Multiplicom
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DMD MASTR

A simple and robust molecular research assay for the identification of all SNVs and CNVs in the *DMD* gene associated with Muscular Dystrophies

Research application

Detection of *DMD* variants associated with

- Duchenne Muscular Dystrophy (DMD)
- Becker Muscular Dystrophy (BMD)
- X-linked dilated cardiomyopathy (XLCM)

Assay characteristics

Genes analyzed	*DMD* transcript NM_004006 (Dp427m isoform)
Genomic region analyzed	23 kb all 79 exons +/- 30 kb flanking region CNVs and SNVs
Number of amplicons	118 including 28 control amplicons
Amplicon length	280-400 bp
Number of plexes	4
DNA amount required	20 ng per multiplex reaction

Workflow

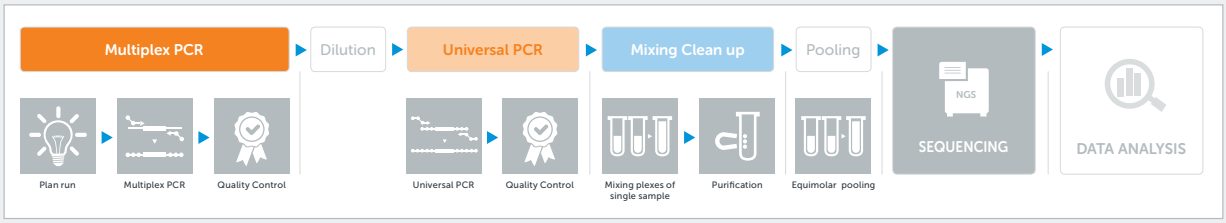
Advised maximum number of samples per run:

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*
For SNV only			
Minimal coverage per allele: 20	*35*	*530**	*972 **
For SNV and CNV			
Minimal coverage per amplicon: 200	*7$*	*107*	*196**

* *only 192 MID combinations available*

$ *for statistically reliable CNV calling, it is advised to analyze minimum 10 samples together. Identical CNVs can not be present in more than 15 % of the samples of a sequencing run.*

Workflow



Order info

Cat. No.	Product Name	Reactions
MR-0120.008	*DMD MASTR*	*8*

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

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