

Sep 17, 2024

## Hybrid selection protocol using 10x Single-Cell RNA-Seq assay library

DOI

**dx.doi.org/10.17504/protocols.io.x54v924jzl3e/v1**

Xian Adiconis<sup>1</sup>, Joshua Z Levin<sup>1</sup>

<sup>1</sup>Broad Institute of MIT and Harvard



xian Adiconis

Broad Institute

OPEN  ACCESS



DOI: [dx.doi.org/10.17504/protocols.io.x54v924jzl3e/v1](https://dx.doi.org/10.17504/protocols.io.x54v924jzl3e/v1)

**Protocol Citation:** Xian Adiconis, Joshua Z Levin 2024. Hybrid selection protocol using 10x Single-Cell RNA-Seq assay library. protocols.io <https://dx.doi.org/10.17504/protocols.io.x54v924jzl3e/v1>

**Manuscript citation:**

Simmons SK, Adiconis X, Haywood N, Parker J, Lin Z, Liao Z, Tuncali I, Al'Khafaji AM, Shin A, Jagadeesh K, Gosik K, Gatzert M, Smith JT, El Kods DN, Kuras Y, Baecher-Allan C, Serrano GE, Beach TG, Garimella K, Rozenblatt-Rosen O, Regev A, Dong X, Scherzer CR, Levin JZ. Experimental and Computational Methods for Allelic Imbalance Analysis from Single-Nucleus RNA-seq Data. bioRxiv [Preprint]. 2024 Aug 16:2024.08.13.607784. doi: 10.1101/2024.08.13.607784. PMID: 39185246; PMCID: PMC11343128.

**License:** This is an open access protocol distributed under the terms of the **Creative Commons Attribution License**, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

**Protocol status:** Working

**We use this protocol and it's working**

**Created:** September 10, 2024

**Last Modified:** September 17, 2024

**Protocol Integer ID:** 107222

**Keywords:** single-cell RNA-seq, 10x Chromium, hybrid selection, targeted sequencing

**Funders Acknowledgement:**  
**Aligning Science Across**  
**Parkinson's**  
**Grant ID: ASAP-000301**

## Abstract

This protocol is for target enrichment of cDNA libraries generated with 10x Genomics single-cell RNA-seq assays. The protocol consists of parts of vendor provided protocols with minor modification. The hybridization and PCR part is based on "CG000059\_DemonstratedProtocolExome\_RevC" (10x Genomics) and the capture part is based on "SureSelectXT Target Enrichment System for Illumina Paired-End Multiplexed Sequencing Library Protocol Version C3, September 2019" (Agilent).

## Materials

### Oligos

A	B	C
Oligo Name	Vendor	Sequence
P5 primer	IDT	5'-AATGATACGGCGACCACCGA-3'
P7 primer	IDT	5'-CAAGCAGAAGACGGCATACGA-3'

### Reagents

A	B	C
Reagents	Vendor	Part Number
xGen® Universal Blocking Oligo – TS-p5, 25 rxn	IDT	1016184
xGen® Universal Blocking Oligo – TS-p7(8nt), 25 rxn	IDT	1016188
SureSelectXT Reagent kit for 16 samples, includes library prep and enrichment reagents for post-capture processing on the HiSeq platform. Includes indexes 1 - 16.	Agilent	G9611A
SureSelect Custom Tier3 3Mb-5.9Mb Probe (up to 180k oligos) sufficient for post-capture processing of 16 samples. With the following configuration: Design/ ELID #: S3333112	Agilent	5191-6910
Dynabeads MyOne Streptavidin T1, 2ml	Thermo Fisher Scientific	65601
Amp Mix	10x Genomics	220129
Agencourt AMPure® XP SPRI beads, 60 ml	Beckman Coulter Genomics	A63881






## Safety warnings

! For hazard information and safety warnings, please refer to the MSDSs (Material Safety Data Sheets).



## Sample preparation


30m

- 1 Use  750 ng of cDNA library generated with the 10x Chromium single-cell RNA-seq assay.
- 2 Add  1  $\mu\text{L}$  each of TS-p5 and TS-p7 blocking oligos.
- 3 If the total volume exceeds  3.4  $\mu\text{L}$ , use a speed-vac and set the temperature at  30  $^{\circ}\text{C}$  to reduce the volume to the desired volume of  3.4  $\mu\text{L}$ .

20m


## Buffer and reaction mix preparation

20m

- 4 Prepare the Hybridization Buffer with reagents from the SureSelectXT kit at  Room temperature  
Prepare the volume for at least 5 reactions to ensure accurate pipetting.

