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Bulk tissue RNA-sequencing - hiPSC-derived astrocytes, neurons and co-cultures

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We use this protocol and it's working

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Abstract

Bulk tissue RNA-sequencing of hiPSC-derived astrocytes, neurons and co-cultures using the Illumina TruSeq Stranded mRNA Library Prep kit

Bulk tissue RNA-sequencing

1 Libraries for sequencing were prepared using the Illumina TruSeq Stranded mRNA Library Prep kit by loading 50 ng of total RNA into the initial reaction; fragmentation and PCR steps were undertaken as per the manufacturer's instructions.

2 Final library concentrations were determined using Qubit 2.0 fluorometer and pooled to a normalized input library.

3 Pools were sequenced using the Illumina NovaSeq 6000 Sequencing system to generate 150 bp paired-end reads with an average read depth of ~137 million paired-end reads per sample.