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Selected Publication

Leung D. et al. (2015) Integrative analysis of haplotype-resolved epigenomes across human tissues. *Nature* 518, 350–354.

Research Aims and Interests

Allelic differences between the two homologous chromosomes can affect the propensity of inheritance in humans; however, the extent of such differences in the human genome has yet to be fully explored. Here we delineate allelic chromatin modifications and transcriptomes among a broad set of human tissues, enabled by a chromosome-spanning haplotype reconstruction strategy. The resulting large collection of haplotype-resolved epigenomic maps reveals extensive allelic biases in both chromatin state and transcription, which show considerable variation across tissues and between individuals, and allow us to investigate *cis*-regulatory relationships between genes and their control sequences. Analyses of histone modification maps also uncover intriguing characteristics of *cis*-regulatory elements and tissue-restricted activities of repetitive elements. The rich data sets described here will enhance our understanding of the mechanisms by which *cis*-regulatory elements control gene expression programs.