

USER GUIDE

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

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



FOR USE WITH

Chromium Next GEM Single Cell 5' Kit v2, 16 rxns PN-1000263  
Chromium Next GEM Single Cell 5' Kit v2, 4 rxns PN-1000265  
Library Construction Kit, 16 rxns PN-1000190  
Chromium 5' Feature Barcode Kit, 16 rxns PN-1000541  
Chromium Single Cell Human TCR Amplification Kit, 16 rxns PN-1000252  
Chromium Single Cell Human BCR Amplification Kit, 16 rxns PN-1000253  
Chromium Single Cell Mouse TCR Amplification Kit, 16 rxns PN-1000254  
Chromium Single Cell Mouse BCR Amplification Kit, 16 rxns PN-1000255  
Chromium Next GEM Chip K Single Cell Kit, 48 rxns PN-1000286  
Chromium Next GEM Chip K Single Cell Kit, 16 rxns PN-1000287  
Dual Index Kit TT Set A, 96 rxns PN-1000215  
Dual Index Kit TN Set A, 96 rxns PN-1000250

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

# Notices

## Document Number

CG000330 • Rev G

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Summary

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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 33.
- Added additional guidance on library quantification on page 71.

General Changes:

Updates for general minor consistency of language and terms throughout.

# Table of Contents

Introduction	6
Chromium Next GEM Single Cell 5' Reagent Kits v2 (Dual Index)	7
10x Genomics Accessories	12
Recommended Thermal Cyclers	12
Additional Kits, Reagents & Equipment	13
Recommended Pipette Tips	14
Protocol Steps & Timing	15
Stepwise Objectives	16
Cell Labeling Guidelines	21
Tips & Best Practices	22
Step 1	29
GEM Generation & Barcoding	30
1.1 Prepare Reaction Mix	31
1.2 Load Chromium Next GEM Chip K	33
1.3 Run the Chromium Controller or X/iX	34
1.4 Transfer GEMs	36
1.5 GEM-RT Incubation	36
Step 2	37
Post GEM-RT Cleanup & cDNA Amplification	38
2.1 Post GEM-RT Cleanup – Dynabeads	39
2.2 cDNA Amplification	41
Step Overview (steps 2.2 & 2.3)	42
2.3 cDNA Cleanup – SPRIselect	43
2.3A Pellet Cleanup (for V(D)J & 5' Gene Expression library)	43
2.3B Transferred Supernatant Cleanup (for Cell Surface Protein/Immune Receptor Mapping library)	43
2.4 cDNA QC & Quantification	44
Step 3	45
V(D)J Amplification from cDNA	46
3.1 V(D)J Amplification 1	47
3.2 Post V(D)J Amplification 1 Cleanup Double Sided Size Selection – SPRIselect	48
3.3 V(D)J Amplification 2	49
3.4 Post V(D)J Amplification 2 Cleanup Double Sided Size Selection – SPRIselect	50
3.5 Post V(D)J Amplification QC & Quantification	51

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Step 4	52
V(D)J Library Construction	53
4.1 Fragmentation, End Repair & A-tailing	54
4.2 Adaptor Ligation	55
4.3 Post Ligation Cleanup – SPRIselect	55
4.4 Sample Index PCR	56
4.5 Post Sample Index PCR Cleanup – SPRIselect	57
4.6 Post Library Construction QC	57
Step 5	58
5' Gene Expression (GEX) Library Construction	59
5.1 GEX Fragmentation, End Repair & A-tailing	60
5.2 GEX Post Fragmentation, End Repair & A-tailing Double Sided Size Selection – SPRIselect	61
5.3 GEX Adaptor Ligation	62
5.4 GEX Post Ligation Cleanup – SPRIselect	62
5.5 GEX Sample Index PCR	63
5.6 GEX Post Sample Index PCR Double Sided Size Selection – SPRIselect	64
5.7 GEX Post Library Construction QC	64
Step 6	65
Cell Surface Protein/Immune Receptor Mapping Library Construction	66
6.1 Sample Index PCR	67
6.2 Post Sample Index PCR Size Selection – SPRIselect	68
6.3 Post Library Construction QC	68
Sequencing	69
Troubleshooting	73
GEM Generation & Barcoding	74
Chromium Controller Errors	76
Appendix	77
Post Library Construction Quantification	78
Agilent TapeStation Traces	79
LabChip Traces	80
Oligonucleotide Sequences	81

# Introduction

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

10x Genomics Accessories

Recommended Thermal Cyclers

Additional Kits, Reagents & Equipment

Protocol Steps & Timing

Stepwise Objectives

Cell Labeling Guidelines

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

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

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

Chromium Next GEM Single Cell 5' GEM Kit v2		
	#	PN
● RT Reagent B	1	2000165
● RT Enzyme C	1	2000085
○ Reducing Agent B	1	2000087
● Poly-dT RT Primer	1	2000007
● Cleanup Buffer	2	2000088
○ Amp Mix	1	2000047
● cDNA Primers	1	2000089

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#### 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

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#### 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

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#### 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

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### 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

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### 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










## Chromium 5' Feature Barcode Kit, 16 rxns PN-1000541 (store at -20°C)

Chromium 5' Feature Barcode Kit		
	#	PN
 Feature cDNA Primers 4	1	2000277
 Feature cDNA Primers 5	1	2000812
 Amp Mix	2	2000047

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## 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

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

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

### TCR Amplification Kit, 16 rxns PN-1000252

**Chromium  
Single Cell  
Human TCR  
Amplification Kit**

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

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### BCR Amplification Kit, 16 rxns PN-1000253

**Chromium  
Single Cell  
Human BCR  
Amplification Kit**

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

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

### TCR Amplification Kit, 16 rxns PN-1000254

**Chromium  
Single Cell  
Mouse TCR  
Amplification Kit**

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

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### BCR Amplification Kit, 16 rxns PN-1000255

**Chromium  
Single Cell  
Mouse BCR  
Amplification Kit**

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

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

Chromium Partitioning Oil			Chromium Recovery Agent		
	#	PN		#	PN
Partitioning Oil	6	2000190	<input type="radio"/> Recovery Agent	6	220016

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


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

Chromium Partitioning Oil			Chromium Recovery Agent		
	#	PN		#	PN
Partitioning Oil	2	2000190	<input type="radio"/> Recovery Agent	2	220016

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

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

Dual Index Kit TT Set A					
	#	PN		#	PN
Dual Index Plate TT Set A	1	3000431			

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

## Dual Index Kit TN Set A

	#	PN
Dual Index Plate TN Set A	1	3000510

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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 listed items have been tested by 10x Genomics and perform optimally with the assay. Substituting materials may adversely affect system performance. This list may not include some standard laboratory equipment.

Supplier	Description	Part Number (US)
<b>Plastics</b>		
Eppendorf	PCR Tubes 0.2 ml 8-tube strips DNA LoBind Tubes, 1.5 ml DNA LoBind Tubes, 2.0 ml	951010022 022431021 022431048
USA Scientific	TempAssure PCR 8-tube strip	1402-4700
Thermo Fisher Scientific	MicroAmp 8-Tube Strip, 0.2 ml MicroAmp 8-Cap Strip, clear	N8010580 N8010535
<b>Kits &amp; Reagents</b>		
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
<b>Equipment</b>		
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
<b>Quantification &amp; Quality Control</b>		
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

## Recommended Pipette Tips

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)
<b>Recommended Pipettes &amp; Pipette tips</b>		
Rainin	<b>Pipettes</b>	
	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
	<b>Pipette Tips</b>	
	Tips LTS 200UL Filter RT-L200FLR	30389240
	Tips LTS 1ML Filter RT-L1000FLR	30389213
	Tips LTS 20UL Filter RT-L10FLR	30389226
<b>Alternate Recommendations</b> <i>(If Rainin pipette tips are unavailable, any of the listed pipette tips may be used)</i>		
Eppendorf	<b>Pipettes</b>	
	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
	<b>Pipette Tips</b> (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 1000 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 &amp; Timing

	Steps	Timing	Stop & Store
3 h	<b>Cell Preparation and Labeling</b> Dependent on cell type and labeling protocol used	~1-2 h	
	<b>Step 1 – GEM Generation &amp; Barcoding</b>		
	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	
6 h	1.5 GEM-RT Incubation	55 min	STOP 4°C ≤ 72 h or -20°C ≤ 1 week
	<b>Step 2 – Post GEM RT Cleanup, cDNA Amplification &amp; QC</b>		
	2.1 Post GEM-RT Cleanup – Dynabead	45 min	
	2.2 cDNA Amplification	50 min	STOP 4°C ≤ 72 h or -20°C ≤ 1 week
	2.3 cDNA Cleanup		
	2.3A Pellet Cleanup	15 min	STOP 4°C ≤ 72 h or -20°C ≤ 4 weeks
10 h plus*	2.3B Supernatant Cleanup	20 min	STOP 4°C ≤ 72 h or -20°C ≤ 4 weeks
	2.4 cDNA Quantification & QC	50 min	
	<b>Step 3 – V(D)J Amplification from cDNA</b>		
	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
10 h plus*	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	
	<b>Step 4 – V(D)J Library Construction</b>		
	4.1 Fragmentation, End Repair & A-tailing	45 min	
	4.2 Adaptor Ligation	25 min	
	4.3 Post Ligation Cleanup – SPRIselect	20 min	
10 h plus*	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	
	<b>Step 5 – 5' Gene Expression (GEX) Library Construction</b>		
	5.1 GEX Fragmentation, End Repair & A-tailing	45 min	
	5.2 GEX Post Fragmentation, End Repair & A-tailing Double Sided Size Selection – SPRIselect	30 min	
10 h plus*	5.3 GEX Adaptor Ligation	25 min	
	5.4 GEX Post Ligation Cleanup – SPRIselect	20 min	
	5.5 GEX Sample Index PCR	40 min	STOP 4°C ≤ 72 h
	5.6 GEX Post Sample Index PCR Double Sided Cleanup – SPRIselect	30 min	STOP 4°C ≤ 72 h or -20°C long-term
	5.7 GEX Post Library Construction QC	50 min	
	<b>Step 6 – Cell Surface Protein/Immune Receptor Mapping Library Construction</b>		
10 h plus*	6.1 Sample Index PCR	30 min	
	6.2 Post Sample Index PCR Size Selection – SPRIselect	20 min	STOP 4°C ≤ 72 h or -20°C long-term
	6.3 Post Library Construction QC	50 min	

\*Time dependent  
on Stop options  
used.

## Stepwise Objectives



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

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

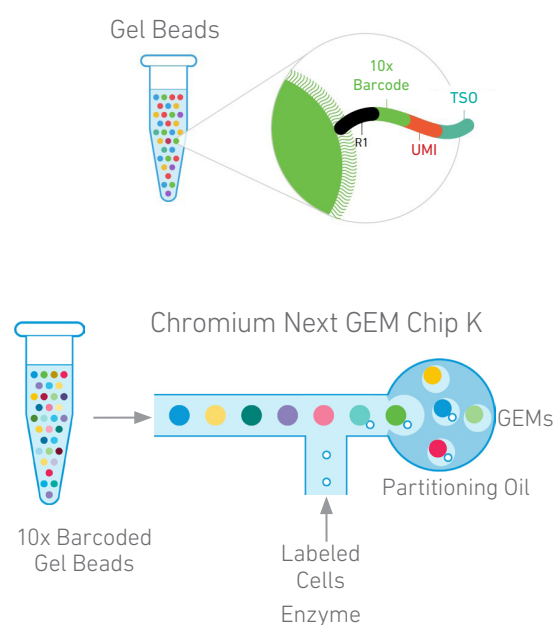
This document outlines the protocols to generate the following libraries:

