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IN BRIEF

TECHNOLOGY

Amplifying single-cell cDNA without bias

Single-cell transcriptomics provides insights into the importance of stochastic transcription and facilitates more complete transcriptome characterization. Many current methods require amplification of cDNA for the analysis of low copy-number transcripts, which introduces bias. These authors optimize the amplification of cDNA libraries that are immobilized on beads. Current protocols include a step that digests primers after cDNA amplification to avoid competition with the cDNA for amplification. However, this step also degrades low copy-number cDNA, which results in amplification bias. The new protocol removes this step and washes the beads instead, which allows amplification of low copy-number transcripts at high efficiency with less bias.

ORIGINAL RESEARCH PAPER Huang, H. *et al.* Non-biased and efficient global amplification of a single-cell cDNA library. *Nucleic Acids Res.* http://dx.doi.org/10.1093/nar/gkt965 (2013)

REGENERATION

Key role for polyploidization in wound healing

The *Drosophila melanogaster* abdominal epithelium provides a good model for understanding how postmitotic diploid cells contribute to repair upon tissue damage. Losick *et al.* show that, after puncture wounds are made in this system, DNA replication without cell division is induced in cells near the wound site, which results in polyploidy. In addition, cells surrounding the wound fuse to form multinucleate cells. The authors postulate that polyploidization is required to restore the tissue mass that is lost upon injury and that cell fusion speeds up re-epithelialization.

ORIGINAL RESEARCH PAPER Losick, V. P. *et al.* Polyploidization and cell fusion contribute to wound healing in the adult *Drosophila* epithelium. *Curr. Biol.* http://dx.doi.org/10.1016/j.cub.2013.09.029 (2013)

DEVELOPMENT

Enhancers 'fine-tune' face and skull shape

These authors identified >4,000 candidate enhancers that are predicted to function in mouse craniofacial development. For three of these candidates they showed that deletions alter the expression of nearby genes that have known roles in craniofacial development. Using micro-computed tomography — a high-resolution three-dimensional imaging method — they accurately measured the skulls of mice that carried these mutations and found subtle but significant effects. These findings have implications for understanding the genetic bases of both normal and abnormal craniofacial morphology.

ORIGINAL RESEARCH PAPER Attanasio, C. *et al.* Fine tuning of craniofacial morphology by distant-acting enhancers. *Science* **342**, 1241006 (2013)

CANCER GENOMICS

Explaining aneuploidy patterns

Aneuploidy — the presence of an abnormal number of chromosomes — is a common feature of cancer cells, but it is unclear how specific patterns of aneuploidy arise. These authors developed a computational method for identifying candidate tumour suppressors and oncogenes on the basis of mutation patterns in tumour samples. They found evidence that there are many cancer-driving genes for which a continuum of oncogenic potential exists, and they propose that the specific combinations of these genes on chromosomes explain the patterns of aneuploidy that arise in cancer.

ORIGINAL RESEARCH PAPER Davoli, T. *et al.* Cumulative haploinsufficiency and triplosensitivity drive aneuploidy patterns and shape the cancer genome. *Cell* http://dx.doi.org/10.1016/j.cell.2013.10.011 (2013)