## 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 $\qquad$ introduction to RNA-seq, so I will only $\qquad$
a brief review. RNA-seq refers to the $\qquad$ of using $\qquad$ parallel
sequencing to obtain global information on an RNA component from an $\qquad$ . This
could be poly(A) RNA (representing mRNA), total RNA, $\qquad$ RNA, or some other
fraction. Here we $\qquad$ 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 $\qquad$ of a genome are expressed

Annotate a $\qquad$

Find splice or alternative splice sites

Examine $\qquad$ in expressed genes

Use de novo assembly in organisms with no $\qquad$ to assemble a set of
cDNAs.

Find genes that are $\qquad$ expressed between treatments, $\qquad$ ,
timepoints, etc.

This lab will $\qquad$ on differential expression and on polymorphism discovery.
$\qquad$ RNA-seq data is an evolving field and there are no truly plug-and-play
$\qquad$ . The basic steps are to:

Perform a quality control analysis of the $\qquad$

Filter reads to remove:
o Reads of $\qquad$ quality
o Adapter contamination
o rRNA or other $\qquad$
$\qquad$ reads to a reference genome or cDNA set.

Normalize read counts between $\qquad$

Fit a statistical $\qquad$ to $\qquad$ for genes that are significantly $\qquad$ expressed.
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