DEC 04, 2017

🌐 Transcriptome sequencing of 19 diverse species of choanoflagellates

📖 eLife

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DOI:

dx.doi.org/10.17504/protocols.io.kwscxee

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Collection Citation: Daniel J. Richter, Parinaz Fozouni, Michael Eisen, Nicole King 2017. Transcriptome sequencing of 19 diverse species of choanoflagellates.

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<https://dx.doi.org/10.17504/protocols.io.kwscxee>

MANUSCRIPT CITATION:

Richter, Daniel J and Fozouni, Parinaz and Eisen, Michael and King, Nicole. Gene family innovation, conservation and loss on the animal stem lineage. 2018;7:e34226
<https://doi.org/10.7554/eLife.34226>

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Protocol status:

Working
This collection of protocols was successfully used to prepare high-quality mRNA sequencing libraries.

Created: Nov 21, 2017

Daniel J. Richter

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ABSTRACT

The origin of animals, which occurred over 600 million years ago, left no evidence in the fossil record. To trace the earliest events in animal prehistory, we compare extant animals to their closest living relatives, the choanoflagellates, in order to reconstruct the gene content of their last common ancestor and how it evolved on the stem lineage leading to animals. In this project, we increase the accuracy of ancestral animal and choanoflagellate gene content reconstructions by sequencing the transcriptomes of 19 species of choanoflagellates selected for their phylogenetic diversity.

Last Modified: Mar 24, 2018

COLLECTION integer ID:
8882

Keywords: choanoflagellates,
animal evolution, mRNA
sequencing, polyA selection,
RNAqueous, Illumina TruSeq

FILES

Protocol

NAME

Modified Qiagen gel extraction with MinElute spin column.

VERSION 1

CREATED BY

Daniel J. Richter Institute of Evolutionary Biology (CSIC-Universitat Pompeu Fabra)

[OPEN](#) →

Protocol

NAME

Modified Qiagen PCR purification (no gel extraction) with MinElute spin column.

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Protocol

NAME

Phenol/chloroform genomic DNA extraction-1.5 ml Eppendorf tube.

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Protocol

NAME

Lysis Buffer for Phenol/ chloroform genomic DNA extraction (makes 20 mL of buffer)

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Protocol

NAME

RNA clean-up by phenol:chloroform

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Protocol

NAME

RNAqueous with TURBO DNA-free and SUPERase-In

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Protocol

NAME

RNAqueous with No DNase, DNA Removal by Acid Phenol:Chloroform

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Protocol

NAME

RNAqueous with DNase Clean-up by Phenol:Chloroform

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Protocol

NAME

TruSeq RNA Preparation with Modification for Four Rounds of Poly-A Selection

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