

**Figure S1.** Splicing changes of alternative exons of six genes in DM1 (samples 1-7) and DM2 (samples 8-16) compared to non-DM muscle samples. For each DM sample the deltaPSI was calculated based on MLPA-based splicing assays described before (Wojciechowska et al., 2014). Samples included in BP\_DM2 sample sets are indicated in red.

circASXL1 exon 4 3' end exon 2 5' end	circCAMSAP1 exon 3 3' end exon 2 5' end	exon 10 3' end circFAM13B exon 8 5' end
хт са ос с т т т т са с о с т сало <mark>о</mark> тат та на алас та с т с о о ат		A GAAT GAAGAAAATAC C CA <mark>g</mark> cac c ca ta ta t c t c c cat ca A Aa AA A A A A A A A A A A A A A A A
Man Margan Man Mala Marga	MMMMMMMMMM/MMM/MMM/MM	IN MININA MARAAMAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
circHIPK3 exon 2 3' end exon 2 5' end	circMBOAT2	circMIB1 exon 6 3' end exon 2 5' end
стасаат ст с оота ста са фота тоос ст са салот с тто		
MMMMMMMMMM		
circNFATC3 exon 3 3' end exon 2 5' end	circPHC3	circPIP5K1C exon 4 5' end
9 9 9 9 A CAT C C TO TTO TO A A OAT C TTO A O C C A O A TO A T	CACCARTANTARCACCARPTCAACCTCTCCACTTCTCC	
MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM		
circSCMH1 exon 10 3' end exon 9 5' end	circSHKBP1 exon 12 3' end exon 11 5' end	circUBAP2_e7-8 exon 8 3' end exon 7 5' end
		те ет есле лте ло е еллсто <mark>р</mark> лттте елсете есле ле есе Ладала Алада. Л
	mmmmhmmmhmmm	MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM
circUBAP2_e9-12 exon 12 3' end exon 9 5' end	circZKSCAN1	circCCDC134 exon 2 5' end
CTOTTCTCCCTCAOAOCCTGAACTOOCATCAAATACTCAC		
MWWWW/WW/WWWWW	MWWWWWWWWWWW	Mappan Halle Mar M Malmas
exon 3 3' end exon 2 5' end	circPDCD11 exon 27 3' end exon 26 5' end	circPROSC
	CACACOOTOTOTTCTTTCO <mark>ATOTTACATCCTOTCCACTO</mark>	LAAT GT CAA CAA AT T G AT G O O AT C T C C C A G C C AT C C A G C C
a Markey Markey Markey Markey	Man	
circCDR1as	circ/BNL1 exon 2.3' end exon 2.5' end	
Mahalman Wm mana haan	MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM	

Figure S2. Results of Sanger sequencing of the predicted back-splice sites of the selected circRNAs.



**Figure S3.** Identification of a new circRNA derived from the *MBNL1* gene. **A)** Agarose gel electrophoresis of the product of PCR performed with the use of circMBNL1-specific primers (right-hand side track). Lower and upper bands represent known circMBNL1 (hsa\_circ\_0001348) and the newly identified circMBNL1', respectively. The size of the upper band does not correspond to a potential concatemer. The left-hand side track is the GeneRuler 1 kb DNA Ladder (Thermo Fisher Scientific). **B**) The results of the Sanger sequencing of PCR products corresponding to upper and lower bands. Sequencing of the lower band confirmed the expected circMBNL1 back-splice site. However, sequencing of the upper band revealed an additional 93-nt long fragment of the downstream intron. The sequences of both circRNAs are shown to the right. **C**) The map showing the localization of MBNL1 circRNAs. The blue (RefSeq) track shows a fragment of *MBNL1* overlapping exon 2. Black tracks indicate known circMBNL1'. The green track depicts exons predicted with high confidence by the GENSCAN online tool.



**Figure S4**. Bar graphs showing the results of circRNA expression analysis performed with the use of different sample sets. A) CL\_DM1, B) BP\_DM1, C) BP\_DM2, D) MM\_DM1. The scheme of the bar graphs is similar to that used in Figure 2.



