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UMN-Mouse-rnaSeq_skeletal_muscle

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Protocol status: Working
We use this protocol and it's working

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Abstract

Protocol for mouse rnaSeq for skeletal muscle

Troubleshooting

1 Description Source name Skeletal muscle Organism Mus musculus Characteristics stain: C57BL/6 age: 6 month Treatment protocol NA Growth protocol NA Extracted molecule total RNA

2 Process Extraction protocol Quadriceps muscle were collected in Trizol solution (Invitrogen, Carlsbad, CA, USA) and RNA isolation was performed following the instructions. cDNA libraries were prepared according to the manufacturer's instructions for the TruSeq Stranded mRNA Sample Prep Kit (Illumina, San Diego, CA). The concentration and size distribution of the completed libraries were determined using an Agilent Bioanalyzer DNA 1000 chip (Santa Clara, CA) and Qubit fluorometry (Invitrogen, Carlsbad, CA). Library strategy RNA-Seq Library source transcriptomic Library selection cDNA Instrument model Illumina HiSeq 4000

3 Data processing Base-calling was performed using Illumina's RTA version 2.7.7. Raw RNA sequencing paired-end reads were processed through the Mayo RNA-Seq bioinformatics pipeline, MAP-RSeq version 3.1.3. In this process, the fast, accurate and splice-aware aligner, STAR (v2.6.1c), was used to align reads to the reference mouse genome build mm10. Subsequently, gene and exon expression quantification was performed using the Subread featureCounts (v1.5.1) [3] package to obtain both raw and normalized (FPKM - Fragments Per Kilobase per Million mapped) reads. Genome_build: mm10 Supplementary_files_format_and_content: a table of raw counts of all samples

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