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In the news

A DISTINCT HUMAN SIGNATURE

A distinct chromatin modification — trimethylation of Lys4 in histone H3 — marks gene promoters, whereas monomethylation of the same residue identifies enhancers, reports a *Nature Genetics* paper.

Previous work has shown that modified histone modifications are associated with transcription-associated regulatory elements. In yeast, flies and mice, active promoters are often marked by trimethylation of a Lys residue in histone H3. Now, Bing Ren and colleagues at the University of California, San Diego, USA, looked systematically for this mark in the human genome.

They used chromatin immunoprecipitation and microarray experiments to analyse the chromatin architecture of ~1% of the human genome, and found that, just as in other species, transcriptional start sites of active promoters were strongly marked by trimethylation of histone H3 Lys4. By contrast, regions likely to be enhancers were monomethylated on the same residue.

“This is the first time that we’ve discovered a histone modification mark that is different between enhancers and promoters. The promoter signature is consistent with previous findings in other organisms, but the enhancer-specific marks are novel”, said Ren (*The Scientist*, 5 Feb 2007).

The study also showed that, similarly to yeast and flies, active human promoters contain nucleosome-free regions at transcriptional start sites. “Because we were actually looking at 38-base pair resolution, we were able to identify these very distinct nucleosome-free regions at active promoters”, said Nathaniel Heintzman, the first author of the study (*The Scientist*, 5 Feb 2007).

The mechanisms underlying these distinct signatures and how these relate to control of gene expression remain to be determined.

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