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HaploCHIPs

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The majority of single nucleotide polymorphisms (SNPs) are found in non-coding DNA and there is often no way to predict their functional significance. In an Advanced Online Publication in Nature Genetics Julian Knight and colleagues at the Wellcome Trust Centre for Human Genetics in Oxford, UK, describe an approach, dubbed HaploCHIP, which uses haplotype-specific chromatin immunoprecipitation (CHIP) to detect differences in the amount of phosphorylated RNA polymerase II (Pol II) bound to different alleles (*Nature Genetics,* 10 March 2003, DOI:10.1038/ng1124). Knight *et al.* tested the HaploCHIP method by studying the imprinted gene *SNRPN*, encoding the small nuclear ribonucleoprotein polypeptide N. CHIP with antibodies against the phosphorylated Pol II protein could distinguish between transcriptional activation of the two *SNRPN* alleles. For accurate and sensitive detection of the relative abundance of the two different alleles they used primer extension and MALDI-TOF mass spectrometry. The HaploCHIP approach revealed a correlation between haplotypes and gene expression at the *TNF*/*LTA* locus *in vivo*. This strategy could be scaled-up for high throughput analysis of other DNA-protein interactions affecting allele-specific expression.

References

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3. Phosphorylation of RNA polymerase II C-terminal domain and transcriptional elongation.