

Resource Summary Report

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Stranded Transcript Count Table Generation from Long Reads

DOI:10.17504/protocols.io.smuec6w

Type: Protocol

Proper Citation

David Eccles 2018. Stranded Transcript Count Table Generation from Long Reads.
protocols.io dx.doi.org/10.17504/protocols.io.smuec6w

Protocol Information

URL: <https://dx.doi.org/10.17504/protocols.io.smuec6w>

Authors: David Eccles

Group: High molecular weight DNA extraction from all kingdoms

Summary: This protocol is for comparing two different samples at the transcript level, using long reads that are mapped to transcripts. Input(s): stranded fastq files (see steps 1-8 of Stranded Mapping from Long Reads), transcript reference fasta file, annotation file Output(s): transcript table, sorted by differential coverage, annotated with gene name / description / location

Affiliations: Malaghan Institute of Medical Research (NZ)

Version: 1

Publication Date: 2018

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