IN BRIEF

⮕ HUMAN GENETICS

Gene expression and functional brain networks

To identify the genes that determine brain connectivity, Richiardi *et al.* mapped microarray-based gene expression data from human brain samples onto functional brain networks that were computed using resting-state fMRI data. Functional brain networks were recapitulated by gene networks based on the correlated expression of 136 genes. These genes were enriched for ion channels, and their expression was associated with axonal connectivity in mice, indicating that functional connectivity is strongly associated with synaptic function.

ORIGINAL RESEARCH PAPER Richiardi, J. *et al.* Correlated gene expression supports synchronous activity in brain networks. *Science* **348**, 1241–1244 (2015)

⮕ MICROBIAL GENETICS

Bimodal regulation of genetic competence

The regulation of genetic competence in *Bacillus subtilis* involves a positive feedback loop, whereby the competence factor ComK activates its own transcription, but only when its levels exceed a certain threshold. Expression 'noise' results in bimodal expression by ensuring that only a subpopulation of cells contain sufficient levels of ComK to trigger autoactivation and a switch to the competent state. Gamba *et al.* identified a novel protein, Kre, that represses *comK* by decreasing mRNA stability. Interestingly, the expression of Kre itself was downregulated by ComK, creating a double negative feedback loop. This study identifies a new level of ComK regulation and demonstrates the importance of mRNA stability in noise control.

ORIGINAL RESEARCH PAPER Gamba, P., Jonker, M. J. & Hamoen, L. W. A novel feedback loop that controls bimodal expression of genetic competence. *PLoS Genet.* http://dx.doi.org/10.1371/journal.pgen.1005047 (2015)

⮕ STEM CELLS

Chimpanzee induced pluripotent stem cells

To facilitate the study of comparative genomics in primates, Romero *et al.* generated a panel of seven induced pluripotent stem cell (iPSC) lines derived from chimpanzees. RNA sequencing and DNA methylation analysis of chimp and human iPSCs and their respective source lines revealed reduced intra-species variation in iPSCs compared with somatic cells, suggesting that differences between individuals were erased during reprogramming. Loss of intra-species variability facilitated the detection of differences between species, as the authors identified more differentially expressed genes and differentially methylated regions between chimpanzee and human iPSCs than other studies using different tissues.

ORIGINAL RESEARCH PAPER Romero, I. G. *et al.* A panel of induced pluripotent stem cells from chimpanzees: a resource for comparative functional genomics. *eLife* http://dx.doi.org/10.7554/eLife.07103 (2015)

⮕ GENETIC TESTING

Low-cost clinical testing for Mendelian diseases

Alkuraya *et al.* describe the Mendeliome Assay, a new low-cost multiplex assay based on next-generation sequencing of 3,070 known Mendelian genes, and demonstrate its utility in more than 2,300 patients with a broad range of suspected diagnoses. The authors suggest that, owing to its practical advantages over whole-exome sequencing, the Mendeliome Assay has potential as a first-tier diagnostic test for genetic diseases.

ORIGINAL RESEARCH PAPER Alkuraya, F. S. *et al.* Comprehensive gene panels provide advantages over clinical exome sequencing for Mendelian diseases. *Genome Biol.* http://dx.doi.org/10.1186/s13059-015-0693-2 (2015)