Clinical and Research Genomics Assignment #2

From Lecture_04-06 (March 29th):

RNA-Sequencing, Single-Cell Expression, Epitranscriptomes, and Gene Fusions

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Assignment: Answer questions about RNA-Sequencing and their methods
Due Date: 10:00AM on April 5th

This week has two sections. First, a True/False section and then an essay question.

(State whether the statement is true or false, then explain with one sentence).

1) There are 20 types of RNA present in cells.
2) Once spliced and 5' capped, an RNA is no longer modified.
3) Gene fusions identified by RNA sequencing always correspond to rearrangements in the DNA as well.

Essay Questions

1) If you were designing an experiment with RNA-Sequencing for each sample:
    a.) How much sequencing is required to assay each sample?
    b.) What are the parameters that affect this depth of sequencing?
    c.) How would you calculate an expression value?

2) Thought experiment. Imagine a cell with 20,000 genes expressed at varying levels, and you have sampled 40 million single-end reads from this sample. Given a measurement of genes X_1, X_2...$X_{20,000}$ at certain levels, what happens to these expression measurements if:
    a.) You double the sequencing depth of the sample?
    b.) You have paired-end instead of single-end reads?
    c.) If genes X_1-$X_{20,000}$ exist at the same levels, but then are present in a cell with an additional 10,000 genes, Y_1-$Y_{10,000}$.

3) What are some of the current functions and roles for the epitranscriptome?

Please hand the assignment on the day of the lecture, or email if you cannot attend.
For any questions, please contact Priyanka Vijay (prv2004@med.cornell.edu), Alexa McIntyre (abm237@cornell.edu), Ebrahim Afshinnekoo (eba2001@med.cornell.edu), or Professor Mason (chm2042@med.cornell.edu).