

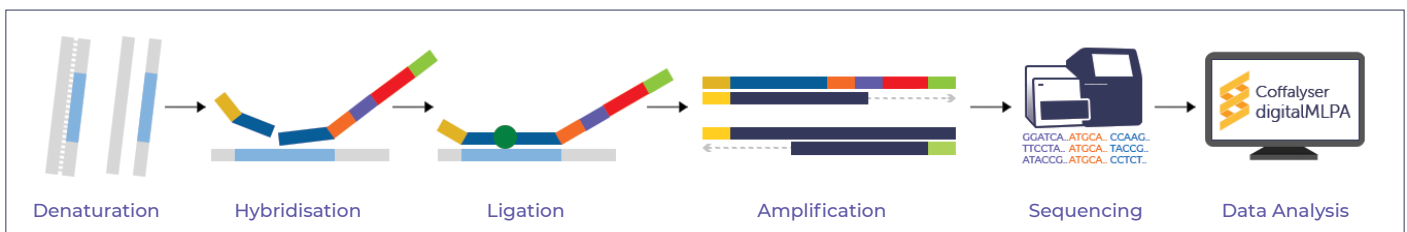
digitalMLPA™

Confidence in Copy
Number Determination



- ✓ **Specific:** unparalleled copy number certainty for complex genetic regions
- ✓ **Cost-effective:** up to 1000 DNA targets in one reaction
- ✓ **Simple:** easy hands-on steps and no library quantification needed
- ✓ **Robust:** only 20 ng of sample DNA needed; uniform coverage generated
- ✓ **Straightforward:** free software, simple analysis, clear-cut results

digitalMLPA is a multiplex PCR followed by Illumina sequencing-based amplicon quantification, for the detection of copy number variations (CNV) and specific single nucleotide variants (SNV). digitalMLPA amplifies ligated probes with a universal PCR primer pair, enabling unbiased amplification. With digitalMLPA, up to 1000 unique sequences can be detected and quantified in a single reaction.



The digitalMLPA technique is similar to SALSA® MLPA®, the gold standard for CNV detection, but with the ability to examine many more targets in a single reaction.

Analysis is done using free, easy-to-use software – so no bioinformatic skills are needed.

NXtec™ probemixes	
Predisposition to Cancer	NXtec D001 Hereditary Cancer Panel 1 Genes associated with a hereditary predisposition to breast, ovarian, colorectal, gastric, prostate, pancreatic and endometrial cancer and melanoma.
Multiple Myeloma	NXtec D006 Multiple Myeloma 1p, 1q, 13q, 17p (<i>TP53</i>), trisomies (3, 5, 7, 9, 11, 15, 19, 21).
Acute Lymphoblastic Leukemia	NXtec D007 Acute Lymphoblastic Leukemia 73 ALL-related genes and 8 ALL-related regions; hyperdiploidy and hypodiploidy.

Call CNVs with confidence and reduce your turnaround time with minimal DNA input.

Features	Advantages
Wide assay coverage	600-1000 DNA targets per reaction
Quick turnaround	Results in 48-72h
Low DNA input	Requires only 20 ng of sample DNA
Highly specific	Can discriminate 1 nt differences, allowing for: <ul style="list-style-type: none"> o reliable gene-pseudogene distinction (e.g. <i>PMS2/PMS2CL</i>) o analysis of complex regions (e.g. <i>PMS2, PTEN</i>) o detection of select SNVs (e.g. <i>BRAF</i> p.V600E, <i>MITF</i> c.952G>A)
Wide range of CNV detection	CNV detection ranging from whole chromosomes to single exons
Simple library prep	No library quantification needed
	No DNA enrichment needed, thus removing associated bias
Uniform coverage for accurate results	Universal PCR primer pair eliminates amplification bias
	Robust even with varying read depths (min. read depth: 400x)
	Efficient amplification of probes in GC-rich regions (e.g. <i>STK11</i>)
Highly-targeted	Sequencing of probes, <i>not</i> sample DNA, meaning: <ul style="list-style-type: none"> o reduced chance of incidental findings o no allelic dropout caused by SNVs interfering with primer binding o simplified data analysis; no dependence on alignment to a reference genome
Extensive quality control	Robust data normalisation due to extensive number of reference probes
	Built-in quality control for enzymatic activity, sample fragmentation, depurination, denaturation, read depth and other reaction conditions
	Free software for quality control and result calculation

Protocol

1. DNA denaturation

- Sample DNA is mixed with a unique barcode solution and denatured.

