Nature Reviews Genetics | AOP, published online 12 April 2012

IN BRIEF

BIOINFORMATICS

Personalized omics profiling

This study describes the 'integrative personal omics profile' (iPOP) of a healthy person — that of Mike Snyder, an author on the paper — which was generated by combining a whole-genome sequence with transcriptomic, proteomic, metabolomic and autoantibody data sampled over 14 months. As well as highlighting the subject's predisposition to type 2 diabetes, the study also identified new immune pathways that are activated by viral infection. Despite the complexity of analysing large and varied data sets, this paper is proof-of-principle that iPOPs are useful for gaining insights into physiological states and for assessing disease risk.

ORIGINAL RESEARCH PAPER Chen, R. *et al.* Personal omics profiling reveals dynamic molecular and medical phenotypes. *Cell* **148**, 1293–1307 (2012)

GENOME BIOLOGY

New family of DNA molecule found in mammals

This paper reports the identification of thousands of extrachromosomal circular DNA molecules in mouse tissues and in mouse and human cell lines. These small 200–400 bp 'microDNAs' map to unique sequences in the genome; these are mostly located in the 5′ untranslated region of genes and in exons and CpG islands. Chromosomal microdeletions due to the excision and loss of microDNAs lead to a considerable degree of mosaicism in the mouse brain and possibly also to the frequent germline mosaicism reported in humans by the 1000 Genomes Project.

ORIGINAL RESEARCH PAPER Shibata, Y. *et al.* Extrachromosomal microDNAs and chromosomal microdeletions in normal tissues. *Science* 8 March 2012 (doi:10.1126/science.1213307)

GENE EXPRESSION

Anti-Shine–Dalgarno regulation of translation

The authors performed an analysis of ribosome pausing in *Escherichia coli* and *Bacillus subtilis* by ribosome profiling — a technique that allows the identification of ribosome-protected mRNA by high-throughput sequencing. They show that ribosome pausing is mediated by Shine–Dalgarno (SD)-like sequences within coding regions; this pausing seems to be due to an altered 16S anti-SD sequence within the ribosome that hybridizes with the SD-like sequence. In coding sequences, SD-like sequences are disfavoured and their inclusion is a way in which translation is controlled.

ORIGINAL RESEARCH PAPER Li, G-W. *et al.* The anti-Shine–Dalgarno sequence drives translational pausing and codon choice in bacteria. *Nature* 28 March 2012 (doi:10.1038/nature10965)

TRANSCRIPTOMICS

Long non-coding RNA stability

Two studies have analysed the half-lives of long non-coding RNAs (lncRNAs). Clark *et al.* used a custom non-coding RNA array to analyse the half-lives of ~800 lncRNAs and ~12,000 mRNAs in the mouse neuro-2a cell line. Tani *et al.* developed a new technique called 5′-bromo-uridine immunoprecipitation chase followed by deep sequencing (BRIC–seq), in which RNAs are labelled by pulse chasing with 5′-bromo-uridine, to survey RNA half-life in HeLa cells. Both groups find that lncRNA half-lives vary over a wide range that is comparable with that of mRNAs; longer half-lives may be indicative of functionality in lncRNAs.

ORIGINAL RESEARCH PAPERS Tani, H. *et al.* Genome-wide determination of RNA stability reveals hundreds of short-lived noncoding transcripts in mammals. *Genome Res.* 27 Feb 2012 (doi:10.1101/gr.130559.111) | Clark, M. B. *et al.* Genome-wide analysis of long noncoding RNA stability. *Genome Res.* 9 March 2012 (doi:10.1101/gr.131037.111)