 read pairs per cell for V(D)J Dual Index library Minimum 20,000 read pairs per cell for 5' Gene Expression Dual Index library Minimum 5,000 read pairs per cell for Cell Surface Protein Dual Index library
Sequencing Type	Paired-end, Dual indexing
Sequencing Read	Read 1: 26 cycles i7 Index: 10 cycles i5 Index: 10 cycles Read 2: 90 cycles

Library Loading

Once quantified and normalized, V(D)J, 5' Gene Expression, and Cell Surface Protein 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	10	1
NextSeq 500	1.5	1
HiSeq 2500 (RR)	10	1
HiSeq 4000	180	1
NovaSeq	150*/300	1
NextSeq 2000	650	1

* Use 150 pM loading concentration for Illumina XP workflow.

Library Pooling

V(D)J, 5' Gene Expression, and Cell Surface Protein libraries may be pooled for sequencing, taking into account the differences in depth requirements between the pooled libraries.

Library Pooling Examples:

Libraries	Sequencing Depth (read pairs per cell)	Library Pooling Ratio
Example 1		
V(D)J library 5' Gene Expression library Cell Surface Protein library	5,000 20,000 5,000	1 4 1
Example 2		
V(D)J library 5' Gene Expression library Cell Surface Protein library	5,000 50,000 5,000	1 10 1

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

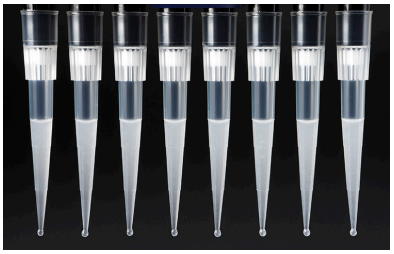
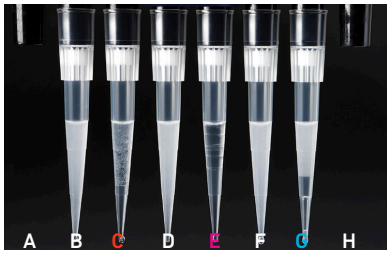
Loupe Browser is an interactive data visualization tool that requires no prior programming knowledge.

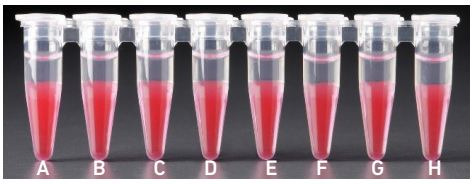
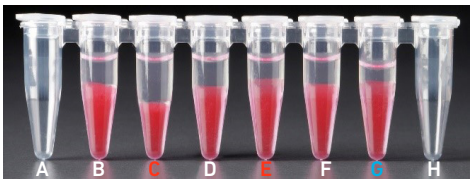
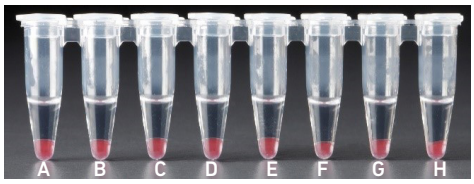
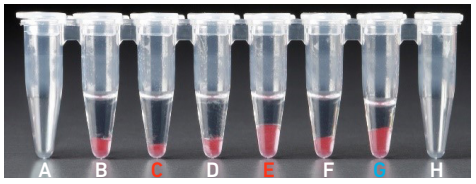
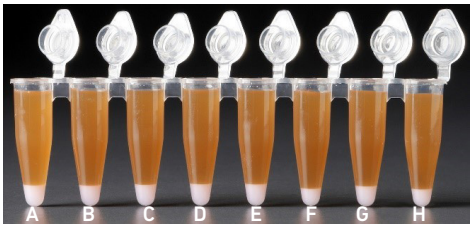
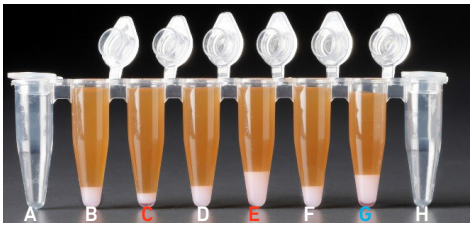
- Input: .cloupe
- Output: Data visualization, including t-SNE and UMAP projections, custom clusters, differentially expressed genes
- Operating System: MacOS, Windows

Troubleshooting

8

GEMs

STEP	NORMAL	REAGENT CLOGS & WETTING FAILURES
1.4 d After Chip K 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 e Transfer GEMs from Chip K Recovery Wells	 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.

