CG000239 Rev F

USER GUIDE

Visium Spatial Gene Expression Reagent Kits

FOR USE WITH

Visium Spatial Gene Expression Slide & Reagent Kit, 16 rxns PN-1000184
Visium Spatial Gene Expression Slide & Reagent Kit, 4 rxns PN-1000187
Visium Gateway Package, 2 rxns PN-1000316
Visium Gateway Slide, 2 rxns PN-1000317
Visium Accessory Kit, PN-1000194
Dual Index Kit TT Set A, 96 rxns PN-1000215

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Notices

Document Number

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Document Revision Summary

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Specific Changes:

- Added additional recommended pipette tips on page 14.

General Changes:

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

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Introduction

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Visium Spatial Gene Expression Reagent Kits

Visium Spatial Gene Expression Slide & Reagent Kit, 16 rxns PN-1000184

Visium Spatial Gene Expression Reagent Kit, 16 rxns PN-1000186 (store at –20°C)

Visium
Spatial Gene Expression Reagent Kit

	#	PN
Permeabilization Enzyme	1	2000214
RT Reagent	1	2000086
RT Enzyme D	1	2000216
Template Switch Oligo	2	3000228
Reducing Agent B	1	2000087
Second Strand Primer	1	2000217
Second Strand Enzyme	1	2000218
Second Strand Reagent	1	2000219
cDNA Primers	1	2000089
Amp Mix	1	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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Visium Spatial Gene Expression Slide Kit, 16 rxns PN-1000185 (store at ambient temperature)

Visium
Spatial Gene Expression Slide Kit

	#	PN
Visium Spatial Gene Expression Slide	4	2000233
*Visium Slide Seals, 40-pack or 20-pack	1	2000284 3000279
Visium Slide Cassette & Gasket, 4-pack	1	2000282

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*Visium Slide Seals may come in varying configurations in different lots.

Visium Spatial Gene Expression Reagent Kits

Visium Spatial Gene Expression Slide & Reagent Kit, 4 rxns PN-1000187

Visium Spatial Gene Expression Reagent Kit, 4 rxns PN-1000189 (store at –20°C)

Visium
Spatial Gene Expression Reagent Kit

	#	PN
Permeabilization Enzyme	1	2000214
RT Reagent	1	2000086
RT Enzyme D	1	2000227
Template Switch Oligo	1	3000228
Reducing Agent B	1	2000087
Second Strand Primer	1	2000217
Second Strand Enzyme	1	2000183
Second Strand Reagent	1	2000219
cDNA Primers	1	2000089
Amp Mix	1	2000103

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

Library Construction Kit

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

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Visium Spatial Gene Expression Slide Kit, 4 rxns PN-1000188 (store at ambient temperature)

Visium
Spatial Gene Expression Slide Kit

	#	PN
Visium Spatial Gene Expression Slide	1	2000233
*Visim Slide Seals, 12-pack or 5-pack	1	2000283 3000279
Visium Slide Cassette & Gasket, 1-pack	1	2000281

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*Visium Slide Seals may come in varying configurations in different lots.

Visium Gateway Reagent Kits

Visium Gateway Package*, 2 rxns PN-1000316
Visium Gateway Slide, 2 rxns PN-1000317

*Contains Tissue Optimization reagents (PN-1000313 and PN-1000314) not used in this protocol.

Visium Gateway Gene Expression Reagent Kit, PN-1000315 (store at –20°C)

Visium
Gateway Gene Expression Reagent Kit

	#	PN
Permeabilization Enzyme	1	2000214
RT Reagent	1	2000086
RT Enzyme D	1	2000227
Template Switch Oligo	1	3000228
Reducing Agent B	1	2000087
Second Strand Primer	1	2000217
Second Strand Enzyme	1	2000183
Second Strand Reagent	1	2000219
cDNA Primers	1	2000089
Amp Mix	1	2000103

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

Library Construction Kit

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

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Visium Gateway Gene Expression Slide Kit, PN-1000312 (store at ambient temperature)

Visium
Gateway Gene Expression Slide Kit

	#	PN
Visium Gateway Gene Expression Slide	1	2000363
Visium Slide Seals, 5-pack	1	3000279
Visium Slide Cassette & Gasket, 1-pack	1	2000281

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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
Dual Index Plate TT Set A	1	3000431

10x Genomics Accessories

Product	Part Number (Kit)	Part Number (Item)
Thermocycler Adaptor	1000194	3000380
Visium Spatial Imaging Test Slide		2000235
10x Magnetic Separator		230003
Slide Alignment Tool		3000433

Recommended Thermal Cyclers

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

Recommended Real Time qPCR Systems

Supplier	Description	Part Number
Applied Biosystems	QuantStudio 12K Flex system	4471087
Bio-Rad	CFX96 Real-time System	1855096

Imaging System Recommendations

The imaging systems listed below were used by 10x Genomics. Any equivalent system with the listed features may be used for imaging. Hardware compatibility may be tested by using the Visium Spatial Imaging Test Slide. Consult the Visium Spatial Gene Expression Imaging Guidelines Technical Note (CG000241) for more information.

Imaging Systems & Specifications	
Microscopes (Any equivalent system with the listed features may be used for imaging)	
Nikon	Nikon Eclipse Ti2 with brightfield and fluorescence capacity (TRITC)
Molecular Devices	ImageXpress Nano Automated Slide Imaging System
Hamamatsu	NanoZoomer S60
Keyence	Keyence BZX800
BioTek	Cytation 7
Thermo Fisher Scientific	EVOS M7000
Leica	Leica DMi8 Versa 8
Microscope Features	
Objectives	• 4X (Plan APO λ; NA 0.20) • 10X (Plan APO λ; NA 0.45) • 20X (Plan APO λ; NA 0.75)
Automated Scanning Stage	Microscope tile scanning functionality is required for imaging tissue sections placed on a Capture Area of a Visium Spatial slide.
Brightfield Features (for H&E staining only)	• Color camera (3 x 8 bit, 2,424 x 2,424 pixel resolution) • White balancing functionality • Minimum Capture Resolution 2.18 µm/pixel • Exposure times 2-10 milli sec
Fluorescence Features*	• Light source (or equivalent) with a wavelength range of 380-680 nm • Monochrome camera (14 bit, 2,424 x 2,424 pixel resolution) • DAPI filter cube (Excitation 392/23, Emission 447/60) • Cy5 filter cube (Excitation 618/50, Emission 698/70) • TRITC filter cube (Excitation 542/20, Emission 620/52) (required for Immunofluorescence Staining & Tissue Optimization protocols only) • Minimum Capture Resolution 2.18 µm/pixel • Exposure times 100 milli sec-2 sec
* Only required for Visium Spatial Tissue Optimization protocol & Visium Imaging Test Slide verification and if performing Immunofluorescence Staining prior to Tissue Optimization and Gene Expression protocols.	
Additional Specifications	
Image Format	Save image as a tiff (preferred) or jpeg
Computer	Computer with sufficient power to handle large images (0.5-5 GB)
Software	Image stitching software (microscope's software or equivalent, like Image J)

Image Capture Guidelines: The 8 mm x 8 mm area that includes the fiducial frame and the Capture Area with the tissue section should be represented by ≥2,000 x 2,000 pixel portion of the image. When setting the microscope for imaging individual Capture Area, the imaging area should be ~1-2 mm beyond the fiducial frame for optimal imaging alignment. Minimize imaging of any adjacent CaptureArea/s when taking images of a specific Capture Area with a tissue section. For lossy compression, such as jpeg, the quality level should be kept high enough to represent the fiducial frame crisply and without artifact.

Additional Kits, Reagents & Equipment

The items in the table below have been validated by 10x Genomics and are highly recommended for the Visium Spatial Reagent Kits protocols. **Substituting materials may adversely affect system performance.** This list does not include standard laboratory equipment such as water baths, centrifuges, vortex mixers, pH meters, freezers etc.

Supplier	Description	Part Number (US)
Plastics		
Eppendorf	PCR Tubes 0.2 ml 8-tube strips DNA LoBind Tubes, 1.5 ml DNA LoBind Tubes, 2.0 ml (when processing more than 2 slides)	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 Simport Scientific LockMailer Tamper Evidence Slide Mailer (alternatively, use a 50-ml centrifuge tube)	N8010580 N8010535 22-038-399
Corning	Self-Standing Polypropylene Centrifuge Tubes (50 ml), sterile	430921
Bio-Rad	Hard-shell PCR Plates 96-well, thin wall (pkg of 50) (alternatively, use any compatible PCR Plate) Microseal 'B' PCR Plate Sealing Film, adhesive (alternatively, use any PCR Plate sealing adhesive)	HSP9665 MSB1001
VWR	Divided Polystyrene Reservoirs	41428-958
Kits & Reagents		
Thermo Fisher Scientific	Nuclease-free Water Low TE Buffer (10 mM Tris-HCl pH 8.0, 0.1 mM EDTA) Tris 1M, pH 7.0, RNase-free Shandon ColorFrost Plus Slides 25 x 75 x1 mm (Optional)	AM9937 12090-015 AM9850G 6776214
Fisher Chemical	Hydrochloric Acid Solution, 0.1N	SA54-1
Roche (US, some Canadian Provinces) Millipore Sigma (Europe, Asia, & some Canadian Provinces)	KAPA SYBR FAST qPCR Master Mix (2X)	KK4600
Beckman Coulter	SPRIselect Reagent Kit	B23318

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

Additional Kits, Reagents & Equipment

The items in the table below have been validated by 10x Genomics and are highly recommended for the Visium Spatial Reagent Kits protocols. **Substituting materials may adversely affect system performance.** This list does not include standard laboratory equipment such as water baths, centrifuges, vortex mixers, pH meters, freezers etc.

Supplier	Description	Part Number (US)
Kits & Reagents		
Millipore Sigma	Ethanol, Pure (200 Proof, anhydrous) Potassium Hydroxide Solution, 8M SSC Buffer 20X Concentrate	E7023-500ML P4494-50ML S66391L
Qiagen	Qiagen Buffer EB	19086
-	Ultrapure/Milli-Q water (from Milli-Q Integral Ultrapure Water System or equivalent)	
Equipment		
VWR	VWR Mini Centrifuge (alternatively, use any equivalent mini centrifuge)	76269-064
Quantification & Quality Control		
Agilent	2100 Bioanalyzer Laptop Bundle (discontinued) (Replacement 2100 Bioanalyzer Instrument/2100 Expert Laptop Bundle) High Sensitivity DNA Kit 4200 TapeStation High Sensitivity D1000 ScreenTape/Reagents High Sensitivity D5000 ScreenTape/Reagents	G2943CA G2939BA/2953CA 5067-4626 G2991AA 5067-5584/ 5067-5585 5067-5592/ 5067-5593
PerkinElmer	LabChip GX Touch HT Nucleic Acid Analyzer DNA High Sensitivity Reagent Kit	CLS137031 CLS760672
KAPA Biosystems	KAPA Library Quantification Kit for Illumina Platforms	KK4824

Choose Bioanalyzer, TapeStation or Lab Chip based on availability & preference.

