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Nitrogen depletion in the fission yeast *Schizosaccharomyces pombe* causes nucleosome loss in both promoters and coding regions of activated genes

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Methods and Resources

Methods

Inference of RhoGAP/GTPase regulation using single-cell morphological data from a combinatorial RNAi screen

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Genome-wide discovery of human heart enhancers

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Population differentiation as a test for selective sweeps

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^{OA}Open Access paper.



Cover Combinations of sequence motifs identified by computational machine learning approaches guide the de novo discovery of tissue-specific regulatory elements in the human genome. Transgenic mouse hearts are stained blue when predicted cardiac regulatory elements demonstrate enhancer properties in vivo. (Cover illustration by Bang Wong, ClearScience, <http://www.clearscience.info>. [For details, see Narlikar et al., pp. 381–392.]