Appendix

Post Library Construction Quantification

Agilent TapeStation Traces

LapChip Traces

Oligonucleotide Sequences

Post Library Construction Quantification

a. Thaw KAPA Library Quantification Kit for Illumina Platforms.

b. Dilute **1 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).

c. 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**

d. Dispense **16 µl** Quantification Master Mix for sample dilutions and DNA Standards into a 96 well PCR plate.

e. Add **4 µl** sample dilutions and **4 µl** DNA Standards to appropriate wells. Centrifuge briefly.

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

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

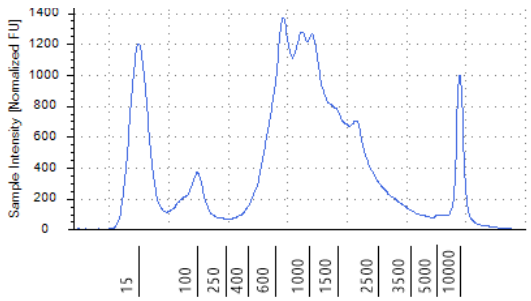
g. Follow the manufacturer's recommendations for qPCR-based quantification. For library quantification for sequencer clustering, determine the concentration based on insert size derived from the Bioanalyzer/TapeStation trace.

Agilent TapeStation Traces

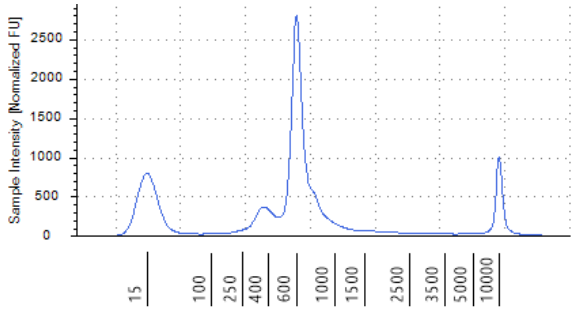
Agilent TapeStation Traces

Agilent TapeStation High Sensitivity D5000 ScreenTape was used. Protocol steps correspond to the Chromium Next GEM Single Cell 5' v2 (Dual Index) User Guide with Feature Barcode technology for Cell Surface Protein & Immune Receptor Mapping (CG000330).

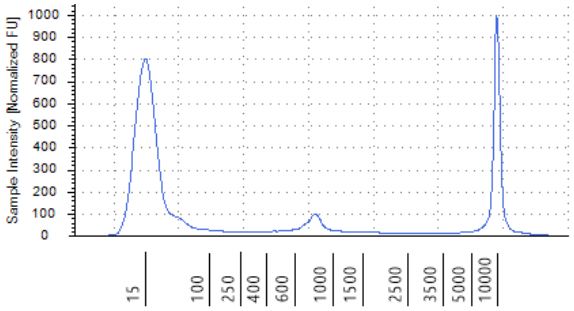
Protocol Step 2.4 – cDNA QC & Quantification



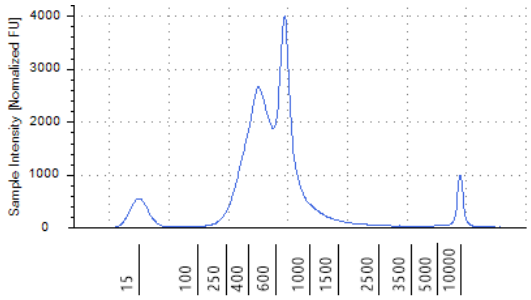
Protocol Step 3.5 – Post TCR Amplification QC