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

### Step 1 GEM Generation & Barcoding

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

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





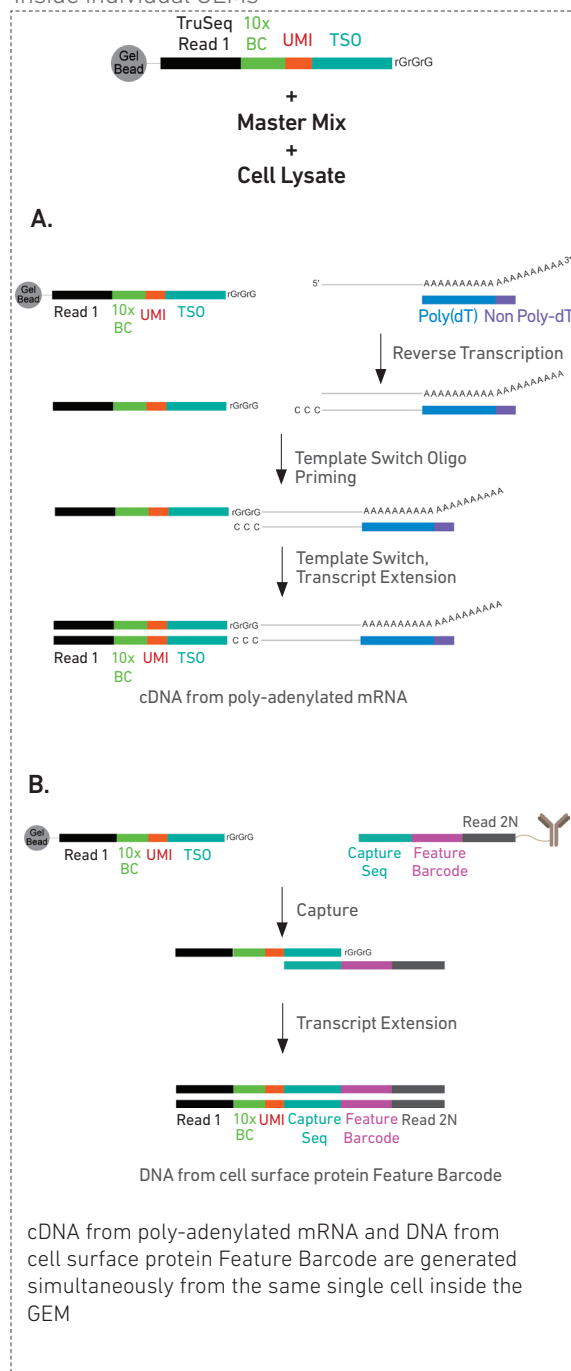
## Step 1 GEM Generation & Barcoding

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

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

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

### Inside individual GEMs



## Step 2

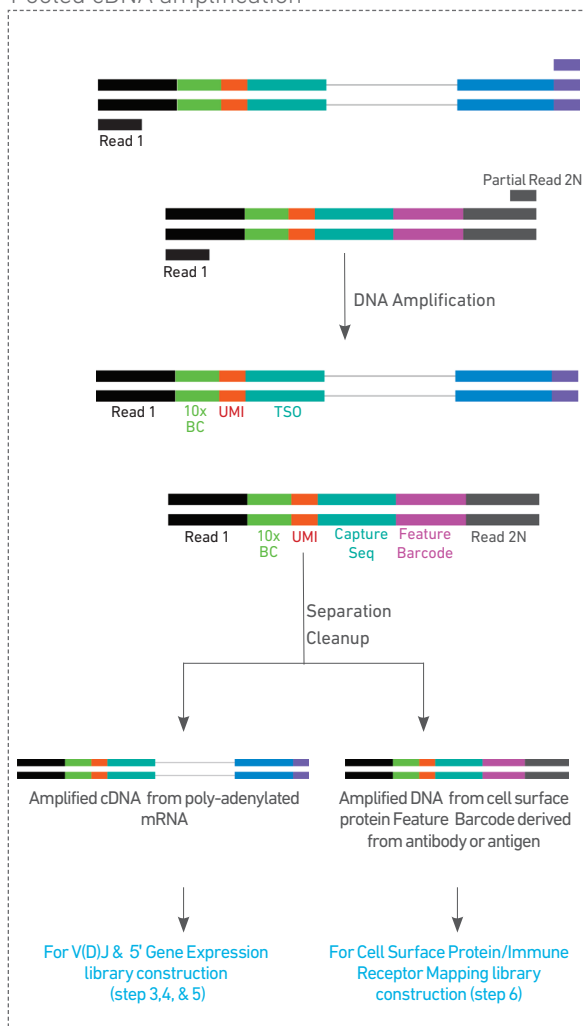
### Post GEM-RT Cleanup & cDNA Amplification

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

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

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

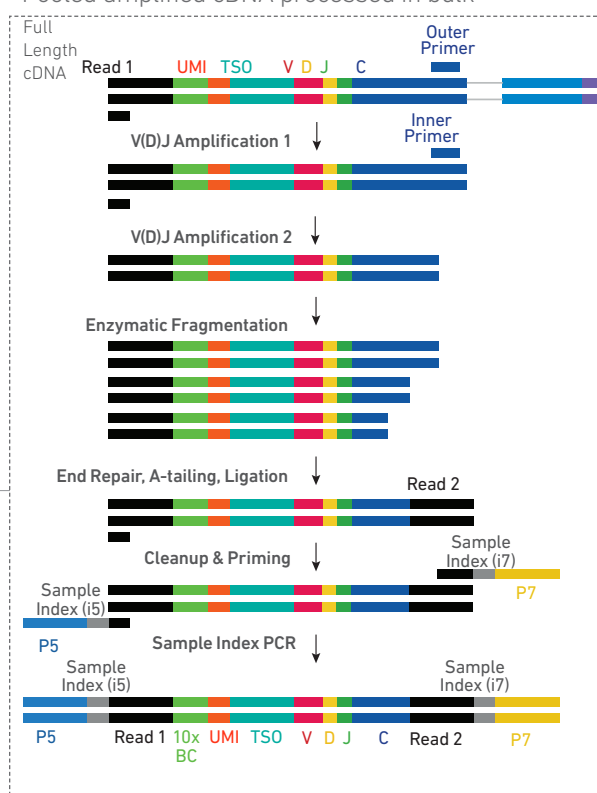
#### Pooled cDNA amplification



### Step 3 V(D)J Amplification from cDNA

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

#### Pooled amplified cDNA processed in bulk

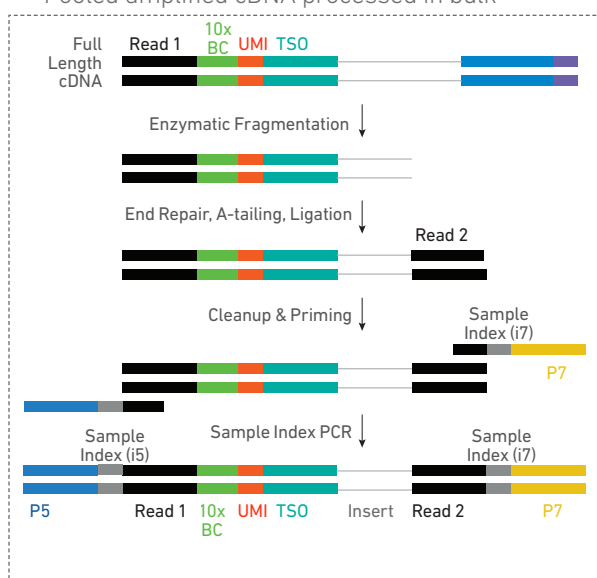


P5, P7, i5 and i7 sample indexes, and an Illumina R2 sequence (read 2 primer sequence) are added via End Repair, A-tailing, Adaptor Ligation, and Sample Index PCR. The final libraries contain the P5 and P7 priming sites used in Illumina sequencing.

### Step 4 V(D)J Library Construction

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

#### Pooled amplified cDNA processed in bulk



### Step 5 5' Gene Expression (GEX) Library Construction

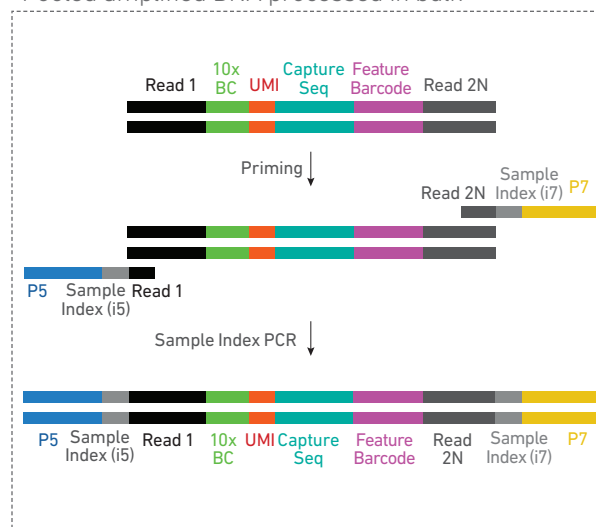
Amplified full-length cDNA from poly-adenylated mRNA is used to generate 5' Gene Expression library. Enzymatic fragmentation and size selection are used to optimize the cDNA amplicon size prior to 5' gene expression library construction. P5, P7, i5 and i7 sample indexes, and Illumina R2 sequence (read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

## Step 6 Cell Surface Protein/ Immune Receptor Mapping Library Construction

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

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

Pooled amplified DNA processed in bulk



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

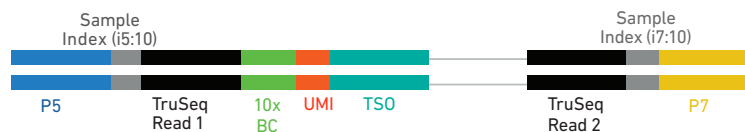
## Step 7 Sequencing

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

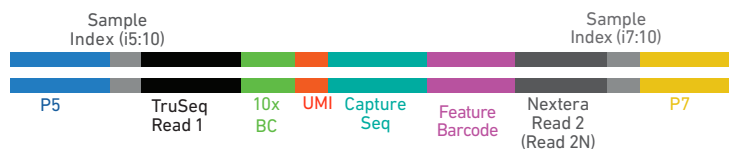
### Chromium Single Cell V(D)J Dual Index Library



### Chromium Single Cell 5' Gene Expression Dual Index Library



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



\*Detects antigen specificity in cells labeled with antibodies and antigen

[See Appendix for Oligonucleotide Sequences](#)

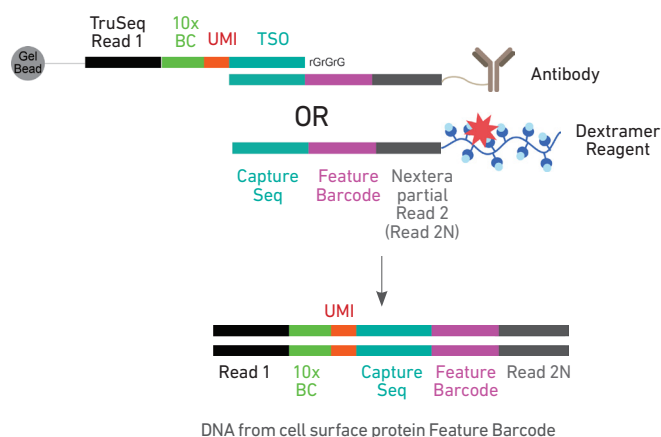
## Cell Labeling Guidelines

### Overview

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

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

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



### Demonstrated Protocols for cell labeling

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

### Cell Surface Protein Library:

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



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

# Tips & Best Practices

TIPS

Icons



Tips & Best Practices section includes additional guidance



Signifies critical step requiring accurate execution



Troubleshooting section includes additional guidance

Version Specific Update



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

Emulsion-safe Plastics

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

Cell Concentration

- Recommended starting point is to load ~1700 cells per reaction, resulting in recovery of ~1000 cells, and a multiplet rate of ~0.8%. The optimal input cell concentration is 700-1,200 cells/ $\mu$ L.
- The presence of dead cells in the suspension may also reduce the recovery rate. Consult the 10x Genomics Single Cell Protocols Cell Preparation Guide and the Guidelines for Optimal Sample Preparation flowchart (Documents CG00053 and CG000126 respectively) for more information on preparing cells.
- Refer to the 10x Genomics Support website for more information regarding cell type specific sample preparation, for example, the Demonstrated Protocol for Enrichment of CD3+ T Cells from Dissociated Tissues for Single Cell RNA Sequencing and Immune Repertoire Profiling (Document CG000123).

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

General Reagent Handling

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

### 50% Glycerol Solution

- Purchase 50% glycerol solution from Ricca Chemical Company, Glycerin (glycerol), 50% (v/v) Aqueous Solution, PN-3290-32.
- OR
- Prepare 50% glycerol solution:
  - i. Mix an equal volume of water and 99% Glycerol, Molecular Biology Grade.
  - ii. Filter through a 0.2- $\mu$ m filter.
  - iii. Store at  $-20^{\circ}\text{C}$  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  $\leq 24$  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.

Chip in Chromium Next GEM Secondary Holder



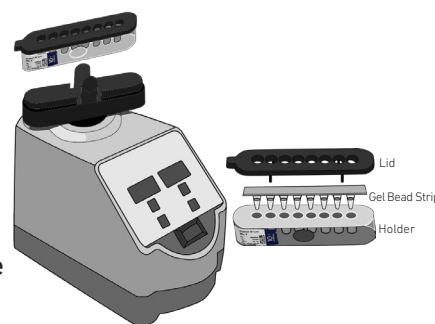
## Chromium Next GEM Chip Loading

- 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.



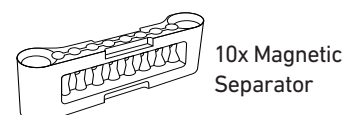
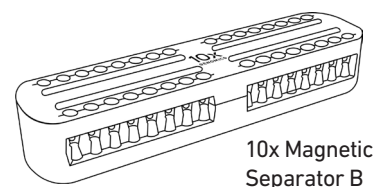
## Gel Bead Handling

- 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  $-80^{\circ}\text{C}$  and avoid more than 12 freeze-thaw cycles. DO NOT store Gel Beads at  $-20^{\circ}\text{C}$ .
- 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.



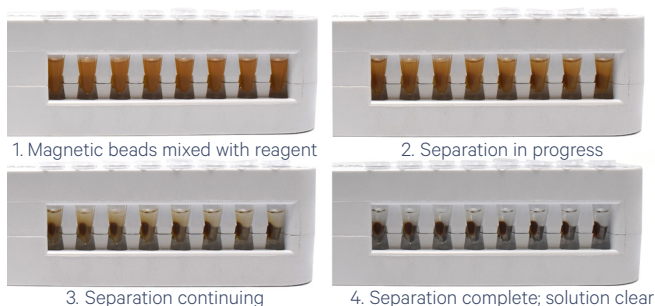
## 10x Magnetic Separator

- 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.



