

IN BRIEF

HUMAN DISEASE**Induced chromosomal proximity and gene fusions in prostate cancer**

Mani, R.-S. *et al. Science* 29 Oct 2009 (doi:10.1126/science.1178124)

A fusion gene that occurs in 50% of prostate cancers has been shown to be triggered by androgen signalling. Stimulating the androgen receptor in prostate cancer cells in culture caused two genes — *TMPRSS2*, which is androgen-regulated, and the transcription factor gene *ERG* — to come into physical proximity. When the same cells were also irradiated to induce dsDNA breaks, analysis by fluorescence *in situ* hybridization (FISH) and reverse transcription PCR (RT-PCR) showed that fusion of these genes takes place and that a corresponding fusion transcript is expressed. The unique dependency of the prostate on androgen signalling could explain the sensitivity of this organ to this gene rearrangement.

GENE REGULATORY NETWORKS**Architecture-dependent noise discriminates functionally analogous differentiation circuits**

Çağatay, T., Turcotte, M., Elowitz, M. B., Garcia-Ojalvo, J. & Süel, G. M. *Cell* **139**, 512–522 (2009)

If two gene regulatory circuits with different topologies can generate similar dynamics, does it matter which of the topologies is used? Çağatay and colleagues engineered a circuit to control competence in *Bacillus subtilis* that differed from the native circuit by incorporating activation of a repressor instead of repression of an activator. Although populations with the synthetic circuit had similar competence dynamics to those with the native circuit, the native circuit caused greater variability in dynamics at the single-cell level, which allowed native populations to respond more effectively to environmental changes. Therefore, the level of circuit noise might influence which topology is selected.

GENETICS OF GENE EXPRESSION**Global patterns of *cis* variation in human cells revealed by high-density allelic expression analysis**

Ge, B. *et al. Nature Genet.* **41**, 1216–1222 (2009)

Expression quantitative trait loci are highly sensitive to cellular differentiation state

Gerrits, A. *et al. PLoS Genet.* **5**, e1000692 (2009)

Cis-acting variants that alter gene expression can be important contributors to complex trait variation. By mapping associations between SNPs and differences in allelic expression (AE) in a lymphoblastoid cell line, Ge and colleagues have generated the highest density map to date of human *cis*-regulatory variants. This study demonstrates the utility of high-density AE mapping and provides a resource for linking gene regulation to disease risk. The authors acknowledge that more tissue types need to be studied. This is also the message of a paper by Gerrits *et al.*, who show the influence of genetic variants on gene expression to be highly sensitive to cell type; they studied closely related haematopoietic cell populations and found that some variants are consistently active but that the majority are cell-type dependent.