

Version 2 ▼

Sep 27, 2022

🌐 A versatile nuclei extraction protocol for single nucleus sequencing in non model species – optimization in various Atlantic salmon tissues.


V.2

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ABSTRACT

Single cell RNA sequencing has rapidly become a standard tool for profiling transcriptomic diversity across thousands of cells (Linnarsson and Teichmann, 2016), and is now being applied to a large diversity of species and tissues. The main limitation of this technology is that it requires the isolation of live cells from fresh tissue, severely restricting its applicability. As a result, single nuclei RNA sequencing (snRNA-seq), which consists of sequencing the RNA of only the nuclei of cells rather than of the whole cell, has been commonly adopted since it allows samples to be stored for several months prior to processing while yielding comparable results to whole cell sequencing (Kulkarni, et al., 2019; Slyper et al. 2021). A critical challenge for snRNA-seq is the successful extraction of high quality nuclei. This has spurred the recent publication of a number of dissociation protocols for nuclei extraction (Drokhlyansky et al. 2020; Eraslan et al. 2021; Melms et al 2021), however, these have largely been optimized for model species such as humans, and more and more single nuclei is being adopted in non-model species.

Here we present a robust protocol that enables the extraction of nuclei from frozen tissue adapted from those shown to work in different tissue types, such as human skin (Drokhlyansky et al. 2020; Eraslan et al. 2021; Melms et al 2021). Our protocol has been used to successfully extract nuclei from an array of different Atlantic salmon (*Salmo salar*) tissues including liver, skin, fin, spleen, head kidney and gill as well as in other species such as sole (*Solea solea*) nose and gonad, rabbit (*Oryctolagus cuniculus*) nasal tissue and nurse shark (*Ginglymostoma cirratum*) spleen. We present the protocol as applied to fin and skin as these are particularly challenging tissues to work with given their toughness and the presence of hard tissue (e.g., scales and bones), connective tissue and fat deposits. We include notes throughout the protocol so that the reader can optimise it for a variety of tissue types. While the protocol has been optimised to work with the Chromium 10x platform, the most commonly used high throughput microfluidic device, but can be used successfully for the extraction of nuclei for other platforms and applications. The aim of this protocol is to capture 7,000 nuclei per single-nuclei RNA sequencing library using the Chromium Single Cell 3' Reagent Kits v2 or v3 (10X Genomics). Given its utility for isolating nuclei from difficult to dissociate tissue types, we anticipate that this protocol will be broadly applicable for snRNA-seq of non-model organisms and unconventional tissue types.

ATTACHMENTS

[hc6dbbap7.docx](#) [figure 1 results.docx](#)

PROTOCOL CITATION

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KEYWORDS

snRNA-seq , aquaculture, non-model species, nuclei

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References:

Drokhlyansky E, Smillie CS, Van Wittenberghe N, Ericsson M, Griffin GK, Eraslan G, Dionne D, Cuoco MS, Goder-Reiser MN, Sharova T, Kuksenko O, Aguirre AJ, Boland GM, Graham D, Rozenblatt-Rosen O, Xavier RJ, Regev A (2020). The Human and Mouse Enteric Nervous System at Single-Cell Resolution.. Cell.
<https://doi.org/10.1016/j.cell.2020.08.003>

Eraslan, G, Drokhlyansky E, Anand S, Subramanian A, Fiskin, E, Slyper M, Wang J, Wittenberghe N. Van; Rouhana, J.M.; Waldman, J.; et al. Single-nucleus cross-tissue molecular reference maps to decipher disease gene function. Science 2022.<https://doi.org/10.1126/science.abc429090>

Kulkarni, A.; Anderson, A.G.; Merullo, D.P.; Konopka, G. Beyond bulk: a review of single cell transcriptomics methodologies and applications. Curr. Opin. Biotechnol. 2019.
<https://doi.org/10.1016/j.copbio.2019.03.001>.