## 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.



## SPRIselect Cleanup & Size Selection

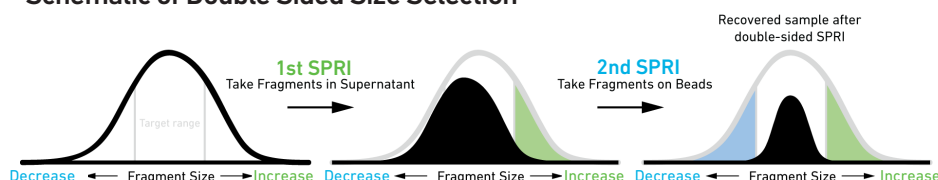
- After aspirating the desired volume of SPRIselect reagent, examine the pipette tips before dispensing to ensure the correct volume is transferred.
- Pipette mix thoroughly as insufficient mixing of sample and SPRIselect reagent will lead to inconsistent results.
- Use fresh preparations of 80% Ethanol.

### Tutorial — SPRIselect Reagent : DNA Sample Ratios

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

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

### 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  $\mu\text{l}$  SPRIselect reagent to 100  $\mu\text{l}$  sample (0.5X).

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

**Step b – Second SPRIselect:** Add 30  $\mu\text{l}$  SPRIselect reagent to supernatant from step a (0.8X).

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

## cDNA Amplification PCR Cycle Numbers

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

Recommended starting point for cycle number optimization.

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

## Enzymatic Fragmentation

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

## Sample Indices in Sample Index PCR

- Choose the appropriate sample index sets to ensure that no sample indices overlap in a multiplexed sequencing run.
- Each well in the Dual Index Plate contains a unique i7 and a unique i5 oligonucleotide.
- Use **ONLY** Dual Index Plate TT, Set A for V(D)J and 5' Gene Expression libraries. Use **ONLY** Dual Index Plate TN, Set A for Cell Surface Protein library.
- Consider sample index compatibility when pooling different libraries; a unique sample index for each of the pooled libraries is required.
- The sample indices of Dual Index Plate TT, Set A are unique from those of Dual Index Plate TN, Set A. Therefore, respective libraries from the two plates may be pooled.

## Index Hopping Mitigation

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

- Remove adaptors during cleanup steps.
- Ensure no leftover primers and/or adaptors 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 adaptors before sequencing.
- Hopped indices can be computationally removed from the data generated from single cell dual index libraries.

# Step 1

## GEM Generation & Barcoding

- 1.1 Prepare Master Mix
- 1.2 Load Chromium Next GEM Chip K
- 1.3 Run the Chromium Controller or X/iX
- 1.4 Transfer GEMs
- 1.5 GEM-RT Incubation

1


## 1.0 GEM Generation & Barcoding

VERSION  
SPECIFIC


### GET STARTED!

Item	10x PN	Preparation & Handling	Storage
------	--------	------------------------	---------

#### Equilibrate to Room Temperature

<input type="checkbox"/>	Single Cell VDJ 5' Gel Bead	1000264/ 1000267	Equilibrate to room temperature 30 min before loading the chip.	-80°C
<input type="checkbox"/>	 RT Reagent B	2000165	Vortex, verify no precipitate, centrifuge briefly.	-20°C
<input type="checkbox"/>	 Poly-dT RT Primer	2000007	Vortex, verify no precipitate, centrifuge briefly.	-20°C
<input type="checkbox"/>	 Reducing Agent B	2000087	Vortex, verify no precipitate, centrifuge briefly.	-20°C

#### Place on ice

<input type="checkbox"/>	 RT Enzyme C	2000085/ 2000102	Centrifuge briefly before adding to the mix.	-20°C
<input type="checkbox"/>	Labeled Cells	Refer to Demonstrated Protocols for Cell Surface Protein Labeling (CG000149, CG000203).		

#### Obtain

<input type="checkbox"/>	Partitioning Oil	2000190	-	Ambient
<input type="checkbox"/>	Chromium Next GEM Chip K <i>Verify name &amp; PN</i>	2000182	-	Ambient
<input type="checkbox"/>	10x Gasket	370017/ 3000072	See Tips & Best Practices.	Ambient
<input type="checkbox"/>	Chromium Next GEM Secondary Holder	3000332	See Tips & Best Practices.	Ambient
<input type="checkbox"/>	10x Vortex Adapter	330002	See Tips & Best Practices.	Ambient
<input type="checkbox"/>	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 <i>Add reagents in the order listed</i>	PN	1X (μl)	4X + 10% (μl)	8X + 10% (μl)
● RT Reagent B	2000165	18.8	82.7	165.4
● Poly-dT RT Primer	2000007	7.3	32.1	64.2
○ Reducing Agent B	2000087	1.9	8.4	16.7
● RT Enzyme C	2000085/ 2000102	8.3	36.5	73.0
<b>Total</b>	-	<b>36.3</b>	<b>159.7</b>	<b>319.3</b>

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.

Chip in Chromium Next GEM Secondary Holder



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

## Cell Suspension Volume Calculator Table

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

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



DO NOT add nuclease-free water directly to single cell suspension. Add nuclease-free water to the Master Mix. Refer to step 1.2b

Cell Stock Concentration (Cells/µl)	Targeted Cell Recovery										
	500	1000	2000	3000	4000	5000	6000	7000	8000	9000	10000
<b>100</b>	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
<b>200</b>	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
<b>300</b>	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
<b>400</b>	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
<b>500</b>	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
<b>600</b>	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
<b>700</b>	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
<b>800</b>	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
<b>900</b>	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
<b>1000</b>	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
<b>1100</b>	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
<b>1200</b>	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
<b>1300</b>	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
<b>1400</b>	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
<b>1500</b>	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
<b>1600</b>	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
<b>1700</b>	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
<b>1800</b>	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
<b>1900</b>	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
<b>2000</b>	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

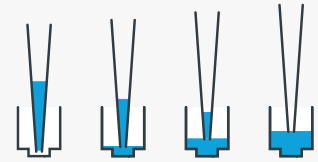
Yellow boxes: Indicate a low transfer volume that may result in higher cell load variability

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**

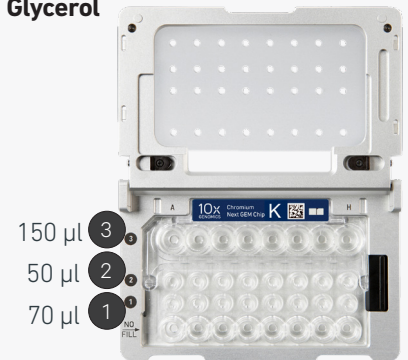
After removing chip from the sealed bag, use in  $\leq 24$  h.  
Open the lid (gasket attached) of the assembled chip and lay flat for loading.  
When loading the chip, raising and depressing the pipette plunger should each take  $\sim 5$  sec.  
When dispensing, raise the pipette tips at the same rate 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)

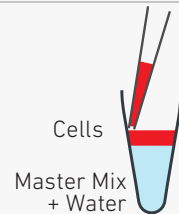
- **70  $\mu$ l** in each unused well in row labeled **1**
- **50  $\mu$ l** in each unused well in row labeled **2**
- **150  $\mu$ l** in each unused well in row labeled **3**



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**

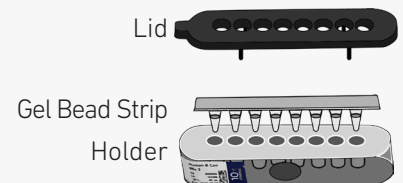
- Refer to the Cell Suspension Volume Calculator Table.
- Add the appropriate volume of **nuclease-free water** to Master Mix.  
Add corresponding volume of **single cell suspension** to Master Mix.  
*Total of **75  $\mu$ l** in each tube.*
- Gently pipette mix the cell suspension before adding to the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

**c. Load Row Labeled 1**

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

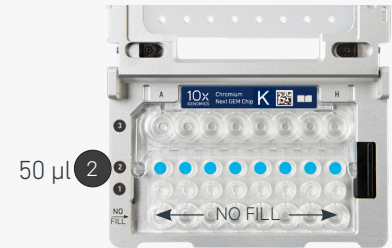
**Master Mix + Sample****d. Prepare Gel Beads**

- Snap the tube strip holder with the Gel Bead strip into a 10x Vortex Adapter. Vortex **30 sec.**
- Centrifuge the Gel Bead strip for  **$\sim 5$  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

**If using Chromium Controller:**

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



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

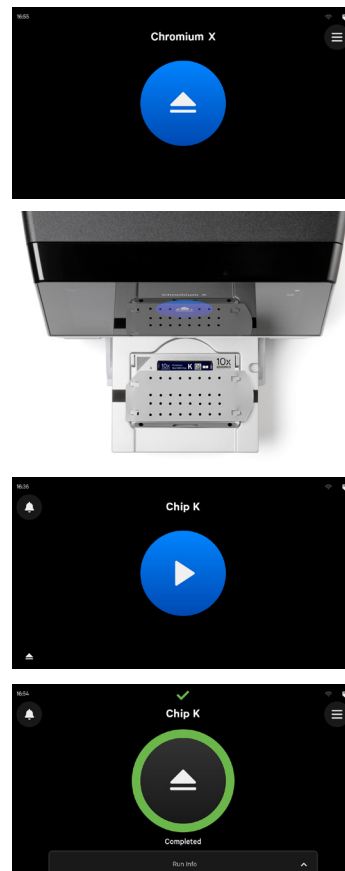
*If the eject button is not touched within 1 min, tray will close automatically. System requires a few seconds before the tray can be ejected again.*

- 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

- Place a tube strip on ice.
- Press the eject button of the Controller and remove the chip.
- Discard the gasket. Open the chip holder. Fold the lid back until it clicks to expose the wells at 45 degrees.
- Check the volume in rows labeled 1-2.  
Abnormally high volume in one well relative to other wells may indicate a clog.
- 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.
- 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.
- Over the course of **~20 sec**, dispense GEMs into the tube strip on ice with the pipette tips against the sidewalls of the tubes.
- 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**.



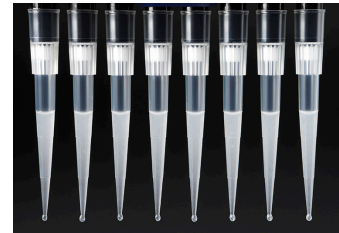
### Expose Wells at 45 Degrees



### 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.

- 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



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

# Step 2

## Post GEM-RT Cleanup & cDNA Amplification

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

## 2.0 Post GEM-RT Cleanup & cDNA Amplification

VERSION  
SPECIFIC

GET STARTED!			
Item	10x PN	Preparation & Handling	Storage
<b>Equilibrate to Room Temperature</b>			
<input type="checkbox"/> <input type="radio"/> Reducing Agent B	2000087	Thaw, vortex, verify no precipitate, centrifuge briefly.	-20°C
<input type="checkbox"/> <input checked="" type="radio"/> Feature cDNA Primers 4	2000277	Thaw, vortex, centrifuge briefly.	-20°C
<input type="checkbox"/> Dynabeads MyOne SILANE	2000048	Vortex thoroughly (≥30 sec) <b>immediately</b> before adding to the mix. If still clumpy, pipette mix to resuspend completely. DO NOT centrifuge before use.	4°C
<input type="checkbox"/> Beckman Coulter SPRIselect Reagent	-	Manufacturer's recommendations.	-
<input type="checkbox"/> Agilent Bioanalyzer High Sensitivity Kit If used for QC and quantification	-	Manufacturer's recommendations.	-
<input type="checkbox"/> Agilent TapeStation ScreenTape and Reagents If used for QC and quantification	-	Manufacturer's recommendations.	-
<b>Place on ice</b>			
<input type="checkbox"/> <input type="radio"/> Amp Mix Retrieve from Single Cell 5' GEM Kit	2000047/ 2000103	Vortex, centrifuge briefly.	-20°C
<b>Thaw at 65°C</b>			
<input type="checkbox"/> <input checked="" type="radio"/> 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
<b>Obtain</b>			
<input type="checkbox"/> <input type="radio"/> Recovery Agent	220016	-	Ambient
<input type="checkbox"/> Qiagen Buffer EB	-	Manufacturer's recommendations.	Ambient
<input type="checkbox"/> Bio-Rad 10% Tween 20	-	Manufacturer's recommendations.	-
<input type="checkbox"/> 10x Magnetic Separator/ 10x Magnetic Separator B		230003/ 2001212	Ambient
<input type="checkbox"/> Prepare 80% Ethanol Prepare 15 ml for 8 reactions	-	Prepare fresh.	Ambient

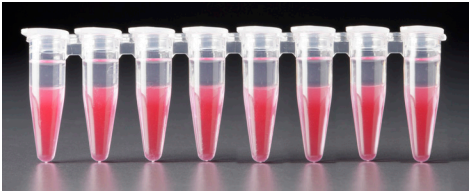
2.1  
Post GEM-RT Cleanup –  
Dynabeads

- 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**.

