WEEK 4 ASSIGNMENT

Introduction to Computational Biology – BIOL 509000 | Fall 1 2020

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Question #1: Of the different histone modifications, how many involve the addition of one or more acetyl groups to the histone? How many involve the addition of one or more methyl groups to the histone?

Three (3) histone modifications involve the addition of one or more acetyl groups to the histone: H3ac, H3K27ac, H3K9ac.
Eight (8) histone modifications involve the addition of one or more methyl groups to the histone: H3K27me3, H3K36me3, H3K4me1, H3K4me2, H3K4me3, H3K79me2, H3K79me3, H3K9me3.

Question #2: What is the role of transcription factor CTCF in gene expression? Is it an activator, repressor or both? Explain.

CTCF is a zinc finger transcription factor that can act both as an activator and repressor. Depending on the cellular context, it can bind a histone acetyltransferase (HAT)-containing complex and function as transcriptional activator or bind a histone deacetylase (HDAC)-containing complex and function as transcriptional repressor.

Question #3: Does H3K4me3 seem to align with the beginning, the end, or the entire length of Ccnd1?

Since the *Ccnd1* gene is encoded on the minus strand, the H3K4me3 marks align predominantly with the beginning (exon 1, intron 1 and exon 2 and intron 2) of the gene (see Fig. 1).

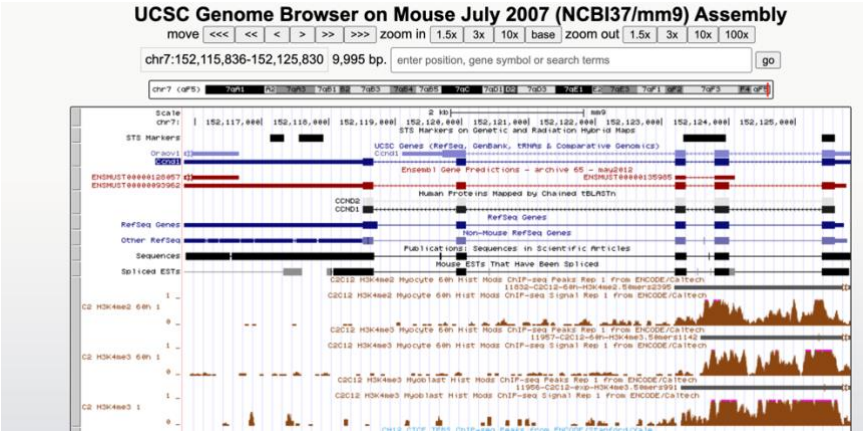

Figure 1. *Ccnd1* and associated H3K4me3 histone marks.

Question #4: Does there seem to be robust H3K27me3 histone modification along the length of this gene, or is it largely missing?

There is no H3K27m3 histone modification track (see Figure 1). Therefore, I assume that these marks are largely missing for *Ccnd1*.

Question #5: How many major peaks do you see for CTCF along the length of Ccnd1? These peaks should be higher than the surrounding (largely negative) regions.

The transcription factor CTCF has 4 major peaks along *Ccnd1*.

