CG000510 Rev D

USER GUIDE

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

with Feature Barcode technology for CRISPR Screening

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' CRISPR Kit, 16 rxns, PN-1000451
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

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

Notices

Document Number

CG000510 • Rev D

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.

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Document Revision Summary

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Title	Chromium Next GEM Single Cell 5' v2 (Dual Index) User Guide with Feature Barcode technology for CRISPR Screening
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Specific Changes:

- Updated 10x Genomics Accessories table to add Magnetic Separator B (PN-2001212) on page 12.
- Updated Thermal Cycler Recommendations on page 12.
- Removed Qubit from Additional Kits, Reagents & Equipment table on page 13.
- Updated the volume of 50% glycerol solution to be added to row labeled 3 on page 34.
- Added additional guidance on library quantification on page 76.

General Changes:

Updates for general minor consistency of language and terms throughout.

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Introduction

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

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

*Not required for this protocol

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

*Not required for this protocol

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

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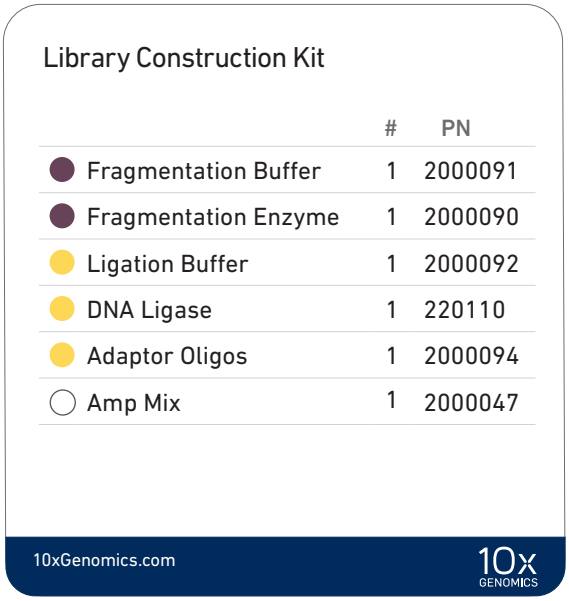
Dynabeads™ MyOne™ SILANE PN-2000048 (store at 4°C)

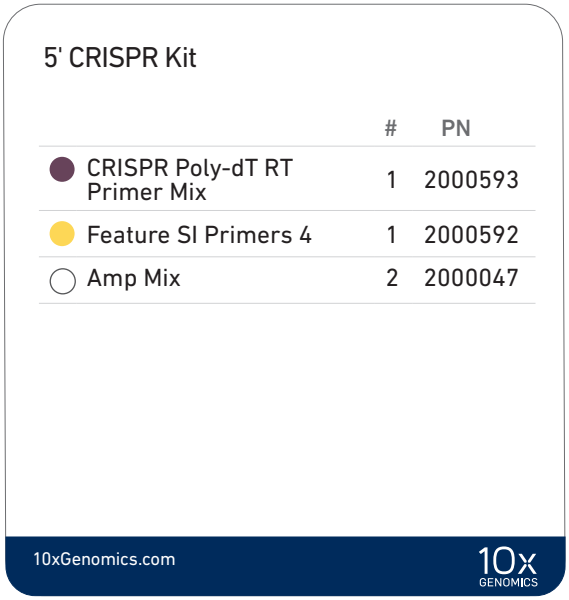
	#	PN
Dynabeads MyOne SILANE	1	2000048

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



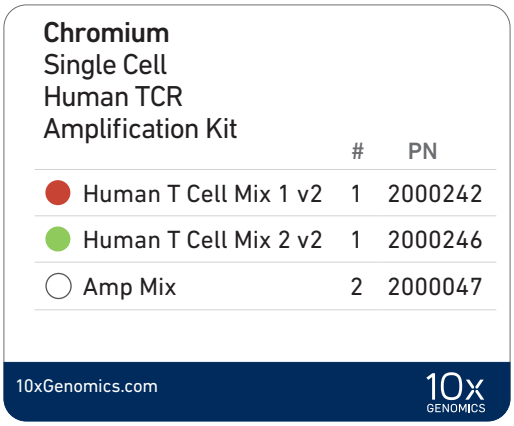
* Depending on the experimental goals, additional Library Construction Kits (PN-1000190) may be required. Refer to 10x Genomics support website for further guidance.

5' CRISPR Kit, 16 rxns PN-1000451 (store at -20°C)

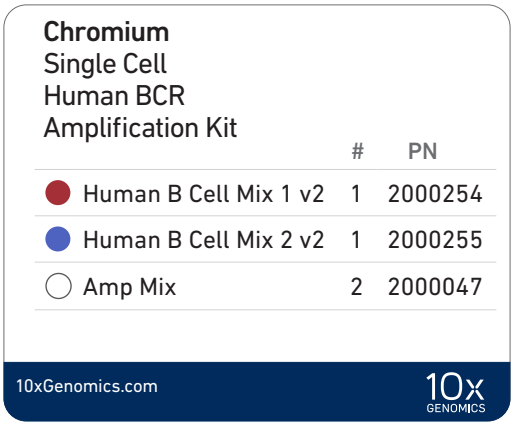


Chromium Single Cell V(D)J Amplification Kits, Human (store at –20°C)

TCR Amplification Kit, 16 rxns PN-1000252

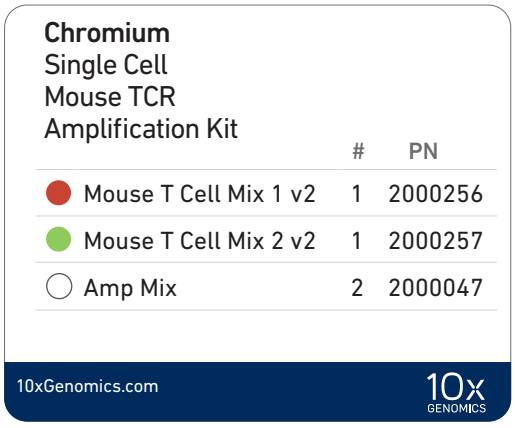


BCR Amplification Kit, 16 rxns PN-1000253

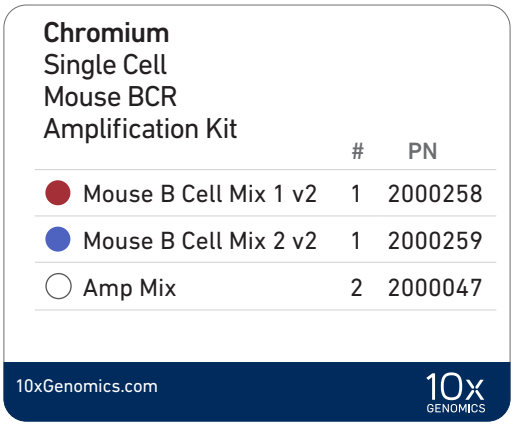


Chromium Single Cell V(D)J Amplification Kits, Mouse (store at –20°C)

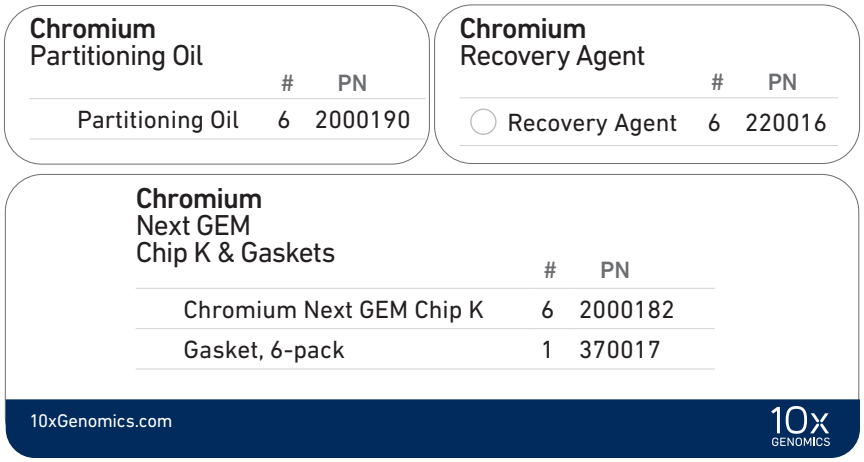
TCR Amplification Kit, 16 rxns PN-1000254



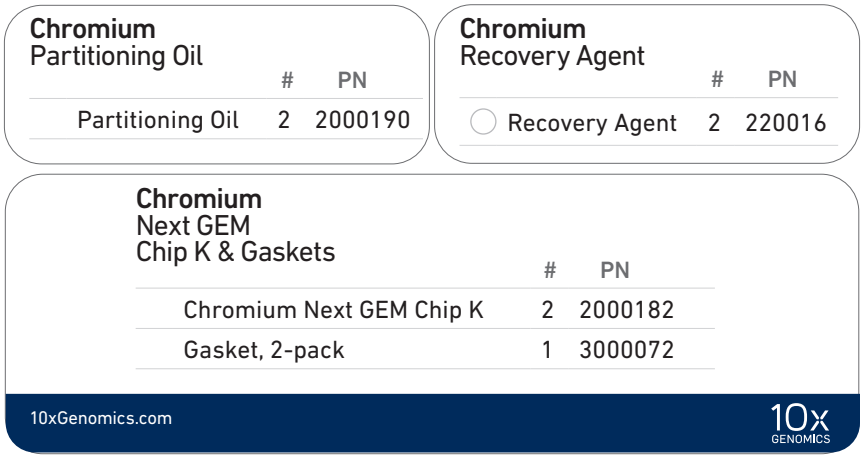
BCR Amplification Kit, 16 rxns PN-1000255



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



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



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

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
10x Magnetic Separator B*	1000709 (Chromium X/iX Accessory Kit)/1000707 (GEM-X Transition Kit)	2001212

**10x Magnetic Separator (PN-230003) and 10x Magnetic Separator B (PN-2001212) can be used interchangeably.*

Recommended Thermal Cyclers

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

Supplier	Description	Part Number
Analytik Jena	Biometra TAdvanced 96 SG/S*	846-x-070-241/846-x-070-251 *(x = 2 for 230 V; 4 for 115 V; 5 for 100 V, 50-60 Hz)*
Eppendorf	Mastercycler X50s/X50a**	6311000010 /6313000018
ThermoFisher	VeritiPro***	A48141
Bio-Rad	PTC Tempo Deepwell	12015392
Bio-Rad	C1000 Touch Thermal Cycler with 96-Deep Well Reaction Module (discontinued)	1851197
Eppendorf	Mastercycler Pro (discontinued)	North America 950030010 International 6321 000.019
Thermo Fisher Scientific	Veriti 96-Well Thermal Cycler (discontinued)	4375786

For select instruments, ramp rates should be adjusted for all steps as described below:

**Analytik Jena Biometra TAdvanced 96 SG/S: 2°C/sec for both heating and cooling*

***Eppendorf Mastercycler X50s/ X50a: 3°C/sec heating and 2°C/sec cooling*

****ThermoFisher VeritiPro requires FW 1.2.0, 96 well tray/retainer (PN 4381850), and "Cover Ramping" enabled*

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	Choose either Eppendorf, USA Scientific or Thermo Fisher Scientific PCR 8-tube strips.	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
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
Quantification & Quality Control			
Agilent	2100 Bioanalyzer Laptop Bundle High Sensitivity DNA Kit 4200 TapeStation High Sensitivity D5000 ScreenTape High Sensitivity D5000 Reagents	Choose Bioanalyzer or TapeStation based on availability & preference.	G2943CA 5067-4626 G2991AA 5067-5592 5067-5593
KAPA Biosystems	KAPA Library Quantification Kit for Illumina Platforms		KK4824

Pipette Tip Recommendations

10x Genomics recommends using only validated emulsion-safe pipette tips for all Single Cell protocols. Rainin pipette tips have been extensively validated by 10x Genomics and are highly recommended for all single cell assays. If Rainin tips are unavailable, any of the listed alternate pipette tips validated by 10x Genomics may be used.

