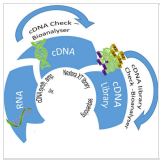

Version 1

Jun 30, 2021

# cDNA library preparation from total RNA extracts of Single-cell marine protists (e.g. Acantharia, Strombidium basimorphum, and Prymnesium parvum) for transcriptome sequencing V.1

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ABSTRACT

Many marine protists are not culturable and therefore challenging to study, nonetheless, they are essential in all marine ecosystems. The development of single-cell techniques is allowing for more marine protists to be studied. Such genomic approaches aim to help to disentangle heterotrophic processes such as phagotrophy from osmotrophy and phototrophic-induced anabolic activities. This information will then support cellular and metabolic modeling by better elucidating the physiological mechanisms and quantifying their importance in different scenarios.

However, single-cell protocols and low input RNA kits for transcriptomics are usually made for and tested with mammalian cells, as such the feasibility and efficiency of single-cell transcriptomics on highly diverse mixotrophic protists is not always known. Often single-cell transcriptomics of microbial eukaryotes shows low transcript recovery rates and large variability.

We report on transcriptomic methods that we have successfully performed on single cells of Acantharia, *Strombidium basimorphum,* and *Prymnesium parvum.*

This protocol follows up after total RNA extraction (from the protocol at dx.doi.org/10.17504/protocols.io.bp6xmrfn) to prepare cDNA libraries for Illumina sequencing. The described protocol uses the SMART-Seq4 kit (Takara #634891) for cDNA synthesis and amplification, but this can also be successfully performed with the NEBNext kit (NEB #E6421). The NEBNext kit protocol is very similar to the protocol described here and generally the manufacture's protocol can be followed but see the notes at step 4 and step 18 of this protocol, and do the final elution after cDNA purification in 10 mM Tris (pH 8.0).

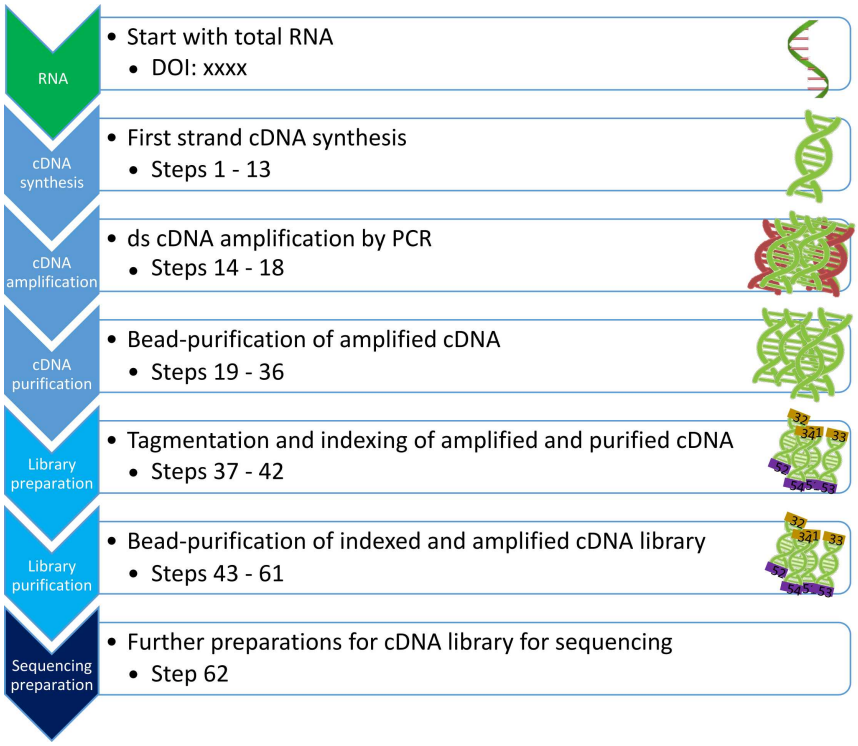
The subsequent cDNA library is prepared following the

Nextera XT DNA Library Preparation

Kit **illumina Catalog #FC-131-1096**



**Citation:** Joost Mansour, Konstantinos Anestis, Fabrice Not, Uwe John (06/30/2021). cDNA library preparation from total RNA extracts of Single-cell marine protists (e.g. Acantharia, Strombidium basimorphum, and Prymnesium parvum) for transcriptome sequencing. https://dx.doi.org/10.17504/protocols.io.bp7vmrn6