2. Probe hybridisation to sample DNA

- A digitalMLPA probemix consisting of up to 1000 probes is added to the denatured DNA/barcode sample mix.

3. Ligation of hybridised probes

- Hybridised digitalMLPA probes are ligated to form a fully amplifiable probe.

4. PCR amplification

- Ligated digitalMLPA probes are all amplified using a single PCR primer pair.

5. Illumina sequencing

- Equal volumes of digitalMLPA PCR reactions are mixed and diluted.
- Diluted PCR products are loaded directly on an Illumina sequencer.

6. Data analysis

- Data analysis software is used for reaction quality control, probe quantification and ratio determination to identify sample aberrations.

Throughput

Illumina instrument ¹	Samples per run ²
iSeq 100	Up to 11
MiSeq System (v3 chemistry), MiniSeq System	Up to 69
All NextSeq, HiSeq and NovaSeq Systems	Up to 384 ³

¹ Besides the instrument, the number of samples also depends on the sequencing kit size used.

² Sample numbers based on 600-probe digitalMLPA assay at an average read depth of 600x.

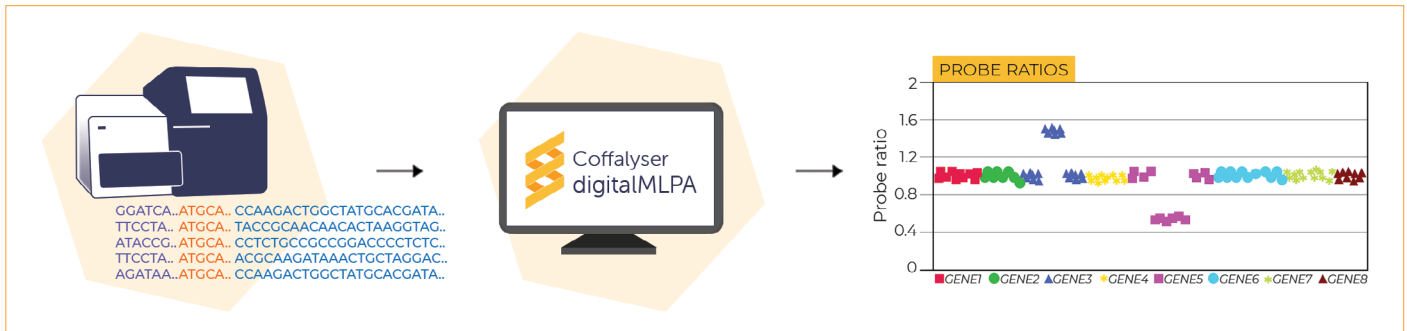
³ Four barcode plates are available to uniquely label 384 (96x4) samples: BP01-IL, BP02-IL (for all probemixes), BP03-IL and BP04-IL (compatible with Nxtec D001 Hereditary Cancer Panel 1 only).

Please read Instructions for use for more detailed instructions.

Coffalyser digitalMLPA™

Data analysis software for clear CNV calling

- ✓ **Simple:** FASTQ files are directly loaded into the software
- ✓ **Smart:** automatic digitalMLPA read and probemix recognition
- ✓ **Reliable:** extensively tested and validated
- ✓ **Safe:** thorough built-in quality control



Coffalyser digitalMLPA is free and easy-to-use software developed by MRC Holland and built specifically for the analysis of digitalMLPA data. The software automatically recognises and extracts digitalMLPA sequence reads from FASTQ files. This is followed by advanced data quality checks, and the return of a clear report displaying all detected aberrant regions.

Interested in digitalMLPA?
For ordering and more information, visit
mrcholland.com or email info@mrcholland.com.