Supplier	Description	Part Number (US)
Recommended Pipettes & Pipette tips		
Rainin	Pipettes:	
	Pipet-Lite Multi Pipette L8-50XLS+	17013804
	Pipet-Lite Multi Pipette L8-200XLS+	17013805
	Pipet-Lite Multi Pipette L8-10XLS+	17013802
	Pipet-Lite Multi Pipette L8-20XLS+	17013803
	Pipet-Lite LTS Pipette L-2XLS+	17014393
	Pipet-Lite LTS Pipette L-10XLS+	17014388
	Pipet-Lite LTS Pipette L-20XLS+	17014392
	Pipet-Lite LTS Pipette L-100XLS+	17014384
	Pipet-Lite LTS Pipette L-200XLS+	17014391
	Pipet-Lite LTS Pipette L-1000XLS+	17014382
	Pipette Tips:	
	Tips LTS 200UL Filter RT-L200FLR	30389240
	Tips LTS 1ML Filter RT-L1000FLR	30389213
	Tips LTS 20UL Filter RT-L10FLR	30389226
Alternate Recommendations (If Rainin pipette tips are unavailable, any of the listed pipette tips may be used)		
Eppendorf	Pipettes:	
	Eppendorf Research plus, 8-channel, epT.I.P.S. Box, 0.5 – 10 µL	3125000010
	Eppendorf Research plus, 8-channel, epT.I.P.S. Box, 10 – 100 µL	3125000036
	Eppendorf Research plus, 8-channel, epT.I.P.S. Box, 30 – 300 µL	3125000052
	Eppendorf Research plus, 1-channel, epT.I.P.S.® Box, 0.1 – 2.5 µL	3123000012
	Eppendorf Research plus, 1-channel, epT.I.P.S.® Box, 0.5 – 10 µL	3123000020
	Eppendorf Research plus, 1-channel, epT.I.P.S.® Box, 2 – 20 µL	3123000039
	Eppendorf Research plus, 1-channel, epT.I.P.S.® Box, 2 – 200 µL	3123000055
	Eppendorf Research plus, 1-channel, epT.I.P.S.® Box, 100 – 1000 µL	3123000063
	Pipette Tips (compatible with Eppendorf pipettes only)	
	ep Dualfilter T.I.P.S., 2-20 µL	0030078535
	ep Dualfilter T.I.P.S., 2-200 µL	0030078551
	ep Dualfilter T.I.P.S., 2-1,000 µL	0030078578
Labcon*	ZAP SLIK 20 µL Low Retention Aerosol Filter Pipet Tips for Rainin LTS	4-1143-965-008
	ZAP SLIK 200 µL Low Retention Aerosol Filter Pipet Tips for Rainin LTS	4-1144-965-008
	ZAP SLIK 1200 µL Low Retention Aerosol Filter Pipet Tips for Rainin LTS	4-1145-965-008
Biotix*	xTIP4 Racked Pipette Tips, Rainin LTS Pipette Compatible, 0.1-20uL	63300931
	xTIP4 Racked Pipette Tips, Rainin LTS Pipette Compatible, 200uL	63300001
	xTIP4 Racked Pipette Tips, Rainin LTS Pipette Compatible, 1200uL	63300004

**Compatible with Rainin pipettes*

Protocol Steps & Timing	Steps		Timing	Stop & Store
3 h	**Cell Preparation and Labeling** (Dependent on cell type and labeling protocol)		~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 or X/iX	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**			
	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	15 min STOP	4°C ≤72 h or –20°C ≤4 weeks
	2.4	cDNA Quantification & QC	50 min	
	*After cDNA Amplification & QC, for V(D)J Amplification and V(D)J Library Construction proceed to steps 3-4. For 5' Gene Expression Library Construction proceed directly to step 5.			
	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	
8 h plus* *Time dependent on Stop options used and protocol steps executed	**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 Frag, End Repair & A-tailing Double Sided – 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	
	5.6	GEX Post Sample Index PCR Double Sided Cleanup – SPRIselect	30 min STOP	4°C ≤72 h
	5.7	GEX Post Library Construction QC	50 min STOP	4°C ≤72 h or –20°C long-term
	Step 6 – 5' CRISPR Screening Library Construction			
	6.1	Guide RNA cDNA Cleanup	20 min	
	6.2	Feature PCR	50 min	
	6.3	Post Feature PCR Cleanup – SPRIselect	20 min	
	6.4	Sample Index PCR	30 min	
	6.5	Post Sample Index PCR Size Selection – SPRIselect	20 min STOP	4°C ≤72 h or –20°C long-term
	6.6	Post Library Construction QC	50 min	

Stepwise Objectives

The Single Cell 5' protocols offer comprehensive, scalable solutions for measuring immune repertoire, gene expression, and CRISPR-mediated perturbations from the same cell. Profile full-length (5' UTR to constant region), paired T-cell receptor (TCR), or B-cell receptor (BCR) transcripts, and CRISPR-mediated perturbations from 500-10,000 individual cells per sample.

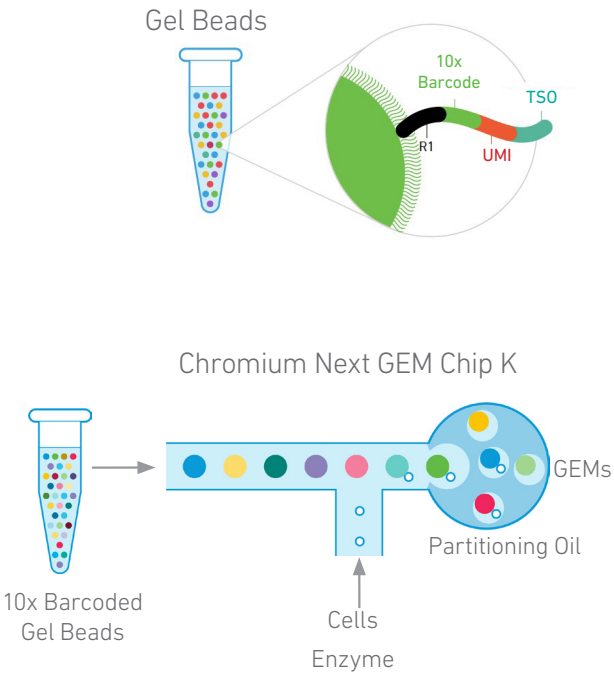
A pool of ~750,000 barcodes are sampled separately to index each cell's transcriptome along with the CRISPR-mediated perturbations. It is done by partitioning thousands of cells into nanoliter-scale Gel Beads-in-emulsion (GEMs), where all generated cDNA (from poly-adenylated mRNAs and single-guide RNAs/sgRNAs) 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 protocol to generate a T-cell library and/or a B-cell library, and/or a 5' Gene Expression, and CRISPR Screening libraries from amplified cDNA from the same cells.

Step 1 GEM Generation & Barcoding

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

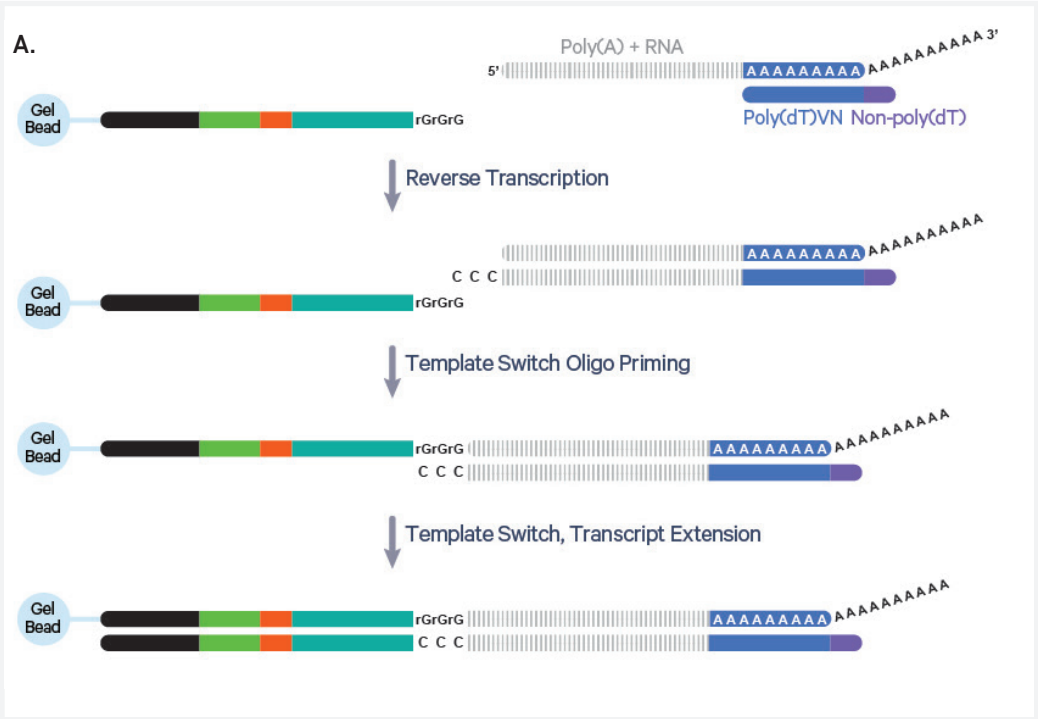
To achieve single cell resolution, cells are delivered at a limiting dilution, such that the majority (~90 – 99%) of generated GEMs contains no cell, while the remainder largely contain a single cell.

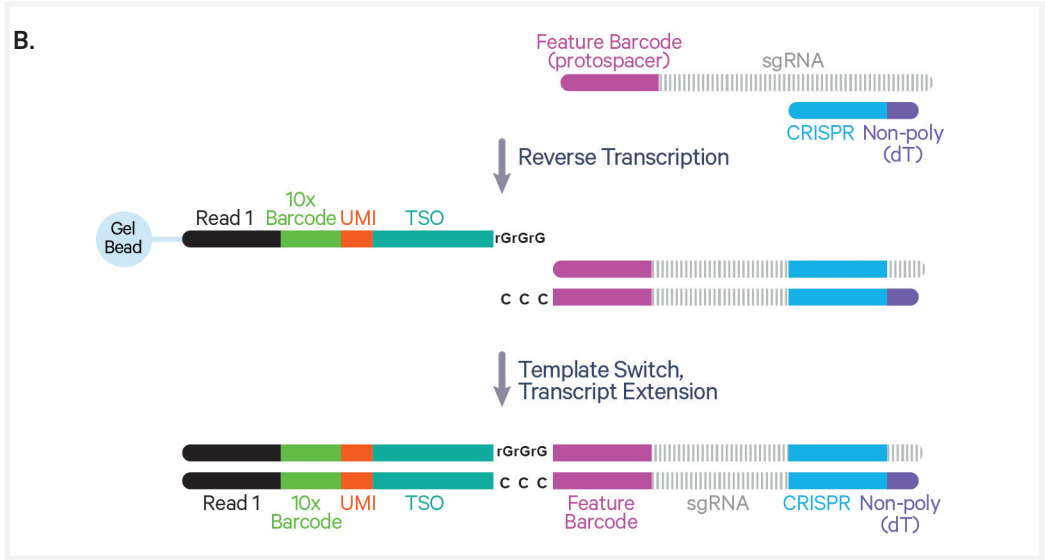


Step 1 GEM Generation & Barcoding

Immediately following GEM generation, the Gel Bead is dissolved and any co-partitioned cell is lysed. Oligonucleotides containing (i) an Illumina R1 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 primer mix (poly(dT) + CRISPR primers). Incubation of the GEMs simultaneously produces 10x Barcoded, full-length cDNA from poly-adenylated mRNA (A) and barcoded DNA from the sgRNA protospacer (Feature Barcode) cDNA, designed to taget gene/s of interest (B).