DOI

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PROTOCOL CITATION

Joost Mansour, Konstantinos Anestis, Fabrice Not, Uwe John 2021. cDNA library preparation from total RNA extracts of Single-cell marine protists (e.g. Acantharia, Strombidium basimorphum, and Prymnesium parvum) for transcriptome sequencing. **protocols.io** https://dx.doi.org/10.17504/protocols.io.bp7vmrn6

MANUSCRIPT CITATION please remember to cite the following publication along with this protocol

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WHAT'S NEW

RNA extraction from single-cells of mixotrophs for subsequent transcriptomics

KEYWORDS

Single-cell, Acantharia, RNA, transcriptomics, cDNA library, Strombidium, Radiolaria, ciliates, RNA-seq



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PARENT PROTOCOLS

In steps of

Single-cell total RNA extraction from marine protists (e.g. Acantharia, Strombidium cf basimorphum, and Prymnesium parvum)

Single-cell total RNA extraction from marine protists (e.g. Acantharia, Strombidium cf basimorphum, and Prymnesium parvum)

GUIDELINES

- Always wear clean RNase-free gloves.
- Clean workspace (and thermocyclers) with ethanol and an RNase Decontamination Solution.
- Work **On ice**
- If possible use a dedicated set of pipettes for RNA and use filter tips.

MATERIALS TEXT

**cDNA synthesis**

- ☒ PCR Tubes & Caps, RNase-free, 0.2 mL (8-strip format) **Thermo Fisher Catalog #AM12230** In 4 steps (x #samples)
- ☒ 1.5 ml reaction tube **Eppendorf** (x2 for mastermix and reaction buffer)
- ☒ Ice **Contributed by users**
- ☒ nuclease free water **Contributed by users** In 3 steps
- ☒ 10X Lysis Buffer **Takara Catalog #634888** Step 5.1
- ☒ RNase Inhibitor **Takara Catalog #2313A** In 2 steps
- ☒ SMART-seq v4 Oligonucleotide (46 µM) **Takarabio Catalog #634888** Step 9.1 (48 µM, 1 µL per sample)
- ☒ 5X Ultra Low First-Strand Buffer **Takarabio Catalog #634888** Step 9.1 (4 µL per sample)
- ☒ SMART-seq CDS Primer II A (12 µM) **Takarabio Catalog #634888** Step 7 (1 µL per sample)
- ☒ SMARTScribe Reverse Transcriptase **Takarabio Catalog #634888** In 2 steps (2 µL per sample)

**cDNA amplification**

- ☒ 1.5 ml reaction tube **Eppendorf** (for mastermix)
- ☒ nuclease free water **Contributed by users** In 3 steps (3 µL per sample)
- ☒ 2X SeqAmp PCR Buffer **Takara Catalog #638526** Step 18.1 (25 µL per sample)
- ☒ SeqAmp DNA Polymerase **Takara Catalog #638504** Step 18.1 (1 µL per sample)



**Citation:** Joost Mansour, Konstantinos Anestis, Fabrice Not, Uwe John (06/30/2021). cDNA library preparation from total RNA extracts of Single-cell marine protists (e.g. Acantharia, Strombidium basimorphum, and Prymnesium parvum) for transcriptome sequencing. https://dx.doi.org/10.17504/protocols.io.bp7vmrn6

PCR Primer II A (12

- µM) **Takara Catalog #634888** Step 18.1 (1 µL per sample)

**cDNA purification**

- 80% Ethanol **Contributed by users** In 2 steps (made from

  100% Molecular grade ethanol **Contributed by users** and

  nuclease free water **Contributed by users** In 3 steps ) (400 µL per sample)
- 50 mL Falcon Tubes **Contributed by users** (for 80% ethanol)
- AMPure XP Beads **Contributed by users** In 3 steps **(this can be substituted for a similar product, we use CleanNGS (GC Biotech, CNGS-0050)**

  Magnetic Stand-
- 96 **Thermofisher Catalog #AM10027** In 2 steps

  PCR Tubes & Caps, RNase-free, 0.2 mL (8-strip format) **Thermo**
- **Fisher Catalog #AM12230** In 4 steps
-

  PCR Tubes, 0.2mL, flat cap, natural, PCR Tube; 0.2mL; Natural; w/flat cap; 1000/Pk. **Thermo Fisher Catalog #3412** Step 6

