FAP MASTR

Research Application

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

FAP MASTR is a disease research panel 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 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 52 amplicons for complete exon coverage of the *APC* and *MUTYH* genes.

Assay Characteristics	
Genes analyzed	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	Illumina MiSeq

Performance	
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* Illumina MiSeq V3: 2,200*

**only 192 MID combinations available.*

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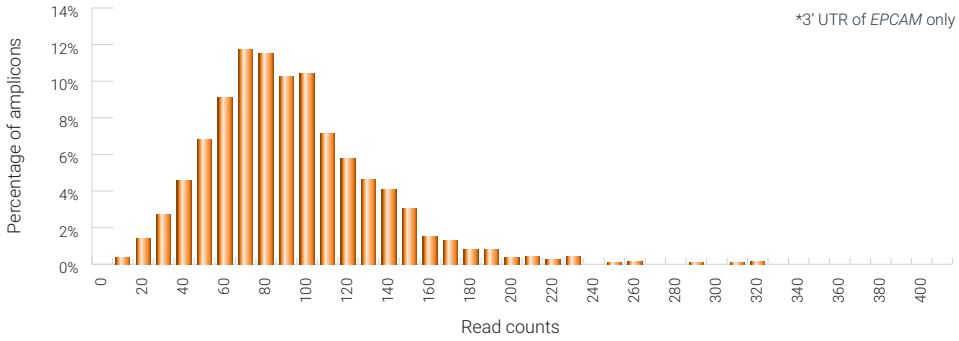
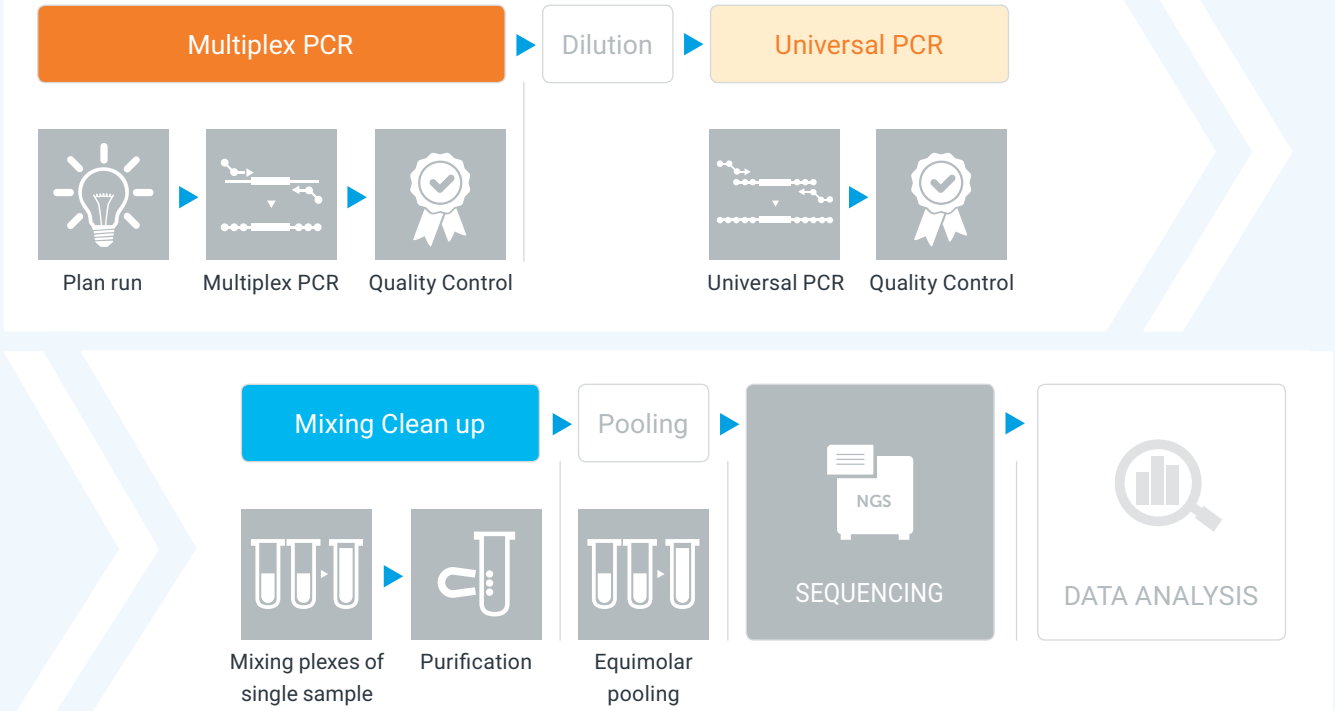
Performance cont.

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 a coverage of 100. The data is based on 22 samples collected from three centers.



MASTR Workflow



Ordering Information

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

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

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

This information is subject to change without notice.

PR7000-0725

Published in the USA, September, 2017
5991-8362ENUC

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