Resource Summary Report

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Hybridization-capture for nanopore sequencing

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Protocol Information

URL: https://dx.doi.org/10.17504/protocols.io.zxyf7pw

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Summary: Large-scale genomic anomalies – structural variations (SVs) – are pervasive in cancer. Due to the scale of the SVs and the repetitive nature of the sequences usually flanking them, they are difficult to measure with conventional short-read sequencing. The long reads possible with nanopore sequencing provide an alternative to advance the understanding of SVs. In this application note, we applied SureSelectXT to nanopore long read sequencing, enriching for CDKN2A and SMAD4 tumor suppressor genes, to improve the depth and variant calling accuracy of nanopore sequencing.This application note focuses on optimizing the SureSelectXT protocol to long-read sequencing and using open-source softwares nanopolish and sniffles to improve the base calling accuracy and detect single nucleotide variants (SNVs) and structural variants (SVs), demonstrating the utility of SureSelect system on third-generation long-read sequencing platforms.

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