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

**Compatible with Rainin pipettes*

Protocol Steps & Timing

1-1.5 days

Steps		Timing	Stop & Store
Step 1 – cDNA Synthesis			
1.1	Tissue Permeabilization	Variable	
1.2	Reverse Transcription	65 min	
Step 2 – Second Strand Synthesis & Denaturation			
2.1	Second Strand Synthesis	25 min	
2.2	cDNA Denaturation	15 min	
Step 3 – cDNA Amplification & QC			
3.1	Cycle Number Determination – qPCR	45 min	
3.2	cDNA Amplification	45-60 min	STOP 4°C ≤72 h or –20°C ≤1 week
3.3	cDNA Cleanup – SPRIselect	20 min	STOP 4°C ≤72 h –20°C ≤4 weeks
3.4	cDNA QC & Quantification	50 min	
Step 4 – Visium Spatial Gene Expression Library Construction			
4.1	Fragmentation, End Repair & A-tailing	50 min	
4.2	Post Fragmentation, End Repair & A-tailing Double Sided Size Selection – SPRIselect	30 min	
4.3	Adaptor Ligation	25 min	
4.4	Post Ligation Cleanup- SPRIselect	20 min	
4.5	Sample Index PCR	40 min	STOP 4°C ≤72 h
4.6	Post Sample Index PCR Double Sided Size Selection- SPRIselect	30 min	STOP 4°C ≤72 h or -20°C long term
4.7	Post Library Construction QC	50 min	

Stepwise Objectives

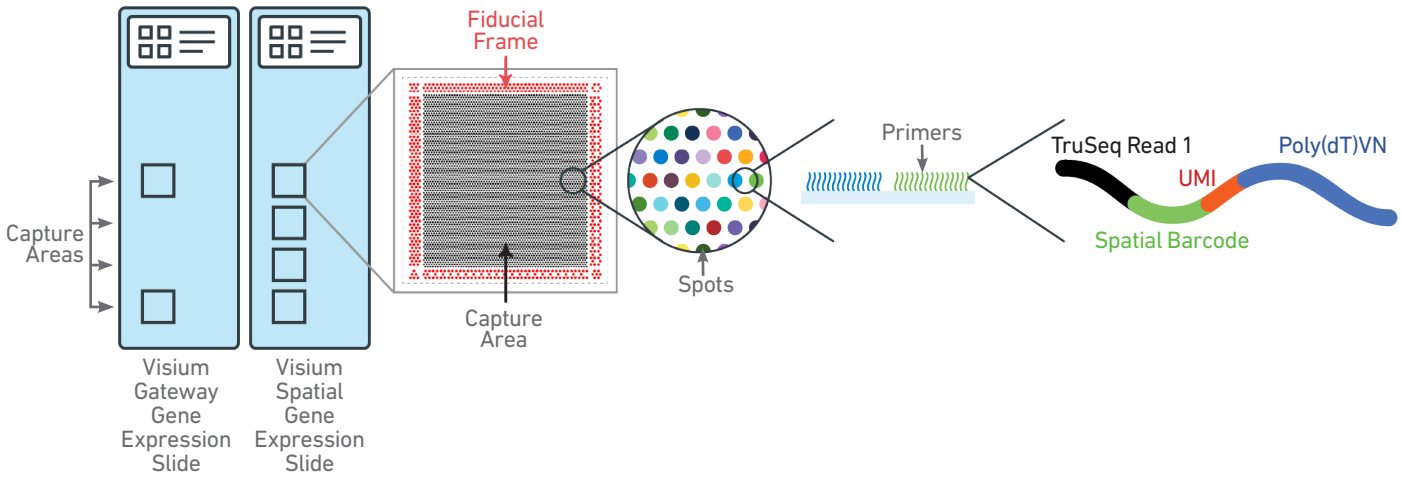
The Visium Spatial Gene Expression Solution measures total mRNA in intact tissue sections and maps the location(s) where gene activity is occurring. Each Visium Spatial or Gateway Gene Expression Slide contains Capture Areas with gene expression spots that include primers required for capture and priming of poly-adenylated mRNA. Tissue sections placed on these Capture Areas are fixed and stained, as described in Tissue Fixation & Staining Demonstrated Protocols – CG000160 or CG000312, permeabilized, and cellular mRNA is captured by the primers on the gene expression spots. All the cDNA generated from mRNA captured by primers on a specific spot share a common Spatial Barcode. Libraries are generated from the cDNA and sequenced and the Spatial Barcodes are used to associate the reads back to the tissue section images for spatial gene expression mapping.

This document outlines the protocol for generating Visium Spatial Single Cell 3' Gene Expression libraries from tissue sections placed on the Capture Areas of a Visium Spatial Gene Expression Slide.

Visium Spatial and Gateway Gene Expression Slides

The Visium Spatial Gene Expression Slide includes 4 Capture Areas (6.5 x 6.5 mm), each defined by a fiducial frame (fiducial frame + Capture Area is 8 x 8 mm). The Visium Gateway Gene Expression Slide includes 2 Capture Areas that are identical in size. The Capture Area has ~5,000 gene expression spots, each spot with primers that include:

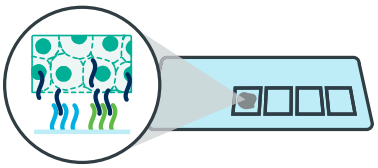
- Illumina TruSeq Read 1 (partial read 1 sequencing primer)
- 16 nt Spatial Barcode (all primers in a specific spot share the same Spatial Barcode)
- 12 nt unique molecular identifier (UMI)
- 30 nt poly(dT) sequence (captures poly-adenylated mRNA for cDNA synthesis).



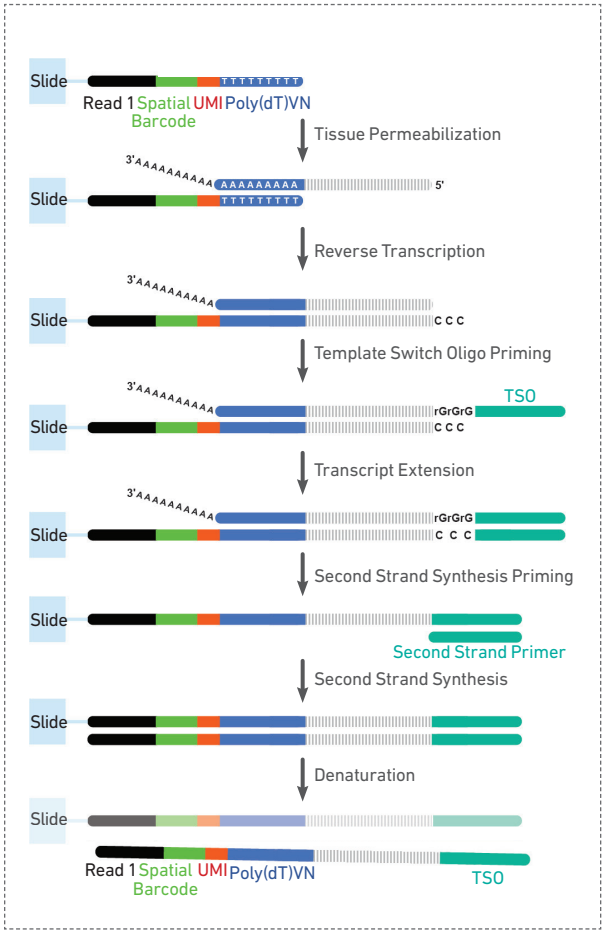
Step 1 Permeabilization & Reverse Transcription

A Permeabilization Enzyme is used to permeabilize the fixed and stained tissue sections on the slide. The poly-adenylated mRNA released from the overlying cells is captured by the primers on the spots. RT Master Mix containing reverse transcription reagents is added to the permeabilized tissue sections. Incubation with the reagents produces spatially barcoded, full-length cDNA from poly-adenylated mRNA on the slide.

Permeabilization



Reactions on slide Capture Areas



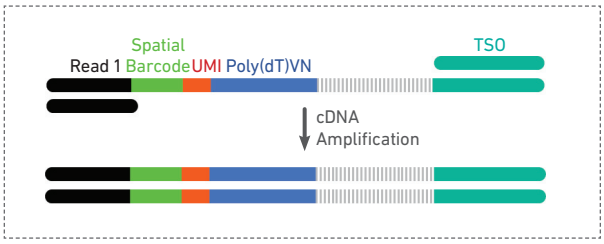
Step 2 Second Strand Synthesis & Denaturation

Second Strand Mix is added to the tissue sections on the slide to initiate second strand synthesis. This is followed by denaturation and transfer of the cDNA from each Capture Area to a corresponding tube for amplification and library construction.

Step 3 cDNA Amplification & QC

After transfer of cDNA from the slide, spatially barcoded, full-length cDNA is amplified via PCR to generate sufficient mass for library construction.

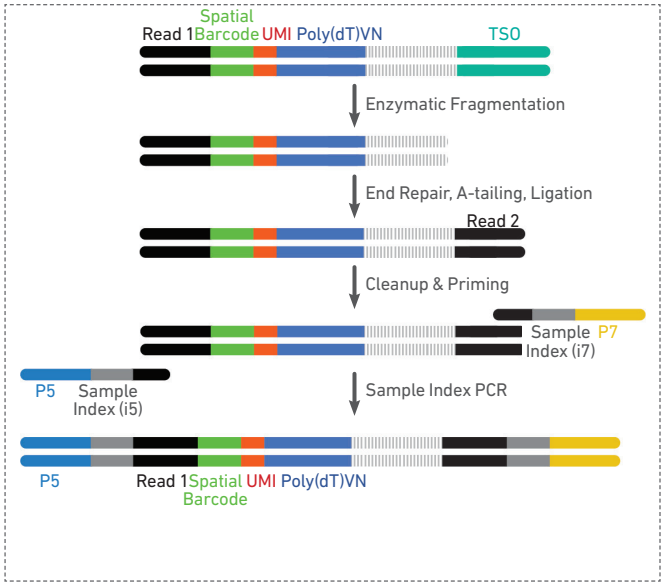
cDNA amplification



Step 4 Visium Spatial Gene Expression Library Construction

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

Amplified cDNA processing (dual index)

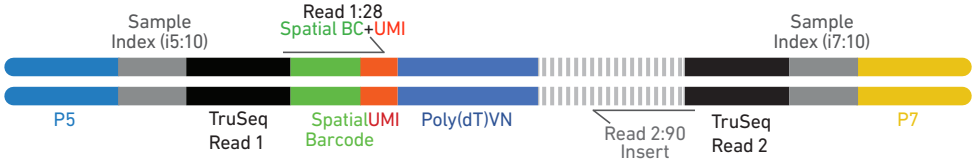


Step 5 Sequencing

A Visium Spatial Gene Expression library comprises standard Illumina paired-end constructs which begin and end with P5 and P7. The 16 bp Spatial Barcode and 12 bp UMI are encoded in Read 1, while Read 2 is used to sequence the cDNA fragment. i7 and i5 sample index sequences are incorporated. TruSeq Read 1 and TruSeq Read 2 are standard Illumina sequencing primer sites used in paired-end sequencing.

Illumina sequencer compatibility, sample indices, library loading and pooling for sequencing are summarized in step 5.

Visium Spatial Gene Expression Library



See Appendix for Oligonucleotide Sequences

Tips & Best Practices

Icons

Tips & Best Practices section includes additional guidance

Signifies critical step requiring accurate execution

Troubleshooting section includes additional guidance

Version Specific Update

VERSION SPECIFIC

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.

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.
- Use a pH meter to adjust pH as necessary during buffer preparation.

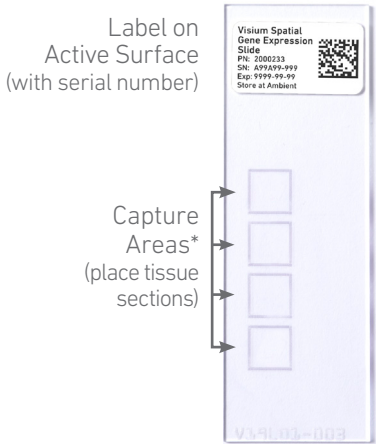
Pipette Calibration

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

Visium Spatial and Gateway Gene Expression Slides

- Includes 2 or 4 Capture Areas (6.5 x 6.5 mm), each with ~5,000 unique gene expression spots.
- Each gene expression spot includes primers with a unique Spatial Barcode (see Stepwise Objectives for additional information).
- The active surface of the slide is defined by a readable label that includes the serial number.
- The tissue sections are always placed on the active surface of the Capture Areas. For more information, consult the Visium Spatial Protocols – Tissue Preparation Guide (Demonstrated Protocol CG000240).

Visium Spatial Gene Expression Slide



Note the serial number on the slide label; required in downstream analysis.

*Visium Gateway Gene Expression Slide contains 2 Capture Areas

Slide Storage

- Always store unused slides in a dry environment at room temperature in their original packaging and keep sealed. DO NOT remove desiccant.
- After tissue placement, store slides in a sealed container. If using an unsealed slide mailer, store in a secondary sealed container, such as a resealable bag.
- Store the sealed container containing slides with tissue at **–80°C** for up to four weeks.