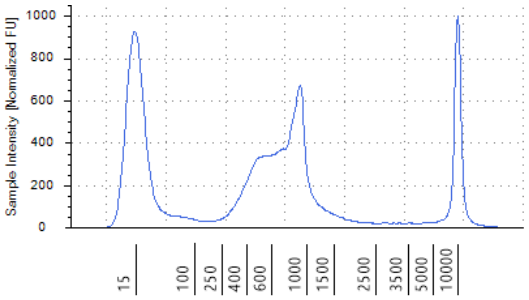
Protocol Step 3.5 – Post BCR Amplification QC



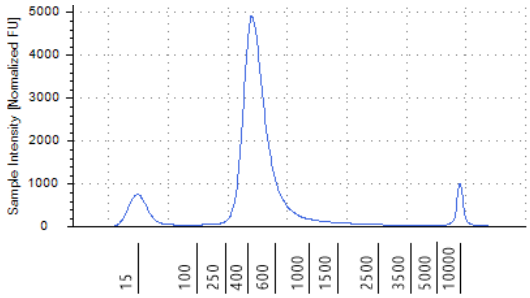
Protocol Step 4.6 – Post Library Construction QC
(PBMCs amplified for TCR)



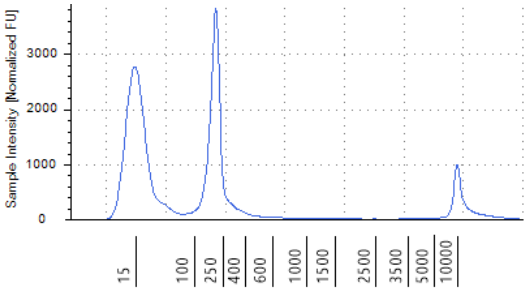
Protocol Step 4.6 – Post Library Construction QC
(PBMCs amplified for BCR)



Protocol Step 5.7 – GEX Post Library Construction QC



Protocol Step 6.3 – Post Library Construction QC



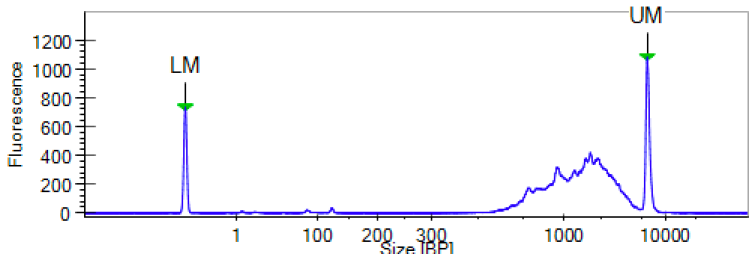
All traces are representative

LabChip Traces

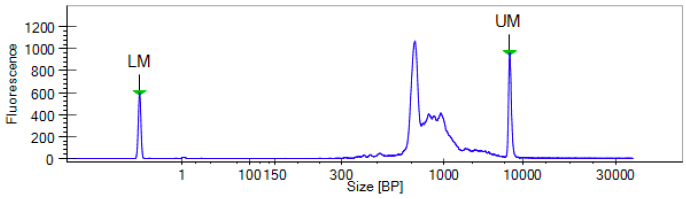
LabChip Traces

DNA High Sensitivity Reagent Kit was used.
Protocol steps correspond to the Chromium Next GEM Single Cell 5' Reagent Kits v2 (Dual Index) with Feature Barcode technology for Cell Surface Protein & Immune Receptor Mapping (CG000330).

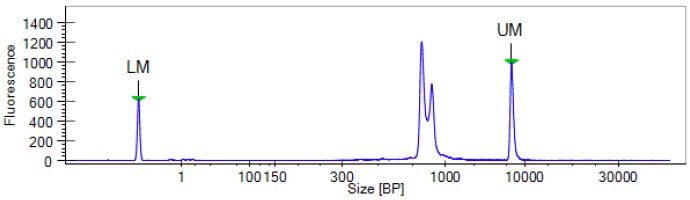
Protocol Step 2.4 – cDNA QC & Quantification



