

High confidence in **copy number determination** with **MLPA** and **digitalMLPA** to support comprehensive **BRCA & HR deficiency testing**

Genetic variants in *BRCA1*, *BRCA2*, *PALB2* and other cancer-associated genes, particularly those involved in the homologous recombination (HR) repair pathway, can give rise to cancer and influence therapeutic decisions. Both copy number variations (CNVs) and promoter methylation, especially of *BRCA1* and *RAD51C*, are emerging biomarkers for guiding clinical interventions, including the use of PARP inhibitors.

**MRC Holland offers over 20 assays** specifically designed for the detection of these genetic alterations, enabling the study of predisposition to breast and ovarian cancer and tumour profiles in these cancer types. These assays are based on the well-established **SALSA® MLPA®** technology and the innovative technique **digitalMLPA™**.

Reliable  
CNV  
detection

Multiple  
targets per  
reaction

High-  
throughput  
solutions

Simple  
data  
analysis

### Germline analysis

digitalMLPA assay	Target genes/regions
<b>NXtec™ D001 Hereditary Cancer Panel 1</b> 582 probes targeting 28 genes associated with a predisposition to 8 common hereditary cancer types, and 5 variants	<i>APC</i> , <i>ATM</i> , <i>BAP1</i> , <i>BARD1</i> , <i>BMPR1A</i> , <i>BRCA1</i> , <i>BRCA2</i> , <i>BRIP1</i> , <i>CDH1</i> , <i>CDK4</i> , <i>CDKN2A</i> , <i>CHEK2</i> , <i>EPCAM</i> , <i>MITF</i> (p.E318K), <i>MLH1</i> , <i>MSH2</i> , <i>MSH6</i> , <i>MUTYH</i> , <i>NBN</i> , <i>PALB2</i> , <i>PMS2</i> , <i>POLE</i> , <i>PTEN</i> , <i>RAD51C</i> , <i>RAD51D</i> , <i>SCG5/GREM1</i> , <i>SMAD4</i> , <i>STK11</i> , <i>TP53</i>
<b>NXtec™ D002 Hereditary Cancer Panel 2</b> 1031 probes targeting 56 genes associated with a predisposition to a wide range of hereditary cancer types, and 8 variants	All D001 targets + <i>CEBPA</i> , <i>DICER1</i> , <i>FH</i> , <i>FLCN</i> , <i>HOXB13</i> , <i>MAX</i> , <i>MEN1</i> , <i>MET</i> , <i>NF1</i> , <i>NF2</i> , <i>NTHL1</i> , <i>PHOX2B</i> , <i>POLD1</i> , <i>PTCH1</i> , <i>RB1</i> , <i>RUNX1</i> , <i>SDHA</i> , <i>SDHAF2</i> , <i>SDHB</i> , <i>SDHC</i> , <i>SDHD</i> , <i>SMARCB1</i> , <i>SUFU</i> , <i>TMEM127</i> , <i>TSC1</i> , <i>TSC2</i> , <i>VHL</i> , <i>WT1</i>

SALSA® MLPA® Probemix	Target genes/regions
<b>P002</b> BRCA1	<i>BRCA1</i>
<b>P087</b> BRCA1 Confirmation	<i>BRCA1</i>
<b>P239</b> BRCA1 region	<i>BRCA1</i> upstream and downstream region, including <i>BRCA1P1</i>
<b>P090</b> BRCA2	<i>BRCA2</i>
<b>P045</b> BRCA2/CHEK2	<i>BRCA2</i> , <i>CHEK2</i> (+c.del1100C)
<b>P077</b> BRCA2 Confirmation	<i>BRCA2</i>
<b>P190</b> CHEK2	<i>CHEK2</i> (+c.del1100C), <i>ATM</i> , <i>TP53</i>
<b>P240</b> BRIP1/CHEK1	<i>BRIP1</i> , <i>CHEK1</i>
<b>P260</b> PALB2-RAD50-RAD51C-RAD51D	<i>PALB2</i> , <i>RAD50</i> , <i>RAD51C</i> , <i>RAD51D</i>
<b>P057</b> FANCD2-PALB2	<i>FANCD2</i> , <i>PALB2</i>
<b>P041</b> ATM-1	<i>ATM</i>
<b>P042</b> ATM-2	<i>ATM</i>
<b>P083</b> CDH1	<i>CDH1</i>
<b>P101</b> STK11	<i>STK11</i>
<b>P056</b> TP53	<i>TP53</i> , <i>CHEK2</i> (+c.del1100C)
<b>P225</b> PTEN	<i>PTEN</i> , <i>PTENP1</i>
<b>P489</b> BARD1	<i>BARD1</i>
<b>P494</b> NBN	<i>NBN</i>
<b>P003</b> MLH1/MSH2	<i>MLH1</i> , <i>MSH2</i> , <i>EPCAM</i>
<b>P248</b> MLH1-MSH2 Confirmation	<i>MLH1</i> , <i>MSH2</i>
<b>P072</b> MSH6-MUTYH	<i>MSH6</i> , <i>MUTYH</i> , <i>MSH2</i> , <i>EPCAM</i>
<b>P008</b> PMS2	<i>PMS2</i> , <i>PMS2CL</i>

