

IN BRIEF

X INACTIVATION

The pluripotency factor Oct4 interacts with Ctf and also controls X-chromosome pairing and counting

Donohoe, M. E. *et al. Nature* **460**, 128–132 (2009)

During early embryogenesis in female mammals the process of silencing one X chromosome, X chromosome inactivation (XCI), is tightly coupled to cellular differentiation. This study advances our understanding of this coupling by showing that a master regulator of pluripotency — the transcription factor OCT4 — also controls XCI. In female mouse embryonic stem cells OCT4 binds to the regulatory non-coding RNA genes *Tsix* and *Xite*. These interactions and protein–protein interactions promote the first steps in XCI — pairing and counting.

GENOME ANNOTATION

Evidence based gene predictions in plant genomes

Liang, C. *et al. Genome Res.* 18 Jun 2009 (doi:10.1101/gr.088997.108)

Rapid and accurate gene annotation can be performed using transcriptional evidence, such as cDNA and protein sequences, but for plant genomes gathering such evidence has lagged behind genome sequencing. These authors designed and tested an evidence-based pipeline for gene annotation — *Gramene* — that is based on the Ensembl pipeline but uses transcriptional evidence from other plant species with previously annotated genomes. Gramene provides greater accuracy than *ab initio* predictions and shows that using cross-species transcriptional data can improve the annotation of new plant genomes.

EPIGENETICS

Assessing the impact of transgenerational epigenetic variation on complex traits

Johannes, F. *et al. PLoS Genet.* **5**, e1000530 (2009)

Changes in DNA methylation are a heritable source of phenotypic variation, but it can be difficult to distinguish their effects from those of sequence polymorphisms. Using parents with few sequence differences but contrasting methylation profiles, a panel of epigenetic recombinant inbred lines of *Arabidopsis thaliana* has been derived. Because changes in methylation were stably inherited and were associated with high heritable variation in flowering time and plant height, this panel is a first step towards identifying epiallelic variants that contribute to complex traits.

EVOLUTION

Evolution of mutational robustness in the yeast genome: a link to essential genes and meiotic recombination hotspots

Keller, P. J. & Knop, M. *PLoS Genet.* **5**, e1000533 (2009)

Using a computer simulation of evolution in diploid sexually reproducing yeast, the authors show that recessive lethal mutations lead to genome architectures in which essential genes are organized as genetically linked clusters. The simulated clustered yeast chromosomes showed similar structural properties and fitnesses to those seen in actual yeast genomes and can purge mutations more efficiently after meiosis than when clustering is absent. These findings suggest that meiotic crossover is important for the robustness of populations to deleterious mutations.