IN BRIEF

TRANSCRIPTOMICS

mRNA-Seq whole-transcriptome analysis of a single cell

Tang, F. *et al. Nature Methods* 6 Apr 2009 (doi:10.1038/nmeth.1315)

Next-generation sequencing enables accurate and in-depth transcriptome analysis (RNA-Seq), but usually requires microgram amounts of RNA, precluding single cell studies. These authors modified a single cell whole-transcriptome amplification method to generate cDNAs as long as 3 kb from poly(A) RNA extracted from a single mouse blastomere, providing sufficient material for at least 100 million sequencing reads. They discovered and quantified many novel transcripts and alternative splicing isoforms, demonstrating that single cell RNA-Seq can overcome some of the technical challenges of investigating gene expression in early development and in rare cell populations.

SMALL RNAS

New class of microRNA targets containing simultaneous 5′-UTR and 3′-UTR interaction sites

Lee, I. *et al. Genome Res.* 31 Mar 2009 (doi: 10.1101/gr.089367.108)

It is well known that post-transcriptional regulation by microRNAs (miRNAs) requires interaction between the 5′ end of the miRNA and the 3′ UTRs of target transcripts. This study reveals that many human miRNAs — particularly those that are conserved in other species — also interact, through their 3′ ends, with the 5′ UTRs of their targets. The authors showed experimentally that both interaction sites can be required for miRNA function. These findings have implications both for improving predictions of miRNA targets — which is important for the potential therapeutic use of miRNAs, to avoid undesired side-effects — and for exploring miRNA evolution.

HUMAN DISEASE

DECIPHER: *D*atabas*e* of *C*hromosomal *I*mbalance and *P*henotype in *H*umans using *E*nsembl *R*esources

Firth, H. V. *et al. Am. J. Hum. Genet.* 2 Apr 2009 (doi:10.1016/j.ajhg.2009.03.010)

Copy number variants underlie many genetic abnormalities, each of which might be very rare. To facilitate the clinical interpretation of such disorders, and to improve phenotype–genotype correlations, an interactive online database (DECIPHER) has been developed. It integrates information about patients across 100 clinical centres, and provides many tools to interpret a range of structural rearrangements; because DECIPHER is integrated with the Ensembl genome browser, each candidate interval can be linked to up-to-date information on gene content and genomic features.