IN BRIEF

GENOME BIOLOGY

Genome-wide characterization of centromeric satellites from multiple mammalian genomes

Alkan, C. *et al. Genome Res.* 16 Nov 2010 (doi:10.1101/gr.111278.110)

Because centromeres have such a complex repeat structure, their assembly and annotation has lagged behind that of other genomic sequences. The authors present an algorithm (RepeatNet) for predicting, identifying and isolating tandem repeat structures from whole-genome shotgun sequence data. RepeatNet identified and confirmed candidate monomer satellite repeats from five out of six mammalian genomes. This tool will be useful for annotating the centromeres of other vertebrates.

GENE EXPRESSION

Global analysis of nascent RNA reveals transcriptional pausing in terminal exons

Oesterreich, F. C., Preibisch, S. & Neugebauer, K. M. *Mol. Cell* **40**, 571–581 (2010)

Splicing-dependent RNA polymerase pausing in yeast

Alexander, R. D. *et al. Mol. Cell* **40**, 582–593 (2010)

Spliceosomes can assemble on precursor mRNA during transcription, but does splicing occur co-transcriptionally? Oesterreich and colleagues show that splicing occurs co-transcriptionally for most intron-containing genes in *Saccharomyces cerevisiae*, as RNA polymerase pausing at terminal exons provides time for splicing to occur. The kinetic analysis by Alexander and colleagues shows that the pause, at 3′ splice sites, depends on a checkpoint imposed by productive splicing.

CANCER GENOMICS

Deep-sequencing identification of the genomic targets of the cytidine deaminase AID and its cofactor RPA in B lymphocytes

Yamane, A. *et al. Nature Immunol.* 28 Nov 2010 (doi:10.1038/ni.1964)

The cytidine deaminase AID facilitates immune-system diversity by hypermutating immunoglobulin genes. Here, ChIP–seq mapping in human B cells showed that AID interacts with thousands of promoter-proximal regions in non-immunoglobulin genes. AID binding is associated with stalled RNA polymerase II, which is required for AID recruitment. These findings explain the genomic instability that occurs following prolonged or abnormal AID expression.

DNA FORENSICS

Estimating human age from T-cell DNA rearrangements

Zubakov, D. *et al. Current Biol.* **20**, R970–R971 (2010)

This paper describes a method for predicting the age of an individual from human blood. During immune system development, the rearrangement of T cell receptor loci produces episomal DNA molecules, the levels of which are known to decrease with age. Zubakov and colleagues show that quantification of these molecules by PCR can accurately predict the age of a sample donor, even with degraded or very small samples. This approach should be useful for identifying disaster victims or providing leads from crime scenes.