# IN BRIEF

## HUMAN DISEASE

### Pathogenic conversions

The authors have investigated the deleterious impact of interlocus gene conversion (IGC) — that is, non-reciprocal recombination between paralogous sequences — in inherited human disease. A genome-wide computational approach carried out on >60,000 known disease mutations in >3,000 genes showed that ~1% of these genes contained pathological mutations resulting from IGC. Thousands of putatively deleterious mutations were also detected, which is unsurprising, given the high number of paralogous sequences that can act as donors in IGC events.

**ORIGINAL RESEARCH PAPER** Casola, C. *et al.* Interlocus gene conversion events introduce deleterious mutations into at least 1% of human genes associated with inherited disease. *Genome Res.* 16 Nov 2011 (doi:10.1101/gr.127738.111)

## FUNCTIONAL GENOMICS

### Predicting phenotype from genotype in yeast

In this study, *Saccharomyces cerevisiae* was used to develop a method for predicting phenotype from genomic sequence. The phenotypic impact of sequence polymorphisms found in 19 strains was predicted computationally based on functional information and data from reverse genetic screens. Strains were ranked with respect to the likelihood of being affected for a particular phenotype; these predictions were then tested by assessing the growth rate and efficiency of 15 strains grown under 20 conditions. Predictions were highly accurate, especially for gene sets that were functionally connected.

**ORIGINAL RESEARCH PAPER** Jelier, R. *et al.* Predicting phenotypic variation in yeast from individual genome sequences. *Nature Genet.* **43**, 1270–1274 (2011)

## TRANSCRIPTION

### Nucleosome fate influenced by RNA polymerase

Direct visualization of yeast RNA polymerase II (RNAPII) and nucleosomes using atomic force microscopy allowed these authors to discover what happens to nucleosomes when they are transcribed. They identified DNA loops that could transfer a nucleosome from downstream to upstream of RNAPII and found that transcription triggers partial dissociation of the histone octamer into a hexamer. The speed of transcription influenced the proportion of histones that became hexamers remained as octamers or, alternatively, were completed removed from the DNA.

**ORIGINAL RESEARCH PAPER** Bintu, L. *et al.* The elongation rate of RNA polymerase determines the fate of transcribed nucleosomes. *Nature Struct. Mol. Biol.* 13 Nov 2011 (doi:10.1038/nsmb.2164)

## GENE REGULATION

### Polycomb and non-coding RNA relocate genes

This study reveals the coordinated action of several modes of transcriptional regulation. The authors found that, in mammals, growth signals alter the methylation of Polycomb 2 protein (PC2), and this leads to the relocation of genes bound by PC2 from repressive Polycomb bodies to transcriptionally active interchromatin granules, or vice versa. They show that this movement is a consequence of methylation altering the binding of PC2 to specific non-coding RNAs that are located in these nuclear compartments.

**ORIGINAL RESEARCH PAPER** Yang, L. *et al.* ncRNA- and Pc2 methylation-dependent gene relocation between nuclear structures mediates gene activation programs. *Cell* **147**, 773–788 (2011)