Clinical and Research Genomics Assignment #5

From Lecture_16-17 (April 18th): Chromatin Accessibility and Noncoding Mutations in Cancer

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Assignment: Answer questions.
Due Date: 10:00AM on April 25th

1. What does ATAC-seq measure and when would you choose ATAC-seq over DNase-seq?

2. You are analyzing ATAC-seq data but your experimental collaborator does not appreciate diamond plots (see Leslie slides). Sketch out a proposed alternative to show log fold change of RNA expression and chromatin accessibility for multiple sites in multiple genes in a single plot.

3. Congratulations, your ATAC-seq analysis predicts an increase in accessibility at the promoter region of a transcription factor during tumor development! What does this suggest and how could you experimentally validate the finding?

4. Unfortunately, your proposed experiment fails to detect the effect under investigation. List five reasons this could have occurred.

5. How could a mutation in a noncoding, non-intronic, non-promoter, non-enhancer region increase oncogene expression?

6. Why study noncoding mutations rather than looking directly at gene expression?

7. How do germline mutations contribute to the development of cancer? Provide an example.

Please hand in the assignment on the day of the lecture or submit it by email beforehand to your TAs. For any questions, please contact Alexa McIntyre (abm237@cornell.edu), Ebrahim Afshinnekoo (eba2001@med.cornell.edu), or Professor Mason (chm2042@med.cornell.edu).