Store Unsealed Slide Mailers in a Secondary Sealed Container

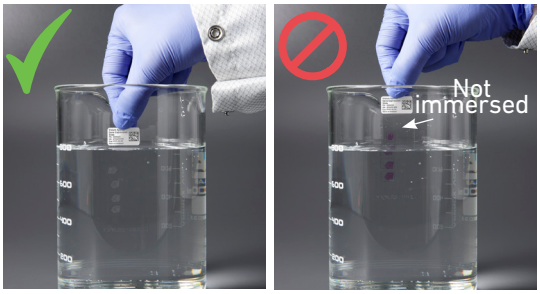
Slide Handling

- Always wear gloves when handling slides.
- Exercise caution when handling slide edges to prevent injury.
- Ensure that the active surface of a slide faces up and is never touched. The orientation of the label on the slide defines the active surface.
- The tissue sections should always be on the active surface of the slide. DO NOT touch the tissue sections on the slide.
- Minimize exposure of the slides to sources of particles and fibers.
- When immersing slides in water, ensure that the tissue sections are completely submerged.
- Keep the slide flat on the bench when adding reagents to the active surface.
- Ensure that no absorbent surface is in contact with the reagents on the slide during incubation.

Active Surface with Tissue Sections

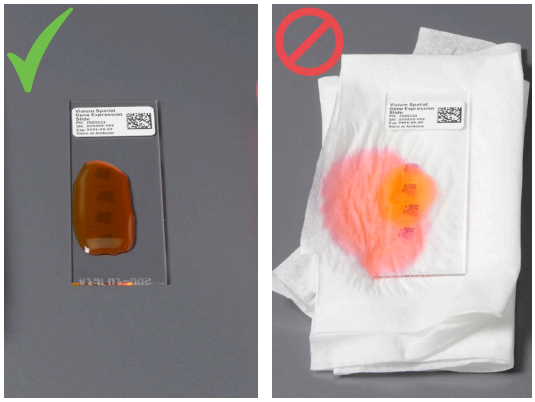
Immersing Slide

Correct | Incorrect



Reagent on Slide

Correct | Incorrect

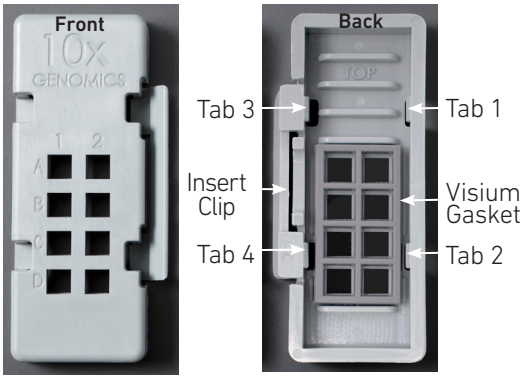


Slides in image are representative.

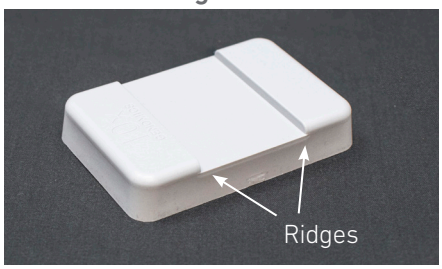
Visium Slide Cassette

- The Visium Slide Cassette encases the slide and creates leakproof wells for adding reagents.
- Place the slides in the Visium Slide Cassette only when specified.
- The Visium Slide Cassette includes a removable Visium Gasket.
- An Insert Clip and four tabs at the back of the Visium Slide Cassette are used for holding the slide in the cassette, as shown.
- The removable Visium Gasket corresponds to the Capture Areas on the slides.
- The Visium Slide Cassette may be assembled using the Slide Alignment Tool or manually. Instructions for both are provided in the following section.
- See Visium Slide Cassette Assembly & Removal instructions for details.
- Ensure that the back of the Visium Slide Cassette is facing the user prior to assembly. The active surface of the slide with tissue sections will face down such that the slide label is no longer readable.
- Practice assembly with a plain glass slide (75 x 25 x 1 mm).
- Applying excessive force to the slide may cause the slide to break.

Visium Slide Cassette



Slide Alignment Tool

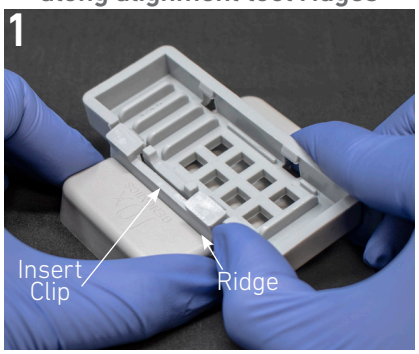


Visium Slide Cassette Assembly

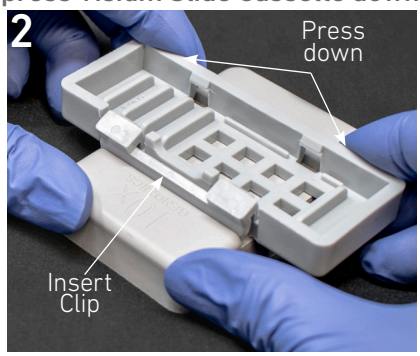
Exercise caution when handling slide edges to prevent injury.

Slide insertion may push Visium Gasket out of alignment with slide cutouts. Adjust if necessary.

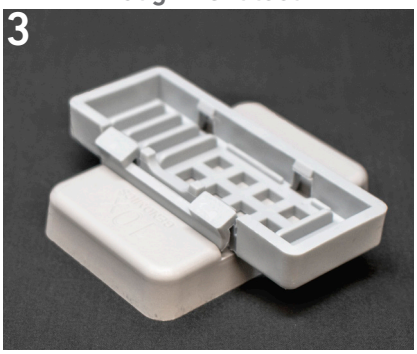
Position Visium Slide Cassette along alignment tool ridges



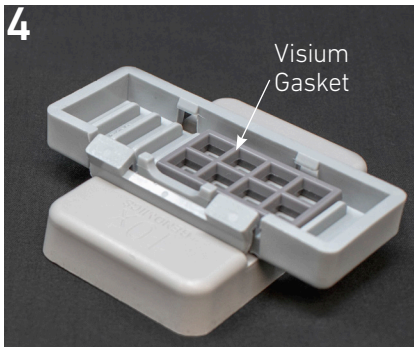
Push Insert Clip along the ridge & press Visium Slide Cassette down



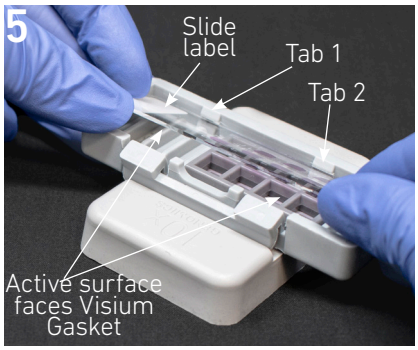
Visium Slide Cassette secured on alignment tool



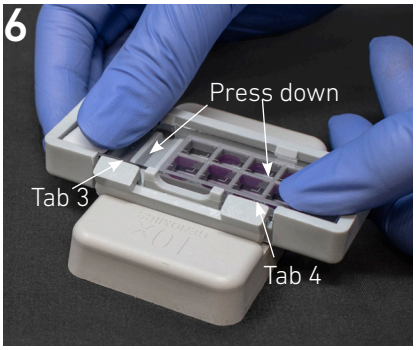
Position Visium Slide Gasket to align with Visium Slide Cassette Cutouts



Insert long edge of slide under tabs 1 & 2; ensure slide is flush



Press slide down until it is flush with the Visium Gasket and under tabs 3 & 4



Remove Visium Slide Cassette while pressing slide against the Visium Gasket

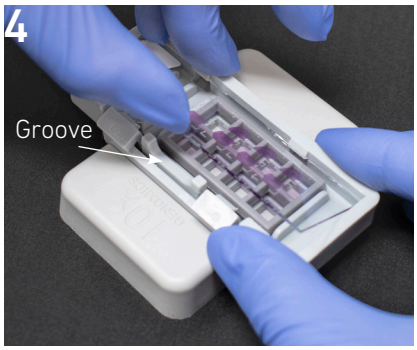
Visium Slide Cassette Removal*

Position Visium Slide Cassette along alignment tool ridges

Push Insert Clip along the ridge & press down

Visium Slide Cassette sits securely on alignment tool

Lift slide at Visium Slide Cassette groove



*Slide removal not needed for the Visium Spatial Gene Expression protocol.

Manual Visium Slide Cassette Assembly & Removal

Assembly

i. Remove the Visium Gasket from the Visium Slide Cassette and re-insert the Visium Gasket, ensuring that the Visium Gasket and Visium Slide Cassette cutouts are aligned.

ii. Align the label on top of the slide to the top of the Visium Slide Cassette, as shown.

iii. Insert the slide under tabs 1 and 2. Ensure that the long edge of the slide is flush with the side of the Visium Slide Cassette.

iv. Press the insert clip **very firmly** by applying even force on the lower part of the insert clip.

v. Place a finger in between tab 3 and the top of the Visium Slide Cassette, and one finger between tab 4 and the bottom of the Visium Slide Cassette. Press down on the slide evenly until the slide is under each tab and release the insert clip.

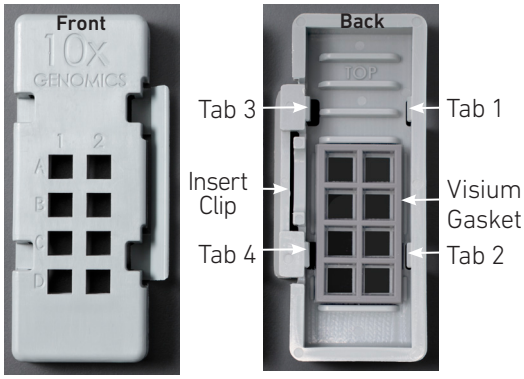
Removal*

vi. Press the insert clip **very firmly** to release the slide from the Visium Slide Cassette.

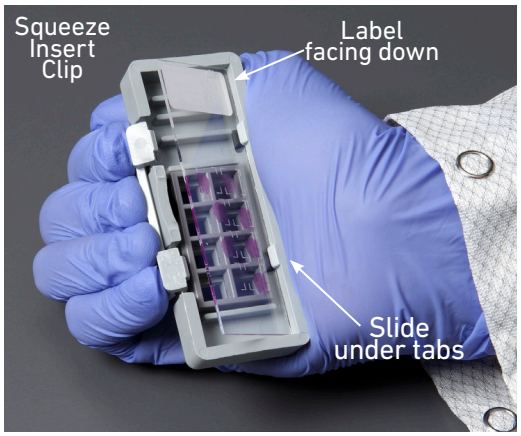
vii. Lift slide at Visium Slide Cassette groove between tabs 3 and 4 until the slide can be removed.

*Slide removal not needed for the Visium Spatial Gene Expression protocol.

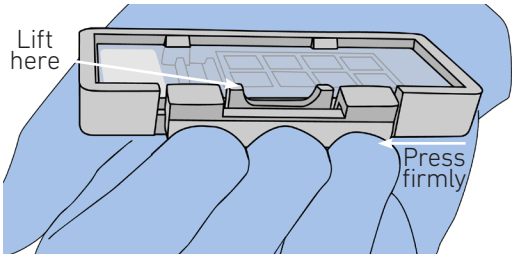
Visium Slide Cassette



Visium Slide Cassette Assembly



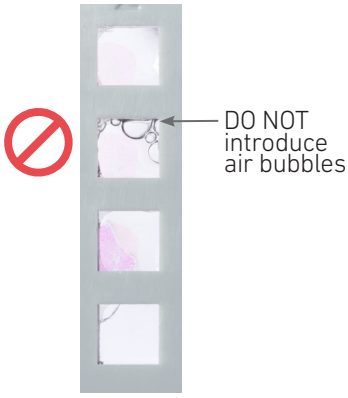
Insert Clip - Press Firmly



Reagent Addition & Removal from Wells

- Place the assembled slide in the Visium Slide Cassette flat on a clean work surface.
- Dispense and remove reagents along the side of the wells without touching the tissue sections and without introducing bubbles.
- Always cover the tissue section completely when adding reagents to the well. A gentle tap may help spread the reagent more evenly.
- Ensure that no bubbles are introduced in the process.