**Figure S5.** Dot plots depicting the cumulative level of 'all' (upper panels) and 'validated' (lower panels) circRNAs in control and DM1 samples of QF and TA. The scheme of the panels is the same as that used in Figure 3.



**Figure S6.** Scatter plots showing correlations of circRNA levels normalized as RPMs (axis X) and FCRs (axis Y). For both QF (on the left-hand side) and TA (right-hand side) samples, the  $R^2$  values are shown above the trendline (red line). Each dot represents an individual circRNA.

	UniProt											
QF	Sublist	<u>Category</u>	¢ <u>Term</u>	\$ RT	Genes		<u>Count</u> \$	<u>%</u> 🗘 <u>F</u>	<u>P-Value</u> ≑	Fold Enrichment	♦ <u>Benjamini</u> ♦	
		UP_KEYWORDS	Phosphoprotein	RT		1	15 8	33,3 4,6	6E-4 2	,1	4,0E-2	
		UP_KEYWORDS	Isopeptide bond	<u>RT</u>	_	5	5 3	27,8 1,2	2E-2 5	,1	4,2E-1	
		UP_KEYWORDS	Alternative splicing	RT		1	14 7	77,8 3,2	2E-2 1	,5	6,2E-1	
ТА	Sublist	<u>Category</u>	≑ <u>Term</u>	\$	RT Ger	es	Cou	<u>nt</u> ≑ <u>%</u> ≎	P-Value	Fold Enrichmer	it 💠 <u>Benjamini</u> 🗘	
		UP_KEYWORDS	Phosphoprotein	ļ	RT		46	68,7	3,5E-6	1,7	5,4E-4	
		UP_KEYWORDS	Alternative splicing	1	RT		52	77,6	1,4E-5	1,5	1,1E-3	
		UP_KEYWORDS	Isopeptide bond	ļ	RT		13	19,4	2,3E-4	3,5	1,2E-2	
		UP_KEYWORDS	Nucleus	1	RT		31	46,3	3,4E-4	1,8	1,3E-2	
		UP_KEYWORDS	Acetylation	1	RT		23	34,3	6,9E-4	2,1	2,1E-2	
cellular component												
QF	Sublist	Categ	lory ¢ <u>Term</u>	\$ RT	Genes	Cour	<u>nt</u> 🗢 <u>%</u>	¢ <u>P-Val</u>	lue 🗘 🕴 🛛	Fold Enrichment	♦ <u>Benjamini</u> ♦	
		GOTERM_CC_DIF	RECT <u>cytoplasm</u>	<u>RT</u>		10	55,6	3,0E-2	1,9		7,6E-1	
		GOTERM_CC_DIF	RECT <u>nucleoplasm</u>	<u>RT</u>		7	38,9	3,4E-2	2,5		5,6E-1	
ТА	Sublist	<u>Category</u>	÷	<u>Term</u>	¢ RT	Genes	<u><u>c</u></u>	<u>ount</u> ≑ <u>१</u>	<u>6</u> ≑ <u>P-Valu</u>	IE Fold Enrichme	<u>int</u> ≑ <u>Benjamini</u> ≑	
		GOTERM_CC_DIRE	CT <u>nucleoplasm</u>		RT	_	24	35	,8 2,9E-5	2,5	3,5E-3	
		GOTERM_CC_DIRE	CT <u>sarcoplasmic reticulu</u>	m membrane	<u>RT</u>	-	4	6,0	) 2,2É-4	33,5	1,3E-2	

**Figure S7.** Summary of the functional association analysis showing the most significant enrichment results for UniProt and Gene Ontology "cellular component" categories in the list of genes differentiated in QF and TA.



**Figure S8.** The maps of genomic regions of the top-MCGs in which both QF and TA consequently generate more than ten distinct circRNA species. The colors of the tracks are shown in Figure 5B.