IN BRIEF

DEVELOPMENT

Transcriptional activation at the maternal-to-zygotic transition

The authors investigated control of transcriptional activation during the maternal-to-zygotic transition (MZT) in *Drosophila melanogaster* by performing chromatin immunoprecipitation followed by sequencing (ChIP–seq) for the transcription factor Zelda. They found pervasive binding of Zelda at genomic regions that are activated in the MZT, and they found that its binding is associated with open chromatin. Their evidence suggests that Zelda is a crucial regulator of MZT and raises the possibility that similar factors could perform this function in other species.

ORIGINAL RESEARCH PAPER Harrison, M. M. *et al.* Zelda binding in the early *Drosophila melanogaster* embryo marks regions subsequently activated at the maternal-to-zygotic transition. *PLoS Genet.* **10**, e1002266 (2011)

TECHNOLOGY

An efficient new targeted resequencing method

Resequencing of targeted genomic regions, such as exons, enables studies of genetic variation in large numbers of samples. This paper presents a new method called oligonucleotide-selective sequencing (OS-seq) in which oligonucleotides are immobilized on a substrate and used to capture sequences of interest before next-generation sequencing is performed on the same substrate. Additional preparation steps that are involved in other methods are avoided, thus increasing speed. To validate the method, OS-seq was successfully used to target the exons of ~350 cancer genes.

ORIGINAL RESEARCH PAPER Myllykangas, S. *et al.* Efficient targeted resequencing of human germline and cancer genomes by oligonucleotide-selective sequencing. *Nature Biotech.* 23 Oct 2011 (doi:10.1038/nbt.1996)

MOLECULAR EVOLUTION

Altering the genetic landscape of the brain

Although half of the human genome is derived from retrotransposons, mobilization of these elements is normally suppressed in somatic cells. By applying their newly developed, high-throughput method for detecting retrotransposon insertion sites (called retrotransposon capture sequencing (RC-seq)), Baillie and colleagues now show that L1, *Alu* and SVA elements are active in the germline and also in the brain. Somatic mobilization of these elements in the brain occurs preferentially in active brain genes, suggesting that insertion mosaicism contributes to normal and abnormal brain functions. Zhang and colleagues examined a different type of genetic landscape: the evolution of human-specific genes that are expressed in the brain. They compared recently evolved genes in humans and mice (those that are specific to the primate or rodent lineages, respectively) and found that young genes in humans are more likely to be expressed during early brain development. Some young genes in humans are also more likely than old genes to be upregulated in newly evolved brain regions, such as the neocortex. The suggestion is that positive selection in newly evolving brain regions has driven accelerated gene origination in the human brain.

ORIGINAL RESEARCH PAPERS Baillie, J. K. *et al.* Somatic retrotransposition alters the genetic landscape of the human brain. *Nature* 30 Oct 2011 (doi:10.1038/nature10531) | Zhang, Y. E. *et al.* Accelerated recruitment of new brain development genes into the human genome. *PLoS Biol.* **9**, e1001179 (2011)