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Xdrop™ - Targeted sequencing enabled into the dark and unknown

Peter Mouritzen

Samplix ApS, Denmark

Abstract

Targeted sequencing data will never be better than the input material generated during the targeted enrichment process! While this may seem trivial, very few targeted enrichment technologies allow maintaining the integrity and quality of the DNA during enrichment. This results in both false positives and false negative results and can significantly impact conclusions. The Xdrop™ innovation, a novel robotized microfluidics-based focused on advancement framework, empowers quick focused on improvement while keeping up the nature of the DNA and subsequently makes it conceivable to dodge the ancient rarities presented with other enhancement advances. Here we show the Xdrop™ framework being utilized to succession incorporated infections and their encompassing obscure chromosomal grouping, long GC rehashes, and we show staging of malignant growth changes from sub-nanograms of DNA. Districts of 40-70 kb are enhanced and sequenced utilizing Illumina, PacBio, and Oxford Nanopore sequencing at high inclusion. Apart from the Xdrop™ reagents, just 0.2-10 ng of input DNA and two adjacent 20-25 bp primers are used for the enrichment of a chromosomal region and it is therefore fast and easy to set up for a new region. The primers are located in the central part of the enriched region which means that partially unknown regions can also be enriched using the system making it relevant for regions with structural variation, CRISPR gene editing, gap closing, variable viruses or bacteria, pseudogenes etc. We also show that the Xdrop™ system can be used for general, unbiased isothermal amplification of small amounts of samples of DNA for any type of downstream sequencing.

Biography:

With more than 20 years of experience in the life science industry, Peter is heading market and application development at Samplix. Here efforts are currently focused on the recently launched Xdrop™ technology which introduces an entirely new concept for target enrichment for both short and long read sequencing. Prior to joining Samplix Peter was Global Head of QIAGEN Genomic Services in Germany and the US and before joining QIAGEN, he was heading R&D at Exiqon overseeing life Science Product Development, Diagnostics, and Services.

Speaker Publications:

1. "Validation of the four-miRNA biomarker panel MiCaP for prediction of long-term prostate cancer outcome"
July 2020Scientific Reports 10(1):10704
DOI: 10.1038/s41598-020-67320-y
2. "Verification of CRISPR editing by XdropTM Indirect Sequence Capture followed by short- and long- read sequencing"
May 2020
DOI: 10.1101/2020.05.28.105718
3. "Elevated miR-615-3p Expression Predicts Adverse Clinical Outcome and Promotes Proliferation and Migration of Prostate Cancer Cells"
September 2019American Journal Of Pathology 189(12)
DOI: 10.1016/j.ajpath.2019.08.007
4. "Novel DNA methylation biomarkers show high sensitivity and specificity for blood-based detection of colorectal cancer—a clinical biomarker discovery and validation study"
December 2019Clinical Epigenetics 11(1)
DOI: 10.1186/s13148-019-0757-3

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