

## Landscaping the epigenome by histone variants

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**Abstract:** In addition to histone modification and DNA methylation, chromatin composition varies with localized enrichment in variant of H3 and H2A core histones. We are studying the function and properties conferred by these variants to nucleosomes and specific domains of chromatin. Patterns of gene expression through the cell cycle requires prompt restoration of epigenetic marks after the dilution caused by DNA replication. We showed that the variant H3.1 is essential for maintenance and propagation of the transcriptional repressive mark histone H3 lysine 27 trimethylation (H3K27me<sub>3</sub>), illustrating the important role played by histone variants in epigenetic regulation of transcription (Jiang and Berger, 2017). New data will be presented on the role of H3 variants in reprogramming transcription.