Inside individual GEMs

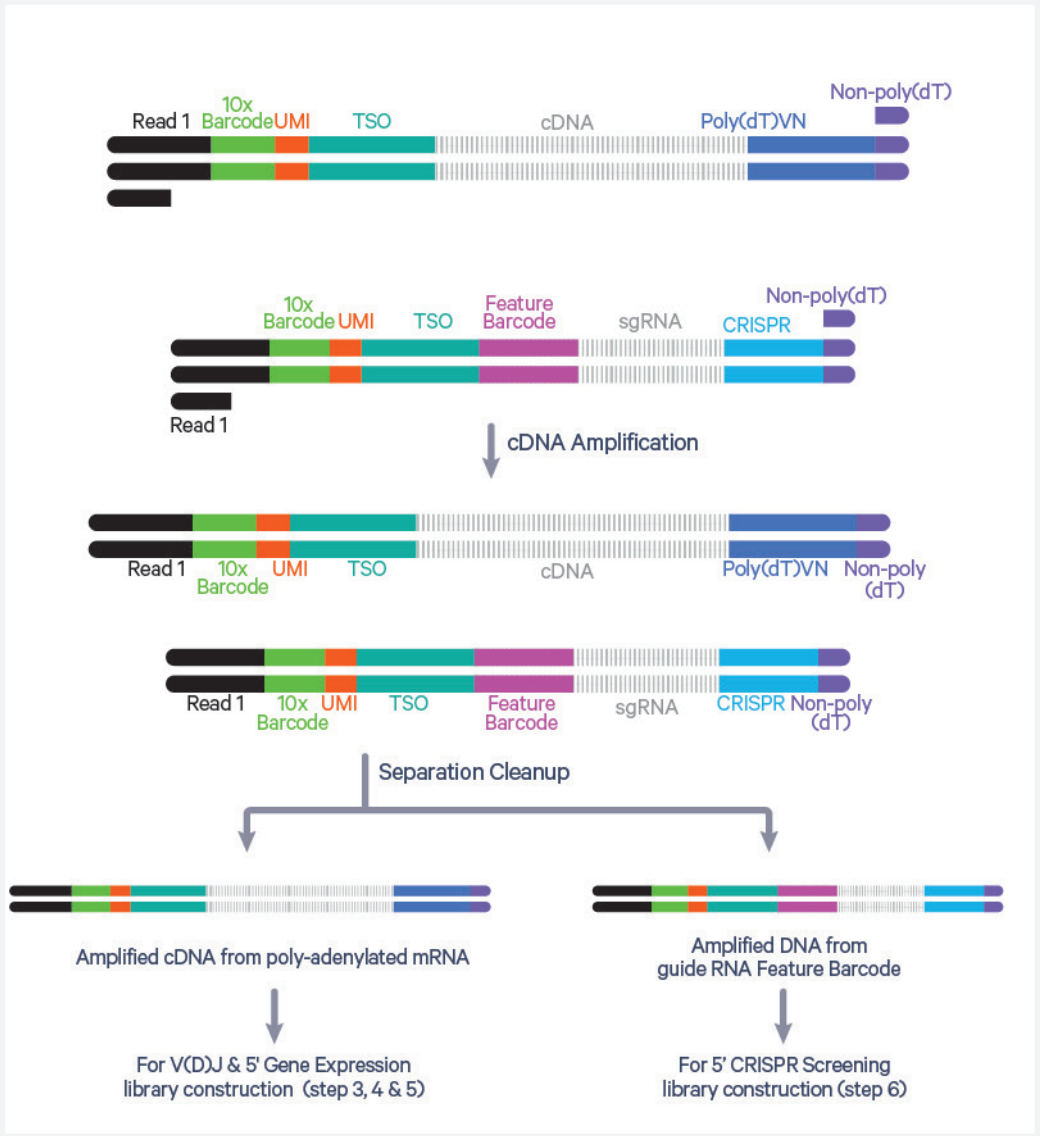




Step 2
Post GEM-RT Cleanup & cDNA Amplification

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 the post GEM-RT reaction mixture, which includes leftover biochemical reagents and primers. 10x Barcoded, full-length cDNA is amplified via PCR with primers against common 5' and 3' ends added during GEM-RT. Amplification generates sufficient material to construct multiple libraries from the same cells, e.g. both T cell and/or B cell libraries (steps 3 and 4), 5' Gene Expression libraries (step 5), and 5' CRISPR Screening libraries (step 6).

Pooled cDNA amplification



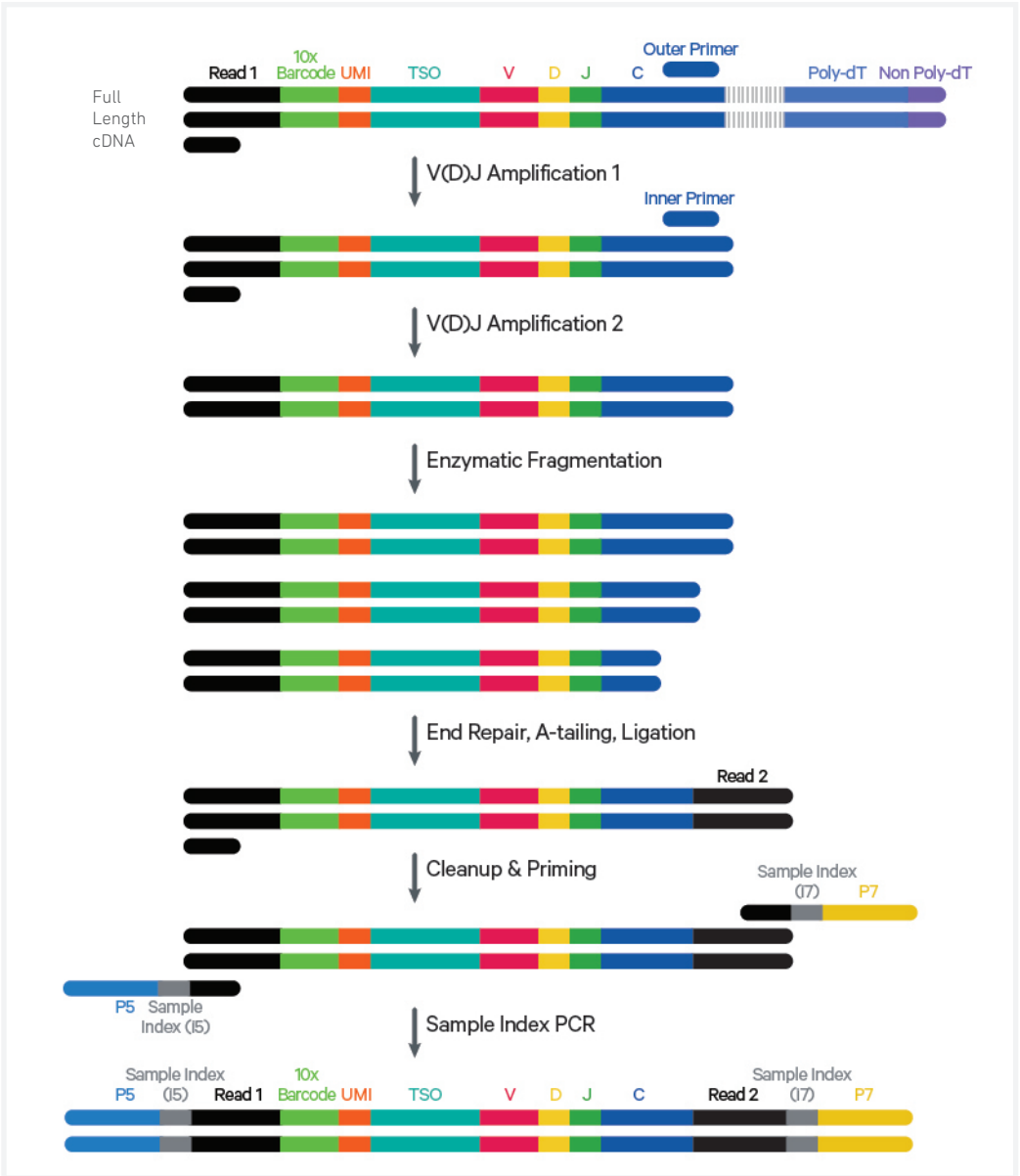
Step 3 V(D)J Amplification from cDNA

Amplified full-length cDNA from poly-adenylated mRNA is used to amplify 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 Ig 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. 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.

Pooled amplified cDNA processed in bulk



Step 5
5' Gene Expression (GEX) Library Construction

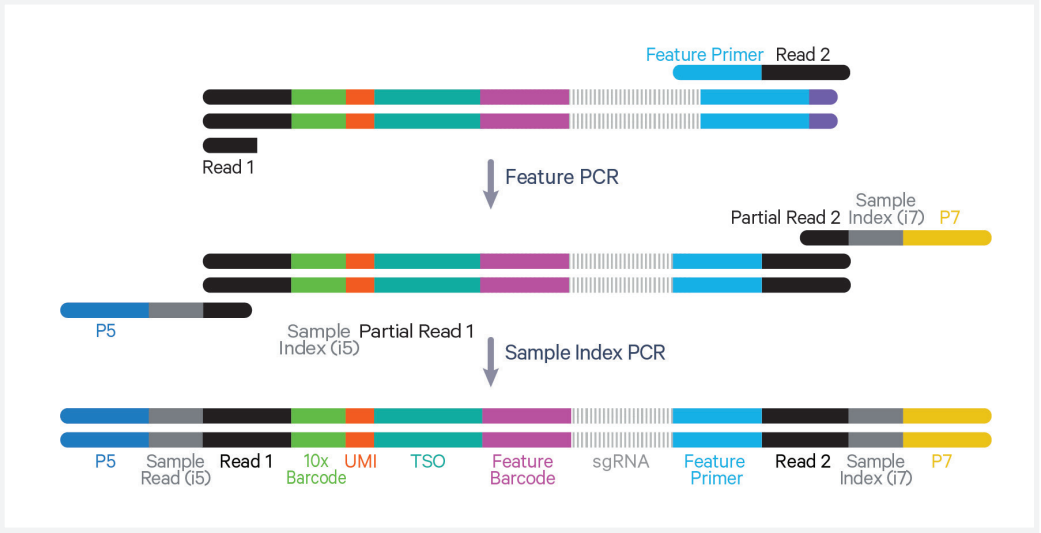
Amplified full-length cDNA from poly-adenylated mRNA is used to generate 5' Gene Expression library. Enzymatic fragmentation and size selection are used to optimize the cDNA amplicon size prior to 5' gene expression library construction. P5, P7, i5 and i7 sample indexes, and Illumina R2 sequence (read 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
5' CRISPR Screening Library Construction

Amplified cDNA from sgRNA molecules is used to generate CRISPR Screening libraries. P5, P7, i7 and i5 sample indexes, and TruSeq Read 2 (read 2 primer sequence) are added via PCR. The final libraries contain the P5 and P7 primers used in Illumina bridge amplification.

Pooled amplified cDNA processed in bulk

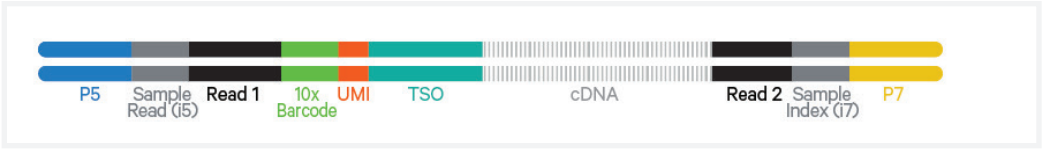


Step 7
Sequencing

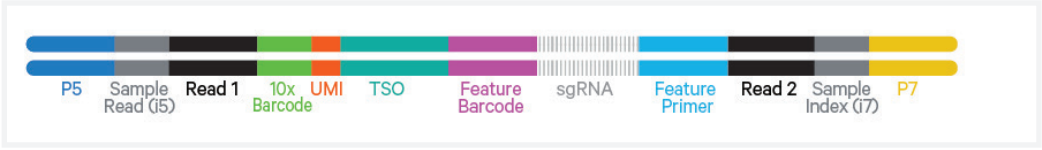
Illumina-ready dual index libraries can be sequenced at the recommended depth & run parameters. Illumina sequencer compatibility, sample indices, library loading and pooling for sequencing are summarized in the Sequencing chapter.

Chromium Single Cell V(D)J Dual Index Library

Chromium Single Cell 5' Gene Expression Dual Index Library



Chromium Single Cell 5' CRISPR Screening Dual Index Library



See Appendix for Oligonucleotide Sequences

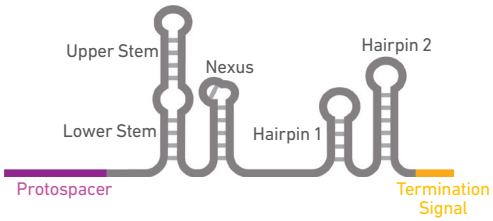
CRISPR Screening Overview

The Chromium Single Cell Immune Profiling Solution with Feature Barcode technology provides a high-throughput and scalable approach to obtain gene expression profiles along with perturbation phenotypes via direct capture of poly-adentylated mRNAs and single-guide RNAs (sgRNAs) from the same single cell (see Stepwise Objectives).

