

The BRCA Hereditary Cancer (HC) MASTR Plus in combination with the MASTR Reporter BRCA HC MASTR Plus application, is a complete research solution (NGS library preparation assay, analysis tool and quality control), for the identification of variants in 25 genes and the 3'UTR of *EPCAM* associated with hereditary breast, ovarian and other related cancers.



Research application

- For the detection of variants (SNVs, small indels) and CNVs, in 26 (25 genes plus the 3'UTR of *EPCAM*) cancer predisposition associated genes on blood-derived DNA using Illumina MiSeq

Assay characteristics

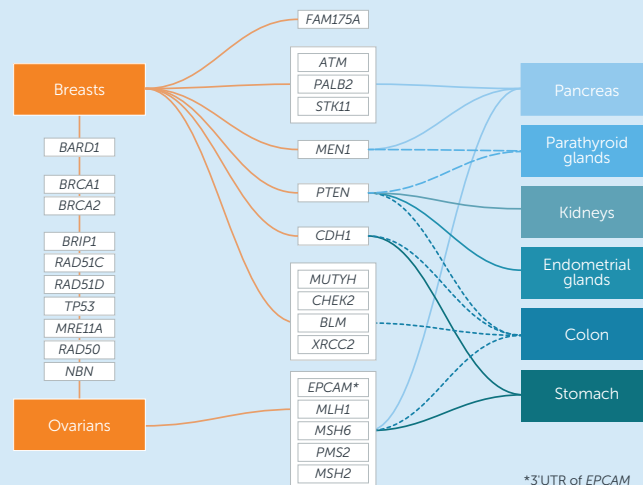
Genes	<i>BRCA1, BRCA2, PALB2, CHEK2, BARD1, BRIP1, RAD51C, RAD51D, TP53, MRE11A, RAD50, NBN, FAM175A, ATM, STK11, MEN1, PTEN, CDH1, MUTYH, BLM, XRCC2, MLH1, MSH6, PMS2</i> and <i>MSH2</i> , and the 3' UTR of <i>EPCAM</i>
Genomic region analyzed	140.5 kb
Number of amplicons	561
Amplicon length	232-430 bp
Number of plexes	5
Verified with NGS System	MiSeq V3
Designed to be compatible with	MiSeq
Compatible analysis options*	MASTR Reporter BRCA HC MASTR Plus application

*Also compatible with analysis tools *Sophia DDM* and *JSI SeqNext*

Performance

Uniformity of amplification (0.2x mean coverage)	96.7 %
On target read count	98.6 %
DNA input	as low as 20 ng per plex
Number of samples/run	Illumina MiSeq V3: 93

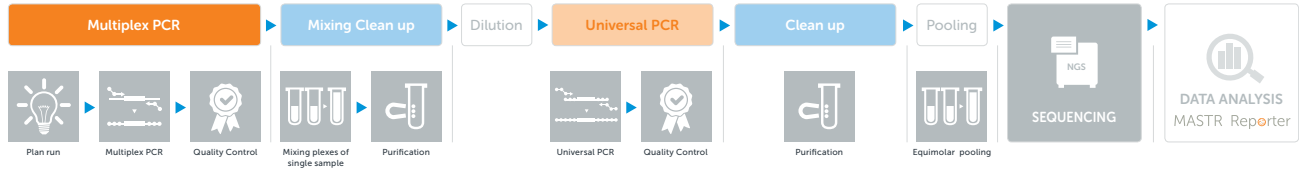
Disease-associated genes



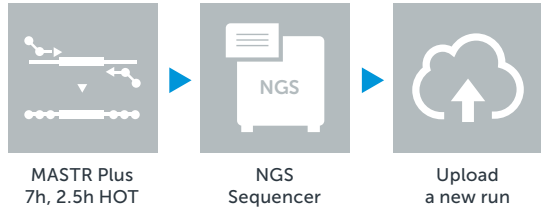
*3' UTR of *EPCAM*

*3' UTR of *EPCAM* only

Workflow



Workflow

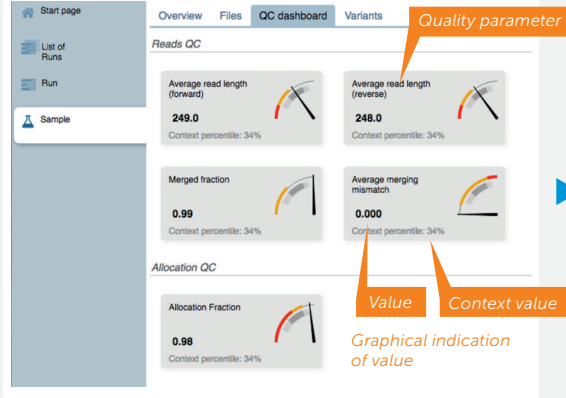


Automated analysis

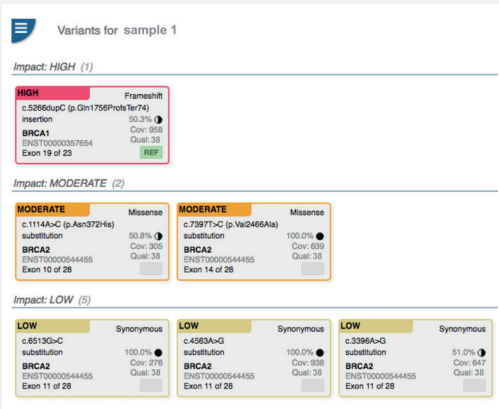
Targeted analysis time/sample \pm 40 min*

* Determined by number of reads in file if CNV analysis was selected

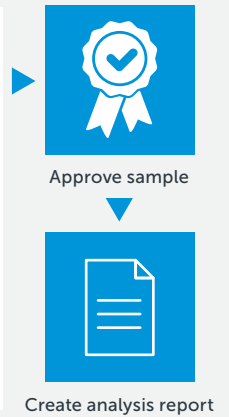
Quality control



Variant calling



Read pile-up views



Order info

Cat. No.	Product Name	Samples
MR-1320.024	BRCA Hereditary Cancer MASTR Plus + MASTR Reporter BRCA Hereditary Cancer MASTR Plus	24

MID (Molecular Identifiers) kits are necessary to complete the workflow.

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