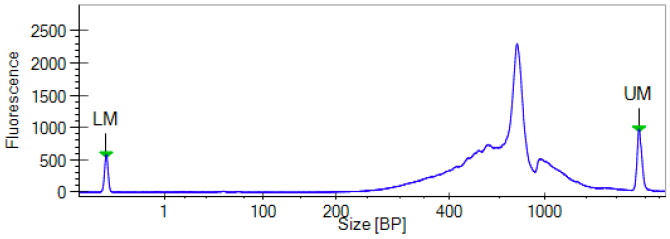
Protocol Step 3.5 – Post TCR Amplification QC



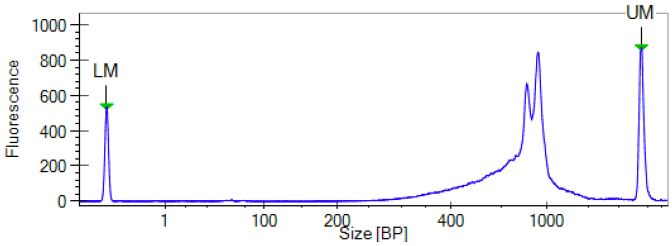
Protocol Step 3.5 – Post BCR Amplification QC



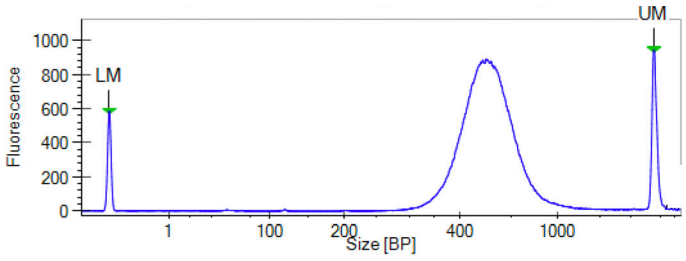
Protocol Step 4.6 – Post Library Construction QC
(PBMCs amplified for TCR)



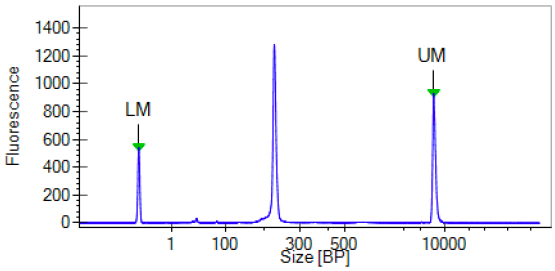
Protocol Step 4.6 – Post Library Construction QC
(PBMCs amplified for BCR)



Protocol Step 5.7 – GEX Post Library Construction QC



Protocol Step 6.3 – Post Library Construction QC



All traces are representative

Oligonucleotide Sequences

Protocol steps correspond to the Chromium Next GEM Single Cell V(D)J Reagent Kits v2 (Dual Index) with Feature Barcode technology for Cell Surface Protein & Immune Receptor Mapping (CG000330).

Protocol Step 1.5 – GEM-RT Incubation

Gel Bead Primer

5'-CTACACGACGCTCTTCCGATCT-N16-N10-TTTCTTATATrGrGrG-3'

Poly-dT RT Primer PN-2000007

5'-AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTVN-3'

Feature Barcode

3'-AAAGAATATACCC-N9-N15-N10-GACAGAGAATATGTGTAGAGGC-5'

GEM-RT Products

cDNA from poly-adenylated mRNA

3'-GATGTGCTGCGAGAAGGCTAGA-N16-N10-AAAGAATATACCC-cDNA_Insert-NVTTTTTTTTTTTTTTTTTTTTTTTTTTTTT-CATGAGACGCAACTATGGTGACGAA-5'

DNA from cell surface protein Feature Barcode

5'-CTACACGACGCTCTTCCGATCT-N16-N10-TTTCTTATATGGG-N9-N15-N10-CTGTCTCTTATACACATCTCCG-3'

3'-GATGTGCTGCGAGAAGGCTAGA-N16-N10-AAAGAATATACCC-N9-N15-N10-GACAGAGAATATGTGTAGAGGC-5'

Protocol Step 2.2 – cDNA Amplification

Feature cDNA Primers 4 -2000277

Amplifies cDNA

Forward Primer: Partial Read 1

5'-CTACACGACGCTCTTCCGATCT-3'

Reverse Primer: Non-poly(dT)

5'-AAGCAGTGGTATCAACGCAGAG-3'