For compatibility with the Chromium Single Cell 5' CRISPR Screening assay, sgRNAs should be engineered for use with standard Cas9 systems with a protospacer on the 5' end (panel A). Compatibility of the assay can be verified by ensuring primer binding is possible with the sgRNA of interest. The assay is also compatible with sgRNA engineered with either Capture Sequence 1* or Capture Sequence 2* within the sgRNA hairpin structure (panel B), or immediately before the sgRNA termination signal (panel C), elongating the 3'-end of the sgRNA. Alternate sgRNA structures for use with other Cas enzymes may be compatible, but have not been tested by 10x Genomics.

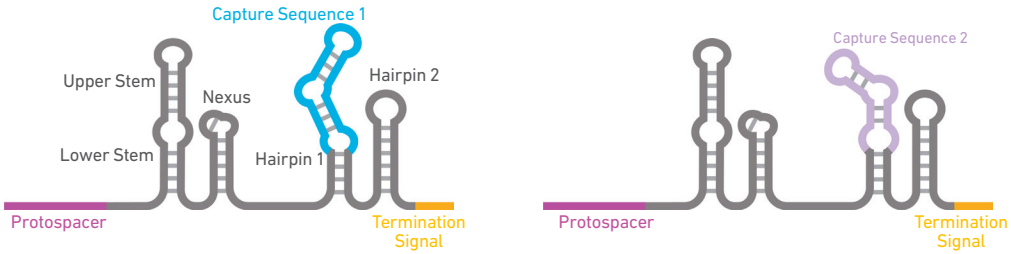
sgRNA compatible with Single Cell 5' CRISPR Assay

A.



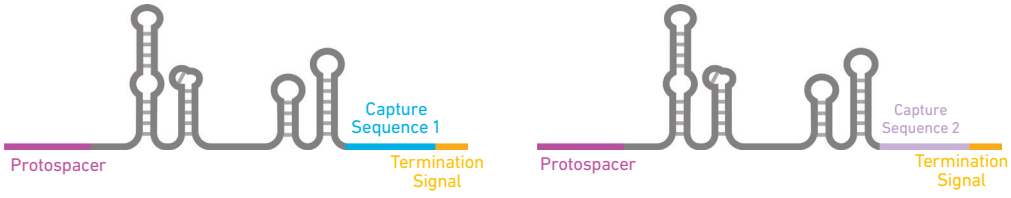
B.

Integrated Capture Sequence 1 or 2 in sgRNA hairpin*



C.

Integrated Capture Sequence 1 or 2 in sgRNA 3'-end*



Also compatible with Chromium Single Cell 3' CRISPR Screening assay.

Performing sgRNA QC by qPCR, NGS, or other methods is recommended prior to proceeding with the Single Cell Immune Profiling and CRISPR Screening Solution.

Experimental Planning Guide

- Refer to the Chromium Single Cell CRISPR Screening – Experimental Planning Guide (Document CG000398).

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 ~1,700 cells per reaction, resulting in recovery of ~1,000 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 Best Practices to Minimize Chromium Next GEM Chip Clogs and Wetting Failure (Documents CG00053 and CG000479 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.

OR

- 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

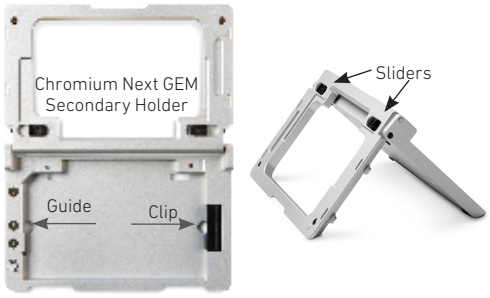
- Follow manufacturer's calibration and maintenance schedules.
- Pipette accuracy is particularly important when using SPRIselect reagents.

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.

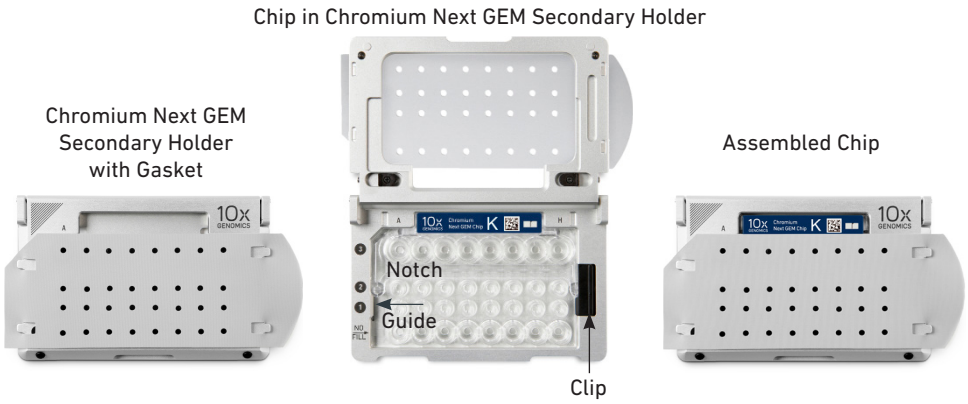
Chromium Next GEM Secondary Holders

- 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 with Gasket

- Close the holder lid. Attach the gasket by holding the tongue (curved end, to the right) and hook the gasket 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.
- Open the chip holder.
- Align notch on the chip (upper left corner) and the open holder with the gasket attached.
- Slide the chip to the left until the chip is inserted under the guide on the holder. Depress the right hand side of the chip until the spring-loaded clip engages.
- Keep the assembled unit with the attached gasket until ready for dispensing reagents into the wells.

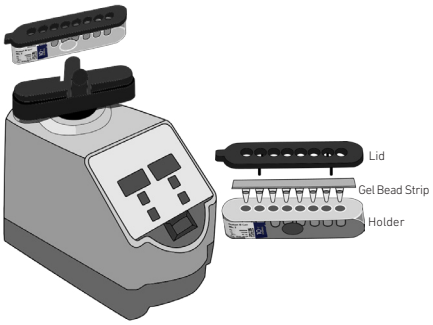


Chromium Next GEM Chip Loading

- Place the assembled chip and holder flat (gasket attached) on the bench with the lid open.
- 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

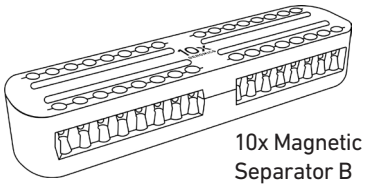
- Use one tube of Gel Beads per sample. DO NOT puncture the foil seals of tubes not used at the time.
- Equilibrate the Gel Beads strip to room temperature before use.
- Store unused Gel Beads at –80°C and avoid more than 12 freeze-thaw cycles. DO NOT store Gel Beads at –20°C.



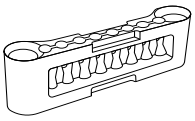
- Snap the tube strip holder with the Gel Bead strip into a 10x Vortex Adapter. Vortex **30 sec**.
- Centrifuge the Gel Bead strip for ~**5 sec** after removing from the holder. Confirm there are no bubbles at the bottom of the tubes and the liquid levels look even. Place the Gel Bead strip back in the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

- Images below are illustrative - actual appearance of magnetic separator may vary. Guidance applies to all 10x Magnetic Separators.
- 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.



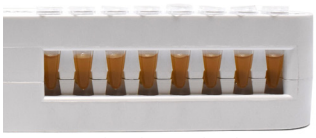
10x Magnetic Separator B



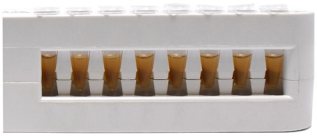
10x Magnetic Separator

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.
- Images below are representative - actual color of magnetic separator may vary. Guidance applies to all 10x Magnetic Separators.



1. Magnetic beads mixed with reagent



2. Separation in progress

3. Separation continuing

4. Separation complete; solution clear

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

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.
- Consider sample index compatibility when pooling different libraries; a unique sample index for each of the pooled libraries is required.

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.

SPRIselect Cleanup & Size Selection

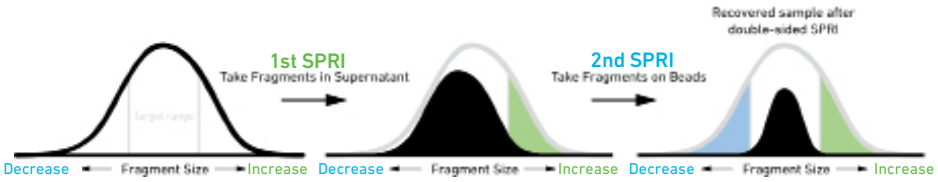
- After aspirating the desired volume of SPRIselect reagent, examine the pipette tips before dispensing to ensure the correct volume is transferred.
- Pipette mix thoroughly as insufficient mixing of sample and SPRIselect reagent will lead to inconsistent results.
- Use fresh preparations of 80% Ethanol.

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

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.

Step 1

GEM Generation & Barcoding

1.1 Prepare Master Mix

1.2 Load Chromium Next GEM Chip K

1.3 Run the Chromium Controller or X/iX

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
☐	**CRISPR poly-dT RT Primer Mix** Verify name & PN	2000593	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
	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
CRISPR poly-dT RT Primer Mix Verify name & PN	2000593	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**

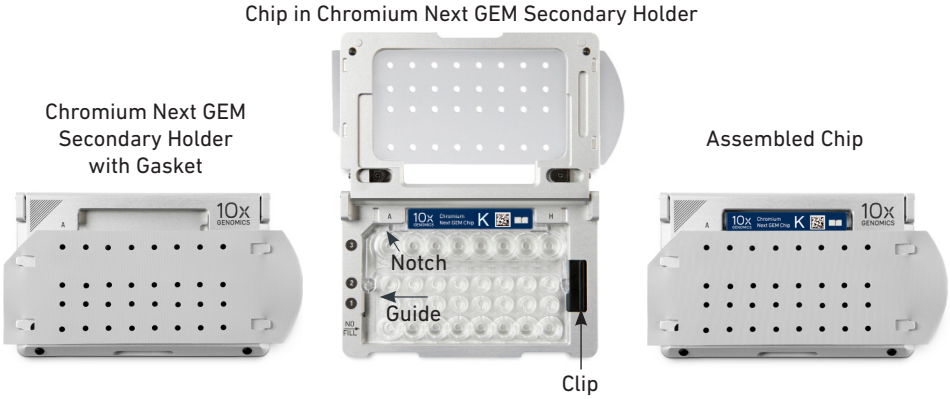
b. Add **36.3 µl** Master Mix into each tube of a PCR 8-tube strip on ice.

Assemble Chromium Next GEM Chip

TIPS

See Tips & Best Practices for chip handling instructions.

- Close the holder lid. Attach the gasket by holding the tongue (curved end, to the right) and hook the gasket 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.
- Open the chip holder.
- Remove the chip from the sealed bag. Use the chip within ≤ 24 h.
- Align notch on the chip (upper left corner) and the open holder with the gasket attached.
- Slide the chip to the left until the chip is inserted under the guide on the holder. Depress the right hand side of the chip until the spring-loaded clip engages.
- Keep the assembled unit with the attached gasket open until ready for and while dispensing reagents into the wells. DO NOT touch the smooth side of the gasket. After loading reagents, close the chip holder. DO NOT press down on the top of the gasket.



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 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

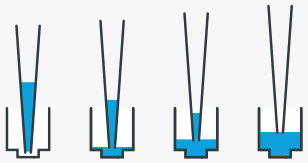
1.2 Load Chromium Next GEM Chip K

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

Open the lid (gasket attached) of the assembled chip and lay flat for loading.

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 pipette centered to each well and the tips slightly submerged.

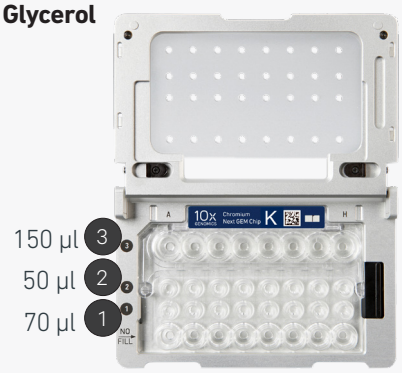


a. Add 50% glycerol solution to each unused well
(if processing <8 samples/chip)

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

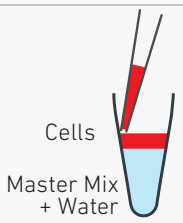
DO NOT add 50% glycerol solution to the bottom row of NO FILL wells.
DO NOT use any substitute for 50% glycerol solution.

