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Genome-wide Nucleosome Occupancy and Depletion at Active Loci

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Nucleosomes are the fundamental repeating unit of chromatin, and are constantly undergoing remodeling events. Relative occupancy of core histones (histones H3 and H4) was measured throughout the *Saccharomyces cerevisiae* genome using chromatin immunoprecipitation (ChIP) coupled with detection using DNA microarray composed of 0.9 kb tiling fragments of yeast genomic elements. The results showed that nucleosome occupancy is generally higher in coding regions than non-coding regions. During rapid mitotic growth, nucleosomes are specifically disrupted at the promoters of transcriptionally active genes. Alterations in the global transcriptional program caused by heat shock or a change in carbon source resulted in recovery nucleosome occupancy at repressed promoters, and a decreased nucleosome occupancy at promoters that became active. It was previously observed that if formaldehyde-fixed chromatin from yeast was subjected to standard phenol-chloroform extraction, non-coding sequences were recovered in the aqueous phase with much greater efficiency than coding sequences. The observed enrichment is strongly and inversely correlated with the histone ChIP data. This simple chromatin fractionation method may have applications in the isolation and identification of mammalian regulatory elements.

References

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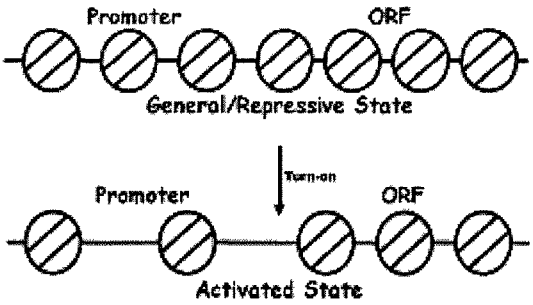

Figure. The genome-wide nucleosome occupancy is heterogeneous. Once a gene is turned-on, nucleosomes are disrupted in active loci. The data suggest two possible mechanisms for differential nucleosome occupancy, a mechanism coupled to transcriptional activity and an intrinsic difference in the ability to load or retain nucleosomes at coding and non-coding regions.