

IN BRIEF

DEVELOPMENT**DMRT1 prevents female reprogramming in the postnatal mammalian testis**

Matson, C. K. *et al. Nature* **476**, 101–104 (2011)

In the mammalian fetus, sex is determined by cells in the gonad differentiating into testicular Sertoli cells or ovarian granulosa cells. It was originally thought that the decision made in the fetus was final, but this paper shows that, in mice, the transcription factor DMRT1 is needed to maintain the male state, even in adults. It was also recently shown that loss of a different transcription factor causes female gonad cells to reprogram into Sertoli cells; such lability in sex determination could explain sexual differentiation disorders.

TRANSLATIONAL GENETICS**Single-step capture and sequencing of natural DNA for detection of *BRCA1* mutations**

Thompson, J. F. *et al. Genome Res.* 15 Jul 2011 (doi:10.1101/gr.122192.111)

This paper presents a method that could be used for low-cost genetic tests. In this approach, which the authors demonstrate for the *BRCA1* gene, genomic DNA is sheared and loaded into a flow cell, and gene-specific primers are used to perform single-molecule sequencing with the Helicos Genetic Analysis System. Because this method removes the need to amplify the DNA sample or to capture the region of interest, it could lower the cost and increase the speed of assays in which specific regions need to be sequenced.

EPIGENETICS**Polycomb eviction as a new distant enhancer function**

Vernimmen, D. *et al. Genes Dev.* **25**, 1583–1588 (2011)

Enhancers are generally thought to regulate gene expression over long distances by promoting the recruitment of the RNA polymerase machinery. This study suggests that another long-range function of enhancers is to remove the repressive Polycomb complex from genes to allow their expression. Using mouse erythroid cells, the authors show that a tissue-specific enhancer is required to clear the Polycomb complex from a CpG island upstream of a developmentally regulated α -globin gene, and it is also needed to recruit an expression-activating histone demethylase to this island.

COMPARATIVE GENOMICS***Trans* genomic capture and sequencing of primate exomes reveals new targets of positive selection**

George, R. D. *et al. Genome Res.* 27 Jul 2011 (doi:10.1101/gr.121327.111)

Primate comparative genomics is currently limited by a lack of reference genomes for most primate species. These authors show that targeted DNA capture methods that have been developed for human exomics can be used to sequence the protein-coding regions of other primate genomes; they demonstrate this for three Old World and one New World species of monkey. The high-quality exome sequences allowed the identification of positively selected genes and those that have undergone lineage-specific loss.