  (x #samples x2)
- 1.5 ml reaction tube **Eppendorf** (for bead aliquot, a 5 mL tube might be preferred)

**cDNA library preparation, indexing, and purification**

PCR Tubes & Caps, RNase-free, 0.2 mL (8-strip format) **Thermo**

- **Fisher Catalog #AM12230** In 4 steps (2x for reagent aliquots)

  PCR Tubes & Caps, RNase-free, 0.2 mL (8-strip format) **Thermo**
- **Fisher Catalog #AM12230** In 4 steps (2x #samples)

  Nextera XT DNA Library Preparation
- Kit **illumina Catalog #FC-131-1096** In 2 steps

  Nextera XT Index Kit v2 Set A (96 indexes 384
- samples) **illumina Catalog #FC-131-2001**
- AMPure XP Beads **Contributed by users** In 3 steps **(This can be substituted for a similar product, we use CleanNGS (GC Biotech, CNGS-0050).**
- 80% Ethanol **Contributed by users** In 2 steps (made from

  100% Molecular grade ethanol **Contributed by users** and

  nuclease free water **Contributed by users** In 3 steps ) (400 µL per sample)
- 1.5 ml reaction tube **Eppendorf** (for bead aliquot, a 5 mL tube might be preferred)

  Magnetic Stand-
- 96 **Thermofisher Catalog #AM10027** In 2 steps

**General lab equipment**

- Micropipettes and filter tips



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- Vortex **Contributed by users**
- PCR Thermocycler **Contributed by users**
- Ice **Contributed by users**

Mini-centrifuge
Centrifuge

**Fisher** **S67601B**

Any standard mini centrifuge with adapters for different tube sizes will suffice

Bioanalyzer
Bioanalyzer

**Agilent** **G2991AA**

Any bioanalyzer will suffice.

Agilent High Sensitivity DNA Kit **Agilent Technologies Catalog #5067-4626** In 2 steps

SAFETY WARNINGS

We have tested this for work to acquire transcriptomes from Acantharia, Strombidinium *basimorphum,* and *Prymnesium parvum.*

Adhere to PPE, as dictated under local Health & Safety regulations.

BEFORE STARTING

Total RNA needs to have been extracted (Protocol: dx.doi.org/10.17504/protocols.io.bp6xmrfn) and when possible quantified and quality checked by Bioanalyzer. If Bioanalyzer analysis was possible, only continue with good quality RNA extracts.

- Thaw reagents (except enzymes).
- Allow reagents that need to be at room temperature to incubate at **Room temperature** (i.e. 5X Ultra Low First-Strand Buffer **Takarabio Catalog #634888** and GC nucleic acids purification beads.
- Set thermocycler programs and pre-heat thermocyclers.



**Citation:** Joost Mansour, Konstantinos Anestis, Fabrice Not, Uwe John (06/30/2021). cDNA library preparation from total RNA extracts of Single-cell marine protists (e.g. Acantharia, Strombidium basimorphum, and Prymnesium parvum) for transcriptome sequencing. https://dx.doi.org/10.17504/protocols.io.bp7vmrn6

- For the cDNA purification step Prepare fresh 80% ethanol from
  100% Molecular grade ethanol **Contributed by users** with
  nuclease free water **Contributed by users**

cDNA synthesis preparations

1 Label for each sample a tube
PCR Tubes & Caps, RNase-free, 0.2 mL (8-strip format) **Thermo Fisher Catalog #AM12230** .

2 Prepare a 72°C incubator (e.g. a thermocycler)

3 Thaw other reagents **On ice** – except SmartScribe Reverse Transcriptase, take that from the freezer only once needed.

4 Thaw your RNA samples **On ice** (as prepared in dx.doi.org/10.17504/protocols.io.bp6xmrfn)

5 Prepare 10X Reaction Buffer (**RB**), **On ice** as follows (1 µL is used per sample (adjust as needed, & write down exact volumes):

5.1
- **19 µl** 10X Lysis Buffer **Takara Catalog #634888** (from SMART-Seq4 kit)
- **1 µl** RNase Inhibitor **Takara Catalog #2313A** (white cap from SMART-Seq4 kit)
- Mix/vortex and spin down (avoid bubbles)

cDNA synthesis 1h 45m

6 Take into clean (labeled)
PCR Tubes, 0.2mL, flat cap, natural, PCR Tube; 0.2mL; Natural; w/flat cap; 1000/Pk. **Thermo Fisher Catalog #3412**
**1 µl to 9.5 ul** of RNA sample & **1 µl** of **RB**
(total 10.5 µL volume, adjust with nuclease free water **Contributed by users** depending on RNA sample)

For single-cells we recommend **5 µl** total RNA. In essence either all total RNA sample can be used, or it is safer to use <50% to allow redo when needed and [RNA] permitting. The total amplification cycles would also be affected by the volume used here.

