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Qiagen unveils new library preparation kit, facilitating multiomic studies and advancing precision medicine

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New kit advances precision medicine by facilitating multiomic studies and Comprehensive Genomic Profiling

German firm Qiagen has announced the launch of its QIAseq Multimodal DNA/RNA Lib Kit. The new kit enables seamless preparation of DNA and RNA libraries for next-generation sequencing (NGS), such as whole genome sequencing (WGS) and whole transcriptome sequencing (WTS), as well as downstream target enrichment based on hybrid-capture from a single sample.

The QIAseq Multimodal DNA/RNA Lib Kit facilitates multiomics, the studies of several omic fields like genomics, transcriptomics and proteomics, aiming to gain a deeper understanding of biological processes and systems – something crucial for studying diseases like cancer.

The kit offers a streamlined and rapid workflow to generate WGS and WTS libraries from a single sample by combining chemistry optimized for DNA and RNA simultaneously. Using traditional methods, separate workflows for DNA and RNA sequencing require a large amount of sample material, labor-intensive library preparation procedures, and long turn-around times.

Researchers can also use the QIAseq Multimodal DNA/RNA Lib Kit for generating DNA-only or RNA-only libraries. It is the first NGS multimodal kit on the market that is compatible with a wide range of input samples, including blood, Formalin-Fixed Paraffin-Embedded (FFPE) samples, and cell-free DNA (cfDNA). This is particularly relevant in translational research, such as in the study of cancers, where different types of samples may be available.

The kit is highly sensitive, enabling detection of both DNA and RNA rare variants. The DNA and RNA libraries generated using the QIAseq Multimodal DNA/RNA Lib Kit are directly compatible with different sequencing platforms such as Illumina instruments and Element Aviti and can be sequenced on other sequencers with an added conversion step (Complete Genomics/MGI, Singular Genomics, and Ultima Genomics).