

GENETICS

Understanding the ABSOLUTE genome

Research led by computational scientists at The Broad Institute in Cambridge, MA, has resulted in ABSOLUTE—a fully quantitative method that can determine tumour purity and cell ploidy of the cancerous cells in a tumour sample. This tool brings scientists closer to pinpointing the precise genetic aberrations in a range of different cancers.

Measuring the absolute copy number per cell has hitherto been challenging because of the heterogeneous nature of tumours. Not only are cancerous cells intermixed with normal cells, which can interfere with accurate DNA measurements, but the cancer cell population itself can undergo subclonal evolution. These features have meant that analyses based on DNA mass or other ‘grouped’ methods were inaccurate.

ABSOLUTE’s power lies in its ability to essentially measure genome alterations on the cellular level. This calculation is achieved by incorporating models of recurrent cancer karyotypes with relative copy-number data and the genome-wide

profiles of DNA concentration using microarray analysis or massively parallel sequencing analysis.

Using this computational technique, the team characterized more than 3,000 tumour samples of 25 different cancers. They found that polyploidy occurred as a result of whole-genome doubling in many epithelial tumours (colorectal, breast, lung, ovarian and oesophageal cancer) rather than by successive partial amplifications.

The structure and history of cancer, in terms of genetic evolution, is arguably the most basic element scientists must understand to design effective therapy. Only once we understand the process of tumorigenesis can we design methods to interfere with it. ABSOLUTE might be one such way we gain these pivotal insights.

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Original article Carter, S. L. *et al.* Absolute quantification of somatic DNA alterations in human cancer. *Nat. Biotechnol.* doi:10.1038/nbt.2203