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Transcriptome sequencing of 19 diverse species of choanoflagellates

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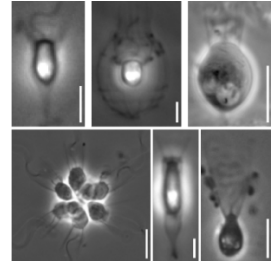
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Protocol status: Working

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

Created: November 21, 2017

Last Modified: March 24, 2018

Collection Integer ID: 8882

Keywords: choanoflagellates, animal evolution, mRNA sequencing, polyA selection, RNAqueous, Illumina TruSeq, diverse species of choanoflagellate, species of choanoflagellate, choanoflagellate, ancestral animal, accuracy of ancestral animal, animal prehistory, last common ancestor, earliest events in animal prehistory, phylogenetic diversity, origin of animal, evidence in the fossil record, extant animal, fossil record, transcriptome, stem lineage, gene content reconstruction, closest living relative, species, diverse species, gene content

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.

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

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