Amplifies DNA from cell surface protein Feature Barcode

Forward Primer: Partial Read 1

5'-CTACACGACGCTCTTCCGATCT-3'

Reverse Primer: Read 2N

5'-CTCGTGGGCTCGGAGATGTG-3'

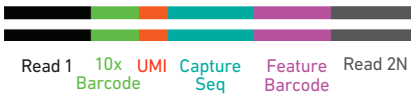
Amplified Products

Amplified cDNA from poly-adenylated mRNA

5'-CTACACGACGCTCTTCCGATCT-N16-N10-TTTCTTATATGGG-cDNA_Insert-GTACTCTGCGTTGATACCACTGCTT-3'

3'-GATGTGCTGCGAGAAGGCTAGA-N16-N10-AAAGAATATACCC-cDNA_Insert-CATGAGACGCAACTATGGTGACGAA-5'

Amplified DNA from cell surface protein Feature Barcode



5'-CTACACGACGCTCTTCCGATCT-N16-N10-TTTCTTATATGGG-N9-N15-N10-CTGTCTCTTATACACATCTCCGAGCCCACGAG-3'

3'-GATGTGCTGCGAGAAGGCTAGA-N16-N10-AAAGAATATACCC-N9-N15-N10-GACAGAGAATATGTGTAGAGGCTCGGGTGCTC-5'

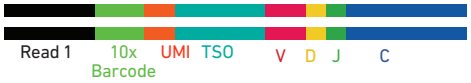
Protocol Step 3.1 – V(D)J Amplification 1

Human T Cell Mix 1 v2 PN-2000242	Forward Primer: PCR Primer 5'-GATCTACACTCTTTCCCTACACGACGC-3'	Reverse Outer Primers: 5'-TGAAGGCGTTTGCACATGCA-3' 5'-TCAGGCAGTATCTGGAGTCATTGAG-3	Outer Primer
Human B Cell Mix 1 v2 PN-2000254	Forward Primer: PCR Primer 5'-GATCTACACTCTTTCCCTACACGACGC-3'	Reverse Outer Primers: 5'-CAGGGCACAGTCACATCCT-3' 5'-TGCTGGACCACGCATTTGTA-3' 5'-GGTTTTGTTGTCGACCCAGTCT-3' 5'-TTGTCCACCTTGGTGTTGCT-3' 5'-CATGACGTCCTTGGAAGGCA-3' 5'-TGTGGGACTTCCACTG-3' 5'-TTCTCGTAGTCTGCTTTGCTCAG-3'	Outer Primer
Mouse T Cell Mix 1 v2 PN-2000256	Forward Primer: PCR Primer 5'-GATCTACACTCTTTCCCTACACGACGC-3'	Reverse Outer Primers: 5'-CTGGTTGCTCCAGGCAATGG-3' 5'-TGTAGGCCTGAGGGTCCGT-3'	Outer Primer
Mouse B Cell Mix 1 v2 PN-2000258	Forward Primer: PCR Primer 5'-GATCTACACTCTTTCCCTACACGACGC-3'	Reverse Outer Primers: 5'-TCAGCACGGGACAAACTCTTCT-3' 5'-GCAGGAGACAGACTCTTCTCCA-3' 5'-AACTGGCTGCTCATGGTGT-3' 5'-TGGTGCAAGTGTGGTTGAGGT-3' 5'-TGGTCACTTGGCTGGTGGTG-3' 5'-CACTTGGCAGGTGAACTGTTTTCT-3' 5'-AACCTTCAAGGATGCTCTTGGGA-3' 5'-GGACAGGGATCCAGAGTTCCA-3' 5'-AGGTGACGGTCTGACTTGGC-3' 5'-GCTGGACAGGGCTCCATAGTT-3' 5'-GGCACCTTGTCCAATCATGTTCC-3' 5'-ATGTCGTTCATACTCGTCCTTGGT-3'	Outer Primer

