

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	<i>DMD</i> 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

Advised maximum number of samples per run:

Workflow

Sequencing System	Illumina MiSeq®		
	Reagent kit		
<i>Flow cell</i>	<i>Nano v2</i> 2 x 251 cycles	v2 2 x 251 cycles	v3 2 x 276 cycles
For SNV only			
<i>Minimal coverage per allele: 20</i>	35	530*	972 *
For SNV and CNV			
<i>Minimal coverage per amplicon: 200</i>	7 ⁵	107	196*

* only 192 MID combinations available

⁵ 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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