Glycerol



b. Prepare Master Mix + Cell suspension

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



c. Load Row Labeled 1

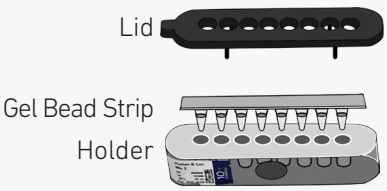
- Gently pipette mix the Master Mix + Cell Suspension
- Using the same pipette tip, dispense **70 µl** Master Mix + Cell Suspension into the bottom center of each well in **row labeled 1** without introducing bubbles.

Master Mix + Sample

d. Prepare Gel Beads

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

Prep Gel Beads



e. Load Row Labeled 2

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

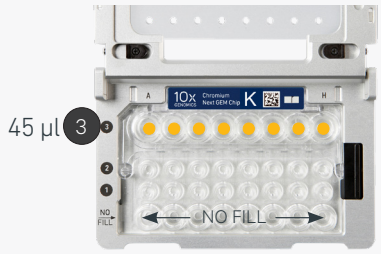
Gel Beads

f. Load Row Labeled 3

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

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

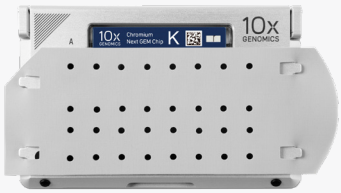
Partitioning Oil



g. Prepare for Run

- Close the lid (gasket already attached). DO NOT touch the smooth side of the gasket. DO NOT press down on the top of the gasket.

Run the chip in the Chromium Controller or X/iX immediately after loading the Partitioning Oil.



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

1.3 Run the Chromium Controller or X/iX

Next GEM

If using Chromium Controller:

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. Press the play button.

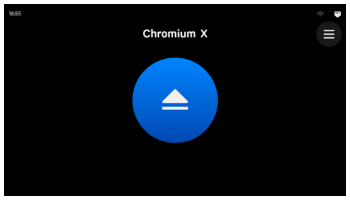
d. At completion of the run **(~18 min),** the Controller will chime. **Immediately** proceed to the next step.

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.

If using Chromium X/iX:

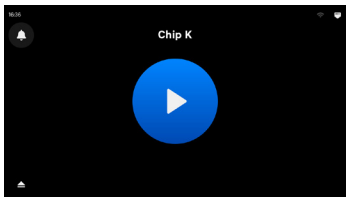
Consult the Chromium X Series (X/iX) User Guide (CG000396) for detailed instrument operation instructions and follow the instrument touchscreen prompts for execution.

a. Press the eject button on Chromium X/iX to eject the tray.
If the eject button is not touched within 1 min, tray will close automatically. System requires a few seconds before the tray can be ejected again.

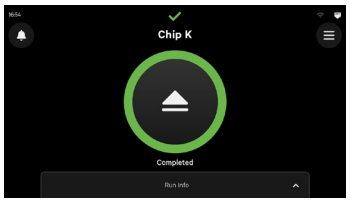


b. Place the assembled chip with the gasket in the tray, ensuring that the chip stays horizontal. Press the button to retract the tray.

c. Press the play button.



d. At completion of the run (~18 min), Chromium X/iX will chime. **Immediately** proceed to the next step.



1.4 Transfer GEMs

a. Place a tube strip on ice.

b. Press the eject button of the instrument 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. Visually compare the remaining volume in rows labeled 1-2. Abnormally high volume in one well relative to other wells may indicate 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.

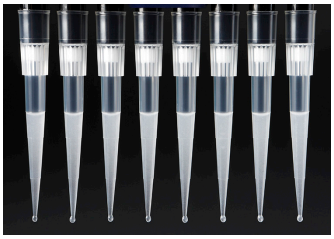
g. Over the course of **~20 sec**, dispense GEMs into the tube strip on ice with the pipette tips against the sidewalls of the tubes.

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

2.4 cDNA QC & Amplification

2.0 Post GEM-RT Cleanup & cDNA Amplification

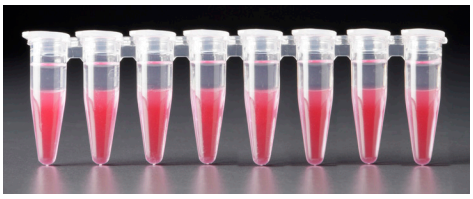
VERSION SPECIFIC

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
☐ ● **cDNA Primers**	2000089	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.	-
Place on ice			
☐ ◯ **Amp Mix** Retrieve from Single Cell 5' GEM Kit	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/ 10x Magnetic Separator B**	-	230003/ 2001212	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

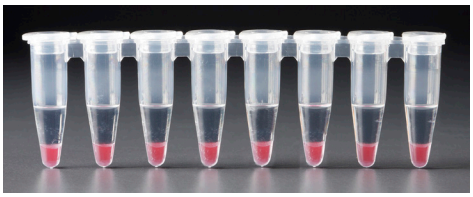


The resulting biphasic mixture contains Recovery Agent/Partitioning Oil (pink) and aqueous phase (clear), with no persisting emulsion (opaque).

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



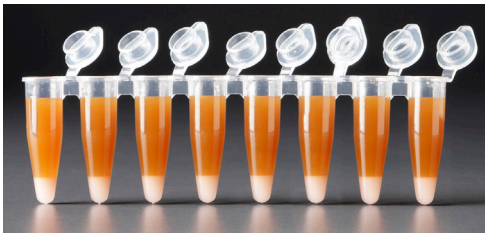
b. Slowly remove and discard **125 µl** Recovery Agent/Partitioning Oil (pink) from the bottom of the tube. DO NOT aspirate any aqueous sample.

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 10x (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.

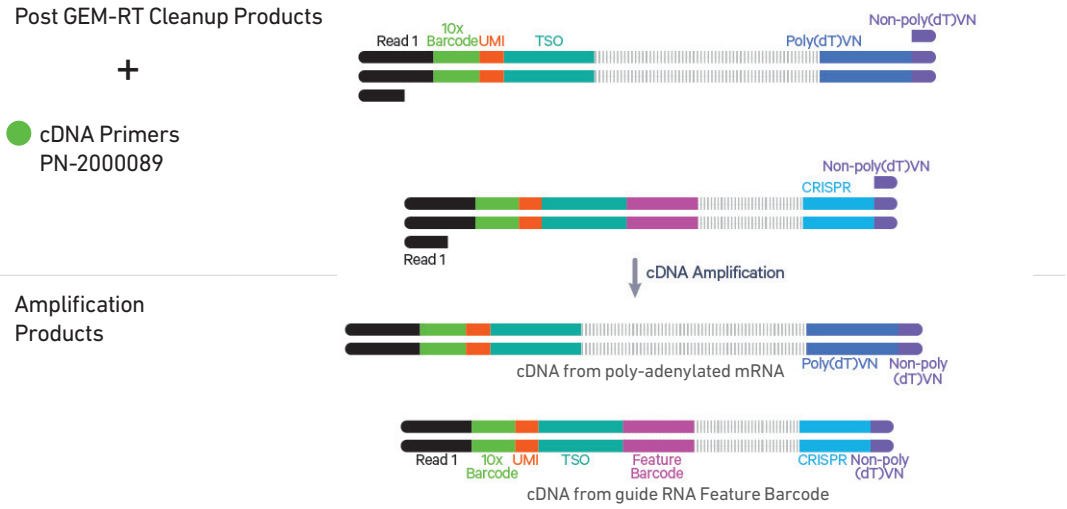
q. Incubate **1 min** at **room temperature**.

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

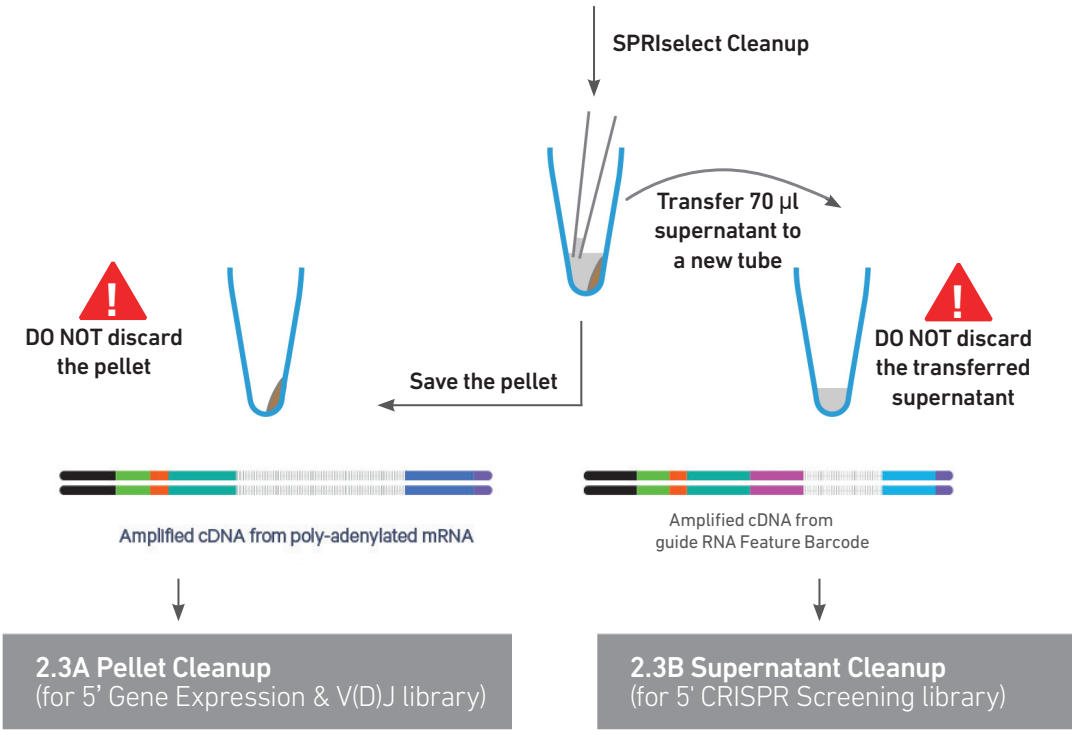
s. Transfer **35 µl** sample to a new tube strip.

Step Overview (steps 2.2 & 2.3)

Amplification Products Generated in Step 2.2 – cDNA Amplification



Step 2.3 – cDNA Cleanup – SPRIselect Overview



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** Retrieve from Single Cell 5' GEM Kit	2000047/ 2000103	50	220	440
● **cDNA Primers** Verify name & PN	2000089	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.

2.3 cDNA Cleanup – SPRIselect

a. Vortex to resuspend the SPRIselect reagent. Add **60 µl** SPRIselect reagent **(0.6X)** to each sample and pipette mix 15x (pipette set to 150 µl).

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

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

d. Transfer and save **70 µl** supernatant in a new tube strip without disturbing the pellet. Maintain at **room temperature**. DO NOT discard the transferred supernatant (cleanup for CRISPR Screening library construction).

e. Remove the remaining supernatant from the pellet without disturbing the pellet. DO NOT discard the pellet (cleanup for V(D)J & 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. 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 **46 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 CRISPR Screening library)

i. Vortex to resuspend the SPRIselect reagent. Add **28 µl** SPRIselect reagent **(1.2X)** to only **70 µl** of the transferred supernatant and pipette mix 15x (pipette set to 80 µl).

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

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

iv. Remove 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 **51 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.

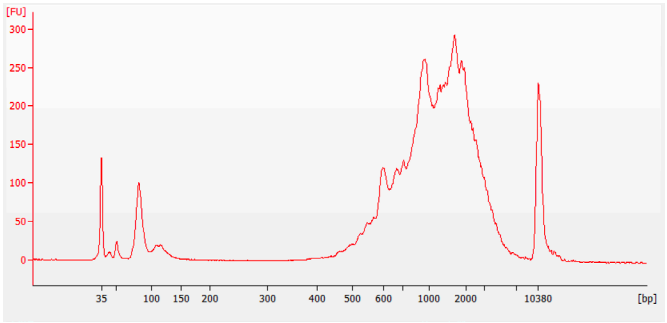
xiii. Transfer **50 µl** sample to a new tube strip.

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 CRISPR Screening Library Construction.

2.4 cDNA QC & Quantification

a. Run **1 µl** undiluted sample 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.