Linnarsson S, Teichmann SA (2016). Single-cell genomics: coming of age.. Genome biology.
<https://doi.org/10.1186/s13059-016-0960-x>

Slyper M, Porter CBM, Ashenberg O, Waldman J, Drokhlyansky E, Wakiro I, Smillie C, Smith-Rosario G, Wu J, Dionne D, Vigneau S, Jané-Valbuena J, Tickle TL, Napolitano S, Su MJ, Patel AG, Karlstrom A, Gritsch S, Nomura M, Waghay A, Gohil SH, Tsankov AM, Jerby-Arnon L, Cohen O, Klughammer J, Rosen Y, Gould J, Nguyen L, Hofree M, Tramontozzi PJ, Li B, Wu CJ, Izar B, Haq R, Hodi FS, Yoon CH, Hata AN, Baker SJ, Suvà ML, Bueno R, Stover EH, Clay MR, Dyer MA, Collins NB, Matulonis UA, Wagle N, Johnson BE, Rotem A, Rozenblatt-Rosen O, Regev A (2020). A single-cell and single-nucleus RNA-Seq toolbox for fresh and frozen human tumors.. Nature medicine.
<https://doi.org/10.1038/s41591-020-0844-1>

MATERIALS TEXT

MATERIAL

[Noyes Spring Scissors - Tungsten Carbide](#) **Fine Science**

Tools Catalog #15514-12 Step 2

[Tungsten Carbide Straight 11.5 cm Fine Scissors](#) **Fine Science**

Tools Catalog #14558-11

[Falcon™ Cell Strainers](#) **Fisher**

→ **40 µm** **Scientific Catalog #08-771-2**

[Corning™ Falcon™ Test Tube with 35µm Cell Strainer Snap](#)

Cap Corning Catalog #352235

[pluriStrainer Mini 20 µm \(Cell](#)

[Strainer\)](#) **pluriSelect Catalog #43-10020-50**

X500 Eppendorf DNA LoBind Tubes, 1.5ml, PCR clean

Cryotube

6-well tissue culture plate (Stem Cell Technologies)

Falcon tubes 15 ml (Corning)

[INCYTO C-Chip™ Disposable](#)

[Hemocytometers](#) **Vwr Catalog #82030-468**

SAMPLING AND STORAGE FOR NUCLEAR ISOLATION

Animals must be appropriately euthanized and immediately processed. Approximately ~ **60 mg** of salmonid tissue is placed in one clearly labelled cryotube and immediately flash frozen in liquid nitrogen. **This step is critical.** The tissue must be preserved as fast as possible for optimal results. In the absence of liquid nitrogen, samples can be frozen in dry ice. Samples can be stored at **-80 °C** for up to a year prior to use. Older samples might still yield viable nuclei but this would need to be tested.

REAGENTS

All reagents should be chilled on ice prior to use.

2X stock of salt-Tris solution makes **10 mL** :

Stocks:

[NaCl \(5 M\) RNase-free](#) **Thermo Fisher**

NaCl: **Scientific Catalog #AM9759**

[UltraPure™ 1 M Tris-HCl Buffer, pH 7.5](#) **Thermo**

Tris-HCl pH 7.5: **Fisher Catalog #15567027**

[Calcium chloride 1 M in aqueous](#)

CaCl₂: [solution](#) **Vwr Catalog #97062-820**

MgCl₂:

[Magnesium chloride solution for molecular biology \(1.00 M\)](#) **Sigma –**

Aldrich Catalog #M1028

[☒ Water for biotechnology nuclease-free](#)

Nuclease-free water: [sterile Vwr Catalog #97062-794](#)

A	B	C
Stock solution (see above)	Volume	Final concentration
NaCl	292 µl	146 mM
Tris-HCL10	100 µl	10 mM
CaCl ₂	10 µl	1 mM
MgCl ₂	210 µl	21 mM
Nuclease-free water	9388 ml	

The following buffers contain RNAse inhibitor

[☒ Protector RNase Inhibitor Sigma](#)

Aldrich Catalog #3335399001

- It is important to use the correct RNAse inhibitor as it can negatively affect library prep, check with the sequencing platform before using another type of RNAse.
- Do not add RNAse until right before nuclear extraction.
- RNAse inhibitor does not need to be used to test nuclear extractions, but it should added for sequencing runs.

