IN BRIEF

GENE EXPRESSION

Secrets of the deep for transcriptomes

The low abundance of many transcripts has limited the analysis of transcriptome complexity. To gain further insight, Mercer *et al.* used array-based capture followed by high-throughput RNA sequencing on human fibroblasts, achieving nearly 5,000-fold coverage of the small (~0.8 Mb) portion of the genome analysed. They found novel spliceoforms of both the tumour suppressor gene *TP53* and of long non-coding RNAs (lncRNAs), such as *HOTAIR*. They also identified pervasive, low-level transcription of regions that were considered to be intergenic and could detect transcripts present at less than one molecule per 1,000 cells.

ORIGINAL RESEARCH PAPER Mercer, T. R. *et al.* Targeted RNA sequencing reveals the deep complexity of the human transcriptome. *Nature Biotech.* 13 Nov 2011 (doi:10.1038/nbt.2024)

RNA INTERFERENCE

Inheritance of an acquired immune response

The possible transgenerational inheritance of acquired traits is a much debated phenomenon. Using infection of *Caenorhabditis elegans* by the flock house virus as a model, Rechav *et al.* showed non-Mendelian inheritance of the induced antiviral response over several generations. The immune memory was mediated by virus-derived small RNAs that function to silence the viral genome. The memory was transmitted independently of the original viral template.

ORIGINAL RESEARCH PAPER Rechav, O. *et al.* Transgenerational inheritance of an acquired small RNA-based antiviral response in *C. elegans*. *Cell* 23 Nov 2011 (doi:10.1016/j.cell.2011.10.042)

DEVELOPMENT

Histone modification pre-patterning

In anamniote vertebrate development, zygotic genome activation (ZGA) occurs after several cell divisions; this allows the investigation of events that precede transcription. Using zebrafish, Linderman *et al.* assayed the levels of histone H3 modifications in embryos before and after ZGA. They showed that both permissive and repressive histone modifications are localized to gene promoters of developmentally regulated and homeostatic genes before transcription begins, indicating pre-patterning of these genes. This implies that histone modifications can be instructive for developmental gene expression.

ORIGINAL RESEARCH PAPER Lindeman, L. C. *et al.* Prepatterning of developmental gene expression by modified histones before zygotic genome activation. *Dev. Cell* 1 Dec 2011 (doi:10.1016/j.devcel.2011.10.008)

DISEASE GENOMICS

Copy number variants and HIV infection control

Pelak *et al.* used genome-wide SNP arrays on >2,000 HIV-1-infected patients to identify copy number variants (CNVs) associated with HIV infection control. Increased copy number of genes encoding two immunoglobulin-like receptors, *KIR3DL1* and *KIR3DS1*, correlated with a lower viral load, although this effect was dependent on epistatic interactions between these receptor genes and those of their HLA ligands. This reinforces a model — for which the authors obtained functional evidence — whereby these receptors, which are present on natural killer cells, influence the immune response to HIV-1-infected cells.

ORIGINAL RESEARCH PAPER Pelak, K. *et al.* Copy number variation of KIR genes influences HIV-1 control. *PLoS Biol.* **9**, e1001208 (2011)