Representative Trace for PBMCs

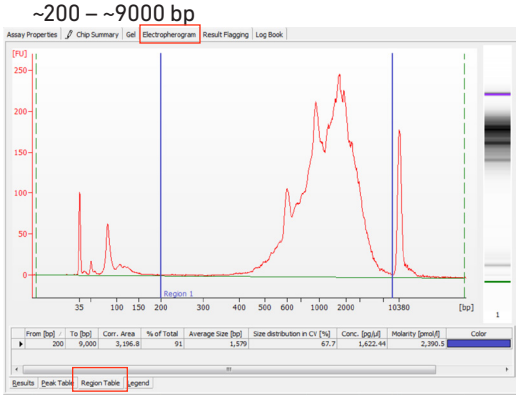


For 5' Gene Expression Library Construction proceed directly to step 5 after step 2.4.

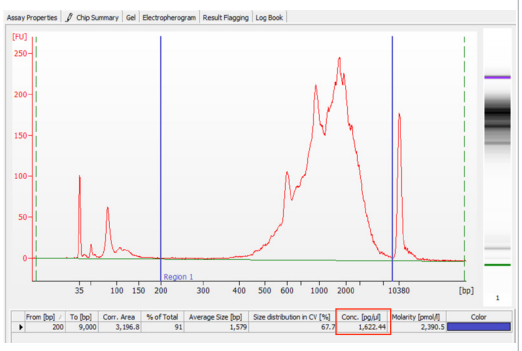
b. If proceeding to 5' GEX Library Construction (step 5), determine cDNA yield for each sample. Example calculation below.

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

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

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

- Agilent TapeStation. See Appendix for representative traces

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.	-
Place on ice			
☐ ◯ **Amp Mix** Retrieve from Single Cell V(D)J Amplification Kits	2000047	Vortex, centrifuge briefly.	–20°C
Obtain			
☐ **Qiagen Buffer EB**	-	Manufacturer's recommendations.	Ambient
☐ **10x Magnetic Separator/ 10x Magnetic Separator B**		230003/ 2001212	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** Retrieve from Single Cell V(D)J Amplification Kits	2000047	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** Retrieve from Single Cell V(D)J Amplification Kits	2000047	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.

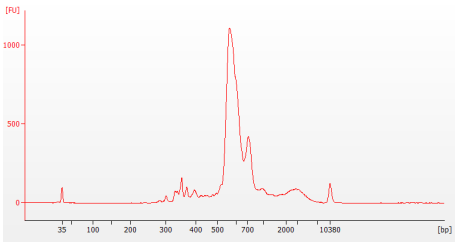
r. Store at **4°C** for up to **72 h** or at **–20°C** for up to **1 week**, or proceed to the next step.

3.5 Post V(D)J Amplification QC & Quantification

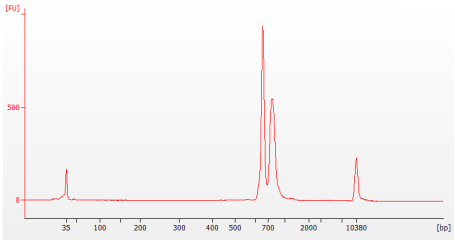
a. Run **1 µl** sample at **1:5 dilution** (Dilution Factor 5) on an Agilent Bioanalyzer High Sensitivity chip.

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

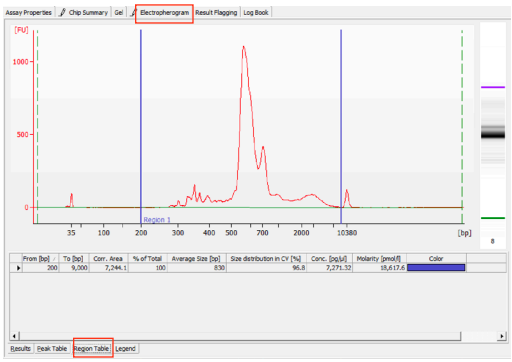


b. Determine yield for each sample. Example calculation below.

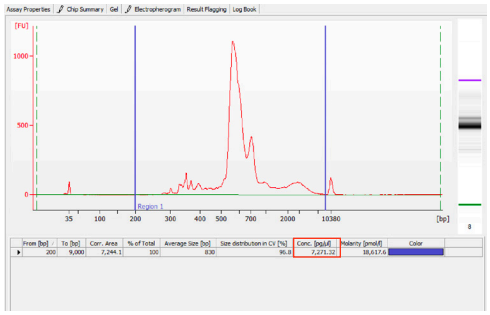
EXAMPLE CALCULATION

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

V(D)J Amplified Product Conc.

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

= **36.35 ng/µl**

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

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

Step 4

V(D)J Library Construction

4.1 Fragmentation, End Repair & A-tailing

4.2 Adaptor Ligation

4.3 Post Ligation Cleanup – SPRIselect

4.4 Sample Index PCR

4.5 Post Sample Index PCR Cleanup – SPRIselect

4.6 Post Library Construction QC

4.0 V(D)J Library Construction

VERSION SPECIFIC

Ensure that Fragmentation Buffer and Fragmentation Enzyme from the same kit are used together. Lots are matched for optimal performance.

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**	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.	-
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
☐ **Qiagen Buffer EB**	-	-	Ambient
☐ **10x Magnetic Separator/ 10x Magnetic Separator B**		230003/ 2001212	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.

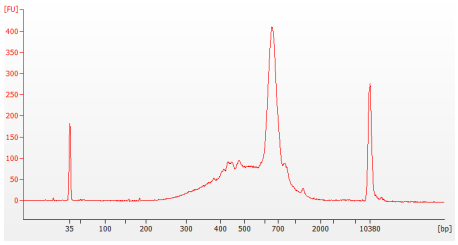
STOP

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

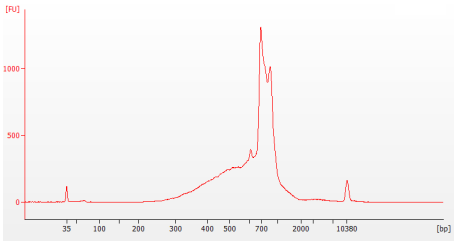
4.6 Post Library Construction QC

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. Select the region between 200-2,000 bp to 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) Dual Index Library Construction

VERSION SPECIFIC

Ensure that Fragmentation Buffer and Fragmentation Enzyme from the same kit are used together. Lots are matched for optimal performance.

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**	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.	-
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/ 10x Magnetic Separator B**		230003/ 2001212	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.

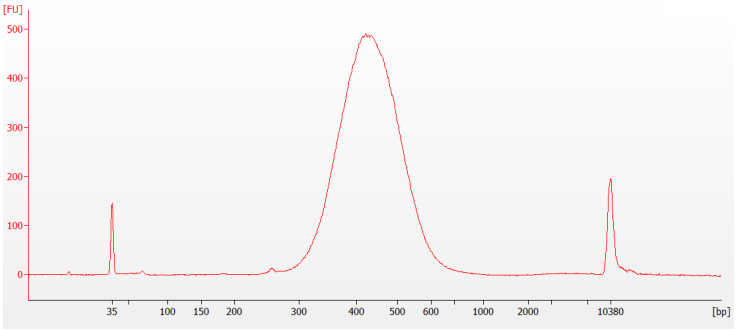
STOP

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.

Representative Trace



b. Select the region between 200-2,000 bp to 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

CRISPR Screening Library Construction

6.1 Guide RNA cDNA Cleanup– SPRIselect

6.2 Feature PCR

6.3 Post Feature PCR Cleanup – SPRIselect

6.4 CRISPR Sample Index PCR

6.5 Post Sample Index PCR Double Sided Size Selection – SPRIselect

6.6 Post Library Construction QC

6.0 CRISPR Screening Library Construction

GET STARTED!

Action	Item	10x PN	Preparation & Handling	Storage
Equilibrate to Room Temperature	**Feature SI Primers 4** Verify name & PN	2000592	Vortex, centrifuge briefly.	–20°C
DUAL INDEX ⚠	**Dual Index Plate TT Set A** Verify name & PN Use indicated plate only	3000431	-	–20°C
	Beckman Coulter SPRIselect Reagent	-	Manufacturer's recommendations.	-
	Agilent TapeStation Screen Tape and Reagents If used for QC		Manufacturer's recommendations.	-
	Agilent Bioanalyzer High Sensitivity kit If used for QC	-	Manufacturer's recommendations.	-
	DNA High Sensitivity Reagent Kit If LabChip used for QC	-	Manufacturer's recommendations.	-
Place on Ice	**Amp Mix** Retrieve from Single Cell 5' CRISPR kit	2000047	Centrifuge briefly.	–20°C
	KAPA Library Quantification Kit for Illumina Platforms	-	Manufacturer's recommendations.	-
Obtain	**Qiagen Buffer EB**	-	-	Ambient
	10x Magnetic Separator/ 10x Magnetic SeparatorB	230003/ 2001212	See Tips & Best Practices.	Ambient
	Prepare 80% Ethanol Prepare 20 ml for 8 reactions	-	Prepare fresh.	Ambient

6.1 Guide RNA cDNA Cleanup – SPRIselect

a. Vortex to resuspend the SPRIselect reagent. Add **50 µl** SPRIselect Reagent (1.0X) to **50 µl** Transfered Supernatant Cleanup (step 2.3B-xiv) and pipette mix 15x (pipette set to 60 µl).

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

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

d. Remove supernatant.

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

f. Remove the ethanol.

g. **Repeat** steps e and f for a total of 2 washes.

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

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

j. Remove from the magnet. Add **40.5 µl** Buffer EB. Pipette mix 15x.

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

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

m. Transfer 40 **µl** sample to a new tube strip.

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

6.2 Feature PCR

a. Prepare Feature PCR Mix on ice. Vortex and centrifuge briefly.

Feature PCR Mix *Add reagents in the order listed*	PN	1X (µl)	4X + 10% (µl)	8X + 10% (µl)
○ **Amp Mix**	2000047	50	220	440
● **Feature SI Primers 4**	2000592	45	198	396
Total	-	**95**	**418**	**836**

b. Transfer **ONLY 5 µl** from Guide RNA cDNA Cleanup (step 6.1m) to a new tube strip.
Note that only **5 µl** of the DNA sample transfer is sufficient for generating CRISPR Screening library. The remaining **35 µl** sample can be stored at **4°C** for up to **72 h** or at **–20°C** for up to **4 weeks,** for generating additional CRISPR Screening libraries.

c. Add **95 µl** Feature PCR Mix to **5 µl** sample.

d. Pipette mix 15x (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 min
Step	**Temperature**	**Time**
1	98°C	00:00:45
2	98°C	00:00:20
3	62°C	00:00:10
4	72°C	00:00:10
5	Go to Step 2, repeat 9X for a total of 10 cycles	
6	72°C	00:01:00
7	4°C	Hold

6.3 Post Feature PCR Cleanup – SPRIselect

a. Vortex to resuspend SPRIselect Reagent. Add **100 µl** SPRIselect Reagent **(1.0X)** 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 **300 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 **1 min**.
DO NOT exceed **1 min** as this will decrease elution efficiency.

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.

6.4 CRISPR Sample Index PCR

DUAL INDEX

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) to **30 µl P**ost Feature PCR cleanup sample (step 6.3m).

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

DUAL INDEX

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

Lid Temperature	Reaction Volume	Run Time
105°C	100 µl	~25 min
Step	**Temperature**	**Time**
1	98°C	00:00:45
2	98°C	00:00:20
3	62°C	00:00:10
4	72°C	00:00:10
5	Go to step 2, repeat 9X for a total of 10 cycles	
6	72°C	00:01:00
7	4°C	Hold

6.5 Post Sample Index PCR Double Sided Size Selection – SPRIselect

a. Vortex to resuspend the SPRIselect reagent. Add **70 µl** SPRIselect Reagent **(0.7X)** 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. DO NOT discard supernatant.

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

e. Vortex to resuspend the SPRIselect reagent. Add **30 µl** SPRIselect Reagent **(1.0X)** to each sample. Pipette mix 15x (pipette set to 150 µl).

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

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

h. Remove the supernatant.

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

j. Remove the ethanol.

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

l. Remove the ethanol.

m. Centrifuge briefly. Place on the magnet•**Low**.

n. Remove remaining ethanol. Air dry for 1 min.

o. Remove from the magnet. Add **40.5 µl** Buffer EB. Pipette mix 15x.

