Mar 19, 2022

Workflow for human placental bulk ATACseq

Scott Lindsay-Hewett[1], Valentina Stanley[1], Mana Parast[1], Louise Laurent[1]

[1]University of California, San Diego

1

dx.doi.org/10.17504/protocols.io.kxygxzyo4v8j/v1

Human BioMolecular Atlas Program (HuBMAP) Method Development Community
Tech. support email: **Jeff.spraggins@vanderbilt.edu**

Scott Lindsay-Hewett

Described here is the workflow used by the Female Reproductive Tissue Mapping Center at UCSD to generate bulk ATACseq data from human placenta.

DOI

dx.doi.org/10.17504/protocols.io.kxygxzyo4v8j/v1

Scott Lindsay-Hewett, Valentina Stanley, Mana Parast, Louise Laurent 2022. Workflow for human placental bulk ATACseq. **protocols.io** https://dx.doi.org/10.17504/protocols.io.kxygxzyo4v8j/v1

protocol ,

Mar 19, 2022

Mar 19, 2022

59632

See accompanying protocols.

Tissue preparation

1 As soon as possible after Cesarean section or vaginal delivery, prepare tissue according to the following protocol:

Human Placenta Tissue Collection and Preservation Methods - UCSD Female Reproductive TMC

For this protocol, use tissue that has been snap-frozen.

Nuclei isolation

2 Isolate nuclei from 4 samples at a time according to the following protocol:

Nuclei isolation from snap-frozen human placental tissue for bulk ATACseq

Proceed to tagmentation immediately.

Tagmentation and library generation

3 Perform tagmentation and library generation according to the following protocol:

Tagmentation and library generation for human placental bulk ATACseq

After passing quality control, proceed to sequencing.

Sequencing

4 For HuBMAP bulk ATACseq samples, the multiplexed pool was sequenced on a NovaSeq 6000 S4 lane using a 100bp paired-end run configuration. Alignment and peak-calling were performed using the ATAC-seq pipeline within the bcbio Python package.

Citation: Scott Lindsay-Hewett, Valentina Stanley, Mana Parast, Louise Laurent Workflow for human placental bulk ATACseq https://dx.doi.org/10.17504/protocols.io.kxygxzyo4v8j/v1