7 Place samples **On ice** and add **1 µl** of



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SMART-seq CDS Primer II A (12 µM) **Takarabio Catalog #634888** (blue cap) to the samples.

We are performing 17+ PCR cycles. If fewer cycles are envisioned **2 µl** of SMART-seq CDS Primer II A (12 µM) **Takarabio Catalog #634888** should be used instead, though keeping the total volume the same by disregarding step 7.1).

7.1 add **1 µl** nuclease free water **Contributed by users** (total volume 12.5 µL)

7.2 Mix gently (vortex) & spin down

8 Incubate samples at **72 °C** for **00:03:00** 3m

Immediately proceed to step 8 after incubation finishes

9 While samples are incubating prepare Master Mix (MM) as below for each sample (+10%; write down exact volumes) **On ice**

9.1

- **4 µl** 5X Ultra Low First-Strand Buffer **Takarabio Catalog #634888** (red cap)
- **1 µl** SMART-seq v4 Oligonucleotide (46 µM) **Takarabio Catalog #634888** (pink cap)
- **5 µl** RNase Inhibitor **Takara Catalog #2313A** (white cap)

10 **Immediately** after the 3 min 72°C incubation from step 8 put samples **On ice** for **00:02:00** 2m
During this incubation time on ice perform steps 11 and 12.

11 Preheat thermocycler to **42 °C**

12 SMARTScribe Reverse Transcriptase **Takarabio Catalog #634888** (purple cap), gently mix it



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without vortexing and add to the prepared Master Mix (from step 9):

12.1 SMARTScribe Reverse Transcriptase **Takarabio Catalog #634888** **2 µl** for each sample (x #samples +10%)

12.2 Mix MM by gentle vortex and spin down

13 Add **7.5 µl** of the MM to the samples (total volume now 20 µL)

13.1 Mix by pipetting and follow with short spindown

14 Incubate samples in pre-heated Thermocyler with heated lid and the following program: 1h 40m

**42 °C** **01:30:00** ,

**70 °C** **00:10:00** ;

**4 °C forever**

15

STOPPING POINT - 4°C overnight

cDNA Amplification

16 Thaw all the reagents (see step 18) **On ice** except the enzyme (Vortex and spin down reagents except for enzyme)

17 Preheat thermocycler to **95 °C**

18 Prepare Mastermix (+10%), one sample is as below:

18.1

- **25 µl** 2X SeqAmp PCR Buffer **Takara Catalog #638526**
- **1 µl** PCR Primer II A (12 µM) **Takara Catalog #634888** (green cap)



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- **3 µl** nuclease free water **Contributed by users**
  SeqAmp DNA
- **1 µl** Polymerase **Takara Catalog #638504** (take out last minute and mix without vortexing, spin down)
- Mix Master Mix well and gently (finger flick) and spin down

19 Add **30 µl** of Mastermix to each sample from cDNA synthesis.
Mix well (pipetting) and spin down gently.

20 Run samples on pre-heated thermocycler with the program:

| A | B | C |
|---|---|---|
| 95°C | 1 min | |
| 98°C | 10 sec | repeat step 2, 18 times |
| 65°C | 30 sec | |
| 68°C | 3 min | |
| 72°C | 10 min | |
| 4°C | forever | |

This thermocycler program is run with 18 cycles and works for us. Nonetheless, it is recommended to test this beforehand. Over-amplification can result in ahigher yield of cDNA, however, it introduces a bias towards more abundant transcripts. We settled on the following number of amplification cycles.

| Species | cDNA kit | Number of cycles |
|---|---|---|
| *Strombidium basimorphum* | SMARTseq-v4 | 18 |
| *Prymnesium parvum* | NEBNext | 25 |
| Acantharia | SMARTseq-v4 | 18 |
| Acantharia | NEBNext | 16 |

21

STOPPING POINT 4°C overnight

## cDNA cleanup/bead purification 43m

22 Preparations: 30m
- Label for each sample two tubes
  PCR Tubes & Caps, RNase-free, 0.2 mL (8-strip format) **Thermo Fisher Catalog #AM12230** . One tube is used for the cDNA after purification, and one is for an aliquot of the purified cDNA for Bioanalyzer.