1X ST buffer solution (ST) -  **10 mL** :

Dilute 2x ST in ultrapure nuclease-free water (1:1)

A	B	C
Stock Solution	Volume	Final concentration
2X ST	3 ml	
Ultrapure nuclease free water	3 ml	
RNAse inhibitor	6ul µl (240 U)	40 Uml

Make fresh and chill prior to use, add RNAse inhibitor right before nuclear isolation. RNAse inhibitor amount can up upped if it's an RNAse Rich tissue, up to 500 U per ml instead, tissue spends very little time in this buffer and is chilled at all time, which is why the amount of RNAse inhibitor can be lower.

Working solution (TST) –  **4 mL** :

[☒ Tween-20 Sigma-](#)

1% Tween-20: **aldrich Catalog #P-7949**

2% BSA:

[☒ Bovine Serum Albumin \(20 mg/mL\) Molecular Biology Grade New England](#)

Biolabs Catalog #B9000S

A	B	C
Stock solution	Volume	Final concentration
2X ST buffer	2 ml	
1% Tween-20	120 µl	
2% BSA	20 µl	
Nuclease-free water	1840 µl	
RNAse inhibitor	20 µl (800 U)	200 U/ml

Make fresh and chill prior to use, add RNAse inhibitor right before nuclear isolation. Dilute the Tween from 10% in stock solution with nucH₂O before making the buffer. RNAse inhibitor amount can be upped if it's an RNAse rich tissue up to 1000 U per ml instead, the nuclear isolation will happen in this buffer so it's more critical in here.

PBS+0.02 BSA (PBS+BSA) – 1 mL :

A	B	C
Stock solution	Volume	Final concentration
Ultra-pure molecular grade PBS	1970 µl	
2% BSA **	20 µl	
RNAse inhibitor	10 µl	200 U/ml

** can top this up this to 2% BSA if the cells are clumping or look degraded. RNAse inhibitor is the most critical in this step as the nuclei will be in this buffer the longest can use up to 1000 U per ml.

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BEFORE STARTING

Sampling and storage for nuclear isolation.

Animals must be appropriately euthanized and immediately processed. Approximately ~ 60 mg of tissue is placed in one clearly labelled cryotube and immediately flash frozen in liquid nitrogen. **This step is critical.** The tissue must be preserved as fast as possible for optimal results. In the absence of liquid nitrogen, samples can be frozen in dry ice. Samples can be stored at -80 °C for up to a year prior to use. Older samples might still yield viable nuclei but this would need to be tested.

All reagents should be chilled on ice prior to use.

Samples should be kept frozen on dry ice until immediately before nuclei isolation, and all sample-handling steps should be performed on ice.

The centrifuge should be pre chilled at **4 °C**.

All reagents are given for 2 nuclear isolations.

Amounts of buffer especially those that contain RNase should be adjusted appropriately for each experiment prepared prior and RNase added immediately before use.

Before using this prep for library preparation do a trial run.

Recommended to do a trial especially on a new tissue type to adjust different parameters without adding RNase. Once parameters are adjusted such as mincing times, filter size and dilution in to final buffer in order to get good quality nuclei.

Nucleus isolation workflow for ST-based buffers

30m

1

Samples should be kept frozen on dry ice until immediately before nuclei isolation, and all sample-handling steps should be performed **On ice**. The centrifuge should be pre-chilled at **4 °C**.

On ice, place a piece of frozen tissue into one well of a 6-well tissue culture plate with **1 mL** TST.

If the sample is stuck to the cryotube, remove using tweezers, preferably while still in dry ice, and place immediately into the culture plate with TST. If the sample needs processing for examples cutting this is best done on dry ice. This is avoided by processing the sample prior to flash freezing.

2 **On ice**, mince tissue initially using Tungsten Carbide scissors for **00:00:30** and then with Noyes Spring Scissors^{10m}

[Noyes Spring Scissors - Tungsten Carbide Fine Science](#)

Tools Catalog #15514-12

for a total of

00:10:00.