### Tumour analysis

SALSA® MLPA® Probemix	Target genes/regions
<b>P078</b> Breast tumour	6q ( <i>ESR1</i> ), 7p ( <i>EGFR</i> ), 8p ( <i>ZNF703</i> , <i>FGFR1</i> , <i>IKBKB</i> ), 8q ( <i>MTDH</i> , <i>MYC</i> ), 11q13 ( <i>CCND1</i> , <i>EMSY</i> ), 16q ( <i>CDH1</i> ), 17q12-q25 ( <i>ERBB2</i> , <i>TOP2A</i> , <i>BIRC5</i> ), 19q ( <i>CCNE1</i> ), 20q ( <i>AURKA</i> )
<b>P483</b> HER gene family	<i>EGFR</i> , <i>ERBB2</i> , <i>ERBB3</i> , <i>ERBB4</i>
<b>P056</b> TP53	<i>TP53</i> , <i>CHEK2</i> (+c.del1100C)
<b>P083</b> CDH1	<i>CDH1</i>
<b>P225</b> PTEN	<i>PTEN</i> , <i>PTENP1</i>
<b>ME053</b> BRCA1-BRCA2-RAD51C	<i>BRCA1</i> , <i>BRCA2</i> , <i>RAD51C</i> methylation profiling
<b>ME011</b> Mismatch Repair Genes	<i>MLH1</i> , <i>MSH6</i> , <i>PMS2</i> methylation, <i>BRAF</i> p.V600E point mutation and <i>EPCAM</i> copy number profiling
<b>ME001</b> Tumour suppressor mix	Methylation profiling of tumour suppressor genes



# digitalMLPA™



## High-throughput analysis of copy number status

- ✓ NGS-based MLPA for the detection of CNVs and targeted variants
- ✓ Only requires a thermocycler and Illumina sequencing platform
- ✓ Up to 1600 targets per reaction
- ✓ 20 ng of DNA input per sample
- ✓ Free analysis software: **Coffalyser digitalMLPA™**

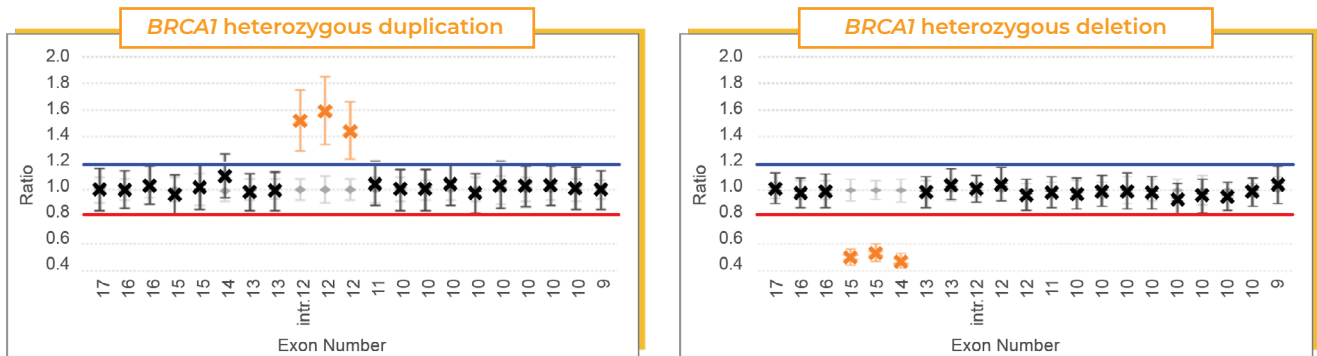


Figure 1. Representation of copy number results using NXtec D002 Hereditary Cancer Panel 2 and Coffalyser digitalMLPA. Probe Ratios sorted by genomic location. A selection of data points is shown.

# SALSA® MLPA®



## The go-to technique for studying CNVs associated with disease

- ✓ Multiplex PCR-based method for CNV and targeted variants detection
- ✓ Only requires a thermocycler and capillary electrophoresis device
- ✓ 40-60 targets per reaction
- ✓ 50 ng of DNA input per sample
- ✓ Free analysis software: **Coffalyser.Net™**

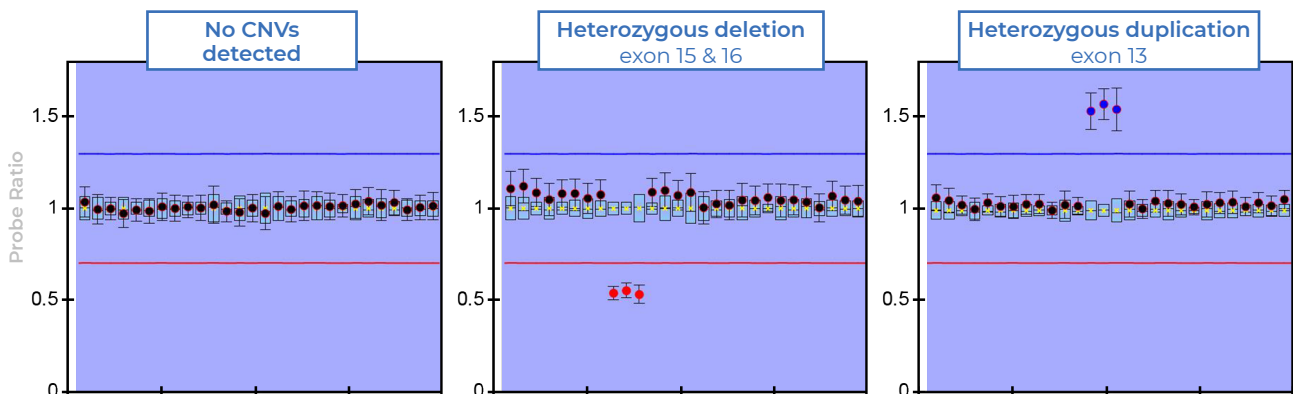


Figure 2. Representation of *BRCA1* copy number results using SALSA® MLPA® Probemix P002 *BRCA1* and Coffalyser.Net. Probe Ratios sorted by genomic location. A selection of data, from *BRCA1* exon 24 (left) to exon 7 (right), is shown.