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BGI Tech develops novel assembly solution

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Singapore: BGI Tech Solutions has introduced its novel assembly solution for facilitating heterozygous genomes research. This marks another technological breakthrough for BGI in heterozygous genome assembly after the completed genome sequencing of oyster, diamondback moth and pear.

BGI Tech aims to provide advanced multi-omics and bioinformatics service solutions for its global customers to achieve their research goals in biomedical, agricultural, and environmental areas.

The availability of a reference genome for a species is the cornerstone for the in-depth understanding of its biological secrets and commercial values. However, a major obstacle that prevents scientists to easily crack the genome of a heterozygous species is the cost-intensive and time-consuming process through traditional assembly approaches.

To overcome the technical difficulties, researchers from BGI Tech developed a novel assembly solution, Ultra-Deep de novo, based upon high-throughput sequencing technology. The new solution adopts BGI's latest assembly software, SOAPdenovo2, and heterozygous sequence processing algorithm. After processing the genomic data produced by ultra-deep sequencing (>200X), the heterozygous regions within the genome can be entirely reserved and classified, with high quality and efficiency.

"Ultra-Deep de novo can serve as a robust tool for researchers to efficiently decode heterozygous genomes." said, Junyi Wang, senior vice president of BGI Tech, "BGI has completed the genome sequencing of more than 570 species to date. Some of the species have not been studied because of the challenges posed by high heterozygosis. We believe that this new solution will be a powerful tool for researchers to crack more heterozygous genomes, and boost the further development of agriculture and human health."