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

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

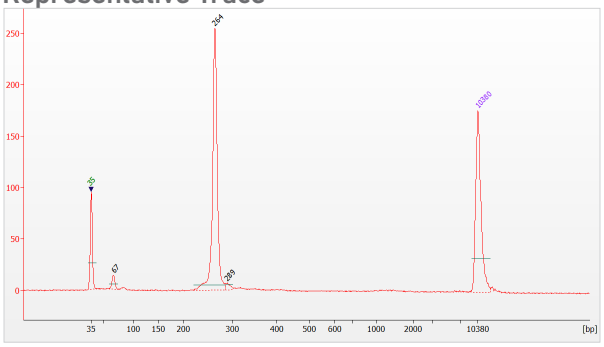
r. Transfer **40 µl** to a new tube strip.

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

6.6 Post Library Construction QC

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

Representative Trace



Select the region between 200-400 bp to determine the average fragment size from the Bioanalyzer trace. This will be used as the insert size for library quantification.

Alternate QC Method:

- Agilent TapeStation
- LabChip

See Appendix for representative trace

See Appendix for Post Library Construction Quantification

Sequencing

7

Sequencing Libraries

Chromium Single Cell V(D)J, 5' Gene Expression, and 5' CRISPR Screening 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 10 bp i5 and i7 index reads. TruSeq Read 1 and TruSeq Read 2 are standard Illumina sequencing primer sites used in paired-end sequencing of V(D)J, 5' Gene Expression, and 5' CRISPR Screening libraries. 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' CRISPR Screening Dual Index Library

Generating and sequencing a 5' Gene Expression library along with the V(D)J library is highly recommended as it greatly enhances cell calling when run with "cellranger multi" command and facilitates downstream troubleshooting during data analysis. If data from GEX library is not required, shallow sequencing (5,000 read pairs/cell) can be used for GEX library as opposed to the typical sequencing recommendation (20,000 read pairs/cell). The minimum GEX sequencing depth needed for accurate cell calling may vary based on the sample type and data quality.

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 6000

*5' CRISPR libraries have not been tested on this sequencer

Sample Indices

Each well of the Dual Index Kit TT Set A (PN-1000215) 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.

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 library Minimum 20,000 read pairs per cell for 5' Gene Expression library Minimum 5,000 read pairs per cell for 5' CRISPR Screening 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 5' CRISPR Screening 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 6000 standard workflow	300	1
*NovaSeq 6000 Xp workflow	150	1
NextSeq 2000	650	1

**The NovaSeq 6000 standard workflow permits loading one library pool across all lanes of the flow cell; whereas the Xp workflow enables sequencing various library pools in each lane of the NovaSeq 6000 flow cell. The recommended loading concentrations for the standard workflow are higher than the Xp workflow. For more information on both workflows, refer to the NovaSeq 6000 Denature and Dilute Guide*

Library quantification should be done with the KAPA DNA Quantification Kit using the average insert size determined by Agilent Bioanalyzer, Perkin Elmer LabChip, or Agilent TapeStation QC. Alternate methods to KAPA qPCR for final library quantification may result in under quantification, and consequently overloading.

Library Pooling

V(D)J, 5' Gene Expression, and CRISPR Screening libraries may be pooled for sequencing, taking into account the differences in depth requirements between the pooled libraries. 5' Gene Expression libraries may be sequenced using enriched library parameters, however the cost of sequencing using enriched library parameters is higher.

DO NOT sequence CRISPR Screening libraries alone.

Library Pooling Example:

Libraries	Sequencing Depth (read pairs per cell)	Library Pooling Ratio
V(D)J library	5,000	1
5' Gene Expression library	20,000	4
5' CRISPR Screening	5,000	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

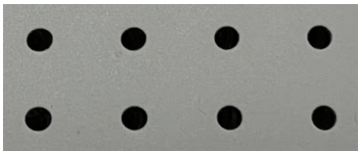
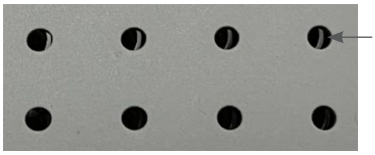
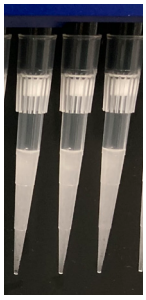
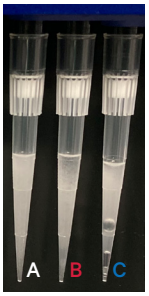
Loupe Browser is an interactive data visualization tool that requires no prior programming knowledge.

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

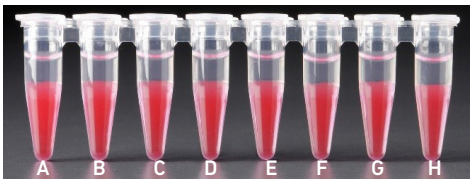
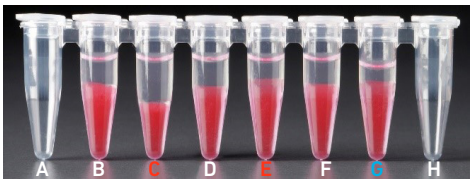
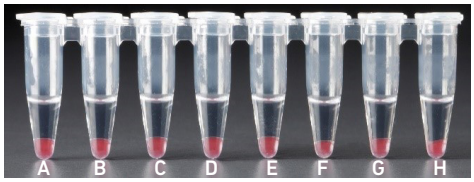
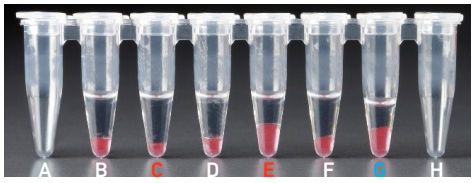
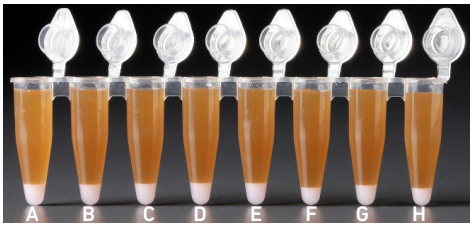
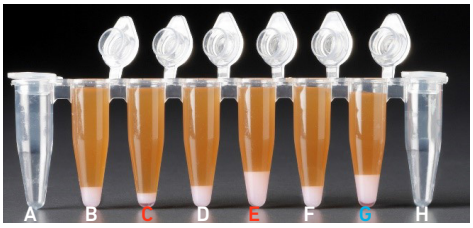
Troubleshooting

8

GEM Generation & Barcoding

STEP	NORMAL	IMPACTED
1.2 Load Chromium Next GEM Chip K	 Gasket holes are aligned with the sample and gel bead wells.	 Gasket holes are misaligned with the gel bead wells. Open and close the chip holder slowly once.
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.	 Adequate emulsion volume (no clog or wetting failure) Wetting failure Low emulsion volume (clog) Pipette tip A shows normal GEM generation, pipette tip B indicates a wetting failure, and pipette tip C shows a clog and wetting failure.

Consult the Best Practices to Minimize Chromium Next GEM Chip Clogs and Wetting Failures (Technical Note CG000479) for more information.

STEP	NORMAL	IMPACTED
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. Replacement reagents and chips may be provided for properly documented clogs or wetting failures if they are associated with runs of unexpired reagents and chips, and are reported within 30 days of the expiration date. Consult the Best Practices to Minimize Chromium Next GEM Chip Clogs and Wetting Failures (Technical Note CG000479) for more information.

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, open and close the lid to ensure the gasket is properly aligned, and try again. If the error message is still received after trying this more than twice, contact support@10xgenomics.com for further assistance.

   ii. If this message is received after a few minutes into the run, the Chromium Next GEM Chip must be discarded. **Do not try running this Chromium Next GEM Chip again as this may damage the Chromium Controller.**

d. **Invalid Chip CRC Value:** This indicates that a Chromium Next GEM Chip has been used with an older firmware version. The chip must be discarded. Contact support@10xgenomics.com for further assistance.

e. **Chip Holder Not Present:** Open the controller drawer and check if chip holder is present. Insert chip properly into chip holder and retry.

f. **Unauthorized Chip:** This indicates that an incompatible non-Next GEM chip has been used with an instrument that only can run Next GEM assays. Use only Chromium Controller (PN-120223;120246) or Chromium Single Cell Controller (PN-120263;120212) to run that chip or chip must be discarded. Contact support@10xgenomics.com for further assistance.

g. **Endpoint Reached Early:** If this message is received, contact support@10xgenomics.com for further assistance.

Chromium X Series Errors

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

There are two types of errors:

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

a. System Error

b. Pressure Error

c. Chip Error

d. Run Error

e. Temperature Error

f. Software Error

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

a. Gasket Error

b. Tray Error

c. Chip Error

d. Unsupported Chip Error

e. Update Error

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

Appendix

Post Library Construction Quantification

Agilent TapeStation Traces

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)	

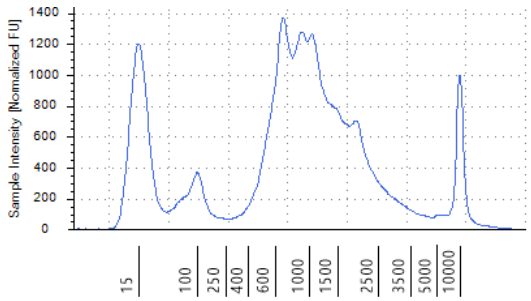
g. Follow the manufacturer's recommendations for qPCR-based quantification. For library quantification for sequencer clustering, determine the concentration based on insert size derived from the Bioanalyzer/TapeStation trace.

Agilent TapeStation

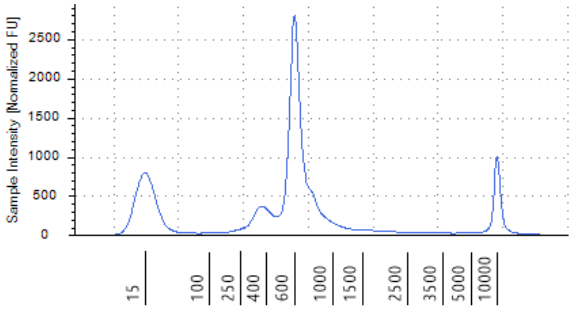
Agilent TapeStation Traces

Agilent TapeStation High Sensitivity D5000 ScreenTape was used.

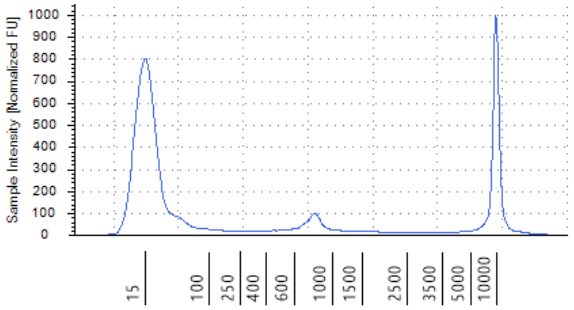
Protocol Step 2.4 – cDNA QC & Quantification



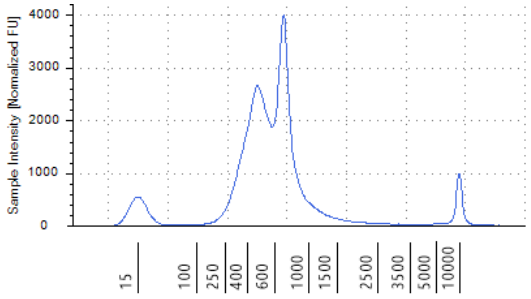
Protocol Step 3.5 – Post TCR Amplification QC



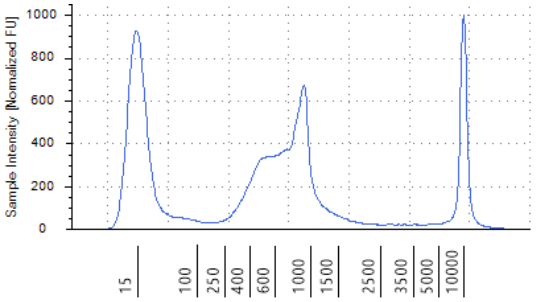
Protocol Step 3.5 – Post BCR Amplification QC



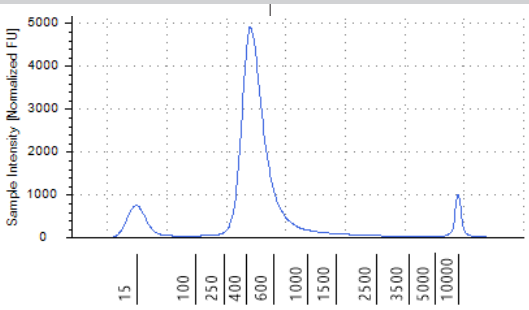
Protocol Step 4.6 – Post Library Construction QC
(PBMCs amplified for TCR)



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



Protocol Step 5.7 – GEX Post Library Construction QC

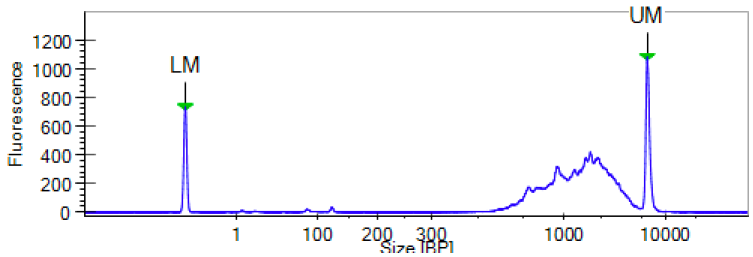


All traces are representative

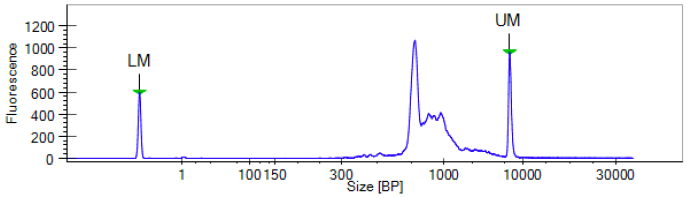
LabChip Traces

LabChip Traces
DNA High Sensitivity Reagent Kit was used.

