Deregulation of Histone Modification Associates to Alternative Splicing of Developmental Genes

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Alternative exon usage is known to affect a large portion of genes in mammalian genomes. Importantly, different splice forms sometimes lead to distinctly different protein functions. We analyzed data from the Human Epigenome Atlas (version 9) whereby we connected the differential usage of exons in various developmental stages of human cells/tissues to differential epigenetic modifications at the exon level. In total, we analyzed 19 different human tissues in adult and cultured cells that mimic early developmental stages. We found that the differential incidence of protein isoforms across developmental stages was often associated with changes in histone marks at exon boundary regions. Many of those genes that are differentially regulated at the exon level were found to be functionally associated with development and metabolism. We concluded that the analysis pipeline was suitable for providing a mechanistic view to cell reprogramming events at molecular level that is meaningful for the study of cell identity, differentiation, and development.