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IN BRIEF

DISEASE GENETICS

Genetic diagnoses from single oocytes

Pre-implantation genetic analyses are typically carried out on growing, multicellular embryos. Hou *et al.* fertilized single human oocytes and extracted the polar bodies, which are products of maternal meiosis that are dispensable for embryonic development. They carried out DNA amplification by multiple annealing and looping-based amplification cycles (MALBAC) followed by high-throughput sequencing of the polar body genomes. From these data, they were able to deduce the presence or absence of chromosomal aneuploidies and single-nucleotide disease variants in the unsampled female pronucleus, which forms the maternally inherited component of the embryonic genome.

ORIGINAL RESEARCH PAPER Hou, Y. *et al.* Genome analyses of single human oocytes. *Cell* **155**, 1492–1506 (2013)

TECHNOLOGY

Mapping small-molecule binding sites

Anders and colleagues have developed a new method called Chem–seq to determine the genomic sites where small molecules interact with target proteins or DNA. Similarly to chromatin immunoprecipitation followed by sequencing (ChIP–seq), Chem–seq integrates ligand affinity capture with massively parallel DNA sequencing. Together with other genome-wide analysis techniques such as ChIP–seq, mapping the interaction sites of small-molecule drugs may provide insights into their mechanisms of action and their specificity.

ORIGINAL RESEARCH PAPER Anders, L. *et al.* Genome-wide localization of small molecules. *Nature Biotech.* http://dx.doi.org/10.1038/nbt.2776 (2013)

ENHANCERS

BRD4 and JMJD6 regulate antipause enhancers

Pausing and pause release of RNA polymerase II (Pol II) in early transcription elongation are key regulatory events for several genes and have important roles in development, homeostasis and disease. Liu and colleagues now show that distal enhancers have a role in regulating pause release. They demonstrate that BRD4 and JMJD6 recruitment to these 'antipause enhancers' in cultured human cells causes removal of a repressive chromatin mark at these enhancers, which allows them to loop to the promoter. This ultimately results in pause release of Pol II and subsequent activation of a large subset of genes.

ORIGINAL RESEARCH PAPER Liu, W. *et al.* Brd4 and JMJD6-associated anti-pause enhancers in regulation of transcriptional pause release. *Cell* **155**, 1581–1595 (2013)

RNA

Characterizing native RNA structures

High-throughput experimental methods to characterize RNA structure typically involve the treatment of *in vitro* refolded RNAs with reagents or nucleases that are sensitive to RNA base pairing followed by high-throughput sequencing. To determine how broadly applicable such data is to RNA structure under native conditions in cells, Rouskin *et al.* used a variation of these methods that used the cell-permeable reagent dimethylsulphate (DMS) in live yeast and human cells. They found that globally, RNAs were substantially more unfolded *in vivo* than *in vitro*. This may reflect the presence of RNA helicases and single-stranded RNA-binding proteins in cells.

ORIGINAL RESEARCH PAPER Rouskin, S. *et al.* Genome-wide probing of RNA structure reveals active unfolding of mRNA structures *in vivo*. *Nature* http://dx.doi.org/10.1038/nature12894 (2013)