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- Vortex the bead stock well ( AMPure XP Beads **Contributed by users** ), this needs to be very well and evenly mixed
- Aliquot beads, **22.5 µl** x samples (plus extra)
- Bring the bead aliquot to **Room temperature** for at least **00:30:00**
- Vortex the bead aliquot until evenly mixed
- Prepare fresh 80% EtOH, 400 µL x samples

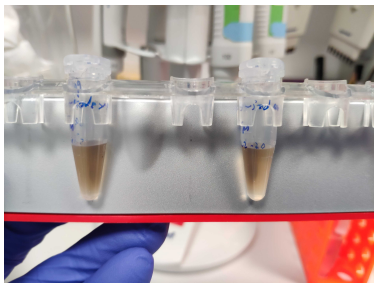
23 Add **22.5 µl** of beads to each sample (amplified cDNA from the previous section)

23.1 Mix by pipetting up and down at least 10 times, and vortex

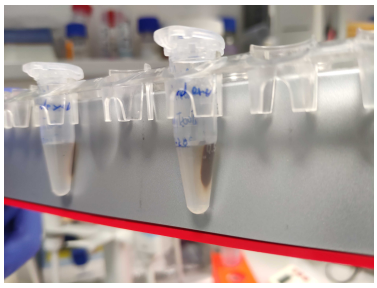
24 Incubate at **Room temperature** **00:08:00** to let cDNA bind to the beads 8m

25 Magnetic Stand- 5m

Briefly spin down and place the samples **on a** 96 **Thermofisher Catalog #AM10027** **for** **00:05:00** or longer. Until the liquid appears completely clear and there are no beads in the supernatant.



Not yet clear, beads have not yet all pelleted



clear, all beads have pelleted

26 Pipet and discard the supernatant (72.5 µL), keeping the samples in the magnetic device

27 Keeping the samples in the magnetic device, **add** **200 µl fresh** 80% Ethanol **Contributed by users** to each sample.

Do not disturb the beads



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27.1 Wait **00:00:30** 30s

27.2 Pipet and discard supernatant containing contaminants (use 100 µL)

28 Repeat the EtOH washing step for a total of 2 washing steps **go to step #27**

29 Briefly spin the samples to collect liquid off the sides

30 Place samples back in the **magnetic device for** **00:00:30** , beads will again be collected on the side 30s

31 Remove all remaining ethanol/supernatant with a pipet (use 10 µL pipet)

32 Place samples at **Room temperature for** **00:02:00 minutes.** (it might take a bit longer) 2m
Until the pellet is no longer shiny, but before a crack appears. It needs to be 'just' dry, matte with no shine.

33 Once the beads are dry add **15 µl of Elution buffer to all samples** to cover the bead pellet

33.1 Remove samples from the magnetic device

33.2 Mix to re-suspend the beads by (multi)pipetting (can scrap of beads from the side)

34 Incubate at **Room temperature for** **00:02:00** **(longer)** to rehydrate 2m

35 Briefly spin the samples to collect liquid off the sides

36 Place the samples back in the **magnetic device for** **00:01:00** , until the solution is completely clear 1m



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37

**Transfer the clear supernatant** containing purified cDNA to ⊠PCR Tubes & Caps, RNase-free, 0.2 mL (8-strip format) **Thermo Fisher Catalog #AM12230** tube (use 10 µL pipet).

