

HNPCC MASTR Plus

Research Application

- For detection of germline variants, SNVs and CNVs, in *MLH1*, *MSH2*, *MSH6*, and *PMS2* and 3' UTR of *EPCAM* in blood-derived DNA.

The HNPCC MASTR Plus is a disease research panel for the identification of variants in 4 genes (*MLH1*, *MSH2*, *MSH6*, and *PMS2*) and 3' UTR of *EPCAM*, which are associated with hereditary non-polyposis colorectal cancer (HNPCC). This panel is ready to use and offers robust performance with minimum hands-on time. It consists of all the reagents necessary to enable multiplex amplification of 84 amplicons for complete exon coverage of the *MLH1*, *MSH2*, *MSH6*, *PMS2* and 3' UTR of *EPCAM*.

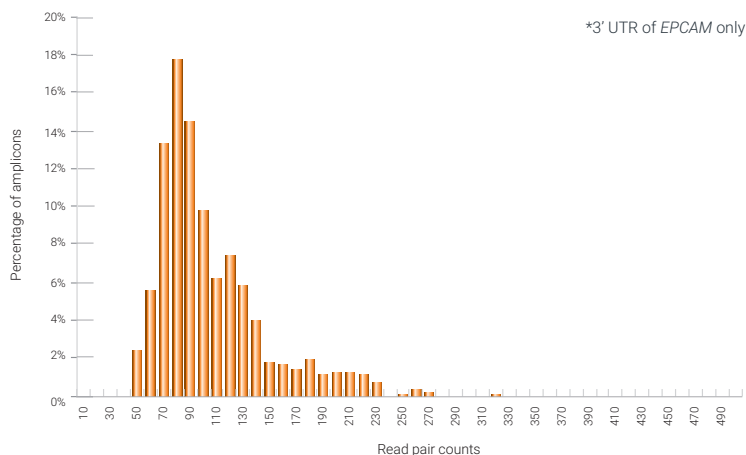
Assay Characteristics	
Genes analyzed	full coding region of <i>MLH1</i> , <i>MSH2</i> , <i>MSH6</i> , and <i>PMS2</i> and 3' UTR of <i>EPCAM</i>
Genomic region analyzed	20 kb
Number of amplicons	84
Amplicon length	277-443 bp
Number of plexes	5
Designed to be compatible with	Illumina MiSeq

Performance	
Uniformity of amplification (0.2x mean coverage)	100 %
On target read count	> 95 %
DNA input	as low as 20 ng per plex reaction
Number of samples/run (20 reads/allele):	Illumina MiSeq V2: 670* Illumina MiSeq V3: 1,229*

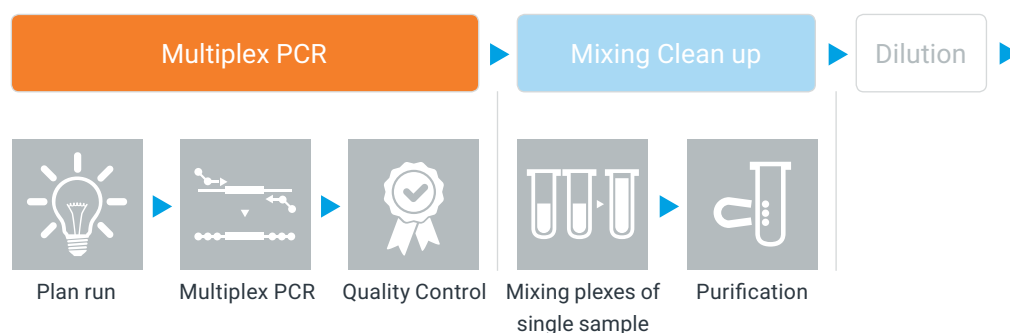
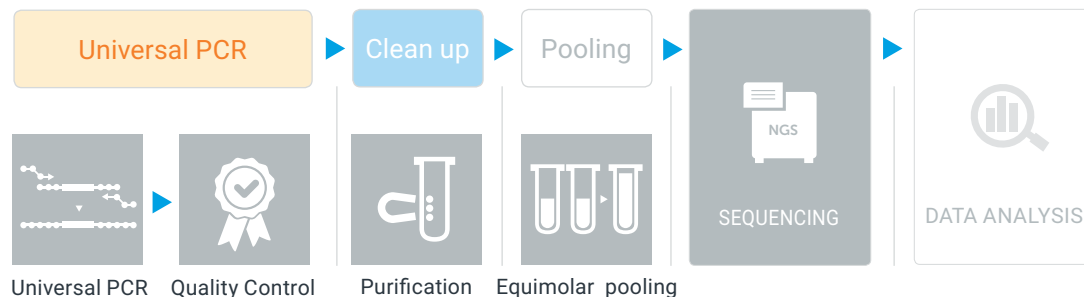
*only 192 MID combinations available.

Performance cont.

Graph presenting the read pair counts for all HNPCC MASTR Plus amplicons, showing their outstanding uniform representation. To allow comparison between samples, the read pair counts were normalized to coverage of 100. The data are based on a 10 samples study, using the Illumina MiSeq System.



MASTR Plus Workflow



Ordering Information

Cat. No.	Product Name	Reactions
MR-0031.024	HNPCC MASTR Plus	5

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

www.agilent.com

Not for EU

genomics@agilent.com

For Research Use Only. Not for use in diagnostic procedures.

This information is subject to change without notice.

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