Reagent Addition/Removal



Visium Slide Seal Application & Removal

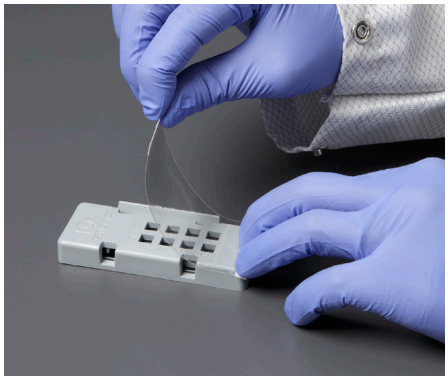
Application

- Place the Visium Slide Cassette flat on a clean work surface.
- Remove the back of the adhesive Visium Slide Seal.
- Align the Visium Slide Seal with the surface of the Visium Slide Cassette and apply while firmly holding the Visium Slide Cassette with one hand.
- Press on the Visium Slide Seal to ensure uniform adhesion.

Removal

- Place the Visium Slide Cassette flat on a clean work surface.
- Pull on the Visium Slide Seal from the edge while firmly holding the Visium Slide Cassette. Ensure that no liquid splashes out of the wells.

Visium Slide Seal Application



Seals in image are representative.

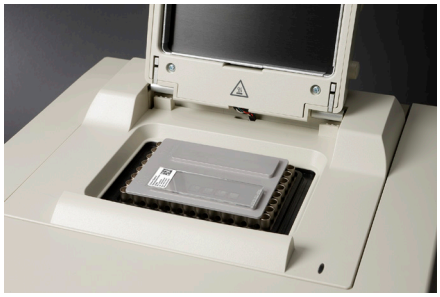
Slide Incubation Guidance

Incubation at a specified temperature

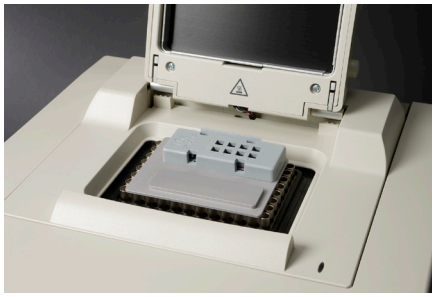
- Position a Thermocycler Adaptor on a thermal cycler that is set at the incubation temperature.
- Ensure that the Thermocycler Adaptor is in contact with the thermal cycler surface uniformly.
- When incubating a slide, position the slide on the Thermocycler Adaptor with the active surface facing up.
- Ensure that the entire bottom surface of the slide is in contact with Thermocycler Adaptor.
- When incubating a slide encased in a Visium Slide Cassette, place the assembled unit on the Thermocycler Adaptor with the wells facing up. The Visium Slide Cassette should always be sealed when on the Thermocycler Adaptor.

Place Thermocycler Adaptor

Incubate Slide



Incubate Assembled Visium Slide Cassette



Incubation at room temperature

- Place the slide/Visium Slide Cassette on a flat, clean, non-absorbent work surface.
- Ensure that no absorbent surface is in contact with the reagents on the slide during incubation.

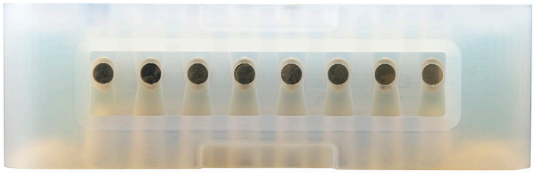
Slide Incubation

Correct

Incorrect

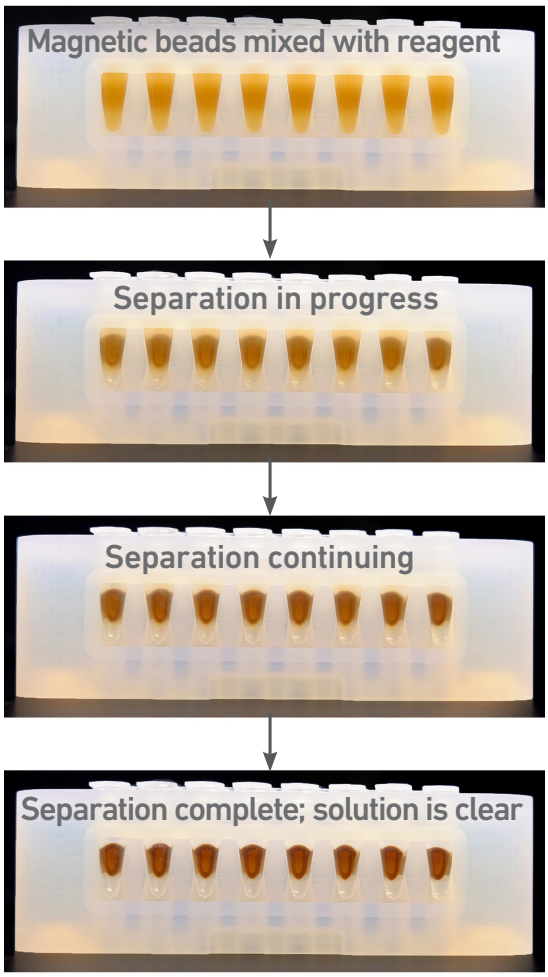
10x Magnetic Separator

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



Magnetic Bead Cleanup Steps

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



SPRIselect Cleanup & Size Selection

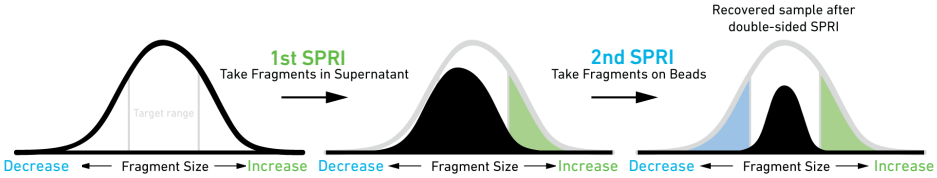
- After aspirating the desired volume of SPRIselect reagent, examine the pipette tips before dispensing to ensure the correct volume is transferred.
- Pipette mix thoroughly as insufficient mixing of sample and SPRIselect reagent will lead to inconsistent results.
- Use fresh preparations of 80% Ethanol.

Tutorial — SPRIselect Reagent:DNA Sample Ratios

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

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

Schematic of Double Sided Size Selection



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

Tutorial — Double Sided Size Selection

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

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

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

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

Enzymatic Fragmentation

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

Sample Indices (i5/i7) 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 TT Set A contains a unique i7 and a unique i5 oligonucleotide.

Sample Preparation, Fixation & Staining Guidelines

Sample Preparation Guidelines

Proper tissue handling and preparation techniques are critical in preserving the morphological quality of the tissue sections and subsequent transcript profiling using Visium Spatial protocols.

Listed below are some key considerations for preparing samples that are compatible with the Visium Spatial protocols.

Consult the Visium Spatial Protocols – Tissue Preparation Guide for complete information (Demonstrated Protocol CG000240).

Key Considerations
Slide Handling (before sectioning)
☐ Equilibrate Visium slides to cryostat temperature before cryosectioning.
☐ Store unused slides in original packaging and keep sealed. DO NOT remove desiccant. If necessary, store original packaging in a secondary container such as a resealable bag.
Freezing and Embedding
☐ Snap freeze samples in a bath of isopentane and liquid nitrogen.
☐ Store frozen samples at **-80°C** in a sealed container for **long-term** storage prior to embedding.
Cryosectioning
☐ Equilibrate OCT tissue block to the cryostat chamber temperature for **30 min**.
☐ Place tissue sections on the Capture Area* within the fiducial frame on the slide.

*Visium Gateway Gene Expression Slide contains 2 Capture Areas

Slide Handling (after sectioning)
☐ Maintain slides containing sections in a low moisture environment.
☐ Keep slides cold and transport slides on dry ice.
☐ DO NOT leave slides at room temperature.
Sample Storage
☐ Store slides individually in a sealed container at **-80°C** for up to **4 weeks** to avoid multiple freeze thaw cycles. If using an unsealed slide mailer, store in a secondary sealed container, such as a resealable bag.

Fixation & Staining Guidelines

Proper tissue fixation and staining should be performed before executing the Permeabilization & cDNA Synthesis steps.

Consult Demonstrated Protocols (available on the 10x Genomics Support website) for fixing and staining tissue sections:

Methanol Fixation, H&E Staining & Imaging for Visium Spatial Protocols (Demonstrated Protocol CG000160)

OR

Methanol Fixation, Immunofluorescence Staining & Imaging for Visium Spatial Protocols (Demonstrated Protocol CG000312)

DO NOT proceed with Permeabilization & Reverse Transcription without performing appropriate fixation, staining, and imaging for the tissue sections on the appropriate Visium slide.

Tissue Optimization Guidelines

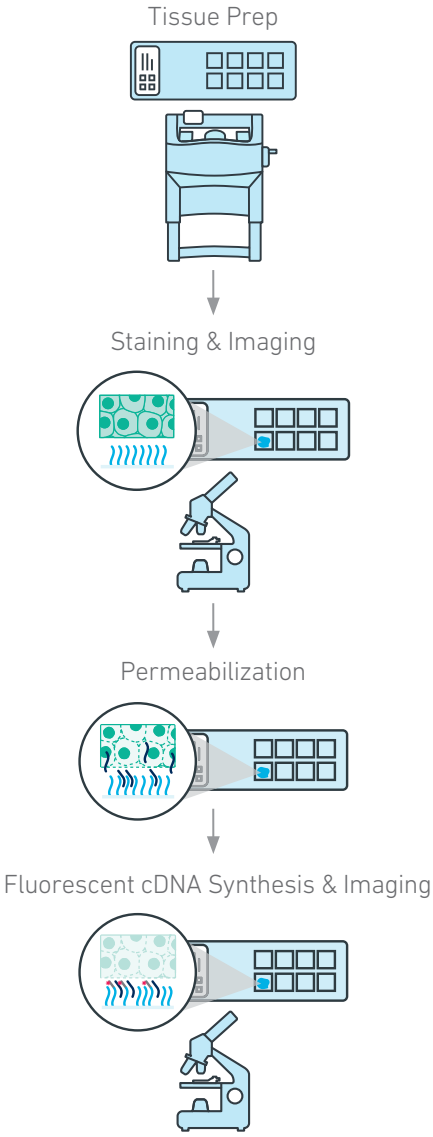
Tissue Optimization Guidelines

Prior to using a new tissue type for generating Visium Spatial Gene Expression libraries, the permeabilization time should be optimized. Failure to optimize the permeabilization time can diminish the efficiency of the assay significantly.

Refer to the Visium Spatial Gene Expression Reagent Kits – Tissue Optimization User Guide (CG000238) for the complete protocol for optimizing permeabilization time for any tissue of interest.

Briefly, previously fixed and stained tissue sections on 7 Capture Areas on a Visium Tissue Optimization slide are permeabilized for different times. mRNA released during permeabilization binds to oligonucleotides on the Capture Areas. Fluorescent cDNA is synthesized on the slide and imaged. The permeabilization time that results in maximum fluorescence signal with the lowest signal diffusion is optimal. If the signal is the same at two time points, the longer permeabilization time is considered optimal.

Tissue Optimization Workflow



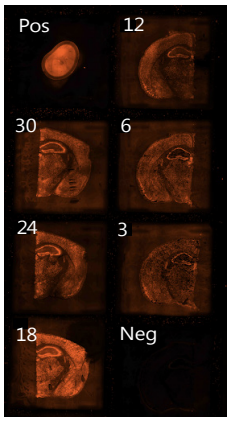
Choose the permeabilization time that results in maximum fluorescence signal with the lowest signal diffusion. If the signal is the same at two time points, choose the longer permeabilization time.

Example: Tissue Permeabilization Time Course

Mouse brain sections were imaged after permeabilization and fluorescent cDNA synthesis, using a Nikon Eclipse Ti2 microscope.

- Positive control: Strong fluorescent signal.
- Negative Control: No fluorescent signal.
- Optimal signal: **18 min**.
  Use for Visium Spatial Gene Expression protocol.

Permeabilization Time Course (min)



Step 1

Permeabilization & Reverse Transcription

1.1 Tissue Permeabilization

1.2 Reverse Transcription

1

1.0 Permeabilization & Reverse Transcription

CHECKLIST – GET STARTED!