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.

Biphasic Mixture

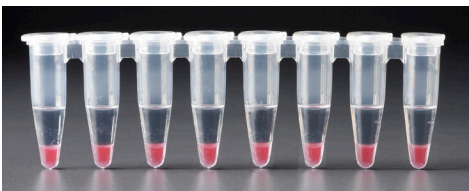


A smaller aqueous phase volume indicates a clog during GEM generation.



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

Remove Recovery Agent



- c. Prepare Dynabeads Cleanup Mix.

Dynabeads Cleanup Mix <i>Add reagents in the order listed</i>	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. <b>DO NOT</b> 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 <i>Add reagents in the order listed</i>	PN	1X (μl)	10X (μl)
Buffer EB	-	98	980
10% Tween 20	-	1	10
○ Reducing Agent B	2000087	1	10
<b>Total</b>	<b>-</b>	<b>100</b>	<b>1000</b>

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

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

**h. Remove the supernatant.****i. Add 300 μl 80% ethanol to the pellet while on the magnet. Wait 30 sec.****j. Remove the ethanol.****k. Add 200 μl 80% ethanol to pellet. Wait 30 sec.****l. Remove the ethanol.****m. Centrifuge briefly. Place on the 10x Magnetic Separator•Low position (magnet•Low).****n. Remove remaining ethanol. Air dry for 2 min.****o. Remove from the magnet. Immediately add 35.5 μl Elution Solution I.****p. Pipette mix (pipette set to 30 μl) without introducing bubbles. Pipette mix 15x. If beads still appear clumpy, continue pipette mixing until fully resuspended.****q. Incubate 1 min at room temperature.****r. Place on the magnet•Low until the solution clears.****s. Transfer 35 μl sample to a new tube strip.**



## 2.2 cDNA Amplification

VERSION  
SPECIFIC

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

cDNA Amplification Mix <i>Add reagents in the order listed</i>	PN	1X (μl)	4X + 10% (μl)	8X + 10% (μl)
○ <b>Amp Mix</b> Retrieve from Single Cell 5' GEM Kit	2000047/ 2000103	50	220	440
● <b>Feature cDNA Primers 4</b> <i>Verify name &amp; PN</i>	2000277	15	66	132
<b>Total</b>	-	<b>65</b>	<b>286</b>	<b>572</b>

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 <i>e.g., Primary Cells</i> Total Cycles	High RNA Content Cells <i>e.g., Cell Lines</i> 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.



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

## Step Overview (steps 2.2 & 2.3)

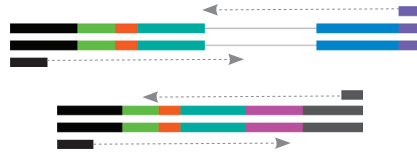
VERSION  
SPECIFIC

### Amplification Products generated in Step 2.2 – cDNA Amplification

Post GEM-RT Cleanup Products

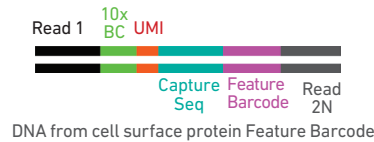
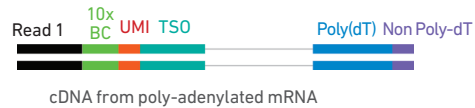
+

Feature cDNA Primers 4  
PN-2000277

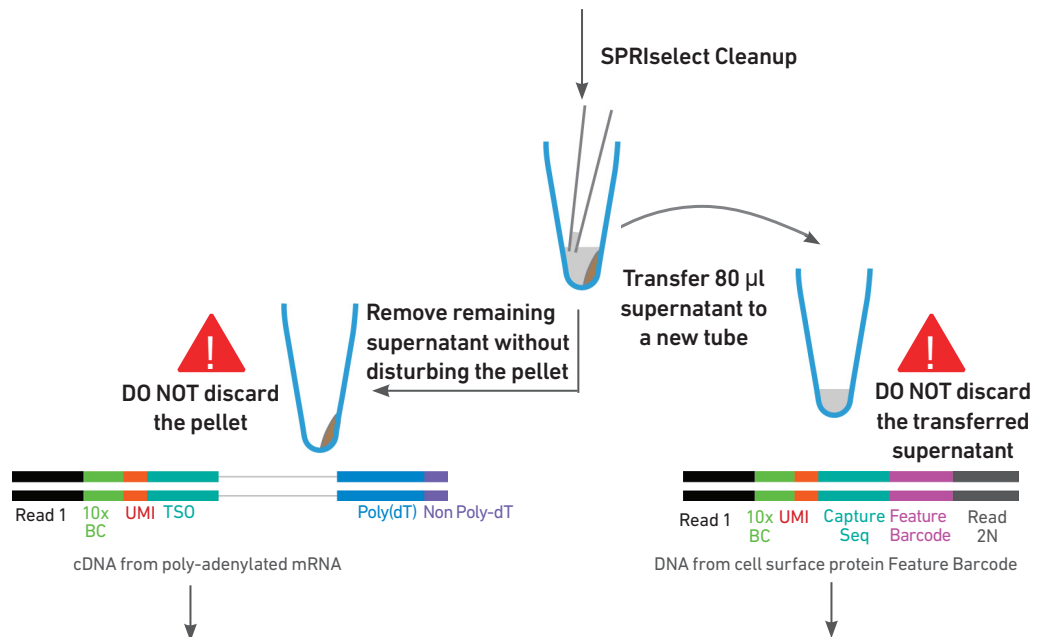


DNA Amplification

Amplification  
Products



### Step 2.3 – cDNA Cleanup – SPRIselect Overview




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




2.3B – Supernatant Cleanup  
(for Cell Surface Protein/Immune  
Receptor Mapping Library)




### 2.3 cDNA Cleanup – SPRIselect

- a. Vortex to resuspend the SPRIselect reagent. Add **60 µl** SPRIselect reagent (**0.6X**) to each sample and pipette mix 15x (pipette set to 140 µl).
- b. Incubate **5 min** at **room temperature**.
- c. Place on the magnet•**High** until the solution clears.
- d.  Transfer and save **80 µl** supernatant in a new tube strip without disturbing the pellet. Maintain at **room temperature**. DO NOT discard the transferred supernatant (cleanup for Cell Surface Protein library construction).
- e. Remove the remaining supernatant from the pellet without disturbing the pellet. DO NOT discard the pellet (cleanup for V(D)J and 5' Gene Expression library construction). **Immediately** proceed to Pellet Cleanup (step 2.3A).

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

- i. Add **200 µl** 80% ethanol to the pellet while still on magnet•**High**. Wait **30 sec**.
- ii. Remove the ethanol.
- iii. **Repeat** steps i and ii for a total of 2 washes.
- iv. Centrifuge briefly and place on the magnet•**Low**.
- v. Remove any remaining ethanol. Air dry for **2 min**. DO NOT exceed **2 min** as this will decrease elution efficiency.
- vi. Remove from the magnet. Add **45.5 µl** Buffer EB. Pipette mix 15x.
- vii. Incubate **2 min** at **room temperature**.
- viii. Place the tube strip on the magnet•**High** until the solution clears.
- ix. Transfer **45 µl** sample to a new tube strip.
- x.  Store at **4°C** for up to **72 h** or at **-20°C** for up to **4 weeks**, or proceed to [step 2.4 for cDNA QC & Quantification](#).

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

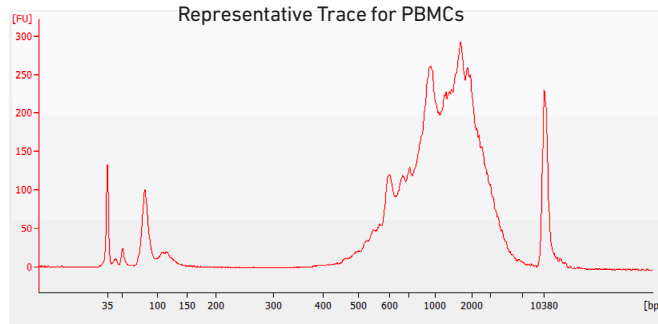
- i. Vortex to resuspend the SPRIselect reagent. Add **70 µl** SPRIselect reagent (**2.0X**) to **80 µl** of the transferred supernatant and pipette mix 15x (pipette set to 150 µl).
- ii. Incubate for **5 min** at **room temperature**.
- iii. Place on the magnet•**High** until the solution clears.
- iv. Remove the supernatant.
- v. Add **300 µl** 80% ethanol to the pellet. Wait **30 sec**.
- vi. Remove the ethanol.
- vii. **Repeat** steps v and vi for a total of 2 washes.
- viii. Centrifuge briefly and place on the magnet•**Low**.
- ix. Remove any remaining ethanol. Air dry for **2 min**. DO NOT exceed **2 min** as this will decrease elution efficiency.
- x. Remove from the magnet. Add **45.5 µl** Buffer EB. Pipette mix 15x.
- xi. Incubate **2 min** at **room temperature**.
- xii. Place the tube strip on the magnet•**High** until the solution clears.
- xiii. Transfer **45 µl** sample to a new tube strip.
- xiv.  Store at **4°C** for up to **72 h** or at **-20°C** for up to **4 weeks**, or proceed directly to [step 6 for Cell Surface Protein/Immune Receptor Mapping Library](#).

## 2.4 cDNA QC & Quantification



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

- a. Run 1  $\mu\text{L}$  undiluted sample from the Pellet Cleanup step 2.3A-x (Dilution Factor 1) on an Agilent Bioanalyzer High Sensitivity chip.  
Run 1  $\mu\text{L}$  undiluted product for input cells with low RNA content (<1pg total RNA/cell), and 1  $\mu\text{L}$  of 1:10 diluted product for input cells with high RNA content.

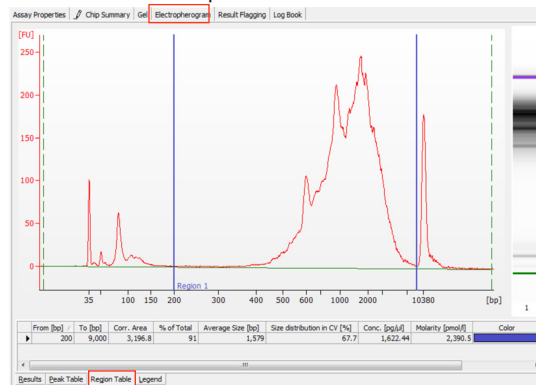


- b. If proceeding to 5' GEX Library Construction (step 5), determine cDNA yield for each sample. Example calculation below.

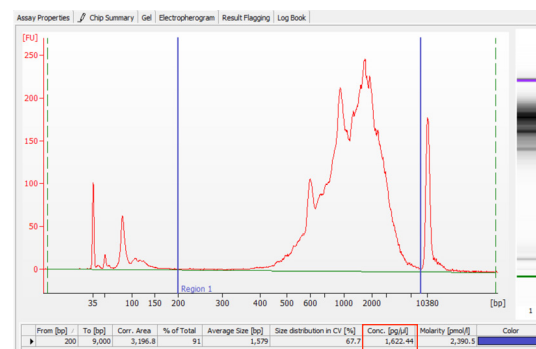
### EXAMPLE CALCULATION

#### 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. =

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

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

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

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

Sample volume for library construction = 20  $\mu\text{L}$

If <50 ng available, carry forward 20  $\mu\text{L}$  sample (2–50 ng) into 5' GEX Library Construction.



DO NOT exceed a mass of 50 ng in the 20  $\mu\text{L}$  carry forward volume.

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

- Agilent TapeStation.
- LabChip

# 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)					
<input type="checkbox"/>		Human T Cell Mix 1 v2	2000242	Thaw, vortex, centrifuge briefly.	-20°C
<input type="checkbox"/>		Human T Cell Mix 2 v2	2000246	Thaw, vortex, centrifuge briefly	-20°C
<input type="checkbox"/>		Human B Cell Mix 1 v2	2000254	Thaw, vortex, centrifuge briefly	-20°C
<input type="checkbox"/>		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)					
<input type="checkbox"/>		Mouse T Cell Mix 1 v2	2000256	Thaw, vortex, centrifuge briefly	-20°C
<input type="checkbox"/>		Mouse T Cell Mix 2 v2	2000257	Thaw, vortex, centrifuge briefly	-20°C
<input type="checkbox"/>		Mouse B Cell Mix 1 v2	2000258	Thaw, vortex, centrifuge briefly	-20°C
<input type="checkbox"/>		Mouse B Cell Mix 2 v2	2000259	Thaw, vortex, centrifuge briefly	-20°C
For all Samples					
<input type="checkbox"/>		Beckman Coulter SPRIselect Reagent	-	Manufacturer's recommendations.	-
<input type="checkbox"/>		Agilent Bioanalyzer High Sensitivity Kit If used for QC and quantification	-	Manufacturer's recommendations.	-
<input type="checkbox"/>		Agilent TapeStation ScreenTape and Reagents If used for QC and quantification	-	Manufacturer's recommendations.	-
Place on ice					
<input type="checkbox"/>		Amp Mix Retrieve from Single Cell V(D)J Amplification Kits	2000047	Vortex, centrifuge briefly.	-20°C
Obtain					
<input type="checkbox"/>		Qiagen Buffer EB	-	Manufacturer's recommendations.	Ambient
<input type="checkbox"/>		10x Magnetic Separator/ 10x Magnetic Separator B		230003/ 2001212	Ambient
<input type="checkbox"/>		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  $\mu$ l 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 <i>Add reagents in the order listed</i>	PN	1X ( $\mu$ l)	4X + 10% ( $\mu$ l)	8X + 10% ( $\mu$ l)
○ <b>Amp Mix</b> Retrieve from Single Cell V(D)J Amplification Kits	2000047	50	220	440
● <b>T Cell Mix 1 v2</b>  or	Human 2000242/ Mouse 2000256 or	48	211.2	422.4
● <b>B Cell Mix 1 v2</b>	Human 2000254/ Mouse 2000258			
<b>Total</b>	-	<b>98</b>	<b>431.2</b>	<b>862.4</b>

- c. Add 98  $\mu$ l V(D)J Amplification 1 Reaction Mix to each tube containing 2  $\mu$ l sample.
- d. Pipette mix 5x (pipette set to 90  $\mu$ l). Centrifuge briefly.
- e. Incubate in a thermal cycler with the following protocol.