Beads that do not pellet can be pipetted for resuspension and then towards the magnet, and incubation continued until there are no more beads in the supernatant

37.1 Make immediately an aliquot for Bioanalyzer analysis to prevent unnecessary freeze-thawing cycles.

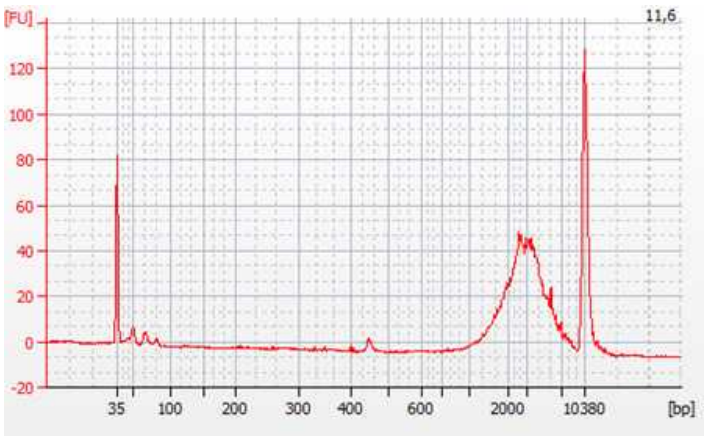
38

STOPPING POINT - Label and store at **-20 °C**

cDNA Sample verification

39

⊠Agilent High Sensitivity DNA Kit **Agilent Technologies Catalog #5067-4626** Check the quality of cDNA by following the manufacture's protocol.




Example of a desirable electrograph. Showing a good cDNA curve, and few primer dimers. Example of an acantharian sample. The peaks on the outsides are markers of the Bioanalyser chip for size and concentration marker

39.1 Quantify and calculate the concentration of cDNA. This is needed for the next cDNA library procedure.



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## cDNA library preparation and indexing – Nextera XT

40 Proceed with cDNA library preparation only for good quality samples from the previous step.

41 Normalize cDNA samples to 30pg/ul

Dilute each sample of amplified and purified cDNA to 30 pg/µL in either Elution buffer or as per the final step of the used protocol for cDNA purification. Work with a minimum of 1 µL amplified cDNA and a total volume of 5 µL.

42 Prepare to work very timely for this protocol

- Preheat a PCR thermocycler to **55 °C** , with preheat lid at 100 °C
- Prepare from the Nextera XT DNA Library Preparation Kit **illumina Catalog #FC-131-1096** the **ATM** and **NT reagents** in sufficient quantity (i.e. 5 ul per sample for each) separated over multiple tubes to facilitate multi-pipetting

43 Nextera XT DNA Library Preparation

Follow the Kit **illumina Catalog #FC-131-1096** manufacturer's protocol for " Tagment genomic DNA", and "Amplify Libraries", with the changes listed below.

Refer to pages 7-9 of the Nextera XT manual (https://emea.support.illumina.com/content/dam/illumina-support/documents/documentation/chemistry_documentation/samplepreps_nextera/nextera-xt/nextera-xt-library-prep-reference-guide-15031942-05.pdf).

44 Changes to manufacturer' s protocol:

- Start the tagmentation with **5 µl** of 30 pg/µl amplified cDNA sample (from step 37)
- all steps indicated as "centrifuge at 280 x g at 20 °C for 1 minute" can be substituted short spindown in a tabletop mini-centrifuge.

45 Store samples at **4 °C** for up to 2 days or proceed immediately with purification

## cDNA library purification 46m

46 Preparations: 30m

- Vortex the bead stock well ( AMPure XP Beads **Contributed by users** ), this needs to be very well and evenly mixed
- Aliquot beads, **30 µl** x samples (plus extra)
- Bring the bead aliquot to **Room temperature** for at least **00:30:00**
- Vortex the bead aliquot until evenly mixed
- Prepare fresh 80% EtOH, 400 µL x #samples

47 Spin down your indexed cDNA samples (total 50 µL)



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48 **Add 30 µL** of AMPure XP Beads **Contributed by users** to each sample 2m

- Mix by pipetting up and down
- Shake/vortex for **00:02:00**

49 Incubate at **Room temperature** **00:05:00** to let cDNA bind to the beads 5m

50 Magnetic Stand-
Briefly spin down and place the samples **on a** 96 **Thermofisher Catalog #AM10027** **for** **00:05:00** or longer. Until the liquid appears completely clear and there are no beads in the supernatant.

51 Pipet and discard the supernatant (80 µL), keeping the samples in the magnetic device

52 Keeping the samples in the magnetic device, **add** **200 µl fresh** 80% Ethanol **Contributed by users** to each sample.