Items	10x PN	Preparation & Handling	Storage
Prepare & equilibrate to 37°C			
☐ **Permeabilization Enzyme**	2000214	Centrifuge briefly and resuspend in 1.2 ml HCl (0.1N), pipette mix, centrifuge briefly, verify no precipitate. Equilibrate to 37°C for 15 min prior to step 1.1c. DO NOT exceed 20 min of preheating. Permeabilization enzyme will be kept at 37°C throughout step 1.1c. Store unused resuspended enzyme at –20°C **immediately** after Tissue Permeabilization. DO NOT freeze-thaw more than 3x. DO NOT keep at 37°C for extended periods.	–20°C
Equilibrate to room temperature			
☐ **RT Reagent**	2000086	Thaw, vortex, verify no precipitate, centrifuge briefly.	–20°C
☐ **Template Switch Oligo**	3000228	Centrifuge briefly, resuspend in 80 µl Low TE Buffer. Vortex 15 sec at maximum speed, centrifuge briefly, leave at room temperature for ≥ 30 min. After resuspension, store at –80°C.	–20°C
☐ **Reducing Agent B**	2000087	Thaw, vortex, verify no precipitate, centrifuge briefly.	–20°C
Place on ice			
☐ **RT Enzyme D**	2000216/ 2000227	Pipette mix, centrifuge briefly.	–20°C
Obtain			
☐ **Nuclease-free Water**	-	-	Ambient
☐ **20X SSC**	-	-	Ambient
☐ **Visium Slide Cassette & Gasket**	2000281/ 2000282	See Tips & Best Practices.	Ambient
☐ **Visium Slide Seals**	2000283/ 2000284/ 3000279	See Tip & Best Practices	Ambient
☐ **Low TE Buffer**	-	-	-
☐ **Hydrochloric Acid Solution (HCl), 0.1N**	-	-	-
Prepare			

0.1X SSC *Store at room temperature*	Stock	Final	50 ml (50 slides)
SSC	20X	0.1X	250 µl
Water (Ultrapure/ Milli-Q)	-	-	49.75 ml

1.1 Tissue Permeabilization

Retrieve the Visium Gene Expression Slide with **fixed & stained** tissue sections. If a coverslip was mounted on the slide for imaging, remove the coverslip. Consult the Demonstrated Protocol used for tissue staining for coverslip removal instructions. Ensure Permeabilization Enzyme is resuspended and is equilibrated to **37°C** for **15 min** prior to step 1.1c.

If Methanol Fixation, Immunofluorescence Staining & Imaging was performed (CG000312), the slide will be in the Visium Slide Cassette with wash buffer in the wells. Using a pipette, remove wash buffer from well corners and proceed immediately to step 1.1c.

DO NOT proceed with Permeabilization & cDNA Synthesis without performing appropriate fixation, staining, and imaging (if applicable) for the tissue sections on the Visium slide.

a. Place a Thermocycler Adaptor in the thermal cycler. Prepare the thermal cycler with the following incubation protocol and start the program.

Lid Temperature	Reaction Volume	Run Time
37°C (may be 50°C if instrument does not enable 37°C)		*
Step	**Temperature**	**Time**
Pre-equilibrate	37°C	Hold
Permeabilization	37°C	*Determined by Tissue Optimization protocol.

TIPS

b. Place the slide in the Visium Slide Cassette. See Tips & Best Practices for assembly instructions. Practice assembly with a blank slide.

c. Add **70 µl** Permeabilization Enzyme along the side of the wells to uniformly cover the tissue sections, without introducing bubbles.

Tap Visium Slide Cassette gently to ensure uniform coverage.

d. Apply Visium Slide Seal on the Visium Slide Cassette and place the Visium Slide Cassette on the Thermocycler Adaptor at **37°C**.

e. Close the thermal cycler lid and incubate for the pre-determined permeabilization time (tissue type specific).

Consult the Visium Spatial Gene Expression Reagent Kits – Tissue Optimization User Guide (CG000238) for the complete protocol for optimizing permeabilization time for any tissue of interest.

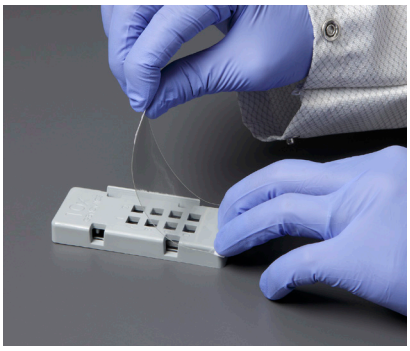
f. Remove the Visium Slide Cassette from the Thermocycler Adaptor and place on a flat, clean work surface.

g. Using a pipette, remove Permeabilization Enzyme from the well corners.

h. Add **100 µl** 0.1X SSC to the wells.

Add Reagent

Apply Visium Slide Seal



1.2 Reverse Transcription

a. Place a Thermocycler Adaptor in the thermal cycler. Prepare a thermal cycler with the following incubation protocol and start the program.

Lid Temperature	Reaction Volume	Run Time
53°C	-	45 min
Step	**Temperature**	**Time**
Pre-equilibrate	53°C	Hold
Reverse Transcription	53°C	00:45:00
Hold	4°C	Hold

b. Prepare RT Master Mix on ice. Pipette mix 10x and centrifuge briefly.

RT Master Mix *Add reagents in the order listed.*	PN	1X (µl)	2X +10% (µl)	4X +10% (µl)	8X +10% (µl)
Nuclease-free Water	-	37.84	83.25	166.50	333.00
● **RT Reagent**	2000086	18.75	41.25	82.50	165.00
● **Template Switch Oligo**	3000228	5.22	11.48	23.00	45.94
○ **Reducing Agent B**	2000087	1.50	3.30	6.60	13.20
● **RT Enzyme D**	2000216/ 2000227	11.69	25.72	51.40	102.87
Total	-	**75.00**	**165.00**	**330.00**	**660.00**

c. Remove 0.1X SSC from the wells.

d. Add **75 µl** RT Master Mix to each well.

e. Apply Visium Slide Seal on the Visium Slide Cassette and place on the Thermocycler Adaptor on the pre-heated thermal cycler. Close the thermal cycler lid.

f. Skip Pre-equilibrate step to initiate Reverse Transcription.

Step 2

Second Strand Synthesis & Denaturation

2.1 Second Strand Synthesis

2.2 Denaturation

2.0 Second Strand Synthesis

CHECKLIST – GET STARTED!

Items	10x PN	Preparation & Handling	Storage
Equilibrate to room temperature			
☐ **Second Strand Reagent**	2000219	Thaw, vortex, centrifuge briefly.	–20°C
☐ **Second Strand Primer**	2000217	Thaw, vortex, centrifuge briefly.	–20°C
Place on ice			
☐ **Second Strand Enzyme**	2000218/ 2000183	Pipette mix, centrifuge briefly.	–20°C
Obtain			
☐ **Nuclease-free Water**	-		Ambient
☐ **Qiagen Buffer EB**	-	Manufacturer's recommendations.	Ambient
☐ **Tris 1 M, pH 7.0** (Tris-HCl)	-	Manufacturer's recommendations.	Ambient
☐ **Visium Slide Seals**	2000283/ 2000284/ 3000279	See Tip & Best Practices.	Ambient
Prepare			

	0.08 M KOH *Store at room temperature*	Stock	Final	500 µl
☐ **0.08 M KOH** (prepare 500 µl/slide)	KOH	8 M	0.08 M	5 µl
	Nuclease-free Water	-	-	495 µl

2.1 Second Strand Synthesis

a. Remove the Visium Slide Cassette from the thermal cycler and place on a flat, clean work surface.

b. Leave the Thermocycler Adaptor on the thermal cycler. Prepare the thermal cycler with the following incubation protocol and start the program.

Lid Temperature	Reaction Volume	Run Time
65°C	-	15 min
Step	**Temperature**	**Time**
Pre-equilibrate	65°C	Hold
Second Strand Synthesis	65°C	00:15:00
Hold	4°C	Hold

c. Remove RT Master Mix from the wells.

d. Add **75 µl** 0.08 M KOH (diluted from stock; ensure accurate dilution) to each well.

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

f. Using a pipette, remove KOH from the wells.

g. Add **100 µl** EB to each well.

h. Prepare Second Strand Mix on ice. Vortex and centrifuge briefly.

Second Strand Mix *Add reagents in the order listed*	PN	1X (µl)	2X +10% (µl)	4X +10% (µl)	8X +10% (µl)
Second Strand Reagent	2000219	69.5	152.9	305.8	611.6
Second Strand Primer	2000217	4.0	8.8	17.6	35.2
Second Strand Enzyme	2000218/ 2000183	1.5	3.3	6.6	13.2
Total	-	**75.0**	**165.0**	**330.0**	**660.0**

i. Using a pipette, remove Buffer EB from the wells.

j. Add **75 µl** Second Strand Mix to each well.

k. Apply Visium Slide Seal on the Visium Slide Cassette and place on the Thermocycler Adaptor on the pre-heated thermal cycler. Close the thermal cycler lid.

l. Skip Pre-equilibrate step to initiate Second Strand Synthesis.

2.2 Denaturation

a. At the end of incubation, using a pipette, remove reagents from the wells.

b. Add **100 µl** Buffer EB to each well.

c. Using a pipette, remove Buffer EB from the wells.

d. Add **35 µl** 0.08 M KOH (diluted from stock) to each well.

e. Incubate **10 min** at **room temperature**.

f. Add **5 µl** Tris (1 M, pH 7.0) to up to 4 tubes in an 8-tube strip (2 tubes will be used for each Visium Gateway Gene Expression slide, 4 tubes will be used for each Visium Spatial Gene Expression slide).

g. Transfer **35 µl** sample from each well to a corresponding tube containing Tris in the 8-tube strip.
DO NOT discard sample. ~**1-2 µl** volume variation is expected.

h. Vortex, centrifuge briefly, and place on ice.

The Visium Slide Cassette and slide may be discarded. Ensure the slide serial number has been recorded, as it is required for downstream analysis.

Step 3

cDNA Amplification & QC

3.1 Cycle Number Determination – qPCR
3.2 cDNA Amplification
3.3 cDNA Cleanup – SPRIselect
3.4 cDNA QC & Quantification

3

3.0 cDNA Amplification & QC

CHECKLIST – GET STARTED!			
Item	**10x PN**	**Preparation & Handling**	**Storage**
Equilibrate to room temperature			
☐ ● **cDNA Primers**	2000089	Thaw, vortex, centrifuge briefly.	–20°C
☐ **Beckman Coulter SPRIselect Reagent**	-	Manufacturer's recommendations.	-
☐ **Agilent TapeStation Screen Tape and Reagents** If used for QC	-	Manufacturer's recommendations.	-
☐ **Agilent Bioanalyzer High Sensitivity kit** If used for QC	-	Manufacturer's recommendations.	-
☐ **DNA High Sensitivity Reagent Kit** If LabChip used for QC	-	Manufacturer's recommendations.	-
Place on ice			
☐ **KAPA SYBR FAST qPCR Master Mix** Minimize light exposure	-	Vortex, centrifuge briefly.	–20°C
☐ ○ **Amp Mix**	2000047/ 2000103	Vortex, centrifuge briefly.	–20°C
Obtain			
☐ **Qiagen Buffer EB**	-	-	Ambient
☐ **Nuclease-free Water**	-	-	-
☐ **qPCR Plate**	-	-	-
☐ **10x Magnetic Separator**	230003	See Tips & Best Practices.	Ambient
☐ **Prepare 80% Ethanol** Prepare 15 ml for up to 4 reactions	-	Prepare fresh.	Ambient
Special Equipment			
☐ **Real Time qPCR System**			

3.1 Cycle Number Determination – qPCR

a. Prepare qPCR Mix on ice. Vortex and centrifuge briefly.

A passive reference dye, such as ROX, may be required. Consult the Roche KAPA SYBR FAST qPCR Kit or the appropriate qPCR system manufacturer for guidance.

qPCR Mix *Add reagents in the order listed.* *Maintain on ice*	PN	3X* + 10% (µl)	5X* + 10% (µl)	9X* + 10% (µl)
		*Includes 1 negative control		
Nuclease-free Water	-	12.2	20.4	36.6
KAPA SYBR FAST qPCR Master Mix Minimize light exposure	-	16.5	27.5	49.5
cDNA Primers	2000089	1.0	1.7	3.0
Total	-	**29.7**	**49.6**	**89.1**

b. Add **9 µl** qPCR Mix to each well in a qPCR plate (a well for negative control may be included).

