IN BRIEF

GENE REGULATION

Human-specific gain of function in a developmental enhancer.

Prabhakar, S. *et al. Science* **321**, 1346–1350 (2008)

Shadow enhancers as a source of evolutionary novelty.

Hong, J.-W., *et al. Science* **321**, 1314 (2008)

These papers combined bioinformatics and experimental biology to find and characterize enhancer sequences. Prabhakar and colleagues identified a highly conserved non-coding region that diverged rapidly between humans and chimps. The human sequence drives limb-specific expression in mice, suggesting that it mediated human hand or foot specializations. Using chromatin immunoprecipitation combined with microarray (ChIP–chip) analysis, Hong and colleagues identified enhancers containing binding sites for the Dorsal transcription factor in the fly genome. Although they are functionally equivalent, distant 'shadow' enhancers evolve more rapidly than gene-proximal ones, suggesting that the former are substrates for adaptive tinkering.

HUMAN GENOMICS

A common sequence motif associated with recombination hot spots and genome instability in humans.

Myers, S. *et al. Nature Genet.* **40**, 1124–1129 (2008)

This paper provides the first evidence that many human meiotic recombination events involve a common mechanism. Taking advantage of the increased information about human recombination from phase 2 of the HapMap project, the authors identified a 13-mer degenerate sequence that is crucial for crossing over for at least 40% of recombination hot spots. This motif also seems to drive genomic instability at some hypervariable minisatellites and at hot spots for disease-causing non-allelic homologous recombination and mitochondrial deletion.

DEVELOPMENT

The NDR/LATS family kinase Cbk1 directly controls transcriptional asymmetry.

Mazanka, E. *et al. PLoS Biol.* **6**, e203 (2008)

These authors have found a new mechanism by which mother and daughter cells acquire different fates in *Saccharomyces cerevisiae*. The distribution of the transcriptional regulator Ace2 changes from uniform to asymmetric during cell division owing to phosphorylation by the protein kinase Cbk1, which causes Ace2 to become trapped in the daughter nucleus and leads to different gene expression programmes in mother and daughter cells.

GENOMICS

Rapid whole-genome mutational profiling using next-generation sequencing technologies.

Smith, D. R. *et al. Genome Res.* 4 Sep 2008 (doi 10.1101/gr.077776.108)

The authors evaluate the utility of next-generation sequencing technologies for identifying mutations. Three sequencing platforms were tested on an engineered strain of the yeast *Pichia stipitis*. With 10–15-fold genome coverage, all three platforms could accurately identify nucleotide variations between the mutant and reference sequence, but deeper coverage will be needed to profile diploid organisms.