IN BRIEF

COMPLEX TRAITS

Genetic maps for sequenced rats

In this study, the rat genome sequencing and mapping consortium used a combined sequencing and genetic mapping approach to analyse 355 quantitative trait loci (QTLs) for 122 phenotypes in 1,407 outbred rats. Although they were able to identify 35 loci that correlate with 31 traits, for ~42% of the loci, a single variant was unable to explain the phenotypic effect of the QTL. Furthermore, when compared with mice, the patterns of genetic variation differed and genetic variants in orthologous genes rarely contributed to similar phenotypes.

ORIGINAL RESEARCH PAPER Baud, A. *et al.* Combined sequence-based and genetic mapping analysis of complex traits in outbred rats. *Nature Genet.* 26 May 2013 (doi:10.1038/ng.2644)

TELOMERES

Telomere length measurement in single cells

Current measurements of telomere length take the average from a population of cells. Here, the authors adapted a quantitative real-time PCR (qPCR)-based method for telomere measurement in order to be able to take measurements in single cells. They optimized a multiplex pre-amplification step that is specific to telomeres, such that when applying qPCR, the ratio of telomere repeats to known multi-copy reference genes could be used to measure telomere length in single cells. The authors show that their method is able to dissect telomere length in heterogenous cell populations, which will aid in the understanding of the role of telomere length in development and disease.

ORIGINAL RESEARCH PAPER Wang, F. *et al.* Robust measurement of telomere length in single cells. *Proc. Natl Acad. Sci. USA* **110**, E1906–E1912 (2013)

GENE REGULATION

mRNA decay factors regulate transcription

Levels of mRNAs depend on the balance of their synthesis and decay; this study reveals a way in which the two processes are intimately connected. Working in yeast, Haimovich *et al.* found that components of the cytoplasmic 5′ to 3′ decay pathway (collectively known as the 'decaysome') shuttle between the cytoplasm and nucleus. In the nucleus, they preferentially associated with chromatin near transcription start sites. The authors show that these factors stimulate transcription initiation and elongation and thus link transcription and decay.

ORIGINAL RESEARCH PAPER Haimovich, G. *et al.* Gene expression is circular: factors for mRNA degradation also foster mRNA synthesis. *Cell* **153**, 1000–1011 (2013)

CHROMOSOME BIOLOGY

Nonrandom chromatid segregation in stem cells

Adult stem cells, such as germline stem cells (GSCs), undergo asymmetric divisions to produce a daughter stem cell and a daughter that differentiates; nonrandom segregation of sister chromatids between daughters has been observed in some cases. In this study, Yadlapalli and Yamashita show direct evidence that genetically identical sister chromatids are segregated in a biased manner in male fruitfly GSCs. The authors used a single-chromosome resolution method based on fluorescence *in situ* hybridization and found biased segregation for the X and Y chromosomes but not for autosomes. Furthermore, they identified proteins that are necessary for nonrandom segregation, including components of the centrosome and proteins associated with the nuclear envelope.

ORIGINAL RESEARCH PAPER Yadlapalli, S. & Yamashita, Y. M. Chromosome-specific nonrandom sister chromatid segregation during stem-cell division. *Nature* 5 May 2013 (doi:10.1038/nature12106)