

Resource Summary Report

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Stranded Transcript Count Table Generation from Long Reads

DOI:10.17504/protocols.io.xu4fnyw

Type: Protocol

Proper Citation

David Eccles 2019. Stranded Transcript Count Table Generation from Long Reads.
protocols.io dx.doi.org/10.17504/protocols.io.xu4fnyw

Protocol Information

URL: <https://dx.doi.org/10.17504/protocols.io.xu4fnyw>

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Summary: This protocol is for comparing different samples at the transcript level, using long reads that are mapped to transcripts. Input(s): demultiplexed fastq files (see protocol Demultiplexing Nanopore reads with LAST), transcript reference fasta file, annotation file Output(s): transcript table, sorted by differential coverage, annotated with gene name / description / location

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Version: 3

Publication Date: 2019

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