**Homework for Epigenomics class**

1. Discuss the mechanisms by which epigenetic changes in gene expression occur. What are the different types and what types of enzymes are involved in the regulation of these changes.
2. List three methods for assaying DNA methylation and provide a brief description of each.
3. Describe how changes in histone modifications can be assayed from paraffin embedded tissue.
4. Discuss how epigenetic changes can be used as biomarkers in colon cancer. Include in your discussion, major points raised in your assigned readings.
5. Describe a method which can distinguish hydroxymethylated cytosines from methylated cytosines.
6. Explain how the BET-domain inhibitor, JQ1 can be used to selectively disrupt oncogenes.
7. Identify the cancer types with the most frequent mutations in the following epigenetic regulators and list the type of mutations:

(You can use the Cosmic database: <http://cancer.sanger.ac.uk/cell_lines/gene/analysis?ln=SMARCA4_ENST00000358026#dist> or any other databases.)

1. SMARCA4
2. ARID2
3. EZH2
4. SMARCB1
5. TET2
6. DNMT1
7. List atleast one cancer type that exhibits aberrant expression of the epigenetic regulators in question 7. (You can use Oncomine <https://www.oncomine.org/resource/login.html>
8. or GEO Profiles <http://www.ncbi.nlm.nih.gov/pubmed?holding=ohiolinklib,mcolib_fft,f1000&otool=ohiolink> . Make sure you reference the study