Lid Temperature	Reaction Volume	Run Time
105°C	100 $\mu$ l	~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	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



Different cycle numbers for T & B cells



- 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



- a. Vortex to resuspend the SPRIselect reagent. Add **50  $\mu$ l** SPRIselect reagent (**0.5X**) to each sample. Pipette mix 15x (pipette set to 140  $\mu$ l).
- 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  $\mu$ l** supernatant to a new tube strip.
- e. Vortex to resuspend SPRIselect reagent. Add **30  $\mu$ l** SPRIselect reagent (**0.8X**) to each sample. Pipette mix 15x (pipette set to 150  $\mu$ l).
- f. Incubate **5 min** at **room temperature**.
- g. Place on the magnet•**High** until the solution clears.
- h. Remove **170  $\mu$ l** supernatant. DO NOT discard any beads.
- i. Add **200  $\mu$ l** 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  $\mu$ l** 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  $\mu$ l** 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 <i>Add reagents in the order listed</i>	PN	1X (μl)	4X + 10% (μl)	8X + 10% (μl)
<input type="radio"/> <b>Amp Mix</b> Retrieve from Single Cell V(D)J Amplification Kits	2000047	50	220	440
<input checked="" type="radio"/> <b>T Cell Mix 2 v2</b>  or  <input checked="" type="radio"/> <b>B Cell Mix 2 v2</b>	Human 2000246/ Mouse 2000257  or Human 2000255/ Mouse 2000259	15	66	132
<b>Total</b>	-	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	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



Different cycle numbers for T & B cells



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

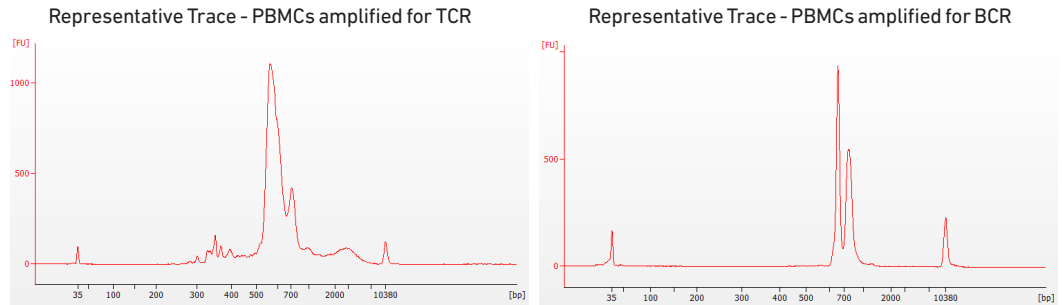
- a. Vortex to resuspend SPRIselect reagent. Add **50 µl** SPRIselect reagent (**0.5X**) to each sample. Pipette mix 15x (pipette set to 145 µl).
- b. Incubate **5 min** at **room temperature**.
- c. Place on the magnet•**High** until the solution clears. DO NOT discard supernatant.
- d. Transfer **145 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.

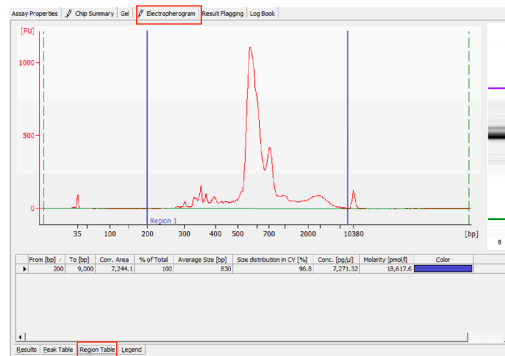


#### b. Determine yield for each sample. Example calculation below.

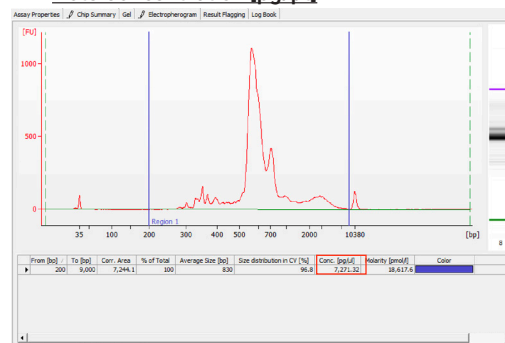
##### EXAMPLE CALCULATION

##### i. Select Region

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



##### ii. Note Concentration [pg/µl]



##### iii. Calculate

Concentration: 7271.32 pg/µl  
Dilution Factor: 5

Amplified Product Conc.

$$\text{Conc. (pg/µl)} \times \text{Dilution Factor} = \frac{7271.32 \times 5}{1000 \text{ (pg/ng)}} = 36.35 \text{ ng/µl}$$

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

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

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 Dual Index 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



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

GET STARTED!			
Item	10x PN	Preparation & Handling	Storage
<b>Equilibrate to Room Temperature</b>			
<input type="checkbox"/> <b>Fragmentation Buffer</b>	2000091	Thaw, vortex, verify no precipitate, centrifuge briefly.	-20°C
<input type="checkbox"/> <b>Adaptor Oligos</b>	2000094	Thaw, vortex, centrifuge briefly.	-20°C
<input type="checkbox"/> <b>Ligation Buffer</b>	2000092	Thaw, vortex, verify no precipitate, centrifuge briefly.	-20°C
<input type="checkbox"/> <b>Dual Index Plate TT Set A</b> <i>Verify name &amp; PN</i>	3000431	-	-20°C
<input type="checkbox"/> <b>Beckman Coulter SPRIselect Reagent</b>	-	Manufacturer's recommendations.	-
<input type="checkbox"/> <b>Agilent Bioanalyzer High Sensitivity Kit</b> If used for QC and quantification	-	Manufacturer's recommendations.	-
<input type="checkbox"/> <b>Agilent TapeStation ScreenTape and Reagents</b> If used for QC and quantification	-	Manufacturer's recommendations.	-
<b>Place on ice</b>			
<input type="checkbox"/> <b>Fragmentation Enzyme</b>	2000090/ 2000104	Centrifuge briefly.	-20°C
<input type="checkbox"/> <b>DNA Ligase</b>	220110/ 220131	Centrifuge briefly.	-20°C
<input type="checkbox"/> <b>Amp Mix</b>	2000047/ 2000103	Vortex, centrifuge briefly.	-20°C
<b>Obtain</b>			
<input type="checkbox"/> <b>Qiagen Buffer EB</b>	-	-	Ambient
<input type="checkbox"/> <b>10x Magnetic Separator/ 10x Magnetic Separator B</b>		230003/ 2001212	Ambient
<input type="checkbox"/> <b>Prepare 80% Ethanol</b> 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 <i>Pre-cool block prior to preparing the Fragmentation Mix</i>	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 <i>Add reagents in the order listed</i>	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



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

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

- 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



- 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



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



#### 4.5

##### Post Sample Index PCR Cleanup – SPRIselect

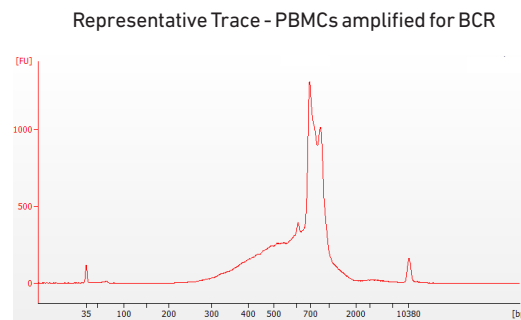
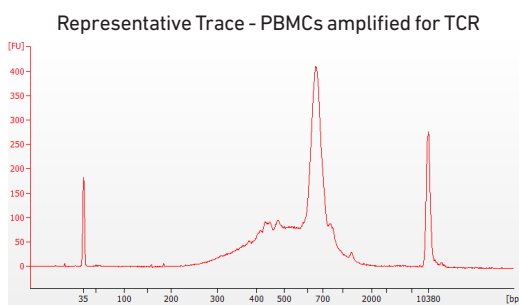
- Vortex to resuspend the SPRIselect reagent. Add **80 µl SPRIselect Reagent (0.8X)** to each sample. Pipette mix 15x (pipette set to 150 µl).
- Incubate **5 min** at **room temperature**.
- Place the magnet•**High** until the solution clears.
- Remove the supernatant.
- Add **200 µl 80% ethanol** to the pellet. Wait **30 sec**.
- Remove the ethanol.
- Repeat** steps e and f for a total of 2 washes.
- Centrifuge briefly. Place on the magnet•**Low**.
- Remove remaining ethanol. Air dry for **2 min**.
- Remove from the magnet. Add **35.5 µl Buffer EB**. Pipette mix 15x.
- Incubate **2 min** at **room temperature**.
- Place on the magnet•**Low** until the solution clears.
- Transfer **35 µl** to a new tube strip.
- Store at **4°C** for up to **72 h** or at **-20°C** for **long-term storage**.



#### 4.6

##### Post Library Construction QC

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



- 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) Library Construction



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

GET STARTED!			
Item	10x PN	Preparation & Handling	Storage
<b>Equilibrate to Room Temperature</b>			
<input type="checkbox"/> <b>Fragmentation Buffer</b>	2000091	Thaw, vortex, verify no precipitate, centrifuge briefly.	-20°C
<input type="checkbox"/> <b>Adaptor Oligos</b>	2000094	Thaw, vortex, centrifuge briefly.	-20°C
<input type="checkbox"/> <b>Ligation Buffer</b>	2000092	Thaw, vortex, verify no precipitate, centrifuge briefly.	-20°C
<input type="checkbox"/> <b>Dual Index Plate TT Set A</b> <i>Verify name &amp; PN</i>	3000431	-	-20°C
<input type="checkbox"/> <b>Beckman Coulter SPRIselect Reagent</b>	-	Manufacturer's recommendations.	-
<input type="checkbox"/> <b>Agilent Bioanalyzer High Sensitivity Kit</b> If used for QC and quantification	-	Manufacturer's recommendations.	-
<input type="checkbox"/> <b>Agilent TapeStation ScreenTape and Reagents</b> If used for QC and quantification	-	Manufacturer's recommendations.	-
<b>Place on ice</b>			
<input type="checkbox"/> <b>Fragmentation Enzyme</b>	2000090/ 2000104	Centrifuge briefly.	-20°C
<input type="checkbox"/> <b>DNA Ligase</b>	220110/ 220131	Centrifuge briefly.	-20°C
<input type="checkbox"/> <b>Amp Mix</b>	2000047/ 2000103	Vortex, centrifuge briefly.	-20°C
<input type="checkbox"/> <b>KAPA Library Quantification Kit for Illumina Platforms</b>	-	Manufacturer's recommendations.	-20°C
<b>Obtain</b>			
<input type="checkbox"/> <b>Qiagen Buffer EB</b>	-	-	Ambient
<input type="checkbox"/> <b>10x Magnetic Separator/ 10x Magnetic Separator B</b>	-	230003/ 2001212	Ambient
<input type="checkbox"/> <b>Prepare 80% Ethanol</b> 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 <i>Pre-cool block prior to preparing the Fragmentation Mix</i>	4°C	Hold
Fragmentation	32°C	00:05:00
End Repair & A-tailing	65°C	00:30:00
Hold	4°C	Hold

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

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

- 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 30  $\mu$ l SPRIselect Reagent (**0.6X**) to each sample. Pipette mix 15x (pipette set to 75  $\mu$ l).
- b. Incubate **5 min** at **room temperature**.
- c. Place on the magnet •**High** until the solution clears. **DO NOT** discard supernatant.
- d. Transfer **75  $\mu$ l** supernatant to a new tube strip.
- e. Add **10  $\mu$ l** SPRIselect reagent (**0.8X**) to each sample. Pipette mix 15x (pipette set to 75  $\mu$ l).
- f. Incubate **5 min** at **room temperature**.
- g. Place on the magnet •**High** until the solution clears.
- h. Remove **80  $\mu$ l** supernatant. **DO NOT** discard any beads.
- i. With the tube strip still on the magnet, add **125  $\mu$ l** 80% ethanol to the pellet. Wait **30 sec**.
- j. Remove the ethanol.
- k. **Repeat** steps i and j for a total of 2 washes.
- l. Centrifuge briefly. Place on the magnet •**Low**.
- m. Remove the ethanol. **DO NOT** over-dry beads to ensure maximum elution efficiency.
- n. Remove from the magnet. Add **50.5  $\mu$ l** 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  $\mu$ l** sample to a new tube strip.

