



CDB SEMINAR

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Monday, January 15, 2007

16:00~17:00 A7F CDB Conference Room

Genome-wide profiling of histone H3.3 replacement patterns

Summary

Chromatin assembly occurs primarily during DNA replication, but at other times the histone H3.3 variant is assembled into chromatin, replacing canonical H3. Genome-wide high-resolution profiling of histone H3.3 replacement patterns in *Drosophila melanogaster* revealed that H3.3 replacement occurs prominently at sites of abundant RNA polymerase II and methylated H3 lysine-4 throughout the genome, suggesting that H3.3 replacement is correlated with transcriptional activity. The deposition and inheritance of actively modified H3.3 in transcriptionally active regions might facilitate maintaining active chromatin. Our genome-wide profiling of H3.3 replacement and nucleosome occupancy patterns also suggests that a process that replaces histones maintains continuous accessibility of cis-regulatory elements and facilitates epigenetic regulation.

Reference:

Mito Y, Henikoff JG, Henikoff S. *Nat Genet* 37:1090-7 (2005)

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