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.*

For the number of samples per run on Life Technologies Ion Torrent Systems, please refer to the Sequence Calculator on the Agilent website.

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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