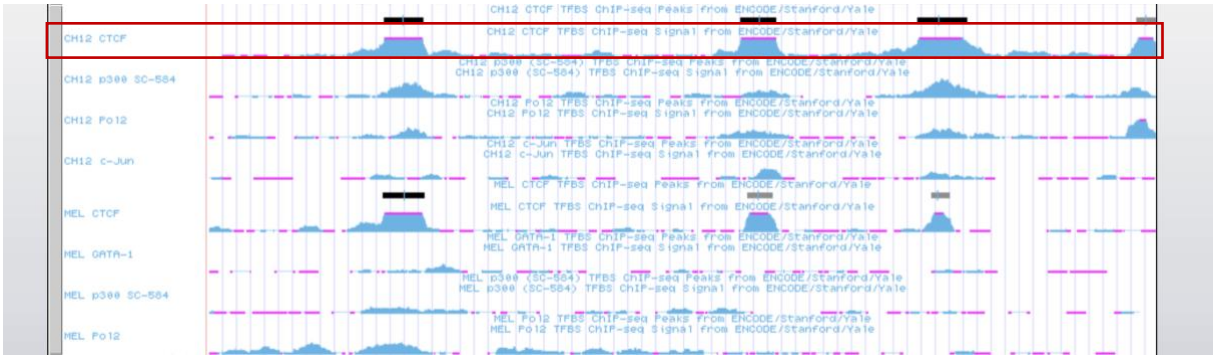

Figure 2. Transcription factor tracks for *Ccnd1*.

Question #6: How many DHS sites (number of bars) are found within Ccnd1?

There have been 6 DHS sites reported for *Ccnd1*.

Figure 3. DHS sites (grey bars) found within *Ccnd1*.

Question #7: Do DHS sites represent portions of the gene where the DNA is or is not tightly associated with histones (is the DNA considered "open" or "closed"?)

The DNaseI-hypersensitive (DHS) sites correspond to open DNA conformation. These sites are sensitive to DNaseI treatment due to an accessible chromatin and correspond to active regulatory sequences.

Question #8: Now search for the gene Ccnd2. How many DHS sites are found in the length of this gene?

The *Ccnd2* gene contains three DHS sites.

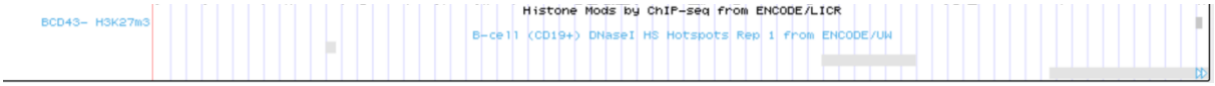

Figure 4. DHS sites (grey bars) found within *Ccnd2*.

Question #9: Finally, search for the gene Ccnd3. How many DHS sites are reported for the length of this gene? Consider the RefSeq gene listing for transcript variant 1. Does H3K4me3 seem to align with the beginning, the end, or the entire length of Ccnd3?

For the length of the *Ccnd3* gene, there have been five DHS sites reported.

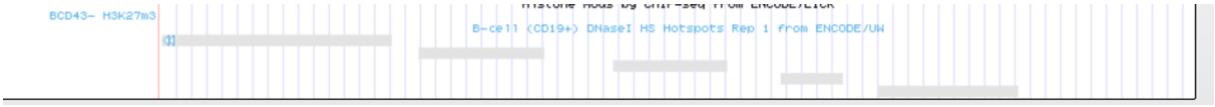

Figure 5. DHS sites (grey bars) found within *Ccnd3*.

H3K4me3 methylation is reported for the beginning of the *Ccnd3* gene which is encoded on the plus strand.

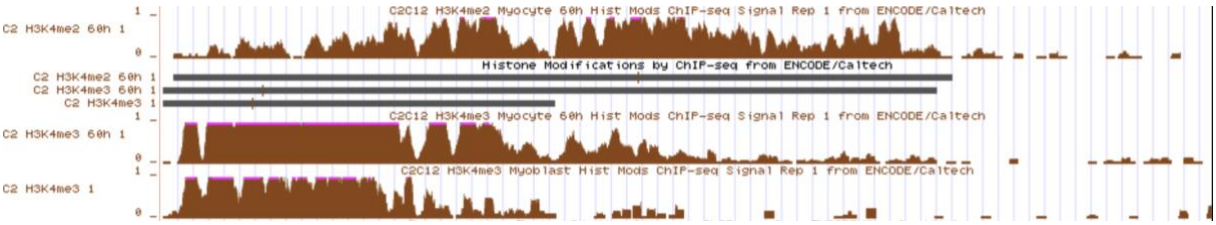

Figure 6. H3K4me3 methylation along *Ccnd3*.