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RNAseq Analysis

1. Adjective _____
2. Verb - Base Form _____
3. Noun _____
4. Adjective _____
5. Noun _____
6. Adjective _____
7. Verb - Base Form _____
8. Noun _____
9. Noun _____
10. Noun - Plural _____
11. Noun _____
12. Adverb _____
13. Noun _____
14. Verb - Base Form _____
15. Verb - Present Ends In Ing _____
16. Noun - Plural _____
17. Noun _____
18. Adjective _____
19. Noun _____
20. Verb - Base Form _____
21. Noun - Plural _____
22. Noun _____
23. Verb - Base Form _____

24. Adjective _____

RNAseq Analysis

Anthony Hall already gave an _____Adjective_____ introduction to RNA-seq, so I will only _____Verb - Base Form_____ a brief review. RNA-seq refers to the _____Noun_____ of using _____Adjective_____ parallel sequencing to obtain global information on an RNA component from an _____Noun_____. This could be poly(A) RNA (representing mRNA), total RNA, _____Adjective_____ RNA, or some other fraction. Here we _____Verb - Base Form_____ on analysis of poly(A) RNA.

There are many questions that can be answered from RNA-seq data. RNA-seq data can be used to:

Determine which _____Noun_____ of a genome are expressed

Annotate a _____Noun_____

Find splice or alternative splice sites

Examine _____Noun - Plural_____ in expressed genes

Use de novo assembly in organisms with no _____Noun_____ to assemble a set of cDNAs.

Find genes that are _____Adverb_____ expressed between treatments, _____Noun_____, timepoints, etc.

This lab will _____Verb - Base Form_____ on differential expression and on polymorphism discovery.

_____Verb - Present ends in ING_____ RNA-seq data is an evolving field and there are no truly plug-and-play _____Noun - Plural_____. The basic steps are to:

Perform a quality control analysis of the _____Noun_____

Filter reads to remove:

o Reads of _____Adjective_____ quality

o Adapter contamination

o rRNA or other _____Noun_____

_____Verb - Base Form_____ reads to a reference genome or cDNA set.

Normalize read counts between _____Noun - Plural_____

Fit a statistical _____Noun_____ to _____Verb - Base Form_____ for genes that are significantly _____Adjective_____

expressed.

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