

IN BRIEF

GENE REGULATION

Transcriptional infidelity promotes heritable phenotypic change in a bistable gene network

Gordon A. J. E. *et al. PLoS Biol.* **7**, e1000044 (2009)

This study shows that transient errors occurring during transcription can have heritable phenotypic consequences for cells. The authors used single-cell analysis of the bistable *lac* operon in *Escherichia coli* to show that transcriptional fidelity affects the rate of switching between two alternative and heritable epigenetic states at this locus. *E. coli* strains defective for transcriptional fidelity showed increased epigenetic switching, indicating that the effects of transient and stochastic RNA errors should be considered in models of molecular noise.

GENETIC VARIATION

Segmental copy number variation shapes tissue transcriptomes

Henrichsen, C. N. *et al. Nature Genet.* 8 Mar 2009 (doi:10.1038/ng.345)

The impact of copy number variation on local gene expression in mouse hematopoietic stem/progenitor cells

Cahan, P. *et al. Nature Genet.* 8 Mar 2009 (doi:10.1038/ng.350)

These studies generated genome-wide maps of mouse copy number variants (CNVs) and showed that this type of variation extensively influences transcript levels in a range of tissues and cell types, with copy number differences generally correlating with expression levels. The findings indicate that CNVs outside transcribed regions have important *cis* effects on the expression of nearby genes, and that CNVs are major contributors to strain-specific variations in gene expression.

FUNCTIONAL PROTEOMICS

Comparative functional analysis of the *Caenorhabditis elegans* and *Drosophila melanogaster* proteomes

Schrimpf, S. P. *et al. PLoS Biol.* **7**, e1000048 (2009)

The first comparison of two model organism proteomes — a new *Caenorhabditis elegans* proteome and a previously generated *Drosophila melanogaster* proteome — provides an overview of the 'core animal proteome'. The abundances of orthologous proteins correlated better than the abundances of the corresponding transcripts across organisms or the abundance of proteins compared with transcripts within an organism, implying that changes in transcript abundance may have been partially compensated for by opposing alterations in protein abundance during evolution.

TRANSCRIPTION

Transcriptional termination enhances protein expression in human cells

West, S. & Proudfoot, N. J. *Mol. Cell* **33**, 354–364 (2009)

Many aspects of transcription and transcript processing are known to affect levels of gene expression, but whether termination also has an effect has remained uncertain in higher eukaryotes. West and Proudfoot show that efficient termination of RNA polymerase II transcription in human cells can enhance expression both at the mRNA and protein level. Termination probably facilitates release of pre-mRNA transcripts from their site of synthesis, and so they escape degradation.