Do not disturb the beads

52.1 Wait **00:00:30**

52.2 Pipet and discard supernatant containing contaminants (use 100 µL pipet)

53 Repeat the EtOH washing step for a total of 2 washing steps **go to step #52**

54 Briefly spin the samples to collect liquid off the sides

55 Place samples back in the **magnetic device for** **00:00:30** , beads will again be collected on the side

56 Remove all remaining ethanol/supernatant with a pipet (use 10 µL pipet)

57 Place samples at **Room temperature for** **00:05:00 minutes.** 5m



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Until the pellet is no longer shiny, but before a crack appears. It needs to be 'just' dry, matte with no shine.

58 Once the beads are dry add **52.5 µl** **of** Resuspension Buffer **Contributed by users** (NexteraXT kit) to all samples to cover the bead pellet

58.1 Remove samples from the magnetic device

58.2 Mix to re-suspend the beads by (multi)pipetting (can scrap of beads from the side)

58.3 Vortex for **00:02:00** followed by a very short spindown 2m

59 Incubate at **Room temperature for** **00:02:00** to rehydrate

60 Briefly spin the samples to collect liquid off the sides

61 Place the samples back in the **magnetic device for** **00:02:00** , until the solution is completely clear 2m

62 **Transfer the clear supernatant (50 uL)** containing your purified cDNA library to PCR Tubes & Caps, RNase-free, 0.2 mL (8-strip format) **Thermo Fisher Catalog #AM12230** tube (use 10 µL pipet).

Beads that do not pellet can be pipetted for resuspension and then towards the magnet, and incubation continued until there are no more beads in the supernatant

62.1 Make immediately an aliquot for Bioanalyser analysis to prevent unnecessary freeze-thawing cycles.

63 ⏸

STOPPING POINT - Label and store at **-20 °C** for sequencing

cDNA library verification

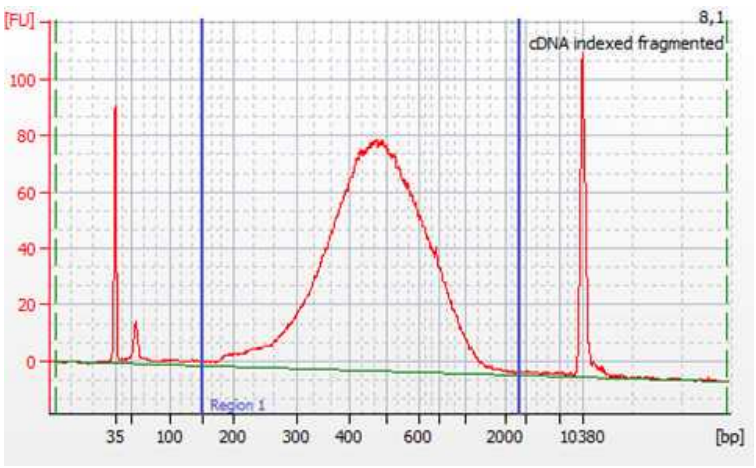


**Citation:** Joost Mansour, Konstantinos Anestis, Fabrice Not, Uwe John (06/30/2021). cDNA library preparation from total RNA extracts of Single-cell marine protists (e.g. Acantharia, Strombidium basimorphum, and Prymnesium parvum) for transcriptome sequencing. https://dx.doi.org/10.17504/protocols.io.bp7vmrn6

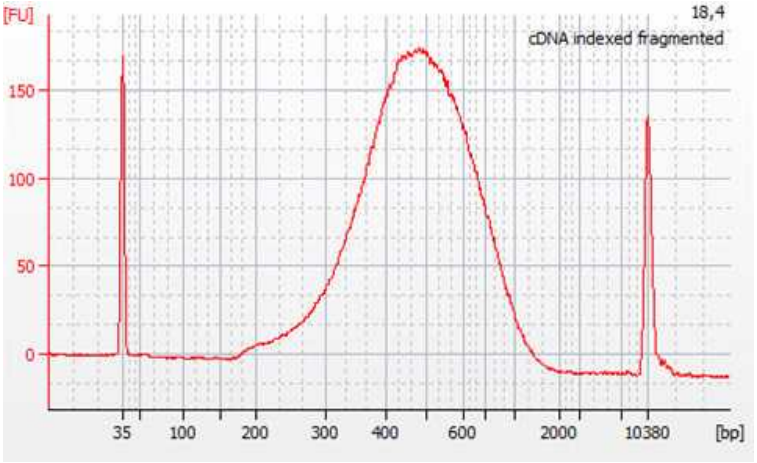
64

Check the quality of the cDNA libraries by

Agilent High Sensitivity DNA Kit **Agilent Technologies Catalog #5067-4626** following the manufacture's protocol. Alternatively, a Bioanalyser DNA 7500 Kit (Agilent #5067-1506) could be used as a more cost-efficient alternative and if sample concentration permitting. See for example the third graph.