Protocol Step 3.3 – V(D)J Amplification 2

Human T Cell Mix 2 v2 PN-2000246	Forward Primer: PCR Primer 5'-GATCTACACTCTTTCCCTACACGACGC-3'	Reverse Inner Primers: 5'-AGTCTCTCAGCTGGTACACG-3' 5'-TCTGATGGCTCAAACACAGC-3'	Inner Primer
Human B Cell Mix 2 v2 PN-2000255	Forward Primer: PCR Primer 5'-GATCTACACTCTTTCCCTACACGACGC-3'	Reverse Inner Primers: 5'-GGGAAGTTTCTGGCGGTCA-3' 5'-GGTGGTACCCAGTTATCAAGCAT-3' 5'-GTGTCCCAGGTCACCATCAC-3' 5'-TCCTGAGGACTGTAGGACAGC-3' 5'-CACGCTGCTCGTATCCGA-3' 5'-TAGCTGCTGGCCGC-3' 5'-GCGTTATCCACCTTCCACTGT-3'	Inner Primer
Mouse T Cell Mix 2 v2 PN-2000257	Forward Primer: PCR Primer 5'-GATCTACACTCTTTCCCTACACGACGC-3'	Reverse Inner Primers: 5'-AGTCAAAGTCGGTGAACAGGCA-3' 5'-GGCCAAGCACACGAGGGTA-3'	Inner Primer
Mouse B Cell Mix 2 v2 PN-2000259	Forward Primer: PCR Primer 5'-GATCTACACTCTTTCCCTACACGACGC-3'	Reverse Inner Primers: 5'-TACACACCAGTGTGGCCTT-3' 5'-CAGGCCACTGTCACACCACT-3' 5'-CAGGTCACATTCATCGTGCCG-3' 5'-GAGGCCAGCACAGTGACCT-3' 5'-GCAGGGAAGTTCACAGTGCT-3' 5'-CTGTTTGAGATCAGTTTGCCATCCT-3' 5'-TGCGAGGTGGCTAGGTACTTG-3' 5'-CCCTTGACCAGGCATCC-3' 5'-AGGTCACGGAGGAACCAGTTG-3' 5'-GGCATCCCAGTGTCACCGA-3' 5'-AGAAGATCCACTTCACCTTGAAC-3' 5'-GAAGCACACGACTGAGGCAC-3'	Inner Primer

V(D)J Amplification Product



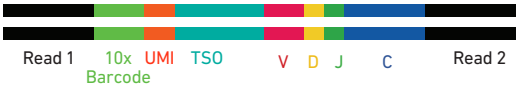
5′–GATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT–N16–N10–TTTCTTATATGGG–cDNA_Insert–Inner_Primer–3′
3′–CTAGATGTGAGAAAGGGATGTGCTGCGAGAAGGCTAGA–N16–N10–AAAGAATATACCC–cDNA_Insert–Inner_Primer–5′

Protocol Step 4.2 – Adaptor Ligation (for V(D)J Library Construction)

Adaptor (Read 2) PN-220026

5′–GATCGGAAGAGCACACGTCTGAACTCCAGTCAC–3′
3′–TCTAGCCTTCTCG–5′

Ligation Product



5′–GATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT–N16–N10–TTTCTTATATGGG–cDNA_Insert–AGATCGGAAGAGCACACGTCTGAACTCCAGTCAC–3′
3′–CTAGATGTGAGAAAGGGATGTGCTGCGAGAAGGCTAGA–N16–N10–AAAGAATATACCC–cDNA_Insert–TCTAGCCTTCTCG–5′

Protocol Step 4.4 – Sample Index PCR (for V(D)J Library Construction)

Dual Indexing

Dual Index Kit TT Set A PN-1000215

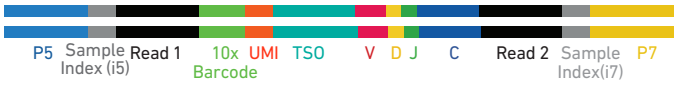
Forward Primer:

5′-AATGATACGGCGACCACCGAGATCTACAC-N10-ACACTCTTTCCCTACACGACGCTC-3′

Reverse Primer:

