Multiplicom
A part of Agilent Technologies

FMF MASTR v2

A simple and robust Research assay for complete mutation analysis in the coding regions of the *MEFV* gene by Next-Generation Sequencing. Mutations of the *MEFV* gene affect normal functioning of the pyrin protein, leading to the inflammatory disorder Familial Mediterranean Fever (FMF).

Application

- For the identification of mutations (SNVs and indels) in the Mediterranean Fever gene (*MEFV*).
- For complete mutational spectrum analysis in one assay
- Ready-to-use kit with simple-to-follow protocols

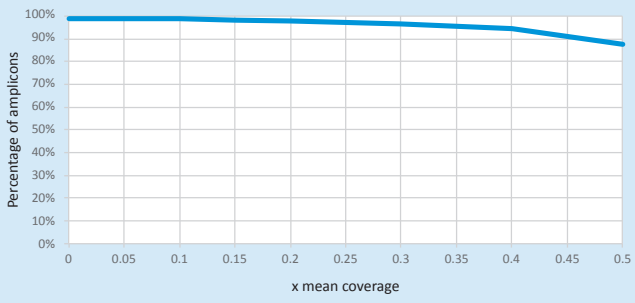
Assay characteristics

Gene analyzed	*MEFV*
Genomic region analyzed	4.2 kb All exons ±30 bp flanking region
Number of amplicons	23
Amplicon length	250-400 bp
Number of plexes	2
DNA amount required	20 ng per multiplex reaction
Compatible with	MiSeq System, Illumina

Performance Parameters

FMF MASTR v2 on MiSeq; germline DNA

	DNA extracted from blood
On target read pair counts	*94.6 %* *[87.6 % - 97.6 %]*
Uniformity of amplification (0.2x mean coverage)	*99.4 %*

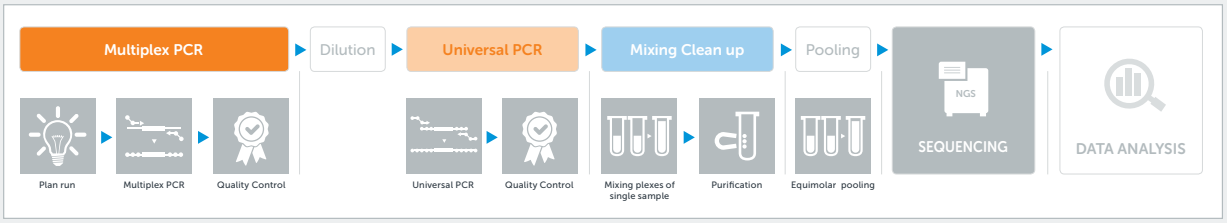


Graph representing the read pair counts for all 23 FMF MASTR v2 amplicons, showing their uniform representation. To allow comparison between samples, the read counts were normalized.

Workflow

Advised maximum number of samples per run

Sequencing System	Illumina MiSeq		
	Reagent Kit		
Flow cell	*Nano v 2* *2 x 251 cycles*	*v2* *2 x 251 cycles*	*v3* *2 x 276 cycles*
SNV variant calling Minimal coverage per allele: 50	*116*	*1753*	*3215*



Order info

Cat. No.	Product Name	Reactions
MR-0071.024	*FMF MASTR v2*	*24*

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

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

Printed in Belgium, December 31, 2017
5991-8953ENN
PR7000-1436

Multiplicom N.V. [a] Galileïlaan 18, B-2845 Niel, Belgium [w] www.agilent.com [e] mtp.customerservice@agilent.com [t] +32 3 289 14 00 [f] +32 3 400 23 16