IN BRIEF

GENOME ENGINEERING

Synthetic genome technology for yeast

The authors have constructed a synthetic chromosome arm of the yeast *Saccharomyces cerevisiae*, laying the groundwork for creating a synthetic eukaryotic genome. A ~90 kb stretch of the right arm of chromosome IX was designed *in silico* to remove unstable elements such as transposons and to facilitate genome manipulations. The synthetic sequence, which was swapped into the endogenous genomic region, also contains an inducible evolution system, SCRaMbLE (synthetic chromosome rearrangement and modification by *loxP*-mediated evolution), which triggers combinatorial rearrangements to allow the study of complex phenotypes.

ORIGINAL RESEARCH PAPER Dymond, J. S. *et al.* Synthetic chromosome arms function in yeast and generate phenotypic diversity by design. *Nature* **477**, 471–476 (2011)

GENE EXPRESSION

Mapping QTLs for genomic stochastic noise

A QTL mapping study in *Arabidopsis thaliana* reveals both the extent to which stochastic noise in gene expression is genetically controlled and the genomic distribution of the variants. The authors mapped polymorphisms underlying stochastic noise in the accumulation of a class of plant defence metabolites and in related transcripts, and they identified noise QTLs that specifically influence transcript or metabolite levels. Similarly, at the whole-transcriptome level, the authors identified QTLs that are responsible for genome-wide stochastic noise that were distinct from those controlling average transcript levels.

ORIGINAL RESEARCH PAPER Jimenez-Gomez, J. M. *et al.* Genomic analysis of QTLs and genes altering natural variation in stochastic noise. *PLoS Genet.* **9**, e1002295 (2011)

TRANSCRIPTOMICS

Measuring gene expression in non-model organisms

This paper describes a high-throughput method for quantifying gene expression in non-model organisms. The new approach — *EcoP151*-tagged digital gene expression (EDGE) — uses a unique tag for each expressed transcript, levels of which are determined from the number of high-throughput sequencing reads for each tag. This method avoids the need for a high-quality reference genome, as required for RNA sequencing (RNA-seq). A validation study showed that EDGE compares favourably to RNA-seq in terms of measuring transcript abundance.

ORIGINAL RESEARCH PAPER Hong, L. Z. *et al.* Digital gene expression for non-model organisms. *Genome Res.* 15 Aug 2011 (doi:10.1101/gr.122135.111)

STEM CELLS

Splicing switch is key to pluripotency

Using human and mouse embryonic stem cells (ESCs), these authors identified an alternatively spliced isoform of the transcription factor FOXP1 that is specific to ESCs and regulates pluripotency. The splicing event alters FOXP1 DNA binding, and this in turn promotes the expression of several transcription factors that are essential for pluripotency. The FOXP1 splice isoform also stimulates the reprogramming of somatic cells and is needed for the efficient production of induced pluripotent stem cells.

ORIGINAL RESEARCH PAPER Gabut, M. *et al.* An alternative splicing switch regulates embryonic stem cell pluripotency and reprogramming. *Cell* **147**, 132–146 (2011)