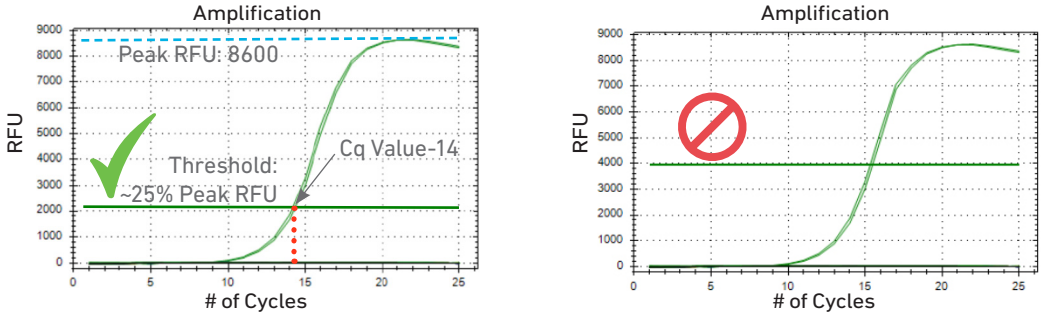
c. Transfer **1 µl** sample from **step 2.2h** to the qPCR plate well containing the qPCR Mix. Pipette mix, centrifuge briefly (if using a negative control, add **1 µl** nuclease-free water to the corresponding well). Seal qPCR plate.

d. Prepare a qPCR system with the following protocol, place the plate, and start the program.

Lid Temperature	Reaction Volume	Run Time
105°C	10 µl	35 min
Step	**Temperature**	**Time**
1	98°C	00:03:00
2	98°C	00:00:05
3	63°C	00:00:30
	Read signal	
4	Go to step 2, for a total of 25 cycles	-

e. Record the Cq Value for each sample.
Set the y-axis to a linear scale. Plot RFU on the y-axis if not using a reference dye, or ΔRn if using a reference dye. The threshold for determining the Cq Value should be set along the exponential phase of the amplification plot, at ~25% of the peak fluorescence value.

Representative qPCR Amplification Plots



3.2 cDNA Amplification

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

cDNA Amplification Mix *Add reagents in the order listed*	PN	1X	2X + 10% (µl)	4X + 10% (µl)	8X + 10% (µl)
○ **Amp Mix**	2000047/ 2000103	50	110	220	440
● **cDNA Primers**	2000089	15	33	66	132
Total	-	**65**	**143**	**286**	**572**

b. Add **65 µl** cDNA Amplification Mix to remaining **~35 µl** sample from step 2.2h.

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

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

Lid Temperature	Reaction Volume	Run Time
105°C	100 µl	~45-60 min
Step	**Temperature**	**Time**
1	98°C	00:03:00
2	98°C	00:00:15
3	63°C	00:00:20
4	72°C	00:01:00
5	Go to Step 2, Use the Cq Value as the total # of cycles. See table below for total # of cycle examples	
6	72°C	00:01:00
7	4°C	Hold

Cycle number examples determined based on rounding the Cq Value.

Cq Value from qPCR	Total Cycles
12.2	12 cycles
13.5	14 cycles
15.7	16 cycles

STOP **e.** 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 cDNA Cleanup – SPRIselect

a. Vortex to resuspend the SPRIselect reagent. Add **60 µl** SPRIselect reagent **(0.6X)** to each sample (100 µl) and pipette mix 15x (pipette set to 150 µl).

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

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

d. Remove the supernatant.

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

f. Remove the ethanol.

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

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

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

j. Remove from the magnet. Add **40.5 µl** Buffer EB. Pipette mix 15x (pipette set to 40 µl).

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

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

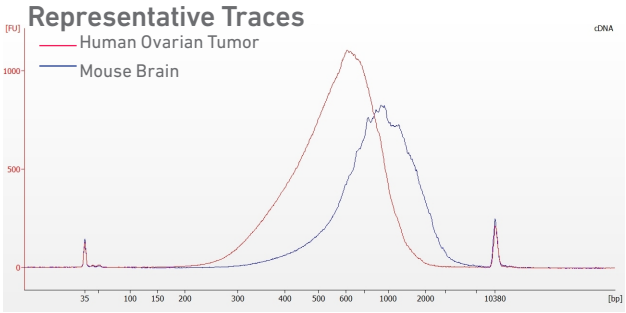
m. Transfer **40 µl** sample to a new tube strip.

STOP

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

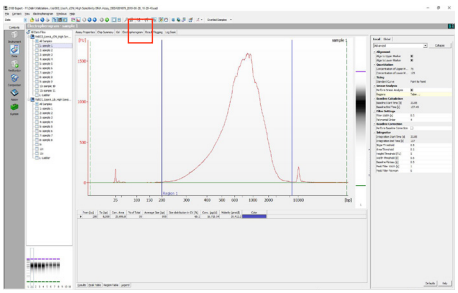
3.4 cDNA QC & Quantification

a. Run 1 µl of sample on an Agilent Bioanalyzer High Sensitivity chip.
cDNA profile may vary depending on tissue type and quality.
Lower molecular weight product (35-150 bp) may be present. This is normal and does not affect sequencing or application performance.

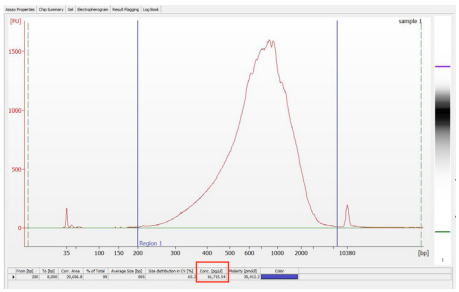


EXAMPLE CALCULATION

i. Select Region
Under the "Electropherogram" view choose the "Region Table". Manually select the region of ~200 – ~9000 bp.



ii. Note Concentration [pg/µl]



iii. Calculate
Multiply the cDNA concentration [pg/µl] reported via the Agilent 2100 Expert Software by the elution volume (40 µl) of the Post cDNA Amplification Reaction Clean Up sample and then divide by 1,000 to obtain the total cDNA yield in ng.

Example Calculation of cDNA Total Yield

Concentration: 16,715.54 pg/µl
Elution Volume: 40

Total cDNA Yield

$$= \frac{\text{Conc'n (pg/µl) x Elution Volume (µl)}}{1000\ \text{(pg/ng)}}$$

$$= \frac{16{,}715.54\ \text{(pg/µl) x 40 (µl)}}{1000\ \text{(pg/ng)}} = 668.6.\ \text{ng}$$

The carry forward cDNA volume is specified in step 4.1.
Refer to step 4.5e for appropriate number of Sample Index PCR cycles based on carry forward cDNA/input mass.

Alternate Quantification Methods:

- Agilent TapeStation
- LabChip

See Appendix for representative traces

Step 4

Spatial Gene Expression Library Construction

4.1 Fragmentation, End Repair & A-tailing
4.2 Post Fragmentation End Repair & A-tailing Double Sided Size Selection – SPRIselect
4.3 Adaptor Ligation
4.4 Post Ligation Cleanup – SPRIselect
4.5 Sample Index PCR
4.6 Post Sample Index PCR Double Sided Size Selection – SPRIselect
4.7 Post Library Construction QC

4.0 Visium Spatial Gene Expression Library Construction

CHECKLIST – GET STARTED!			
Item	**10x PN**	**Preparation & Handling**	**Storage**
Equilibrate to room temperature			
☐ ● **Fragmentation Buffer**	2000091	Vortex, verify no precipitate, centrifuge briefly.	–20°C
☐ ● **Adaptor Oligos**	2000094	Vortex, centrifuge briefly.	–20°C
☐ ● **Ligation Buffer**	2000092	Vortex, verify no precipitate, centrifuge briefly.	–20°C
☐ **Dual Index Plate TT Set A**	3000431	-	–20°C
☐ **Beckman Coulter SPRIselect Reagent**	-	Manufacturer's recommendations.	-
☐ **Agilent TapeStation Screen Tape and Reagents** If used for QC		Manufacturer's recommendations.	-
☐ **Agilent Bioanalyzer High Sensitivity kit** If used for QC	-	Manufacturer's recommendations.	-
☐ **DNA High Sensitivity Reagent Kit** If LabChip used for QC	-	Manufacturer's recommendations.	-
Place on ice			
☐ ● **Fragmentation Enzyme**	2000090/ 2000104	Pipette mix, centrifuge briefly before using.	–20°C
☐ ● **DNA Ligase**	220110/ 220131	Pipette mix, centrifuge briefly before using.	–20°C
☐ ○ **Amp Mix**	2000047/ 2000103	Vortex, centrifuge briefly.	–20°C
☐ **KAPA Library Quantification Kit for Illumina Platforms**	-	Manufacturer's recommendations.	-
Obtain			
☐ **Qiagen Buffer EB**	-		Ambient
☐ **10x Magnetic Separator**	230003	See Tips & Best Practices.	Ambient
☐ **Prepare 80% Ethanol** Prepare 20 ml for 8 reactions	-	Prepare fresh.	Ambient

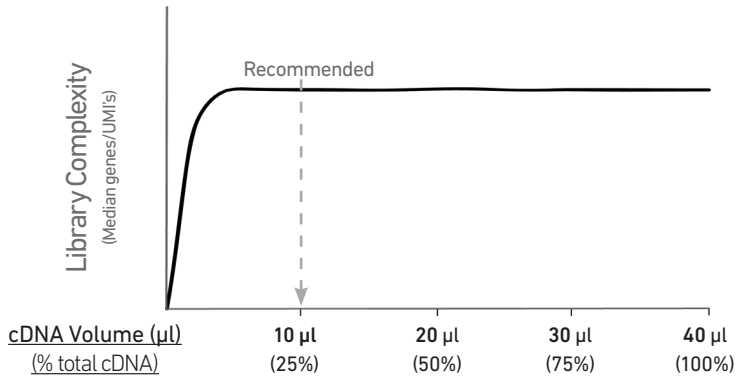
Ensure that Fragmentation Buffer and Fragmentation Enzyme from the same kit are used together. Lots are matched for optimal performance.

Step Overview (Step 4.1d)

Correlation between input & library complexity

A Visium Spatial Gene Expression library is generated using a fixed proportion (10 µl, 25%) of the total cDNA (40 µl) obtained at step 3.3. The complexity of this library will be comparable to one generated using a higher proportion (>25%) of the cDNA. The remaining proportion (30 µl, 75%) of the cDNA may be stored at **4°C** for up to **72 h** or at **–20°C** for longer-term storage (up to **4 weeks**).

Correlation: cDNA input & Library Complexity



Note that irrespective of the total cDNA yield (ng), which may vary based on tissue type, coverage of Capture Area by tissue section, and tissue thickness, this protocol has been optimized for a broad range of input mass (ng), as shown in the example below. The total number of SI PCR cycles (step 4.5d) should be optimized based on carrying forward a fixed proportion (10 µl, 25%) of the total cDNA yield calculated during Post cDNA Amplification QC & Quantification (step 3.4).

Example: Library Construction Input Mass & SI PCR Cycles

Tissue Type	Tissue Covered Capture Area (%)	Total cDNA Amplification Cycles	Total cDNA Yield (ng)	cDNA Input into Fragmentation		SI PCR Cycle Number
				Volume (µl)	Mass (ng)	
High RNA Content	10%	17	412	10	102	16
	60%	15	928	10	232	13
Low RNA Content	10%	17	128	10	32	17
	75%	15	536	10	134	15

4.1 Fragmentation, End Repair & A-tailing

a. Prepare a thermal cycler with the following incubation protocol and start the program.

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

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

Fragmentation Mix *Add reagents in the order listed*	PN	1X (µl)	2X + 10% (µl)	4X + 10% (µl)	8X + 10% (µl)
Fragmentation Buffer	2000091	5	11	22	44
Fragmentation Enzyme	2000090/ 2000104	10	22	44	88
Total	-	**15**	**33**	**66**	**132**

c. Transfer ONLY **10 µl** purified cDNA sample from cDNA Cleanup (step 3.3m) to a tube strip maintained on ice.
Note that only **10 µl** (25%) cDNA sample is sufficient for generating Visium Spatial Gene Expression library. The remaining **30 µl** (75%) cDNA sample can be stored at **4°C** for up to **72 h** or at **–20°C** for up **to 4 weeks** for generating additional libraries.

d. Add **25 µl** Buffer EB to each sample.

e. Add **15 µl** Fragmentation Mix to each sample.

f. Pipette mix 15x (pipette set to 35 µl) on ice. Centrifuge briefly.

g. Transfer into the pre-cooled thermal cycler **(4°C)**.

h. Skip pre-cool block step to initiate Fragmentation.

