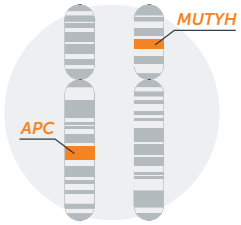
Multiplicom
A part of Agilent Technologies

# FAP MASTR

FAP MASTR is a molecular research assay for the identification of variants in the complete coding regions of the *APC* and *MUTYH* genes, which are associated with familial adenomatous polyposis (FAP). This assay 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 52 amplicons for complete exon coverage of the *APC* and *MUTYH* genes.




## Research application

- For detection of germline variants and SNVs in *APC* and *MUTYH* in blood-derived DNA.

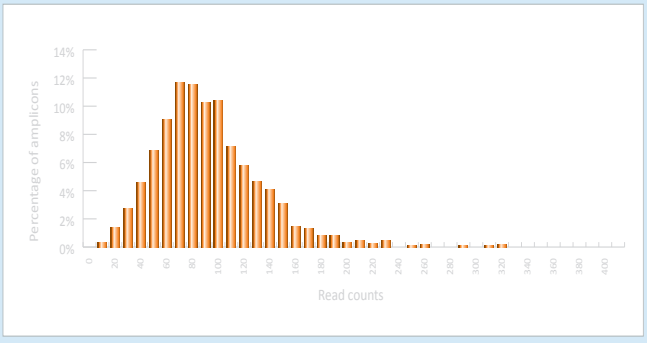
## Assay characteristics

| | |
|---|---|
| Genes | Full coding region of *APC* and *MUTYH* |
| Genomic region analyzed | 14.7 kb |
| Number of amplicons | 52 |
| Amplicon length | 245-455 bp |
| Number of plexes | 3 |
| Designed to be compatible with | MiSeq |

## Performance Characteristics

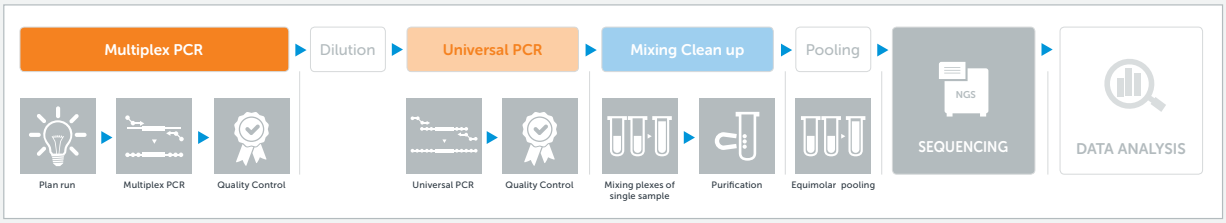
| | |
|---|---|
| Uniformity of amplification (0.2X mean coverage) | 99.7 % |
| On target read count | > 96 % |
| DNA input | as low as 20 ng per plex reaction |
| Number of samples/run (20 reads/allele): | Illumina MiSeq V2: 1,200*<br>Illumina MiSeq V3: 2,200* |

**only 192 MID combinations available.*




*Graph presenting the read counts for all FAP MASTR amplicons, showing their outstanding uniform representation. To allow comparison between samples, the read counts were normalized to coverage of 100. The data are based on 22 samples collected from three centers.*

## Workflow




## Order info

| Cat. No. | Product Name | Reactions |
|---|---|---|
| *MR-0040.008* | *FAP MASTR* | *3* |

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


Printed in Belgium, December 31, 2017
5991-8384ENN
PR7000-1409

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

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