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IN BRIEF

RNA

Getting in shape — bacterial mRNA structure functions beyond information transfer

A team of researchers from Germany has combined three different sequencing technologies — parallel analysis of mRNA structure (PARS), ribosome profiling and RNA sequencing (RNA-seq) — to determine structural features in mRNA that regulate gene expression in *Escherichia coli*. Coding sequences had a high propensity for forming secondary structures; however, only a small subset were found to influence translation fidelity *in vivo*. By combining high-throughput sequencing with RNA structure-probing approaches, the authors were able to obtain a high-resolution transcriptome-wide view that identified structural features implicated in a variety of cellular processes such as the regulation of translation and mRNA degradation.

ORIGINAL RESEARCH PAPER Del Campo, C. *et al.* Secondary structure across the bacterial transcriptome reveals versatile roles in mRNA regulation and function. *PLoS Genet.* **11**, e1005613 (2015)

EPIGENOMICS

Sex matters

Epigenomic differences between men and women must be taken into account when designing and analysing future studies, say the authors of a recent epigenome-wide association study. Singmann *et al.* analysed autosomal DNA methylation levels in whole-blood samples taken from 1,799 European men and women and found that 1,184 CpG sites were differentially methylated between men and women across all autosomes. Some of the differentially methylated loci also exhibited differential gene expression between men and women, while some were enriched among imprinted genes. Findings were replicated in three independent European cohorts. The finding of substantial epigenomic differences between men and women, combined with previous studies that have shown divergence between males and females with respect to disease risk and incidence, highlight the importance of considering gender in study designs and analyses.

ORIGINAL RESEARCH PAPER Singmann, P. *et al.* Characterization of whole-genome autosomal differences of DNA methylation between men and women. *Epigenetics Chromatin* **8**, 43 (2015)

GENETIC VARIATION

A new foundation for non-coding variant analysis

A novel analysis published in *Nature Genetics* reveals >60,000 common variants that directly influence transcription factor occupancy and regulatory DNA accessibility *in vivo*. The authors systematically combined regulatory DNA genotyping with allelically resolved genomic DNase I hypersensitive site sequencing (DNase-seq) of more than 114 cell and tissue types and states sampled from 166 individuals, to identify regulatory variants that directly influence the chromatin architecture of individual regulatory regions in an allele-specific manner. Maurano *et al.* then created *in vivo* profiles of the variation affecting diverse transcription factor families to discriminate nearly 500,000 common regulatory variants that may affect transcription factor occupancy across the human genome. The results highlight that genetic variation in regulatory DNA is predominantly interpreted in a cell type-specific fashion and provide a new foundation for the analysis and interpretation of common disease- and trait-associated variants that localize within regulatory DNA.

ORIGINAL RESEARCH PAPER Maurano, M. T. *et al.* Large-scale identification of sequence variants influencing human transcription factor occupancy *in vivo*. *Nat. Genet.* http://dx.doi.org/10.1038/ng.3432 (2015)