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

a. Vortex to resuspend SPRIselect reagent. Add **30 µl** SPRIselect **(0.6X)** reagent to each sample. Pipette mix 15x (pipette set to 75 µl).

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

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

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

e. Vortex to resuspend SPRIselect reagent. Add **10 µl** SPRIselect reagent **(0.8X)** to each sample. Pipette mix 15x (pipette set to 80 µl).

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

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

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

i. Add **125 µl** 80% ethanol to the pellet. Wait **30 sec.**

j. Remove the ethanol.

k. **Repeat** steps i and j for a total of 2 washes.

l. Centrifuge briefly. Place on the magnet•**Low** until the solution clears. Remove remaining ethanol. DO NOT over dry to ensure maximum elution efficiency.

m. Remove from the magnet. Add **50.5 µl** Buffer EB to each sample. Pipette mix 15x.

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

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

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

4.3 Adaptor Ligation

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

Adaptor Ligation Mix *Add reagents in the order listed*	PN	1X (µl)	2X + 10% (µl)	4X + 10% (µl)	8X + 10% (µl)
Ligation Buffer	2000092	20	44	88	176
DNA Ligase	220110/ 220131	10	22	44	88
Adaptor Oligos	2000094	20	44	88	176
Total	-	**50**	**110**	**220**	**440**

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

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

Lid Temperature	Reaction Volume	Run Time
30°C (lid may be turned off if instrument does not enable 30°C)	100 µl	15 min

Step	Temperature	Time
1	20°C	00:15:00
2	4°C	Hold

4.4 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**. DO NOT exceed **2 min** as this will decrease elution efficiency.

j. Remove from the magnet. Add **30.5 µl** Buffer EB. Pipette mix 15x.

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

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

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

4.5 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-1000215 Dual Index Plate TT Set A well ID) used.

b. Add **50 µl** Amp Mix (PN-2000047 or 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	~25-40 min
Step	**Temperature**	**Time**
1	98°C	00:00:45
2	98°C	00:00:20
3	67°C	00:00:30
4	72°C	00:00:20
5	Go to step 2, see below for # of cycles	
6	72°C	00:01:00
7	4°C	Hold

The total cycles should be optimized based on 25% carry forward cDNA yield/input calculated during Post cDNA Amplification QC & Quantification (step 3.4)

Recommended cycle numbers

cDNA Input	Total Cycles
0.25-25 ng	17-19
25-150 ng	15-17
150-500 ng	13-15
500-1,000 ng	11-13
1,000-1,500 ng	9-11
>1500 ng	8

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

4.6 Post Sample Index PCR Double Sided Size Selection – SPRIselect

a. Vortex to resuspend the 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 the SPRIselect reagent. Add **20 µl** SPRIselect Reagent **(0.8X)** to the transferred supernatant. Pipette mix 15x (pipette set to 150 µl).

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

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

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

i. With the tube still in 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**. Remove remaining ethanol.

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

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

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

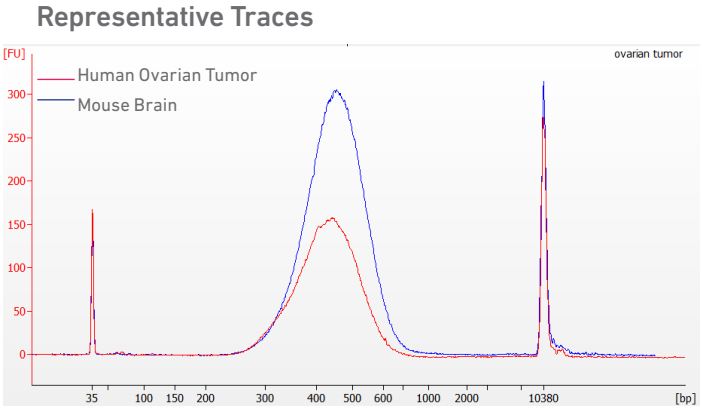
p. Transfer **35 µl** to a new tube strip.

STOP

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

4.7 Post Library Construction QC

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



A smaller peak (~200-600 bp) may be present in some tissue types (e.g. mouse brain).

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

Alternate QC Method:

- Agilent TapeStation
- LabChip

See Appendix for representative traces

See Appendix for Post Library Construction Quantification

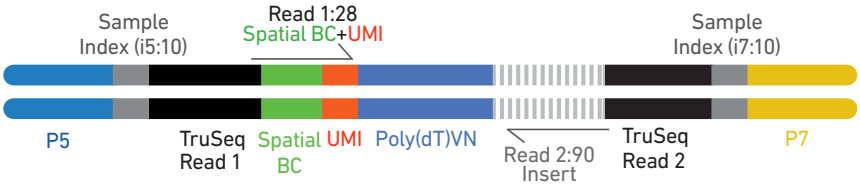
Sequencing

5

Sequencing Libraries

Visium Spatial Gene Expression libraries comprise standard Illumina paired-end constructs that are flanked with P5/P7, necessary for binding to the Illumina flow cell. TruSeq Read 1 is used for priming and sequencing the 16 bp Spatial Barcode and 12 bp UMI, and TruSeq Read 2 is used for priming and sequencing the cDNA insert. The two 10 bp sample indexes are sequenced in the i5 and i7 read respectively. Sequencing these libraries produce a standard Illumina BCL data output folder.

Visium Spatial Gene Expression Library



Sequencing Depth

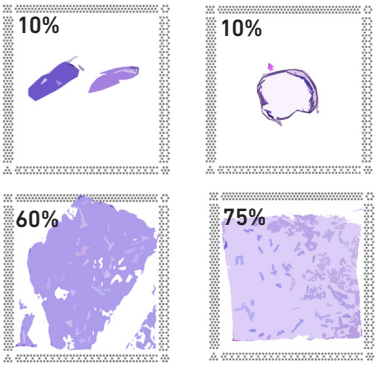
Calculating sequencing depth requires estimating the approximate Capture Area (%) covered by tissue. This may be performed visually or by using the Visium Manual Alignment Wizard in Loupe Browser for a more accurate measurement. See examples below for estimating coverage area visually. If using Loupe Browser, the number of spots covered by tissue will be displayed during the "Identify Tissue" step. For more information, consult the 10x Genomics Support website.

Sequencing Depth/spot	Minimum 50,000 read pairs per tissue covered spot on Capture Area
Sequencing Depth/sample	See example calculation below

Example: Sequencing Depth for a Sample

- Estimate the approximate Capture Area (%) covered by the tissue section.
- **Calculate total sequencing depth=** (Coverage Area x total spots on the Capture Area) x 50,000 read pairs/spot
- **Example calculation for 60% coverage:** (0.60 x 5,000 total spots) x 50,000 read pairs/spot= 150 million total read pairs for that sample

Estimated Coverage Area (%) Examples



Sequencing Type & Run Parameters

Use the sequencing run type and parameters indicated.

Dual Index Library
Paired-end, dual indexed sequencing

Read 1: 28 cycles
i7 Index: 10 cycles
i5 Index: 10 cycles
Read 2: 90 cycles

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
- HiSeq 2500 (Rapid Run)
- HiSeq 3000/4000
- NovaSeq
- iSeq

Sample Indices

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

Library Loading

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

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

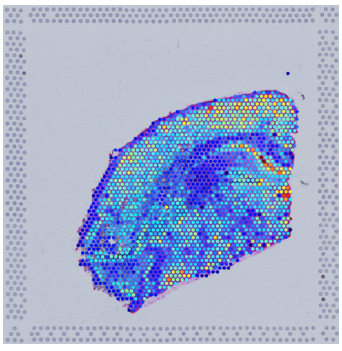
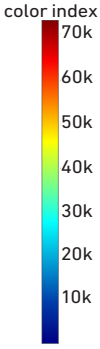
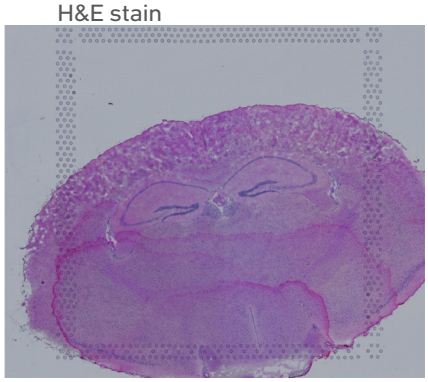
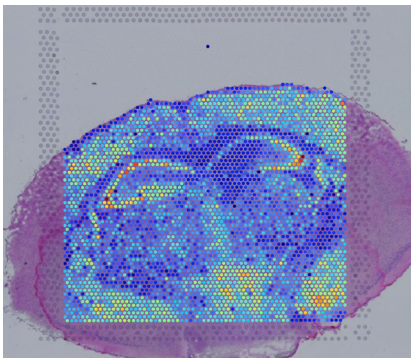
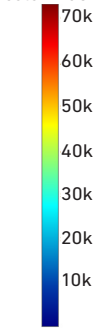
** Use 150 pM loading concentration for Illumina XP workflow.

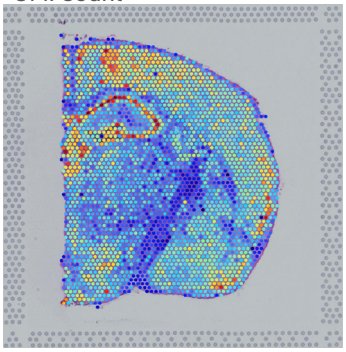
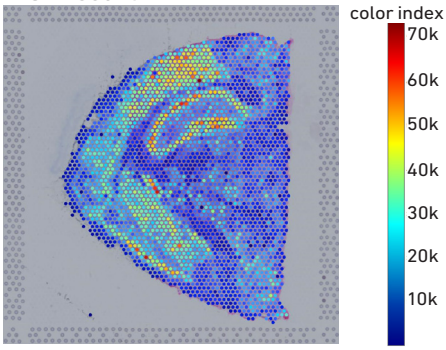
Library Pooling

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

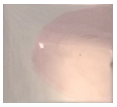
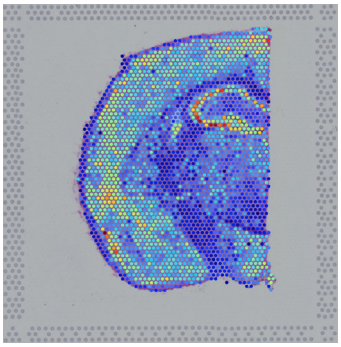
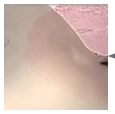
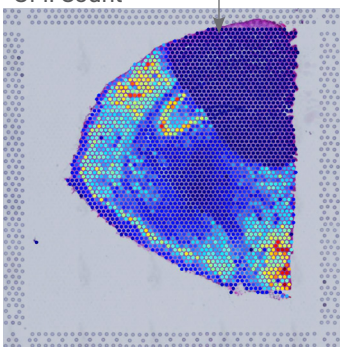
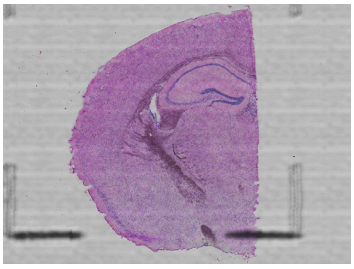
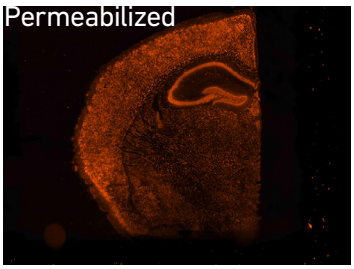
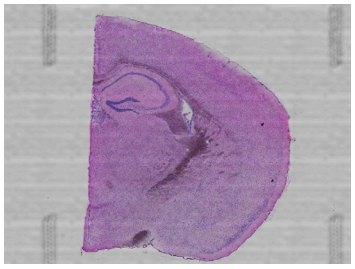
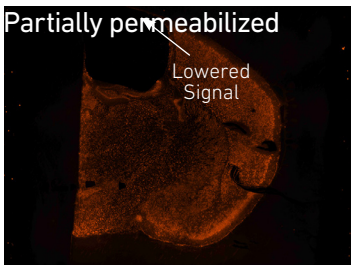
Troubleshooting

6

STEP	NOTES
Tissue Folding – Impact on UMI Count	Folded tissue H&E stain UMI count   Folded tissue section can result in OCT induced tissue damage, impacting permeabilization, and diminishing assay sensitivity. However, the data derived from the rest of the tissue portions (not folded) can be analyzed.
Tissue Placement – Impact on UMI Count	Fiducials are obstructed H&E stain  UMI Count   Fiducial obstruction may result in image analysis failure. Placement must be correct before the workflow begins. If necessary, software will prompt users to manually align tissue images during analysis.

