



Samplix workflow

The Xdrop™ introduces a new approach for genomic analysis. Our innovative technology enables Indirect Sequence Capture via targeted enrichment of genomic regions in droplets. Using the Xdrop™ instrument, cartridges, and reagents, single DNA molecules are partitioned into millions of picolitre size droplets. The Xdrop™ workflow includes Indirect Sequence Capture using double emulsion droplets (steps 1-6) and multiple displacement amplification using single emulsion droplets (steps 7-9). Samplicons, comprising the amplified Target DNA, are compatible with both long- and short-read sequencing platforms (10).

In the first step, the sample is mixed with primers for the Detection Sequence, used to identify the Region of Interest, and droplet PCR (dPCR) reagents (1). This mix is partitioned into millions of double emulsion droplets using the Xdrop™ instrument and the advanced microfluidics dPCR cartridge (2). These droplets are highly stable and are suitable for standard PCR cycling, flow cytometry analysis and sorting. Droplets containing the Region of Interest are identified by the Detection Sequence (3), a short amplicon (~150 bp) placed within or adjacent to the Region of Interest. Droplets are stained with an intercalating dye (4) and positive droplets are identified by their fluorescence and physically separated from negative droplets using a standard cell sorter (5). Native DNA is released from double emulsion droplets (6) resulting in an enrichment of long single molecules comprising kilobases of DNA information.

For downstream DNA amplification of the single molecules, each long fragment derived from the enrichment is partitioned into thousands of single emulsion droplets (7) for high fidelity multiple displacement amplification in droplets (dMDA) (8). Samplicons, i.e., amplified enriched fragments around the region of interest, are then released from the single emulsion droplets (9). The Xdrop™ enriched DNA (100-1000 fold) is compatible with downstream analyses, such as long- and short-read sequencing (10).