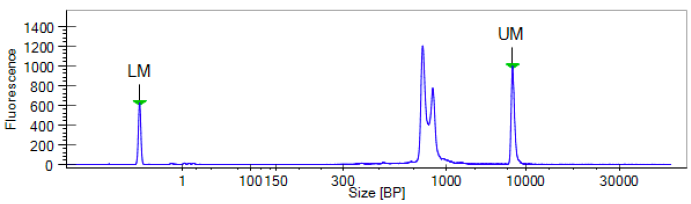
Protocol Step 2.4 – cDNA QC & Quantification



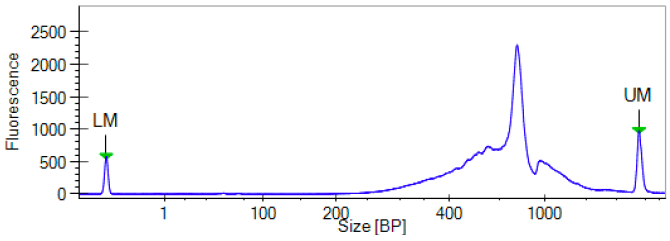
Protocol Step 3.5 – Post TCR Amplification QC



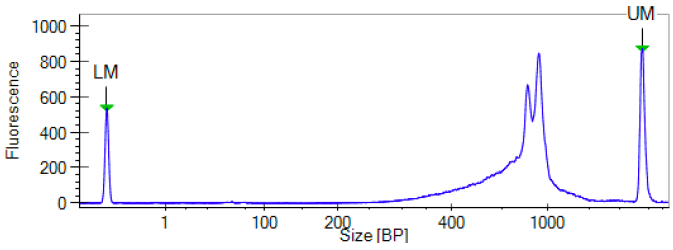
Protocol Step 3.5 – Post BCR Amplification QC



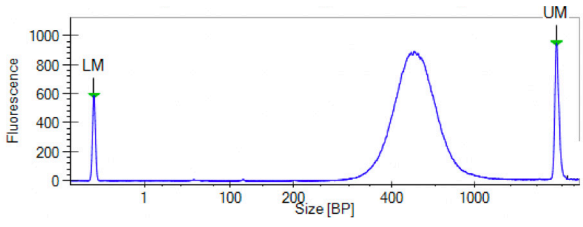
Protocol Step 4.6 – Post Library Construction QC
(PBMCs amplified for TCR)



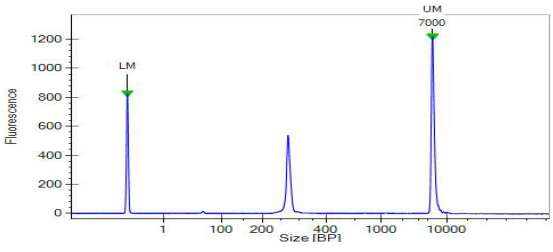
Protocol Step 4.6 – Post Library Construction QC
(PBMCs amplified for BCR)



Protocol Step 5.7 – GEX Post Library Construction QC



Protocol Step 6.5 – CRISPR Post Library Construction QC



All traces are representative

Oligonucleotide Sequences

Protocol Step 1.5 – GEM-RT Incubation

Gel Bead Primer

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

CRISPR Poly-dT RT Primer Mix PN-2000593

5'-AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTVN-3'

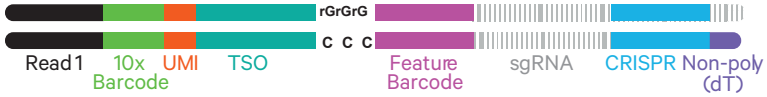
5'-AAGCAGTGGTATCAACGCAGAGTACCAAGTTGATAACGGACTAGCC-3'

GEM-RT Products

cDNA from poly-adenylated mRNA

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

cDNA from guide RNA Feature Barcode

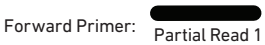


5'-CTACACGACGCTCTTCCGATCT-N16-N10-TTTCTTATATGGG-FeatureBarcode-sgRNA-AATAAGGCTAGTCCGTTATCAACTTG-3'

3'-GATGTGCTGCGAGAAGGCTAGA-N16-N10-AAAGAATATACCC-FeatureBarcode-sgRNA-TTATTCCGATCAGGCAATAGTTGAACGAGACGCAACTATGGTGACGAA-5'

Protocol Step 2.2 – cDNA Amplification

cDNA Primers -2000089

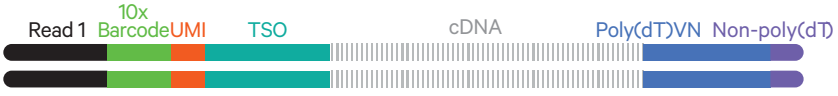


5'-CTACACGACGCTCTTCCGATCT-3'

5'-AAGCAGTGGTATCAACGCAGAG-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 cDNA from sgRNA

5'-CTACACGACGCTCTTCCGATCT-N16-N10-TTTCTTATATGGG-FeatureBarcode-sgRNA-AATAAGGCTAGTCCGTTATCAACTTGCTCTGCGTTGATACCACTGCTT-3'

3'-GATGTGCTGCGAGAAGGCTAGA-N16-N10-AAAGAATATACCC-FeatureBarcode-sgRNA-TTATTCCGATCAGGCAATAGTTGAACGAGACGCAACTATGGTGACGAA-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 Amplified 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 Oligos PN-2000094

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

Ligation Product

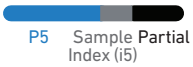
5′–GATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT-N16-N10-TTTCTTATATGGG-cDNA_Insert-AGATCGGAAGAGCACACGTCTGAACTCCAGTCAC–3′
3′–CTAGATGTGAGAAAGGGATGTGCTGCGAGAAGGCTAGA-N16-N10-AAAGAATATACCC-cDNA_Insert-TCTAGCCTTCTCG–5′

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

Dual Indexing

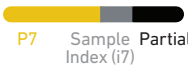
Dual Index Kit TT Set A PN-1000215

Forward Primer:



5′-AATGATACGGCGACCACCGAGATCTACAC-N10-ACACTCTTTCCCTACACGACGCTC-3′

Reverse Primer:



5′-CAAGCAGAAGACGGCATACGAGAT-N10-GTGACTGGAGTTCAGACGTGT-3′

Sample Index PCR Product

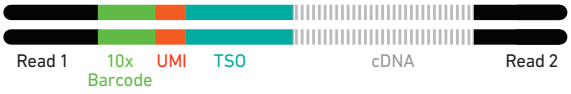
5′-AATGATACGGCGACCACCGAGATCTACAC-N10 -ACACTCTTTCCCTACACGACGCTCTTCCGATCT-N16-N10-TTTCTTATATGGG-Insert-AGATCGGAAGAGCACACGTCTGAACTCCAGTCAC-N10-ATCTCGTATGCCGTCTTCTGCTTG-3′
3′-TTACTATGCCGCTGGTGGCTCTAGATGTG-N10-TGTGAGAAAGGGATGTGCTGCGAGAAGGCTAGA-N16-N10-AAAGAATATACCC-Insert-TCTAGCCTTCTCGTGTGCAGACTTGAGGTCAGTG-N10-TAGAGCATACGGCAGAAGACGAAC-5′

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

Adaptor Oligos PN-2000094

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

Ligation Product



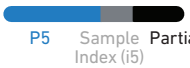
5′–CTACACGACGCTCTTCCGATCT-N16-N10-TTTCTTATATGGG-cDNA_Insert-AGATCGGAAGAGCACACGTCTGAACTCCAGTCAC–3′
3′–GATGTGCTGCGAGAAGGCTAGA-N16-N10-AAAGAATATACCC-cDNA_Insert-TCTAGCCTTCTCG–5′

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

Dual Indexing

Dual Index TT Set A PN-1000215

Forward Primer:

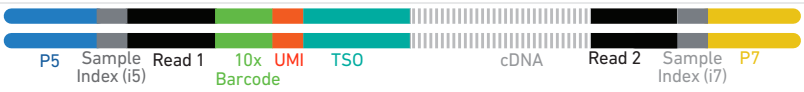


5′-AATGATACGGCGACCACCGAGATCTACAC-N10-ACACTCTTTCCCTACACGACGCTC-3′

Reverse Primer:

5′-CAAGCAGAAGACGGCATACGAGAT-N10-GTGACTGGAGTTCAGACGTGT-3′

Sample Index PCR Product



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

Protocol Step 6.2 –Guide Feature PCR (for 5' CRISPR Screening Library Construction)

Feature SI Primers 4
PN-2000592

Forward primer: Read 1

5'-GATCTACACTCTTTCCCTACACGACGC-3'

CRISPR Enrichment Primer: Partial Read 2 Feature Primer

5'-GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCAAGTTGATAACGGACTAGCCTTATT-3'

Feature PCR Product

5'-GATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT-N16-N10-TTTCTTATATGGG-FeatureBarcode_sgRNA-AATAAGGCTAGTCCGTTATCAACTTGAGATCGGAAGAGCACACGTCTGAACTCCAGTCAC-3'
3'-CTAGATGTGAGAAAGGGATGTGCTGCGAGAAGGCTAGA-N16-N10-AAAGAATATACCC-FeatureBarcode_sgRNATTATTCCGATCAGGCAATAGTTGAACTCTAGCCTTCTCGTGTGCAGACTTGAGGTCAGTG-5'

Protocol Step 6.4 – Sample Index (for 5' CRISPR Screening Library Construction)

Dual Indexing
Dual Index TT
Set A
PN-1000215

Forward Primer: P5 Sample Index (i5) Partial Read 1

5'-AATGATACGGCGACCACCGAGATCTACAC-N10-ACACTCTTTCCCTACACGACGCTC-3'

Reverse Primer: P7 Sample Index (i7) Partial Read 2

5'-CAAGCAGAAGACGGCATACGAGAT-N10-GTGACTGGAGTTCAGACGTGT-3'

Sample Index PCR Product

5''-AATGATACGGCGACCACCGAGATCTACAC-N10-ACACTCTTTCCCTACACGACGCTCTTCCGATCT-N16-N10-TTTCTTATATGGG-FeatureBarcode_sgRNA-AATAAGGCTAGTCCGTTATCAACTTGAGATCGGAAGAGCACACGTCTGAACTCCAGTCAC-N10-ATCTCGTATGCCGTCTTCTGCTTG-3'
3'-TTACTATGCCGCTGGTGGCTCTAGATGTG-N10-TGTGAGAAAGGGATGTGCTGCGAGAAGGCTAGA-N16-N10-AAAGAATATACCC-FeatureBarcode_sgRNA-TTATTCCGATCAGGCAATAGTTGAACTCTAGCCTTCTCGTGTGCAGACTTGAGGTCAGTG-N10-TAGAGCATACGGCAGAAGACGAAC-5