

## IN BRIEF

**TRANSLATIONAL GENETICS****Whole-genome sequencing diagnostics for newborns**

This paper describes a system for the differential diagnosis of ~3,500 genetic disorders in newborns in just 50 hours using whole-genome sequencing (WGS). The rapid turnaround was achieved by decreasing the length of the WGS process and automating the bioinformatic analysis of results. The authors demonstrated the use of this system in a neonatal intensive care unit by providing prospective molecular diagnoses. Crucial time savings could be made using this system in the treatment of newborns with severe genetic conditions.

**ORIGINAL RESEARCH PAPER** Saunders, C. J. *et al.* Rapid whole-genome sequencing for genetic-disease diagnosis in neonatal intensive care units. *Sci. Transl. Med.* **4**, 154ra135 (2012)

**NON-CODING RNA****Bacterial ncRNAs alter gene expression in worms**

This study shows that endogenous bacterial non-coding RNAs (ncRNAs) can affect gene expression in animals that eat the bacteria. Liu and colleagues showed that the *Escherichia coli* ncRNAs OxyS and DsrA suppress the expression of two *Caenorhabditis elegans* genes — *che-2* and *F42G9.6*, respectively — when bacteria are ingested by worms that express these ncRNAs. These effects on gene expression have resulting effects on worm physiology, resulting in impaired chemosensation in the case of *che-2* and decreased lifespan in the case of *F42G9.6*.

**ORIGINAL RESEARCH PAPER** Liu, H. *et al.* *Escherichia coli* noncoding RNAs can affect gene expression and physiology of *Caenorhabditis elegans*. *Nature Commun.* **3**, 1073 (2012)

**TRANSCRIPTION****MYC provides a global boost**

MYC is a transcription factor that is commonly overexpressed in cancer, but its key oncogenic transcriptional targets have remained elusive. Two new studies manipulated MYC expression levels in normal mouse cells and human cancer cells and analysed the effects on MYC occupancy and gene expression genome-wide. In all cell types, they found that, on upregulation, MYC widely associates with the promoters of already active genes to enhance transcriptional output further, particularly through releasing paused RNA polymerase II. Thus, MYC seems to function as a global amplifier of the transcriptional output of a particular cell type.

**ORIGINAL RESEARCH PAPERS** Lin, C. Y. *et al.* Transcriptional amplification in tumor cells with elevated c-Myc. *Cell* **151**, 56–67 (2012) | Nie, Z. *et al.* c-Myc is a universal amplifier of expressed genes in lymphocytes and embryonic stem cells. *Cell* **151**, 68–79 (2012)

**EVOLUTION****Coevolution revealed**

Barrière *et al.* used the conserved expression pattern of the GABA transporter *unc-47* in the nematodes *Caenorhabditis elegans* and *Caenorhabditis briggsae* to investigate how gene expression patterns are conserved in genetically diverged species. By expressing the distinct *cis*-regulatory elements from one species in the other, the resultant altered expression patterns revealed the influence of the *trans* environment. The study showed that on rapid evolution of *C. briggsae*, compensatory mutations in *cis* elements and their associated *trans* factors maintained expression patterns.

**ORIGINAL RESEARCH PAPER** Barrière, A., Gordon K. L. & Ruvinsky, I. Coevolution within and between regulatory loci can preserve promoter function despite evolutionary rate acceleration. *PLoS Genet.* **8**, e1002961 (2012)