IN BRIEF

GENE REGULATION

Surveying non-specific binding

The binding of proteins to nucleic acids through interactions that do not involve specific DNA or RNA sequence motifs is likely to have widespread functional consequences but it has not been broadly characterized. These authors developed a method that uses affinity purification mass spectrometry to identify such interactions. They used oligonucleotide probes that were designed as 'generic nucleic acids' and identified interacting proteins from human cells. This approach identified 746 proteins with high confidence, a large proportion of which were not previously known to bind nucleic acids.

ORIGINAL RESEARCH PAPER Dürnberger, G. *et al.* Experimental characterization of the human non-sequence-specific nucleic acid interactome. *Genome Biol.* **14**, R81 (2013)

GENOMICS

Filling gaps in the human genome

The physical map of the human genome is incomplete owing to difficulties in cloning and assembling some regions — a problematic situation given that many unlocalized regions contain genes. This study uses a method in which patterns of genetic variation in genomes from admixed populations can be used to determine the genomic locations of 'missing' regions. The authors find that using Latino genomes, in which ancestry is derived from three or more continents, is a powerful approach: it allowed them to localize almost 20 Mb of unmapped sequence.

ORIGINAL RESEARCH PAPER Genovese, G. *et al.* Mapping the human reference genome's missing sequence by three-way admixture in Latino genomes. *Am. J. Hum. Genet.* http://dx.doi.org/10.1016/j.ajhg.2013.07.002 (2013)

DEVELOPMENT

Order from chaos for transcription

For a given gene, there is typically great intercellular variability in transcriptional activity among genetically identical cells. How can this noise be compatible with the precise expression patterns underlying coordinated cell fate changes during development? Little *et al.* used quantitative fluorescence microscopy to analyse the expression of four patterning genes in *Drosophila melanogaster* embryos at the syncytial (multinuclear) stage. They found that despite high noise levels in transcriptional activity, subsequent cytoplasmic diffusion and accumulation of the resultant mRNAs and proteins provided a form of spatiotemporal averaging to account for the observed precise expression patterns.

ORIGINAL RESEARCH PAPER Little, S. C., Tikhonov, M. & Gregor, T. Precise developmental gene expression arises from globally stochastic transcriptional activity. *Cell* **154**, 789–800 (2013)

EPIGENETICS

An economical route to DNA methylation profiling

Stevens *et al.* sought a cost-effective alternative to whole-genome bisulphite sequencing (WGBS) for a high-resolution, whole-genome characterization of DNA methylation. They devised a statistical algorithm for combining DNA methylation data from two relatively economical methods based on methylated DNA immunoprecipitation (MeDIP–seq) or methylation-sensitive restriction enzymes (MRE–seq). This method, termed methylCRF, showed comparable resolution, coverage and accuracy to WGBS at <10% of the cost.

ORIGINAL RESEARCH PAPER Stevens, M. *et al.* Estimating absolute methylation levels at single-CpG resolution from methylation enrichment and restriction enzyme sequencing methods. *Genome Res.* **23**, 1541–1553 (2013)