STEP	CORRECT	INCORRECT
Tissue Staining – Impact on UMI Count	Even H&E staining	Uneven H&Estaining
	UMI Count 	UMI Count 

Ensure that staining reagents are applied to the tissue uniformly and adequate washes are performed. A gentle tap may help spread the reagent uniformly. Uneven staining may diminish sensitivity and spatial resolution. However, the data derived from the evenly stained tissue portions can be analyzed.

STEP	CORRECT	INCORRECT
1.1 Tissue Permeabilization – Reagent Coverage	 Visium Slide Cassette Well Tissue section covered completely UMI Count 	 Visium Slide Cassette Well Tissue section not covered UMI Count 
	Ensure that permeabilization reagents are applied to the tissue uniformly. Uneven permeabilization will diminish sensitivity and spatial resolution. However, the data derived from the optimally permeabilized tissue portions can be analyzed.	
1.1 Tissue Permeabilization – Time	Optimal  	Sub-optimal  
	Ensure that permeabilization times are optimized for each tissue type using the Visium Spatial Tissue Optimization protocol prior to beginning this workflow. Sub-optimal permeabilization will diminish sensitivity and spatial resolution.	
2.2 Denaturation – Partial	Cover the tissue section uniformly with 35 µl 0.08 M KOH to prevent partial denaturation.	
3.1 No Cq Value	Ensure that correct KOH dilution (0.08 M) is used at step 2.2d. Confirm that the Quantification Master Mix is prepared using the KAPA SYBR FAST Master Mix (2x) Kit. DO NOT use an alternative SYBR qPCR Master Mix. Using an alternative Master Mix may result in poor performance.	
3.4 Flat cDNA Trace (Cq value observed)	Flat cDNA trace, even though Cq value was observed at step 3.1. Failure to properly neutralize KOH by addition of Tris (1 M, pH 7.0) at step 2.2f negatively impacts cDNA amplification efficiency (no impact on qPCR amplification, hence Cq value is observed).	

Appendix

Post Library Construction Quantification

Agilent TapeStation Traces

LabChip Traces

Oligonucleotide Sequences

7

Post Library Construction Quantification

a. Thaw KAPA Library Quantification Kit for Illumina Platforms.

b. Dilute **2 µl** sample with deionized water to appropriate dilutions that fall within the linear detection range of the KAPA Library Quantification Kit for Illumina Platforms. (For more accurate quantification, make the dilution(s) in duplicate).

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. Prepare a qPCR system with the following protocol. Insert the plate and start the program.

Lid Temperature	Reaction Volume	Run Time
-	20 µl	35 min
Step	**Temperature**	**Time**
1	95°C	00:03:00
2	95°C	00:00:05
3	67°C Read signal	00:00:30
4	Go to Step 2, 29X (Total 30 cycles)	

h. 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.

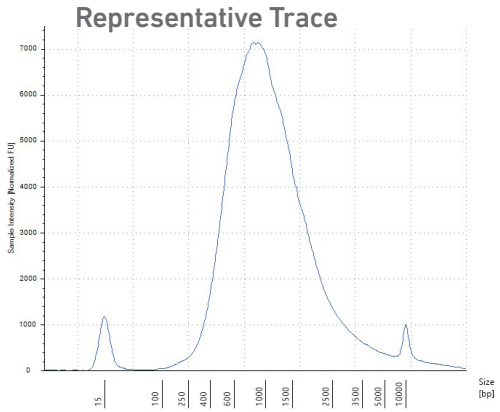
Agilent TapeStation Traces

Agilent TapeStation Traces

Agilent TapeStation High Sensitivity D5000 ScreenTape was used.
Protocol steps correspond to the Visium Spatial Gene Expression Reagent Kits User Guide (CG000239).

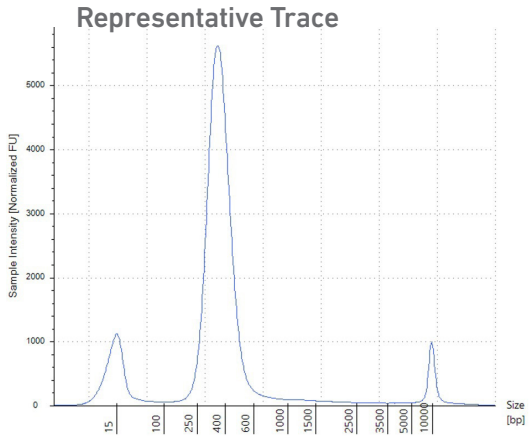
Protocol Step 3.4 – cDNA QC & Quantification

Run 2 µl sample mixed with 2 µl loading buffer.



Protocol Step 4.7 – Post Library Construction QC

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



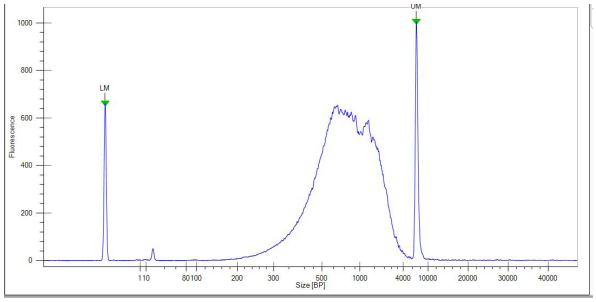
LabChip Traces

LabChip Traces

DNA High Sensitivity Reagent Kit was used.
Protocol steps correspond to the Visium Spatial Gene Expression Reagent Kits User Guide (CG000239).

Protocol Step 3.4 – cDNA QC & Quantification

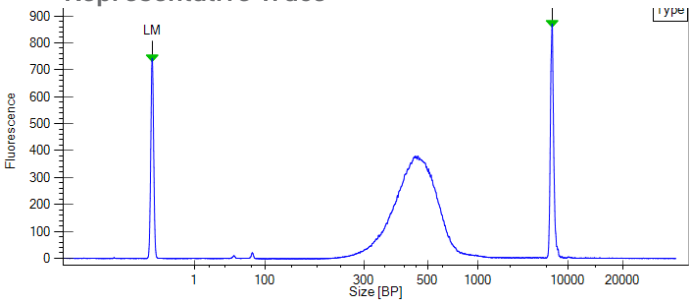
Representative Trace



Run 10 µl undiluted sample.
cDNA yield calculation is same as Agilent Bioanalyzer traces.

Protocol Step 4.7 – Post Library Construction QC

Representative Trace



Run 10 µl diluted sample (1:10 dilution).

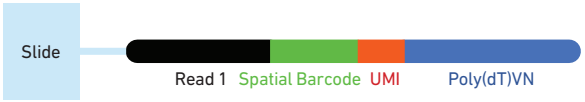
Oligonucleotide Sequences

Protocol steps correspond to the Visium Spatial Gene Expression Reagent Kits User Guide (CG000239)

Protocol Step 1.2 – Reverse Transcription

Slide Primers

5'-CTACACGACGCTCTTCCGATCT-N16-N12-TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTVN-3'



Template Switch Oligo PN -3000228

5'-AAGCAGTGGTATCAACGCAGAGTACATrGrGrG-3'

cDNA

5'-CTACACGACGCTCTTCCGATCT-N16-N12-TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTVN-cDNA_Insert-CCCATGTACTCTGCGTTGATACCACTGCTT-3'

Protocol Step 2.1 – Second Strand Synthesis

Second Strand Primer PN -2000217

5'-AAGCAGTGGTATCAACGCAGAG-3'

Second Strand

3'-GATGTGCTGCGAGAAGGCTAGA-N16-N12-AAAAAAAAAAAAAAAAAAAAAAAAAAAAAABN-cDNA_Insert-GGGTACATGAGACGCAACTATGGTGACGAA-5'

Protocol Step 3.2 – cDNA Amplification

cDNA Primers PN-2000089

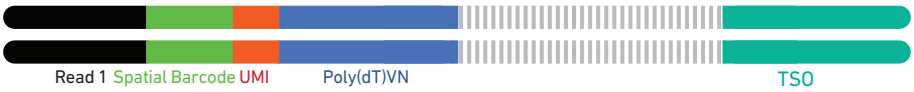
Forward Primer:

5'-CTACACGACGCTCTTCCGATCT-3'

Reverse Primer:

5'-AAGCAGTGGTATCAACGCAGAG-3'

Amplification Products



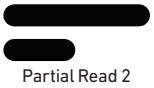
5'-CTACACGACGCTCTTCCGATCT-N16-N12-TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTVN-cDNA_Insert-CCCATGTACTCTGCGTTGATACCACTGCTT-3'
3'-GATGTGCTGCGAGAAGGCTAGA-N16-N12-AAAAAAAAAAAAAAAAAAAAAAAAAAAAAABN-cDNA_Insert-GGGTACATGAGACGCAACTATGGTGACGAA-5'

Oligonucleotide Sequences

Protocol steps correspond to the Visium Spatial Gene Expression Reagent Kits User Guide (CG000239)

Protocol Step 4.3 – Adaptor Ligation

Adaptor Oligos
PN -2000094



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

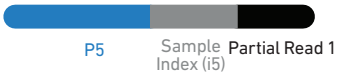
Ligation
Product

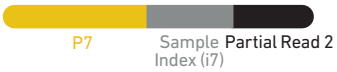
5'-CTACACGACGCTCTTCCGATCT-N16-N12-TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTVN-cDNA_Insert-AGATCGGAAGAGC ACACGTCTGAACTCCAGTCAC-3'
3'-GATGTGCTGCGAGAAGGCTAGA-N16-N12-AAAAAAAAAAAAAAAAAAAAAAAAAAAAAABN - cDNA_Insert-TCTAGCCTTCTCG-5'

Protocol Step 4.5 – Sample Index PCR

Dual Indexing

Dual Index TT
Set A
PN-1000215

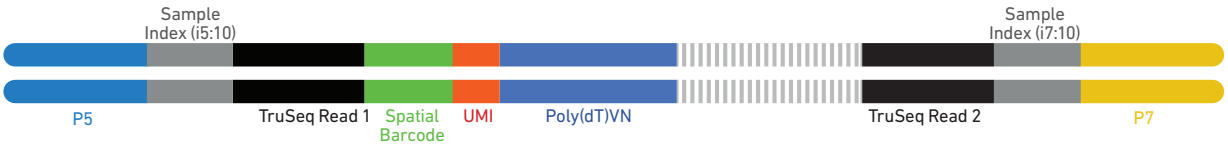




5'-AATGATACGGCGACCACCGAGATCTACAC-N10-ACACTCTTTCCCTACACGACGCTC-3'

5'-CAAGCAGAAGACGGCATACGAGAT-N10- GTGACTGGAGTTCAGACGTGT-3'

Sample Index
PCR Product



5'-AATGATACGGCGACCACCGAGATCTACAC--N10-ACACTCTTTCCCTACACGACGCTCTTCCGATCT-N16-N12-TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTVN- cDNA_Insert-AGATCGGAAGAGCACACGTCTGAACTCCAGTCAC-N10-ATCTCGTATGCCGTCTTCTGCTTG-3'
3'-TTACTATGCCGCTGGTGGCTCTAGATGTG--N10-TGTGAGAAAGGGATGTGCTGCGAGAAGGCTAGA-N16-N12-AAAAAAAAAAAAAAAAAAAAAAAAAAAAAABN- cDNA_Insert-TCTAGCCTTCTCGTGTGCAGACTTGAGGTCAGTG-N10-TAGAGCATACGGCAGAAGACGAAC-5'