

HGNC approved gene symbol	Transcript	OMIM gene ID	Median depth	% covered >10x	% covered >20x	% covered >30x	% covered >50x
<i>ACTA1</i>	NM_001100.3	102610	165	100	100	100	100
<i>ANOS2**</i>	NM_213599.2	608662	160	100	100	100	100
<i>CAPN3**</i>	NM_000070.2	114240	118	100	100	100	100
<i>CAV3**</i>	NM_033337.2	601253	159	100	100	100	100
<i>COL6A1</i>	NM_001848.2	120220	122	100	100	100	98
<i>COL6A2</i>	NM_001849.3	120240	114	100	100	100	97
<i>COL6A3</i>	NM_004369.3	120250	202	100	100	100	100
<i>COLQ</i>	NM_005677.3	603033	126	100	100	100	100
<i>DAG1</i>	NM_001165928.3	128239	292	100	100	100	100
<i>DES</i>	NM_001927.3	125660	143	100	100	100	100
<i>DMD**</i>	NM_004006.2	300377	119	100	100	100	100
<i>DNAJB6</i>	NM_058246.3	611332	137	100	100	100	100
<i>DOK7</i>	NM_173660.4	610285	245	100	100	100	100
<i>DPM3</i>	NM_018973.3	605951	190	100	100	100	100
<i>DYSF**</i>	NM_003494.3	603009	122	100	100	100	100
<i>EMD**</i>	NM_000117.2	300384	107	100	100	100	100
<i>FHL1</i>	NM_001159702.2	300163	97	100	100	100	99
<i>FKRP**</i>	NM_024301.4	606596	187	100	100	100	100
<i>FKTN</i>	NM_001079802.1	607440	164	100	100	100	100
<i>FLNC</i>	NM_001458.4	102565	129	100	100	100	100
<i>GAA</i>	NM_000152.3	606800	136	100	100	100	100
<i>GFPT1</i>	NM_001244710.1	138292	161	100	100	100	99
<i>GNE</i>	NM_001128227.2	603824	162	100	100	100	100
<i>ISPD</i>	NM_001101426.3	614631	148	100	100	100	99
<i>ITGA7</i>	NM_002206.2	600536	125	100	100	100	99
<i>LAMA2</i>	NM_000426.3	156225	162	100	100	100	100
<i>LDB3</i>	NM_007078.2	605906	116	100	100	100	100
<i>LMNA**</i>	NM_170707.2	150330	105	100	100	100	100
<i>MICU1**/**</i>	NM_006077.3	605084	***	100	100	100	100
<i>MYH7</i>	NM_000257.3	160760	163	100	100	100	100
<i>MYOT**</i>	NM_006790.2	604103	192	100	100	100	100
<i>NEB</i>	NM_001271208.1	161650	178	100	100	100	100
<i>PLEC</i>	NM_000445.3	601282	180	100	100	100	99
<i>POMGNT1</i>	NM_001243766.1	606822	135	100	100	100	100
<i>POMT1</i>	NM_007171.3	607423	152	100	100	100	100
<i>POMT2</i>	NM_013382.5	607439	112	100	100	100	98
<i>RAPSN</i>	NM_005055.4	601592	109	100	100	100	100
<i>RYR1</i>	NM_000540.2	180901	109	100	99	99	98
<i>SELENON (SEPN1)</i>	NM_020451.2	NA	132	89	89	88	87
<i>SGCA**</i>	NM_000023.2	600119	131	100	100	100	100
<i>SGCB**</i>	NM_000232.4	600900	140	100	100	100	100
<i>SGCD**</i>	NM_000337.5	601411	132	100	100	100	100
<i>SGCG**</i>	NM_000231.2	608896	127	100	100	100	100
<i>SMCHD1***</i>	NM_015295.2	614982	***	100	100	100	100
<i>TCAP**</i>	NM_003673.3	604488	141	100	100	100	100
<i>TPM3</i>	NM_152263.2	191030	175	100	100	100	100
<i>TRIM32**</i>	NM_012210.3	602290	256	100	100	100	100
<i>TTN</i>	NM_001267550.1	188840	333	100	100	100	100

* Muscular dystrophies / myopathies

** Core genes (if necessary additional Sanger sequencing will be performed for 100% coverage)

***For these genes Sanger sequencing is performed

MLPA for *DMD* is included in the gene panel Muscle Disorders