### 5.3 GEX Adaptor Ligation



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

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

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

- Vortex to resuspend SPRIselect Reagent. Add **80 µl** SPRIselect Reagent (**0.8X**) to each sample. Pipette mix 15x (pipette set to 150 µl).
- Incubate **5 min** at **room temperature**.
- Place on the magnet•**High** until the solution clears.
- Remove the supernatant.
- Add **200 µl** 80% ethanol to the pellet. Wait **30 sec**.
- Remove the ethanol.
- Repeat steps e and f for a total of 2 washes.
- Centrifuge briefly. Place on the magnet•**Low**.
- Remove any remaining ethanol. Air dry for **2 min**.
- Remove from the magnet. Add **30.5 µl** Buffer EB. Pipette mix 15x.
- Incubate **2 min** at **room temperature**.
- Place on the magnet•**Low** until the solution clears.
- Transfer **30 µl** sample to a new tube strip.

## 5.5 GEX Sample Index PCR



- Choose the appropriate sample index sets to ensure that no sample indices overlap in a multiplexed sequencing run.  
Record the 10x sample index name (PN-3000431 Dual Index Plate TT Set A well ID) used.
- Add **50 µl** Amp Mix (PN-2000047/2000103) to **30 µl** sample.
- 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.
- 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

### Recommended cycle numbers

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.

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



- 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

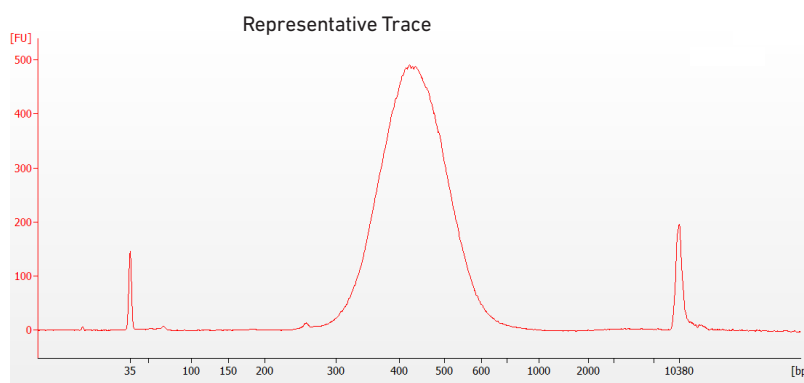
- a. Vortex to resuspend SPRIselect reagent. Add **60 µl** SPRIselect reagent (**0.6X**) to each sample. Pipette mix 15x (pipette set to 150 µl).
- b. Incubate **5 min** at **room temperature**.
- c. Place on the magnet•**High** until the solution clears. DO NOT discard supernatant.
- d. Transfer **150 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.
- r. Store at **4°C** for up to **72 h** or at **-20°C** for **long-term** storage.



## 5.7

### GEX Post Library Construction QC

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



- b. 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

## Cell Surface Protein/Immune Receptor Mapping Library Construction

- 6.1** Sample Index PCR
- 6.2** Post Sample Index PCR Size Selection – SPRIselect
- 6.3** Post Library Construction QC

## 6.0 Cell Surface Protein/ Immune Receptor Mapping Library Construction

VERSION  
SPECIFIC



GET STARTED!			
Item	10x PN	Preparation & Handling	Storage
<b>Equilibrate to Room Temperature</b>			
<input type="checkbox"/> <b>Dual Index Plate TN Set A</b>	3000510	-	-20°C
Verify name & PN			
<input type="checkbox"/> <b>Beckman Coulter SPRIselect Reagent</b>	-	Manufacturer's recommendations.	-
<input type="checkbox"/> <b>Agilent Bioanalyzer High Sensitivity Kit</b> If used for QC	-	Manufacturer's recommendations.	-
<input type="checkbox"/> <b>Agilent TapeStation ScreenTape and Reagents</b> If used for QC and quantification	-	Manufacturer's recommendations.	-
<b>Place on ice</b>			
<input type="checkbox"/> <input type="radio"/> <b>Amp Mix</b> Retrieve from 5' Feature Barcode Kit	2000047	Vortex, centrifuge briefly.	-20°C
<input type="checkbox"/> <b>KAPA Library Quantification Kit for Illumina Platforms</b>	-	Manufacturer's recommendations.	-20°C
<b>Obtain</b>			
<input type="checkbox"/> <b>Qiagen Buffer EB</b>	-	Manufacturer's recommendations.	Ambient
<input type="checkbox"/> <b>10x Magnetic Separator/ 10x Magnetic Separator B</b>		230003/ 2001212	Ambient
<input type="checkbox"/> <b>Prepare 80% Ethanol</b> Prepare 20 ml for 8 reactions	-	Prepare fresh.	Ambient

## 6.1 Sample Index PCR



- Choose the appropriate sample index sets to ensure that no sample indices overlap in a multiplexed sequencing run. Record the 10x sample index name (PN-3000510 Dual Index Plate TN Set A well ID; verify name and part number) used.
- Prepare Sample Index PCR Mix.

Sample Index PCR Mix <i>Add reagents in the order listed</i>	PN	1X (μl)	4X + 10% (μl)	8X + 10% (μl)
Nuclease-free Water		25	110	220
<input type="radio"/> Amp Mix Retrieve from 5' Feature Barcode Kit	2000047	50	220	440
<b>Total</b>	-	<b>75</b>	<b>330</b>	<b>660</b>

- Transfer **ONLY 5 μl** sample from the Transferred Supernatant Cleanup (step 2.3B-xiv) to a new tube strip.  
Note that only **5 μl** of the DNA sample is adequate for generating Cell Surface Protein library. The remaining DNA sample can be stored at **4°C** for up to **72 h** or at **-20°C** for up to **4 weeks** for generating additional Cell Surface Protein libraries.
- Add **75 μl** Sample Index PCR Mix to the **5 μl** Transferred Supernatant Cleanup sample.
- Add **20 μl** of an individual sample index (Dual Index Plate TN Set A) to each well and record the well ID. Pipette mix 5x (pipette set to 90 μl). Centrifuge briefly.
- Incubate in a thermal cycler with the following protocol.

Lid Temperature	Reaction Volume	Run Time
105°C	100 μl	~30 min
Step	Temperature	Time
1	98°C	00:00:45
2	98°C	00:00:20
3	54°C	00:00:30
4	72°C	00:00:20
5	Go to step 2, repeat 7X (total 8 cycles)*	
6	72°C	00:01:00
7	4°C	Hold

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

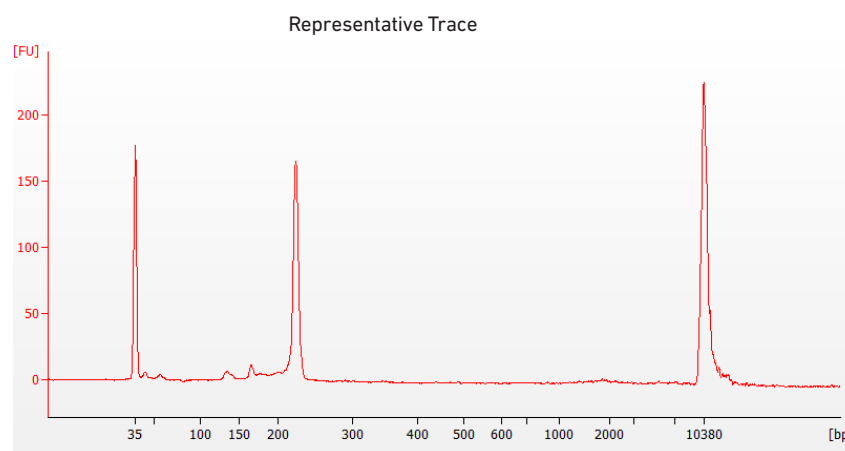
6.2  
[Post Sample Index](#)  
[PCR Size Selection –](#)  
[SPRIselect](#)

- a. Vortex to resuspend the SPRIselect reagent. Add **120 µl** SPRIselect Reagent (**1.2X**) to each sample. Pipette mix 15x (pipette set to 150 µl).
- b. Incubate **5 min** at **room temperature**.
- c. Place the magnet•**High** until the solution clears. Remove the supernatant.
- d. Add **300 µl** 80% ethanol to the pellet. Wait **30 sec**.
- e. Remove the ethanol.
- f. Add **200 µl** 80% ethanol to the pellet. Wait **30 sec**.
- g. Remove the ethanol.
- h. Centrifuge briefly. Place on the magnet•**Low**. Remove remaining ethanol.
- i. Remove from the magnet. Add **35.5 µl** Buffer EB. Pipette mix 15x.
- j. Incubate **2 min** at **room temperature**.
- k. Place on the magnet•**Low** until the solution clears.
- l. Transfer **35 µl** to a new tube strip.
- m. Store at **4°C** for up to **72 h** or at **–20°C** for **long-term** storage.



6.3  
[Post Library Construction](#)  
[QC](#)

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



Select the region between 150–300 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** ([See Appendix for representative traces](#))

- Agilent TapeStation
- LabChip

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

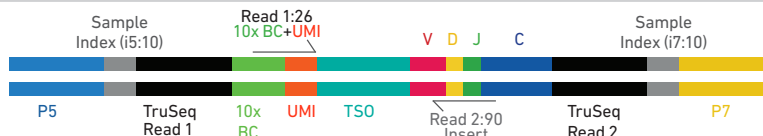
# Sequencing



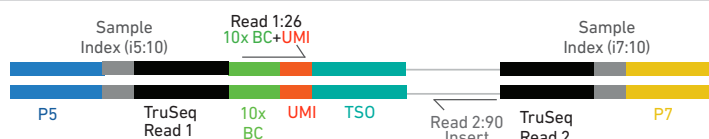
## Sequencing Libraries

Chromium Single Cell V(D)J, 5' Gene Expression, and Cell Surface Protein Dual Index libraries comprise standard Illumina paired-end constructs which begin with P5 and end with P7. These libraries include 16 bp 10x Barcodes encoded at the start of TruSeq Read 1. Sample index sequences are incorporated as the i5 and i7 index read for V(D)J and 5' Gene Expression libraries; as i5 and i7 index read N for Cell Surface Protein library. TruSeq Read 1, TruSeq Read 2, and Nextera Read 2 (Read 2N) are all standard Illumina sequencing primer sites. TruSeq Read 1 and TruSeq Read 2 are used in paired-end sequencing of V(D)J and 5' Gene Expression libraries. TruSeq Read 1 and Nextera Read 2 (Read 2N) are used for paired-end sequencing of Cell Surface Protein library. Sequencing these libraries produce a standard Illumina BCL data output folder.

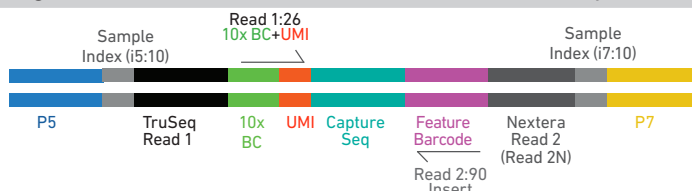
### Chromium Single Cell V(D)J Dual Index Library



### Chromium Single Cell 5' Gene Expression Dual Index Library



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



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)/3000/4000
- NovaSeq 6000

## Sample Indices

Each well of the Dual Index Kit TT Set A (PN-1000215) and Dual Index Kit TN Set A (PN-1000250) contains a mix of one unique i7 and one unique i5 sample index. If multiple samples are pooled in a sequence lane, the sample index name (i.e. the Dual Index plate well ID) is needed in the sample sheet used for generating FASTQs with "cellranger mkfastq". If multiple libraries are pooled in a sequence lane, a separate sample index is needed with each library (see [Tips & Best Practices](#)).

## Library Sequencing Depth & Run Parameters

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

## Library Loading

Once quantified and normalized, V(D)J, 5' Gene Expression, and Cell Surface Protein libraries should be denatured and diluted as recommended for Illumina sequencing platforms. Refer to Illumina documentation for denaturing and diluting libraries. Refer to the 10x Genomics Support website, for more information.

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.

