



Studies of promoter and enhancer usage for medical applications



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Cellular response to biological stimulus requires coordinated induction of genes, facilitated by dynamic regulation of promoters and enhancers. Exploiting the fact that active promoters and enhancers are transcribed and can be measured in the same experiment using Cap Analysis of Gene Expression (CAGE), we have measured enhancer and promoter usage in a large number of systems undergoing state change (differentiation, development, response to activators, growth signals, small molecules or pathogens) in order to expose common mechanisms in transitioning cells. A key observation is that enhancers are often among the earliest elements to respond to stimulus, prompting us to further analyze dynamic enhancers for function relevant to disease. Focusing on adipogenesis and its link to obesity related traits, we identified groups of transcription factors, enhancers and non-coding RNAs with distinct expression patterns during adipocyte formation, and could link specific transcript groups to hypertrophic adipose tissue, which in turn is strongly linked to type 2 diabetes and insulin resistance. We also identified enhancers active during adipogenesis that overlapped with genetic variants associated with adipose tissue distribution, and went on to characterize one such enhancer and its role in adipocyte formation, showing that the enhancer was activated by insulin and that disrupting it decreased adipogenesis, thus providing a likely causal effect of the genetic variant in the locus. Finally, in another application we analyze large scale data on transcriptional response after drug treatment, and use this Information to predict combinations of drugs that facilitate cell conversion.