IN BRIEF

SMALL RNAS

RNA-mediated mechanism for memory storage

This study describes a mechanism by which small RNAs expressed in neurons may contribute to long-term memory. The authors discovered an abundance of PIWI-interacting RNAs (piRNAs) in *Aplysia* neurons that seem to control the epigenetic regulation of the transcription factor cyclic AMP-responsive element-binding protein 2 (CREB2) — a repressor of long-term memory function. In response to serotonin, piRNAs facilitates methylation of the *CREB2* promoter, thereby silencing gene expression. This results in enhanced long-term synaptic changes in the functional state of neurons, suggesting that piRNAs regulate memory storage through an epigenetic mechanism and showing a role for piRNAs outside of the germ line.

ORIGINAL RESEARCH PAPER Rajasethupathy, P. *et al.* A role for neuronal piRNAs in the epigenetic control of memory-related synaptic plasticity. *Cell* **149**, 693–707 (2012)

COMPLEX TRAITS

Meta-analysis for mouse association mapping

Linkage analysis and association mapping in mouse models have played an important part in the discovery of disease genes and mechanisms. Limited power and resolution in mapping panels can be an issue, and previous studies have therefore attempted to combine data from different panels. This paper presents a new meta-analysis-based method that weights each study according to its level of informativeness, thereby increasing the power and resolution in a locus-specific manner. The authors propose that their method will allow researchers to increase the power of their studies using publicly available databases.

ORIGINAL RESEARCH PAPER Furlotte, N. A. *et al.* Increasing association mapping power and resolution in mouse genetic studies through the use of meta-analysis for structured populations. *Genetics* 13 Apr 2012 (doi:10.1534/genetics.112.140277)

GENE REGULATION

X chromosome spatial organization

This study presents a detailed analysis of the three-dimensional organization of a 4.5 Mb region of the mouse X chromosome, including the area that controls the expression of *Xist*, a non-coding transcript that is required for X chromosome inactivation. The authors used chromosome conformation capture carbon copy (5C) and super-resolution microscopy to show that the region is organized into discrete topologically associating domains (which they term TADs). The TADs are an important feature of *cis*-regulatory architecture, and disrupting their boundaries results in misregulation of transcription.

ORIGINAL RESEARCH PAPER Nora, E. P. *et al.* Spatial partitioning of the regulatory landscape of the X-inactivation centre. *Nature* 11 Apr 2012 (doi:10.1038/nature11049)

GENOTYPING

Predicting genotypes from gene expression data

These authors demonstrate that, using a Bayesian approach, it is possible to predict SNP genotypes from RNA expression data alone. They used expression quantitative trait loci (eQTLs) identified in previous studies and showed that the predicted genotypes could be used to identify individuals in large cohorts. Much gene expression data is publicly available, so this ability to predict genotypes accurately from such data may raise privacy concerns similar to those arising from sharing cohort genotype information.

ORIGINAL RESEARCH PAPER Schadt, E. E., Woo, S. & Hao, K. Bayesian method to predict individual SNP genotypes from gene expression data. *Nature Genet.* **44**, 603–608 (2012)