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^{OA}Open Access paper.



Cover A distribution of short reads from high-throughput DNA sequencing combined with chromatin immunoprecipitation (ChIP) can reveal positions of nucleosomes on a genome-scale. In this issue, positions of nucleosomes containing the H2A.Z histone variant or H3 tri-methylation at lysine 4 were identified from ChIP-sequencing data. Analysis of the nucleosomal sequences highlights the differences in nucleosome positioning mechanisms between yeast and human and suggests a novel mechanism for organization of H2A.Z nucleosomes. (Cover illustration by Peter Park, Michael Tolstorukov, and Wonyeop Seok. [For details, see Tolstorukov et al., pp. 967–977.]