Instrument	Loading Concentration (pM)	PhiX (%)
MiSeq	10	1
NextSeq 500	1.5	1
HiSeq 2500 (RR)	10	1
HiSeq 4000	180	1
NextSeq 2000	650	1
*NovaSeq 6000 standard workflow	300	1
*NovaSeq 6000 Xp workflow	150	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 Pooling

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

Library Pooling Examples:

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

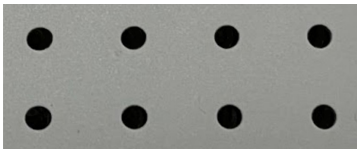
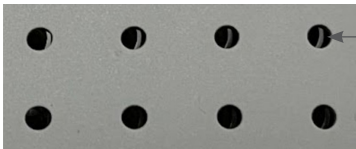


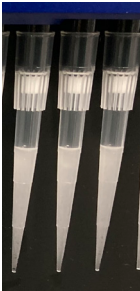
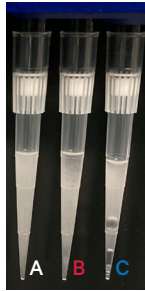




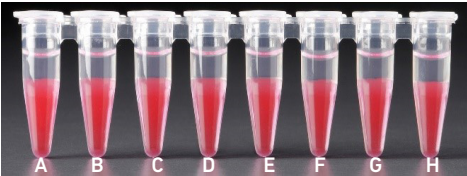
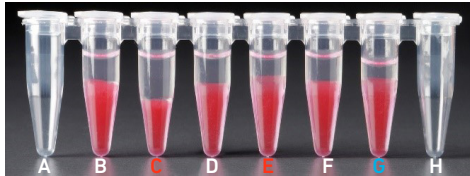
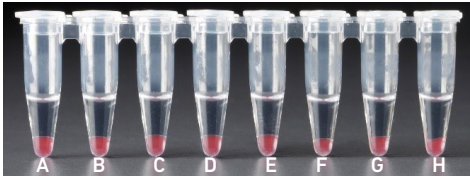
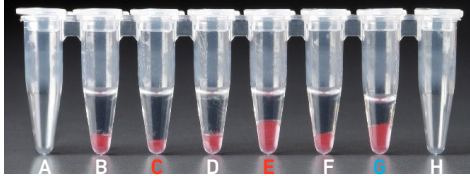
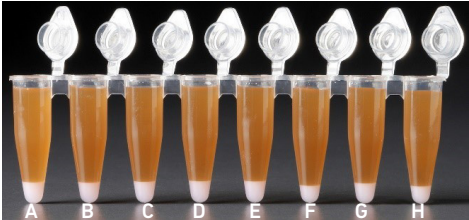
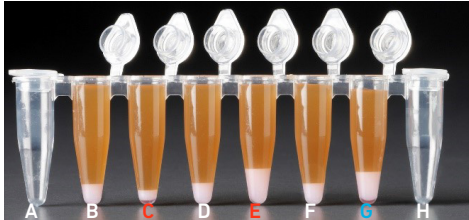
# Troubleshooting



## GEM Generation & Barcoding

STEP	NORMAL	IMPACTED
<b>1.2</b> Load Chromium Next GEM Chip K	 <p>Gasket holes are aligned with the sample and gel bead wells.</p>	 <p>Misaligned gasket holes &amp; chip wells</p> <p>Gasket holes are misaligned with the gel bead wells. Open and close the chip holder slowly once.</p>
<b>1.4 d</b> After Chip K is removed from the Controller and the wells are exposed	 <p>All 8 recovery wells are similar in volume and opacity.</p>	 <p>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.</p>
<b>1.4 e</b> Transfer GEMs from Chip K Recovery Wells	 <p>All liquid levels are similar in volume and opacity without air trapped in the pipette tips.</p>	 <p>             ○ Adequate emulsion volume (no clog or wetting failure)              ● Wetting failure              ● Low emulsion volume (clog)           </p> <p>Pipette tip A shows normal GEM generation, pipette tip B indicates a wetting failure, and pipette tip C shows a clog and wetting failure.</p>

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

STEP	NORMAL	IMPACTED
<b>2.1 a</b> After transfer of the GEMs + Recovery Agent	 <p>All liquid levels are similar in the aqueous sample volume (clear) and Recovery Agent/Partitioning Oil (pink).</p>	 <p>Tube <b>G</b> indicates a reagent clog has occurred. There is a decreased volume of aqueous layer (clear).            Tube <b>C</b> and <b>E</b> indicate a wetting failure has occurred. There is an abnormal volume of Recovery Agent/Partitioning Oil (pink).</p>
<b>2.1 b</b> After aspiration of Recovery Agent/ Partitioning Oil	 <p>All liquid volumes are similar in the aqueous sample volume (clear) and residual Recovery Agent/Partitioning Oil (pink).</p>	 <p>Tube <b>G</b> 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 <b>C</b> and <b>E</b> indicate a wetting failure has occurred. There is an abnormal residual volume of Recovery Agent/Partitioning Oil (pink).</p>
<b>2.1 d</b> After addition of Dynabeads Cleanup Mix	 <p>All liquid volumes are similar after addition of the Dynabeads Cleanup Mix.</p>	 <p>Tube <b>G</b> indicates a reagent clog has occurred. There is an abnormal ratio of Dynabeads Cleanup Mix (brown) to Recovery Agent/Partitioning Oil (appears white).            Tube <b>C</b> and <b>E</b> indicate a wetting failure has occurred. There is an abnormal ratio of Dynabeads Cleanup Mix (brown) to Recovery Agent/Partitioning Oil (appears white).</p>

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](mailto: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](mailto: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](mailto: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](mailto: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](mailto: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](mailto:support@10xgenomics.com) for further assistance.
- g. **Endpoint Reached Early:** If this message is received, contact [support@10xgenomics.com](mailto: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](mailto: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](mailto: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

9

## Post Library Construction Quantification

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

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

- d. Dispense **16 µl** Quantification Master Mix for sample dilutions and DNA Standards into a 96 well PCR plate.
- e. Add **4 µl** sample dilutions and **4 µl** DNA Standards to appropriate wells. Centrifuge briefly.
- f. Incubate in a thermal cycler with the following protocol.

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

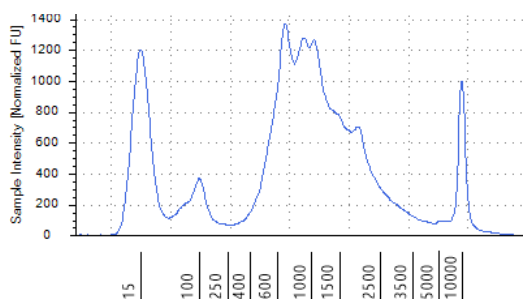
- g. Follow the manufacturer's recommendations for qPCR-based quantification. For library quantification for sequencer clustering, determine the concentration based on insert size derived from the Bioanalyzer/TapeStation trace.

## Agilent TapeStation Traces

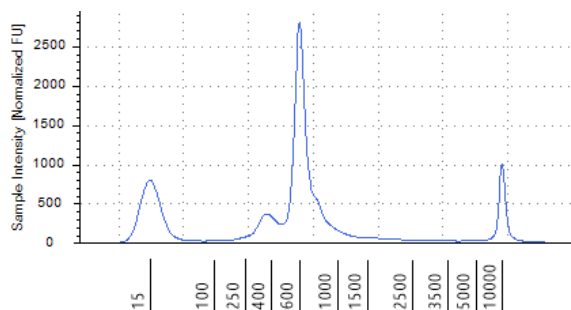
### Agilent TapeStation Traces

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

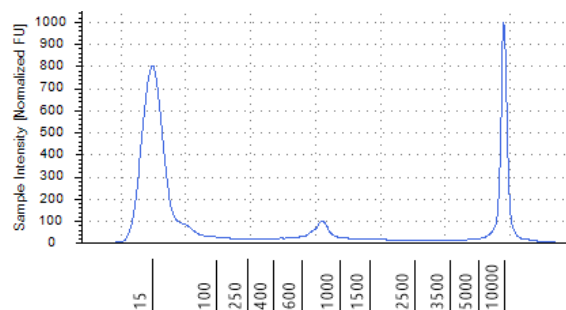
#### Protocol Step 2.4 – cDNA QC & Quantification



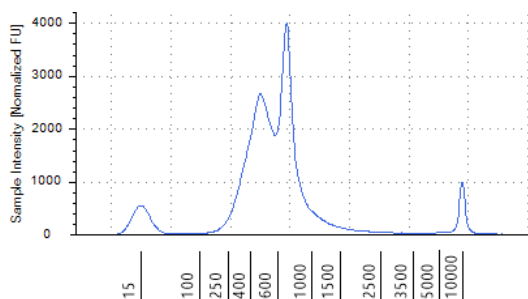
#### Protocol Step 3.5 – Post TCR Amplification QC



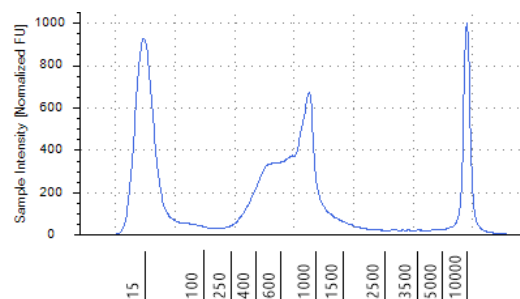
#### Protocol Step 3.5 – Post BCR Amplification QC



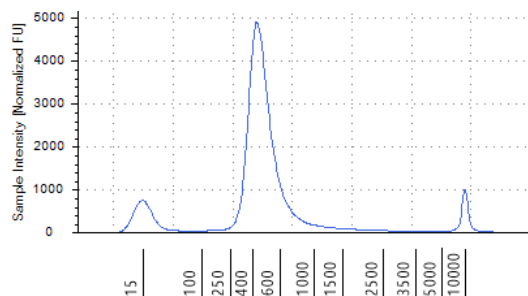
#### Protocol Step 4.6 – Post Library Construction QC (PBMCs amplified for TCR)



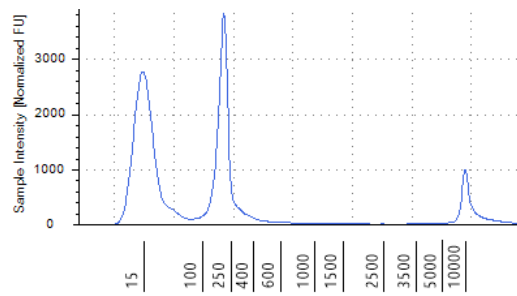
#### Protocol Step 4.6 – Post Library Construction QC (PBMCs amplified for BCR)



#### Protocol Step 5.7 – GEX Post Library Construction QC



#### Protocol Step 6.3 – Post Library Construction QC



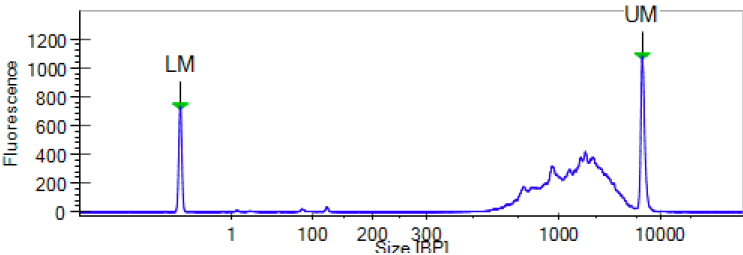
All traces are representative

# LabChip Traces

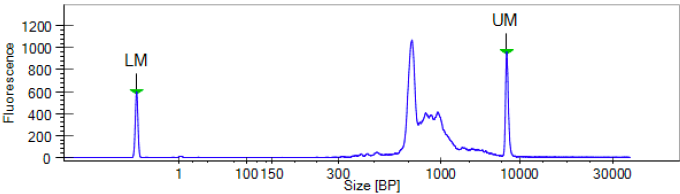
## LabChip Traces

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

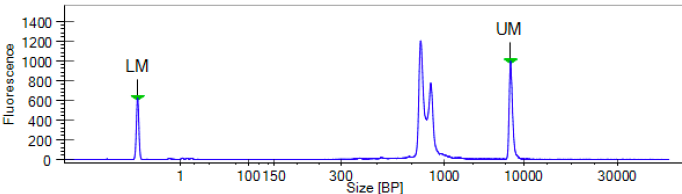
### Protocol Step 2.4 – cDNA QC & Quantification



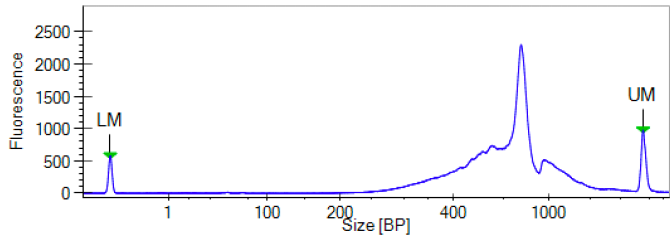
### Protocol Step 3.5 – Post TCR Amplification QC



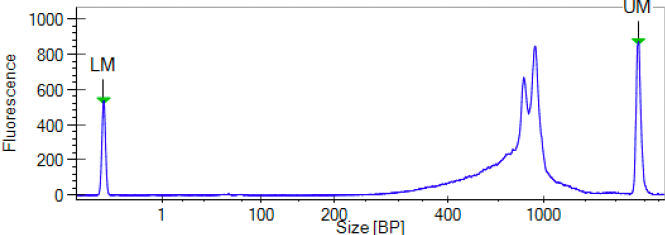
### Protocol Step 3.5 – Post BCR Amplification QC



