Clinical and Research Genomics Assignment #3

RNA-Sequencing, Epigenomes, DNA Modifications, and Chromatin Dynamics
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Assignment: Answer questions about epigenomics and DNA modifications
Due before April 22nd 5PM

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Epigenome and DNA Modifications

Analyze and Contextualize DNA Methylation data from a RRBS experiment

If you do not already have it installed, install the free statistical program R on your computer:
http://www.r-project.org/
You can use the slides on this blog to understand the algorithms that we have discussed in class:
http://zvfak.blogspot.com/2013/03/epiworkshop-2013-dna-methylation.html
If you have trouble getting the package for R from the tutorial, you can download it here:
http://code.google.com/p/methylkit/
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Utilize the tutorial to familiarize yourself with R and the program.
Then, from the test dataset within the package, your assignment is to:
1. Check if there is an indication of PCR bias in the experiment.
2. Calculate # of differentially methylated cytosines (DMCs)
3. Annotate the DMCs with genes and discuss implications of that annotation.
4. Check correlation between samples.
5. Cluster samples to see if replicates cluster together

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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), Evan Afshin (eba2001@med.cornell.edu), or Professor Mason (chm2042@med.cornell.edu)