5′-CAAGCAGAAGACGGCATACGAGAT-N10-GTGACTGGAGTTCAGACGTGT-3′

Sample Index PCR Product



5′-AATGATACGGCGACCACCGAGATCTACAC-N10-ACACTCTTTCCCTACACGACGCTCTTCCGATCT-N16-N10-TTTCTTATATGGG-Insert-AGATCGGAAGAGCACACGTCTGAACTCCAGTCAC-N10-ATCTCGTATGCCGTCTTCTGCTTG-3′
3′-TTACTATGCCGCTGGTGGCTCTAGATGTG-N10-TGTGAGAAAGGGATGTGCTGCGAGAAGGCTAGA-N16-N10-AAAGAATATACCC-Insert-TCTAGCCTTCTCGTGTGCAGACTTGAGGTCAGTG-N10-TAGAGCATACGGCAGAAGACGAAC-5′

Protocol Step 5.3 –GEX Adaptor Ligation (for 5′ Gene Expression (GEX) Library Construction)

Adaptor (Read 2) PN-220026

5′–GATCGGAAGAGCACACGTCTGAACTCCAGTCAC–3′
3′–TCTAGCCTTCTCG–5′

Ligation Product

5′–CTACACGACGCTCTTCCGATCT–N16–N10–TTTCTTATATGGG–cDNA_Insert–AGATCGGAAGAGCACACGTCTGAACTCCAGTCAC–3′
3′–GATGTGCTGCGAGAAGGCTAGA–N16–N10–AAAGAATATACCC–cDNA_Insert–TCTAGCCTTCTCG–5′

Protocol Step 5.5 – Sample Index PCR (for 5' Gene Expression (GEX) Library Construction)

Dual Indexing

Dual Index Kit
TT Set A
PN-1000215

Forward Primer:

5'-AATGATACGGCGACCACCGAGATCT-N10-ACACTCTTTCCCTACACGACGCTC-3'

Reverse Primer:

5'-CAAGCAGAAGACGGCATACGAGAT-N10-GTGACTGGAGTTCAGACGTGT-3'

Sample Index PCR Product

5'-AATGATACGGCGACCACCGAGATCTACAC-N10-ACACTCTTTCCCTACACGACGCTCTTCCGATCT-N16-N10-TTTCTTATATGGG-cDNA _ Insert-AGATCGGAAGAGCACACGTCTGAACTCCAGTCAC-N10-ATCTCGTATGCCGTCTTCTGCTTG-3'

3'-TTACTATGCCGCTGGTGGCTCTAGATGTG-N10-TGTGAGAAAGGGATGTGCTGCGAGAAGGCTAGA-N16-N10-AAAGAATATACCC-cDNA _ Insert-TCTAGCCTTCTCGTGTGCAGACTTGAGGTCAGTG-N10-TAGAGCATACGGCAGAAGACGAAC-5'

Protocol Step 6.1 – Sample Index PCR (for Cell Surface Protein/Immune Receptor Mapping Library Construction)

Dual Indexing

Dual Index Kit
TN Set A
PN-1000250

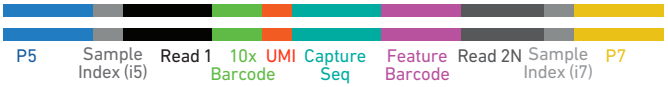
Forward Primer:

5'-AATGATACGGCGACCACCGAGATCT-N10-ACACTCTTTCCCTACACGACGCTC-3'

Reverse Primer:

5'-CAAGCAGAAGACGGCATACGAGAT-N10-GTCTCGTGGGCTCGG-3'

Sample Index PCR Product



5'-AATGATACGGCGACCACCGAGATCTACAC-N10-ACACTCTTTCCCTACACGACGCTCTTCCGATCT-N16-N10-TTTCTTATATGGG-N9-N15-N10-CTGTCTCTTATACACATCTCCGAGCCCACGAGAC-N10-ATCTCGTATGCCGTCTTCTGCTTG-3'

3'-TTACTATGCCGCTGGTGGCTCTAGATGTG-N10-TGTGAGAAAGGGATGTGCTGCGAGAAGGCTAGA-N16-N10-AAAGAATATACCC-N9-N15-N10-GACAGAGAATATGTGTAGAGGCTCGGGTGCTCTG-N10-TAGAGCATACGGCAGAAGACGAAC-5'