

IN BRIEF

FUNCTIONAL GENOMICS**Mouse ENCODE**

The authors outline the focus of the encyclopaedia of mouse DNA elements (Mouse ENCODE), which is already underway. The project will functionally annotate the mouse genome using the same experimental pipelines that were established for human ENCODE. Mouse ENCODE aims to add value to human ENCODE by enabling comparative studies to be carried out, by allowing annotation of tissue types and developmental stages that are not accessible to human ENCODE and by providing resources for translational research.

ORIGINAL RESEARCH PAPER Stamatoyannopoulos, J. A. *et al.* An encyclopedia of mouse DNA elements (Mouse ENCODE). *Genome Biol.* **13**, 418 (2012)

EPIGENETICS**Chromatin inheritance during DNA replication**

Petruk *et al.* studied how the histone marks H3K4me3 and H3K27me3 are inherited to daughter chromosomes during DNA replication in *Drosophila melanogaster* embryos. Using various methods to track protein dynamics following replication fork passage, they made the surprising observation that reloaded histones are initially unmodified at these amino acids. Instead, they found that the Trithorax (TRX) and Enhancer of Zeste (E(Z)) histone methyltransferases remain stably associated with DNA during replication to re-establish the H3K4me3 and H3K27me3 patterns later. In this system at least, TRX and E(Z), rather than the histone modifications they catalyse, seem to be the bona fide epigenetic marks.

ORIGINAL RESEARCH PAPER Petruk, S. *et al.* TrxG and PcG proteins but not methylated histones remain associated with DNA through replication. *Cell* **150**, 922–933 (2012)

EVOLUTIONARY GENOMICS**Introgression in natural populations**

In this study, the evolutionary forces acting on four wild populations of the house mouse *Mus musculus* were analysed by high-density SNP-genotyping arrays. Statistical analysis showed evidence for selective sweeps at rare and newly mutated alleles, indicating positive selection. Furthermore, positive selection was shown to result in a high percentage of introgression, resulting in the permanent incorporation of genetic material from one subspecies to another. Thus, introgression of haplotypes has a larger role in adaptive processes than was previously thought.

ORIGINAL RESEARCH PAPER Staubach, F. *et al.* Genome patterns of selection and introgression of haplotypes in natural populations of the house mouse (*Mus musculus*). *PLoS Genet.* **8**, e1002891 (2012)

TECHNOLOGY**Genome-wide mapping of 5-formylcytosine**

Raiber *et al.* mapped the genome-wide distribution of the DNA demethylation intermediate 5-formylcytosine (5fC) in mouse embryonic stem cells by developing a method to covalently tag and purify 5fC-containing DNA fragments that is then followed by high-throughput sequencing. They found enrichment of 5fC in CpG islands of promoters and exons and found that it co-localizes with chromatin features of active transcription. A lack of thymine DNA glycosylase (TDG) — an enzyme that removes 5fC — resulted in increased 5fC levels and aberrant DNA methylation patterns in differentiated cells. Overall, this study supports a role for DNA demethylation via 5fC in epigenetic reprogramming and gene regulation during development.

ORIGINAL RESEARCH PAPER Raiber, E. A. *et al.* Genome-wide distribution of 5-formylcytosine in ES cells is associated with transcription and depends on thymine DNA glycosylase. *Genome Biol.* **13**, R69 (2012)