Clinical and Research Genomics Assignment #2

From Lecture_04-05 (March 16th):

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 March 23rd

This week has two sections: short-answer questions and a data exercise.

Reading and Problem Sets:
Chapters 7 and 8 from "Computational Genomics With R."
Chapter 7: http://compgenomr.github.io/book/processingReads.html
Chapter 8: http://compgenomr.github.io/book/rna-seq-analysis-overview.html
For more background information on genomics and R, see Chapters 1-4.

Questions:
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?

Please hand the assignment on the day of the lecture, or email if you cannot attend.
For any questions, please contact Chandrima Bhattacharya (chb4004@med.cornell.edu), Ebrahim Afshinnekoo (eba2001@med.cornell.edu), or Professor Mason (chm2042@med.cornell.edu)