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

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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





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

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## **Bulk tissue RNA-sequencing**

- 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.
- 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.