Workflow for bulk RNAseq of human placenta

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

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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 stored in RNAlater.

Total RNA isolation

2 Isolate total RNA using a bead beater to disrupt the tissue, followed by organic extraction and ethanol precipitation. Use the following protocol:

Total RNA extraction from frozen placenta tissue

After passing quality control, proceed to library construction.

Library construction

3 Construct libraries using the KAPA RNA HyperPrep Kit with RiboErase (HMR), according to the following protocol:

Library construction for human placenta bulk RNAseq

After passing quality control, proceed to sequencing.

Sequencing

4 For HuBMAP bulk RNAseq samples, the multiplexed pool was sequenced on a NovaSeq 6000 S4 lane using a 100bp paired-end run configuration. Reads were aligned using STAR, and transcript abundances were quantified using RSEM.

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