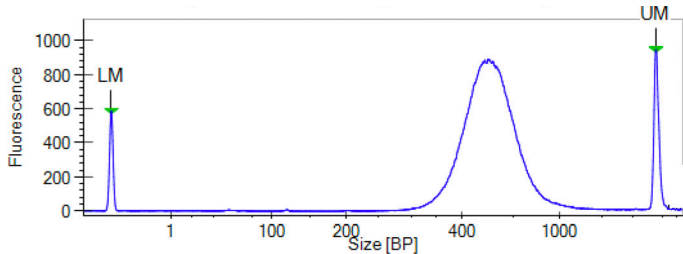
### Protocol Step 4.6 – Post Library Construction QC (PBMCs amplified for TCR)



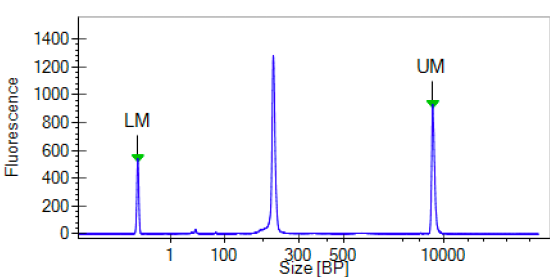
### Protocol Step 4.6 – Post Library Construction QC (PBMCs amplified for BCR)



### Protocol Step 5.7 – GEX Post Library Construction QC



### Protocol Step 6.3 – Post Library Construction QC



All traces are representative



## Oligonucleotide Sequences

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

### Protocol Step 1.5 – GEM-RT Incubation

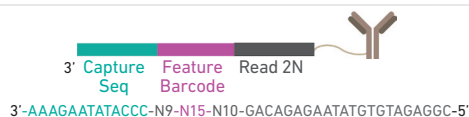
Gel Bead Primer



Poly-dT RT Primer  
PN-2000007



Feature Barcode

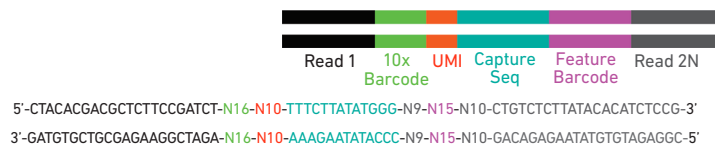


GEM-RT Products

cDNA from poly-adenylated mRNA



DNA from cell surface protein Feature Barcode



### Protocol Step 2.2 – cDNA Amplification

Feature cDNA

Primers 4 -2000277

[Amplifies cDNA](#)

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

Reverse Primer: Non-poly(dT)  
5'-AAGCAGTGGTATCAACGCAGAG-3'

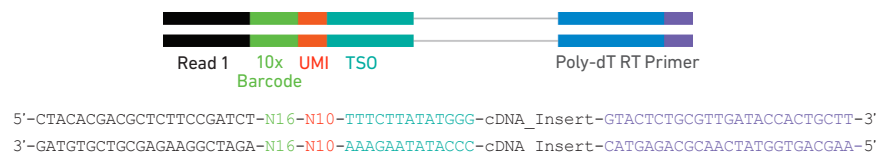
[Amplifies DNA from cell surface protein Feature Barcode](#)

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

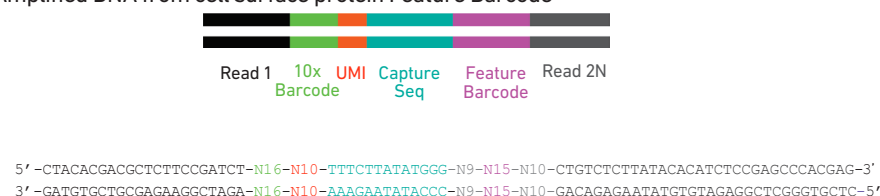
Reverse Primer: Read 2N  
5'-CTCGTGGGCTCGAGATGTG-3'

Amplified Products









Amplified cDNA from poly-adenylated mRNA











Amplified DNA from cell surface protein Feature Barcode



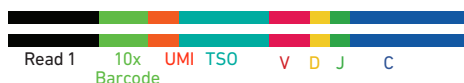
## Protocol Step 3.1 – V(D)J Amplification 1

Human T Cell Mix 1 v2 PN-2000242	Forward Primer:  PCR Primer 5'-GATCTACACTCTTCCCTACACGACGC-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'-GATCTACACTCTTCCCTACACGACGC-3'	Reverse Outer Primers: 5'-CAGGGCAGTCACATCCT-3' 5'-TGCTGGACCACGCATTGTGA-3' 5'-GGTTTTGTGTCGACCCAGTCT-3' 5'-TTGTCCACCTTGGTGTGCT-3' 5'-CATGACGTCCTTGAAGGCA-3' 5'-TGTGGGACTTCCACTG-3' 5'-TTCTCGTAGTCTGCTTTGCTCAG-3'	 Outer Primer
Mouse T Cell Mix 1 v2 PN-2000256	Forward Primer:  PCR Primer 5'-GATCTACACTCTTCCCTACACGACGC-3'	Reverse Outer Primers: 5'-CTGGTTGCTCCAGGCAATGG-3' 5'-TGTAGGCTGAGGGTCCGT-3'	 Outer Primer
Mouse B Cell Mix 1 v2 PN-2000258	Forward Primer:  PCR Primer 5'-GATCTACACTCTTCCCTACACGACGC-3'	Reverse Outer Primers: 5'-TCAGCACGGGACAACTCTTCT-3' 5'-GCAGGAGACAGACTCTTCTCCA-3' 5'-AACTGGCTGCTCATGGTG-3' 5'-TGGTGCAAGTGTGGTTGAGGT-3' 5'-TGGTCACTTGGCTGGTGGT-3' 5'-CACTTGGCAGGTGAAGTGTCTTCT-3' 5'-AACCTTCAAGGATGCTCTTGGGA-3' 5'-GGACAGGGATCCAGAGTTCCA-3' 5'-AGGTGACGGTCTGACTTGGC-3' 5'-GCTGGACAGGGCTCCATAGTT-3' 5'-GGCACCTTGTCCAATCATGTTCC-3' 5'-ATGTCGTTTCTACTCGTCTTGGT-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'-GATCTACACTCTTCCCTACACGACGC-3'	Reverse Inner Primers: 5'-AGTCTCTCAGCTGGTACACG-3' 5'-TCTGATGGCTCAAACACACG-3'	 Inner Primer
Human B Cell Mix 2 v2 PN-2000255	Forward Primer:  PCR Primer 5'-GATCTACACTCTTCCCTACACGACGC-3'	Reverse Inner Primers: 5'-GGGAAGTTTCTGGCGGTCA-3' 5'-GGTGGTACCCAGTTATCAAGCAT-3' 5'-GTGTCCAGGTACCATCAC-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'-GATCTACACTCTTCCCTACACGACGC-3'	Reverse Inner Primers: 5'-AGTCAAAGTCGGTGAACAGGCA-3' 5'-GGCCAAGCACAGAGGTA-3'	 Inner Primer
Mouse B Cell Mix 2 v2 PN-2000259	Forward Primer:  PCR Primer 5'-GATCTACACTCTTCCCTACACGACGC-3'	Reverse Inner Primers: 5'-TACACACAGTGTGGCCTT-3' 5'-CAGGCCACTGTACACCACT-3' 5'-CAGGTCACATTATCATGTCGGC-3' 5'-GAGGCCAGCACAGTGACCT-3' 5'-GCAGGGAAGTTACAGTGCT-3' 5'-CTGTTGAGATCAGTTTGCCATCCT-3' 5'-TGCGAGGTGGCTAGGTAAGT-3' 5'-CCCTTGACCAAGGCATCC-3' 5'-AGGTCACGGAGGAACCAAGTTG-3' 5'-GGCATCCCAGTGTACCCGA-3' 5'-AGAAGATCCACTTACCTTGAAC-3' 5'-GAAGCACACGACTGAGGCAC-3'	 Inner Primer

### V(D)J Amplification Product



5'-GATCTACACTCTTTCCCTACACGACGCTCTCCGATCT-N16-N10-TTCTTTATATGGG-cDNA\_Insert-Inner\_Primer-3'  
 3'-CTAGATGTGAGAAAGGGATGTGCTGCGAGAAGGCTAGA-N16-N10-AAAGAATATACCC-cDNA\_Insert-Inner\_Primer-5'

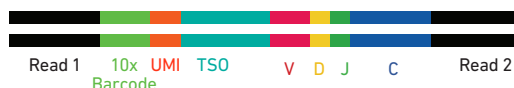
### Protocol Step 4.2 – Adaptor Ligation (for V(D)J Library Construction)

Adaptor  
Oligos  
PN-2000094

Read 2

5'-GATCGGAAGAGCACACGTCTGAACTCCAGTCAC-3'  
 3'-TCTAGCCTTCTCG-5'

### Ligation Product



5'-GATCTACACTCTTTCCCTACACGACGCTCTCCGATCT-N16-N10-TTCTTTATATGGG-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

Forward Primer:

P5 Sample Partial Read 1  
Index (i5)

5'-AATGATACGGCGACCACCGAGATCTACAC-N10-ACACTCTTTCCCTACACGACGCTC-3'

Reverse Primer:

P7 Sample Partial Read 2  
Index (i7)

5'-CAAGCAGAAGACGGCATACGAGAT-N10-GTGTGAGGAGTTCCAGACGTGT-3'

Dual Index Kit  
TT Set A  
PN-1000215

### Sample Index PCR Product



5'-AATGATACGGCGACCACCGAGATCTACAC-N10-ACACTCTTTCCCTACACGACGCTCTCCGATCT-N16-N10-TTCTTTATATGGG-Insert-AGATCGGAAGAGCACACGTCTGAACTCCAGTCAC-N10-ATCTCGTATGCCCTCTTCGCTTG-3'  
 3'-TTACTATGCCGCTGGTGGCTCTAGATGTG-N10-TGTGAGAAAGGGATGTGCTGCGAGAAGGCTAGA-N16-N10-AAAGAATATACCC-Insert-TCTAGCCTTCTCGTGTGCAGACTTGAAGTCAAGT-N10-TAGAGCATACGGCAGAAGACGAAC-5'

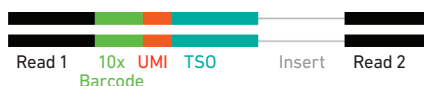
### Protocol Step 5.3 – GEX Adaptor Ligation (for 5' Gene Expression (GEX) Library Construction)

Adaptor Oligos  
PN-2000094

Read 2

5'-GATCGGAAGAGCACACGTCTGAACTCCAGTCAC-3'  
 3'-TCTAGCCTTCTCG-5'

### Ligation Product



5'-CTACACGACGCTCTCCGATCT-N16-N10-TTCTTTATATGGG-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

Forward Primer:



Reverse Primer:



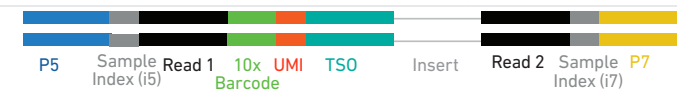
Dual Index Kit

TT Set A

PN-1000215

5'-AATGATACGGCGACCACCGAGATCTACAC-N10-ACACTCTTTCCCTACACGACGCTC-3'

5'-CAAGCAGAAGACGGCATACGAGAT-N10-GTGAAGTTCAGACGTGT-3'

Sample Index  
PCR Product

5'-AATGATACGGCGACCACCGAGATCTACAC-N10-ACACTCTTTCCCTACACGACGCTCTCCGATCT-N16-N10-TTCTTATATGGG-cDNA \_ Insert-AGATCGGAAGAGCACAGTCCTGAACCTCAGTCAC-N10-ATCTCGTATGCCGCTTCTGCTTG-3'

3'-TTACTATGCCGCTGGTGGCTCTAGATGTG-N10-TGTGAGAAAGGGATGTCTGCGAGAAGGCTAGA-N16-N10-AAAGAATATACCC-cDNA \_ Insert-TCTAGCCTTCTCGTGTGCAGACTTGAGGTCAGTG-N10-TAGAGCATACGGCAGAGACGAAC-5'

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

#### Dual Indexing

Forward Primer:



Reverse Primer:



Dual Index Kit

TN Set A

PN-1000250

5'-AATGATACGGCGACCACCGAGATCTACAC-N10-ACACTCTTTCCCTACACGACGCTC-3'

5'-CAAGCAGAAGACGGCATACGAGAT-N10-GTCTCGTGGGCTCGG-3'

Sample Index  
PCR Product

5'-AATGATACGGCGACCACCGAGATCTACAC-N10-ACACTCTTTCCCTACACGACGCTCTCCGATCT-N16-N10-TTCTTATATGGG-N9-N15-N10-CTGTCTCTTATACACATCTCCGAGCCACGAGAC-N10-ATCTCGTATGCCGCTTCTGCTTG-3'

3'-TTACTATGCCGCTGGTGGCTCTAGATGTG-N10-TGTGAGAAAGGGATGTCTGCGAGAAGGCTAGA-N16-N10-AAAGAATATACCC-N9-N15-N10-GACAGAGATATGTGTAGAGGCTCGGCTCTG-N10-TAGAGCATACGGCAGAGACGAAC-5'