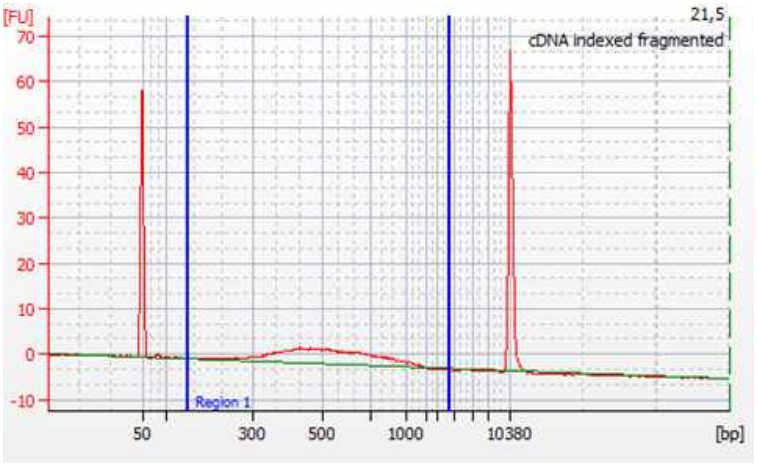

Example electrograph for a good cDNA library run with a Bioanalyser High Sensitivity DNA Kit (Agilent #5067-4626). Though primer-dimers are here still present and a follow up (repeat) cleaning is recommended. The region for smear analysis is indicated between blue lines. Example of an acantharian sample. The peaks on the outsides are markers.




Example electrograph for a desirable cDNA library run with a Bioanalyser High Sensitivity DNA Kit (Agilent #5067-4626). Example of an acantharian sample. The peaks on the outsides are markers.



**Citation:** Joost Mansour, Konstantinos Anestis, Fabrice Not, Uwe John (06/30/2021). cDNA library preparation from total RNA extracts of Single-cell marine protists (e.g. Acantharia, Strombidium basimorphum, and Prymnesium parvum) for transcriptome sequencing. https://dx.doi.org/10.17504/protocols.io.bp7vmrn6




Example electrograph for a desirable cDNA library run with a Bioanalyser DNA 7500 Kit (Agilent #5067-1506) instead of a Bioanalyser High Sensitivity DNA Kit (Agilent #5067-4626). This still allows for smear analysis though the concave parabola is less clear. This is more cost-effective than using a high sensitivity kit. Example of an acantharian sample The peaks on the outsides are markers.

64.1 Quantify and calculate the concentration of cDNA by smear analysis. This is needed for the normalization of samples for sequencing.

### 4.4.3 Follow up steps: library quality control; sample normalization/dilution and pooling for sequencing

65 The quality and quantity control of the generated cDNA libraries is performed using the Agilent High Sensitivity DNA kit (Agilent #5067-4626). In case primer-dimers or adapters are still present, an additional step of cleaning with magnetic beads is to be performed. A bead to sample ratio of 0.7:1 was found to be efficient in eliminating both primer dimers and remaining adapters.

The cDNA libraries are normalized to equal molarity, as well as fragment size before the final pooling and subsequent sequencing. Calculate nM cDNA of each sample as: nM DNA = [ng/µL] x $10^6$ / (660 x fragment length bp). Where the concentration in ng/µL and the average fragment length in base pairs are obtained from Bioanalyzer smear analysis.

The molarity upon which the cDNA libraries are normalized is determined based on the yield of cDNA, as well as the requirements for the subsequent sequencing (e.g. >0.5 nM). The final pool of all the samples should again be checked using the Bioanalyzer in order to verify that the normalization process was successful.

The pools are ready for Illumina sequencing.



**Citation:** Joost Mansour, Konstantinos Anestis, Fabrice Not, Uwe John (06/30/2021). cDNA library preparation from total RNA extracts of Single-cell marine protists (e.g. Acantharia, Strombidium basimorphum, and Prymnesium parvum) for transcriptome sequencing. https://dx.doi.org/10.17504/protocols.io.bp7vmrn6