The RNA-seqlopedia – an overvie nd of the choices necessary to carry out a success periment

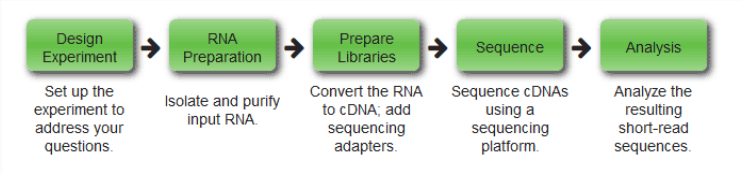
RNA-seq produces millions of sequences from complex RNA samples. With this powerful appr

1. Measure gene expression.
2. Discover and annotate complete transcripts.
3. Characterize alternative splicing and polyadenylation.

The RNA-seqlopedia provides an overview of RNA-seq and of the choices necessary to carry out a successful RNA-seq experiment.

RNA-seqlopedia is written by the Cresko Lab of the University of Oregon and was funded by grant R24 RR032670 (NIH, National Center for Research Resources).

A typical RNA-seq experiment consists of the following steps:



Each of the five chapters below are dedicated to one of these steps.

1. Experimental Design
2. RNA Preparation
3. Library Preparation
4. 4Sequencing
5. Analysis
6. References

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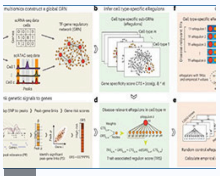

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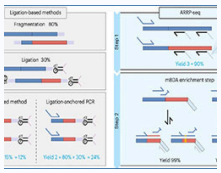

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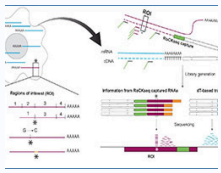

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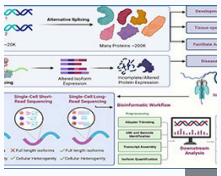

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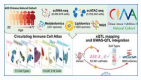

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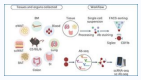

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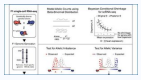

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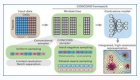
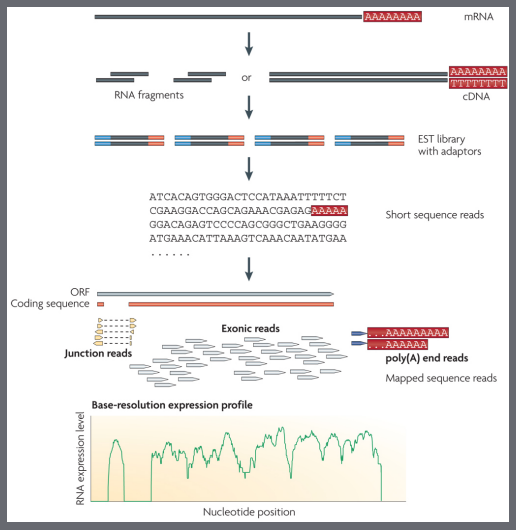


CONCORD – revealing a coherent cell-state landscape across single-cell datasets

WHAT IS RNA-SEQ?

long RNAs are first converted into a library of cDNA fragments through either RNA fragmentation or DNA fragmentation. Sequencing adaptors (blue) are subsequently added to each cDNA fragment and a short sequence is obtained from each cDNA using high-throughput sequencing technology. The resulting sequence reads are aligned with the reference genome or transcriptome, and classified as three types: exonic reads, junction reads and poly(A) end-reads. These three types are used to generate a base-resolution expression profile for each gene. Nat Rev Genet 10(1):57-63 (2009)



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