

# Sequencing and de novo assembly of the red cusk-eel (*Genypterus chilensis*) transcriptome

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© 2014 Elsevier B.V. The red cusk-eel (*Genypterus chilensis*) is an endemic fish species distributed along the coasts of the Eastern South Pacific. Biological studies on this fish are scarce, and genomic information for *G. chilensis* is practically non-existent. Thus, transcriptome information for this species is an essential resource that will greatly enrich molecular information and benefit future studies of red cusk-eel biology. In this work, we obtained transcriptome information of *G. chilensis* using the Illumina platform. The RNA sequencing generated 66,307,362 and 59,925,554 paired-end reads from skeletal muscle and liver tissues, respectively. De novo assembly using the CLC Genomic Workbench version 7.0.3 produced 48,480 contigs and created a reference transcriptome with a N50 of 846. bp and average read coverage of 28.3. x. By sequence similarity search for known proteins, a total of 21,272 (43.9%) contigs were annotated for their function. Out of these annotated contigs, 33.5% G