This step is only necessary for fin, skin or similar hard tissues, for softer tissues just use spring scissors for **00:10:00**.

2.1



5m

⌚ 00:05:00 into the mincing gently pipette up and down with a p1000 pipette using a low retention filtered tip. The time in the dissociation buffer is critical. See image for how to assess the timing is correct by looking at your nuclei.

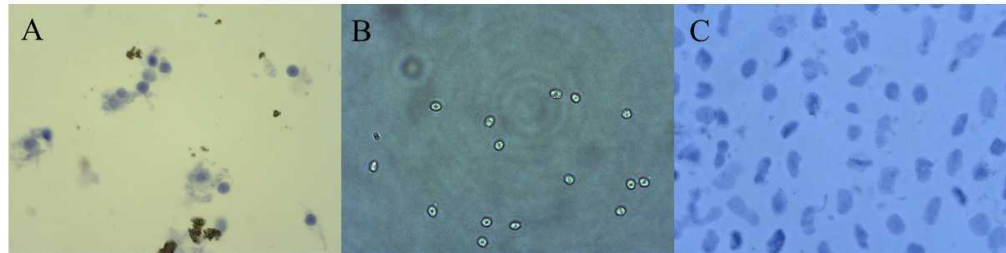



Image from different dissociation trials in Atlantic salmon tissues x40 magnification stained with trypan blue. **A.** Head kidney nuclei not had sufficient time in dissociation buffer, will clog microfluidic device. **B.** Blood nuclei perfectly dissociated minimal clumping ideal for sequencing. **C.** Liver nuclei too long in dissociation buffer, nuclear membrane started to degrade. Can still be sequenced but not ideal. Note when staining nuclei with trypan blue assess nuclear quality as soon as possible as the nuclei will quickly degrade when not on ice.

3 Pass lysate through a 40 µm cell strainer .

3.1

Add a further  1 mL of TST to the cell strainer immediately.

3.2

Add  3 mL of freshly prepared ST buffer to the lysate.

3.3

Add the  5 mL of lysate to a marked 15 ml falcon tube (Corning) on ice.

4

5m

Centrifuge at  500 x g, 4°C, 00:05:00 in a swinging bucket centrifuge.

5

Resuspend the pellet gently using a p1000 pipette in PBS-BSA.

Resuspension volume depends on the size of the pellet, usually within the range of **100 µL** - **1000 µL** (**1 mL** if there are many nuclei). For skin and fin, **400 µL** is recommended.

6 Filter the nucleus solution a second time.

The size of the filter is tissue dependant, e.g. for tissues such as liver and head kidney a **40 µm** Falcon™ cell strainer will suffice, whereas for gill, a **30 µm** filter would be better giving the higher amount of tough debris that could clog the microfluidic device. In addition, for harder tissues that produce a lot of debris such as fin and skin (this is due to the presence of fat layers and scales in skin and the presence of bones in the fin) then **20 µm** is recommended. The lysate may not pass through at once, pipetting very gently up and down with a wide bore pipette can help it through.

7 Count the nuclei using a C-chip disposable haemocytometer.

In this step, it is also possible to visualise the nuclei and ascertain the level of debris present as well as the integrity of the nuclear membrane.

8 The nuclei are also counted using a Bio-Rad TC20 to confirm results from the disposable haemocytometer and to count the proportion of viable cells.

Nuclei are identified as “dead”, therefore a good nuclei isolation will have a small percentage of live cells. 1-4% of live cells is ideal, but below 12% is acceptable. High proportions of live cells indicates incomplete nuclear isolation and could be an indication of high amounts of debris or insufficient lysis time.

9 Load the nucleus suspension into a Chromium Chip and into the Chromium Controller, aiming to recover 7,000 nuclei as per 10x recommendations with a concentration of between 700 to 1200 nuclei per µL.

In the case of some tissues such as fin, readjust the target recovery to 5000 especially with juvenile fish or tissues such as fin and skin as nuclei yields are on the low side.

