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BGI launches tool for tumor xenograft research

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Singapore: Beijing Genomics Institute (BGI), the world's largest genomics organization, has successfully developed a new filtering tool, PDXomics, which performs accurate and specific classification of the mixed reads derived from the host and tumor xenografts. Through the full utilization of this robust tool, researchers could develop the specific patient-derived xenografts (PDX) and advance the oncology drug discovery, biomarker development and their future applications.

Xenograft models serve as an important tool for many areas of biomedical research, including oncology, immunology and HIV pathology. There has been a recent increase in the use of tumor-specific PDX engrafted into immune-compromised rodents such as the most common athymic nude or NOD/SCID mice for preclinical modelling. However, the progress has been greatly hampered by the contamination resulted from the inevitable mixing between the host and the xenografts.

Considering the high degree of homology between human and mouse genomes, it is very difficult to minimize the contamination by the present physical or biochemical techniques, such as conservative sectioning, cell sorting or laser capture micro-dissection. In an effort to address the problem, researchers from BGI developed a fast, accurate and specific tool to classify the xenograft-derived sequence read data.

Researchers evaluated the tool on genomic data from three pairs of xenografts and case-matched primary tumor samples. The sequence reads were directly mapped to a mixed reference-set that contains both of human genome and mouse genome. When classifying the reads located in the DNA collinear regions of human and mouse, the result showed that

PDXomics could specifically filter mouse reads from the mixed reads as well as keep human's.

Currently, there are two major traditional methods for analyzing the reads: one is processing the reads set with human genome as a reference; the other is processing the reads set first with mouse genome as a reference, then removing the mapped reads and processing the remaining reads with human genome again. To evaluate the accuracy and quality of PDXomics, researchers compared the analysis results with the two traditional methods, and they found that the PDXomics could significantly reduce the false-positive rate (FPR) of identified single-nucleotide mutations, and improve the accuracy of variation detection.

Zonghui Peng, director, DEPT of Pharma & Biotech, BGI, said, "Over the past two decades, the applications of PDX have made great impact on the development of translational medicine. With the rapid development of next-generation sequencing (NGS) technology, PDXomics will be a robust tool in the optimization and screening of xenograft models in the near future, with the benefits of fast turnaround time, low cost and high efficiency."