10m

A	B	C
	1x ( $\mu\text{l}$ )	5x ( $\mu\text{l}$ )
Hyb1 (orange)	6.63	33.15
Hyb2 (red)	0.27	1.35
Hyb3 (yellow)	2.65	13.25
Hyb4 (black)	3.45	17.25
Total	13	65

- 5 Prepare the block mix at  4  $^{\circ}\text{C}$

10m

A	B
	1x ( $\mu\text{l}$ )
Indexing Block1 (green)	2.5
Block 2 (blue)	2.5
H2O	0.6
Total	5.6



## Sample and block denaturing

5m

- 6 Add 5.6  $\mu\text{L}$  Block mix to the concentrated 3.4  $\mu\text{L}$  sample, mix well and transfer to the 0.2ml PCR tube strip (Axygen), and place into a thermocycler following

Thermocycler Conditions: (Lid@ 105  $^{\circ}\text{C}$  , 100  $\mu\text{l}$ )

95  $^{\circ}\text{C}$  , 00:05:00

65  $^{\circ}\text{C}$  , 00:00:00 hold

## Hybridization

1d

- 7 While step 6 mix is incubated at 65  $^{\circ}\text{C}$  for 00:05:00 , prepare the following at

Room temperature

A	B
	1x ( $\mu\text{l}$ )
Hybridization Buffer (Step 4)	13
25% RNase Block solution (for $\geq 3\text{Mb}$ )	0.5 $\mu\text{l}$ RNase Block (purple)+1.5 $\mu\text{l}$ H <sub>2</sub> O=2 $\mu\text{l}$
Capture library( $\geq 3\text{ Mb}$ )	5
Total	20

Mix well by high speed vortexing for 00:00:05 , spin down briefly, add into the sample and block mix at 65  $^{\circ}\text{C}$  , mix by pipetting 8-10x, use a new cap strip to seal the tubes

Incubate at 65  $^{\circ}\text{C}$  for 16:00:00 to 24:00:00

## Library capture

2h

- 8 In a strip tube, use 50  $\mu\text{L}$  MyOne Streptavidin T1 beads per sample, wash with 200  $\mu\text{L}$  SureSelect Binding buffer 3 times, resuspend in 200  $\mu\text{L}$  SureSelect Binding buffer.

- 9 Bring the washed beads from step 8 near the thermocycler, add the 65  $^{\circ}\text{C}$  reaction mix (~ 27  $\mu\text{L}$  left) right into the 200  $\mu\text{L}$  beads, gentle pipetting mix, incubate at Room temperature for 00:30:00 , pipetting mix 6 times every 00:05:00



- 10 Place on a magnet stand to pellet the beads and remove the supernatant once the solution appears clear. Resuspend the beads in 200  $\mu$ L SureSelect Wash buffer 1, incubate at Room temperature for 00:15:00 15m
- 11 Meanwhile, pre-warm SureSelect Wash buffer 2 at 65  $^{\circ}$ C in strip tubes with 200  $\mu$ L per well and 3 wells per reaction on a 96-well heating block (or a thermocycler with reaction volume capacity of 200  $\mu$ L ) 5m
- 12 Place step 10 reaction mix on a magnet stand to pellet the beads and remove the supernatant once the solution appears clear.
- 13 Resuspend the beads in 200  $\mu$ L pre-warmed SureSelect Wash buffer 2, incubate at 65  $^{\circ}$ C for 00:10:00 Place the reaction mix on a magnet stand to pellet the beads and remove the supernatant once the solution appears clear. 15m
- 14 Repeat step 13 two more times and total three washes with pre-warmed SureSelect Wash buffer 2. And make sure all the wash buffer has been removed in the final wash. 30m
- 15 Resuspend the beads in 30  $\mu$ L H<sub>2</sub>O and keep on ice. 5m

## Enrichment PCR

2h

- 16 On ice, assemble the following mix 30m

A	B
Amp Mix	50
P5 primer (10 $\mu$ M)	2
P7 primer (10 $\mu$ M)	2
*cDNA containing beads	30
H2O	16
Total	100

Thermocycler Conditions: (Lid@ 105  $^{\circ}$ C , 100  $\mu$ L)

98  $^{\circ}$ C , 00:00:45

then 9 cycles of



🔥 98 °C , ⌚ 00:00:15





🔥 60 °C , ⌚ 00:00:30

🔥 72 °C , ⌚ 00:00:30

then

🔥 72 °C , ⌚ 00:01:00

🔥 4 °C , ⌚ 00:00:00 hold

- 17 Place the PCR reaction tube on a magnet stand, wait until it clears and recover  100  $\mu$ L 5m  
supernatant to a new PCR tube strip.
- 18 Add  180  $\mu$ L SPRI beads (1.8x) to the recovered PCR product, mix well by pipetting, pellet the beads on a magnet stand, after supernatant removal, wash with  300  $\mu$ L 80% ethanol twice, elute with  20  $\mu$ L buffer EB (10 mM Tris-HCl, pH 8.5). 15m
- 19 QC with Quant-it (Thermo Fisher Scientific) and BioAnalyzer DNA HS assay (Agilent). 1h

## Protocol references

1. "CG000059\_DemonstratedProtocolExome\_RevC"

[https://assets.ctfassets.net/an68im79xiti/Zm2u8VIFa8qGYW4SGKG6e/4bddcc3cd60201388f7b82d241547086/CG000059\\_DemonstratedProtocolExome\\_RevC.pdf](https://assets.ctfassets.net/an68im79xiti/Zm2u8VIFa8qGYW4SGKG6e/4bddcc3cd60201388f7b82d241547086/CG000059_DemonstratedProtocolExome_RevC.pdf)

2. "SureSelectXT Target Enrichment System for Illumina Paired-End Multiplexed Sequencing Library Protocol Version C3, September 2019"

newer version at <https://www.agilent.com/cs/library/usermanuals/public/G7530-90000.pdf>