## Poster M-9

**Bioinformatics analysis on ChIP-on-chip data to survey global RNA pol II binding and histone H3 acetylation patterns and the effects induced by HDAC inhibition**


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**Short Abstract:** This poster will present our strategy to analyze data from a ChIP-on-chip experiment, a technology to study the binding status of a protein to DNA. The association of acetylated histone H3 and RNA polymerase II to human promoter regions under normal and HDAC inhibitor treated conditions will be reported.

**Long Abstract:**

Eukryotic chromosomes exist in a highly compact state called chromatin. To facilitate the formation and maintenance of chromatin, DNA is associated with various proteins, including histones. A nucleosome is created from a histone octomer which serve as a core for DNA wrapping. Histones can be posttranslationally modified. One of the best known modifications is histone acetylation, carried out by histone acetyltransferases. To counteract, histone deacetylases (HDACs) remove acetyl groups from acetylated histones. Acetylated and deacetylated histones are known to be coupled with transcription activation and repression, respectively, probably by controlling the accessibility of transcription factors and members of the transcription machinery to DNA.

To study the relationship among histone acetylation, RNA polymerase II binding and transcript levels on a genome scale, we have undertaken a study to investigate the global, genome wide binding patterns of RNA polymerase II and acetylated histone H3 (Lys9/14) and connect these binding patterns to gene expression data. And for the first time, the effects of an HDAC inhibitor (HDACI) on these association patterns were studied. In this study, we utilized the ChIP-on-chip technology, which examines the association status of a particular protein with DNA. The microarray (Hu19k) used in our study contains roughly 19k probes and covers about 13k human genes, mostly promoter regions. Due to the large amount of data accumulated in the study, a systematic approach was needed to guide data mining efforts. This poster will detail, step-by-step, our analysis strategy to perform binding strength calculations tailored for RNA pol II and acetylated histone H3, to classify binding sites in the context of gene structure and to identify relationships between binding and gene functions and transcript levels. We discovered that RNA pol II and acetylated histone H3 were associated with a similar set of promoters and both RNA pol II binding and histone acetylation status showed positive correlations with transcript levels. We will describe the primary effects of LAQ824, a potent HDAC pan-inhibitor, on the status of RNA pol II binding

and histone acetylation and propose a potential mechanism through which LAQ824 could influence different sets of promoters/genes in different cell types and elaborate how our findings could explain the different effects observed in different cell types upon HDACI treatment.