

## Supplemental data

### Experimental procedure

**Two-dimensional gels and mass spectrometry.** Samples were diluted in isoelectric focusing buffer (7M urea, 2M thiourea, 4% CHAPS, 1% DTT), absorbed into 17 cm ReadyStrip™ IPG strips (Bio-Rad Laboratories, Hercules, CA), and separated with a pH range of 4 to 7 following the manufacturer's instructions. Amounts of 200 µg of cytosolic proteins and 30 µg of phosphoproteins were used. Isoelectric focusing was performed on a Protean IEF Cell (Bio-Rad Laboratories) with the following program: 200 V for 1 hour, 500 V for 1 hour, 5000 V ramp for 5 hours and 5000 V until it rate up to 80,000 VH. For the second dimension, IPG strips were overlaid onto 10% SDS-PAGE gels and electrophoresed with the Protean II apparatus (Bio-Rad Laboratories). SDS-PAGE gels were fixed in a 10% methanol and 7% acetic acid solution for 30 minutes, before being stained with Sypro Ruby protein gel stain (Sigma-Aldrich) overnight at room temperature under agitation. Thereafter, gels were washed in a fixing solution for 30 min, and imaged on an AlphaImager™ (AlphaInnotech, San Leandro, CA). Each experiments samples (healthy and GRMD) were ran independently repeated 3 times for the cytosolic experiment and 2 times for the phosphoprotein experiment due to sample availability, and representative 2-D gels were used for the figure 2 and to excise protein spots.

In-gel digests were performed using a standard method<sup>33</sup>. Briefly, sample cleanup was performed using ZipTip (Millipore Corporation, Billerica, MA). Tandem mass spectra were collected on an Applied Biosystems/SciEX QSTAR XL with oMALDI2 ion source. Spectra were analyzed using Mascot 2.0 (Matrix Science, UK) and the NCBI non-redundant protein sequence dog database (release 2008.03.28; 34217 sequences). MS/MS tolerance was  $\pm 0.2$  Da. SYPRO Ruby-stained gels were analyzed with PDQuest software (Version 8.0, Bio-Rad Laboratories) for gel-to-gel matching and identifying differences between dystrophic and healthy dog muscle samples. The gel images were normalized in the PDQuest software using the local regression model to even out differences in staining intensities between gels. Each matched protein spot was assigned a unique SSP (sample spot protein) number in the PDQuest software. A minimum of 1.42-fold change was considered for the up-regulated proteins and 0.7-fold for down-regulated proteins.

### Result

**2-D gel-based proteomic analysis revealed differentially expressed proteins in canine dystrophic muscle.** To identify protein changes associated with DMD, two-dimensional (2-D) gel analysis coupled with mass spectrometry was performed on the *Vastus lateralis* muscle removed from 4-month-old healthy and dystrophic dogs. In the experiment using the crude cytosolic fraction of muscle (Figure 1A), 146 protein spots were detected by PDQuest, of which 95 corresponded to differentially expressed proteins. Among these, 5 were chosen (spots 1-5, Figure 2A-top panel), according to their high level of dysregulation, for further identification by mass spectrometry (Figure 1B). Peptides were searched against the protein database using SEQUEST. Among the 5 proteins identified, 2 are involved in contractile function ( $\alpha$ -tubulin 1 and 2; spots 1 and 5, respectively), 2 are serum proteins (haptoglobin and serum albumin; spots 2 and 4, respectively) and 1 is a mitochondrial protein involved in energy metabolism (ubiquinol cytochrome c reductase, spot 3).

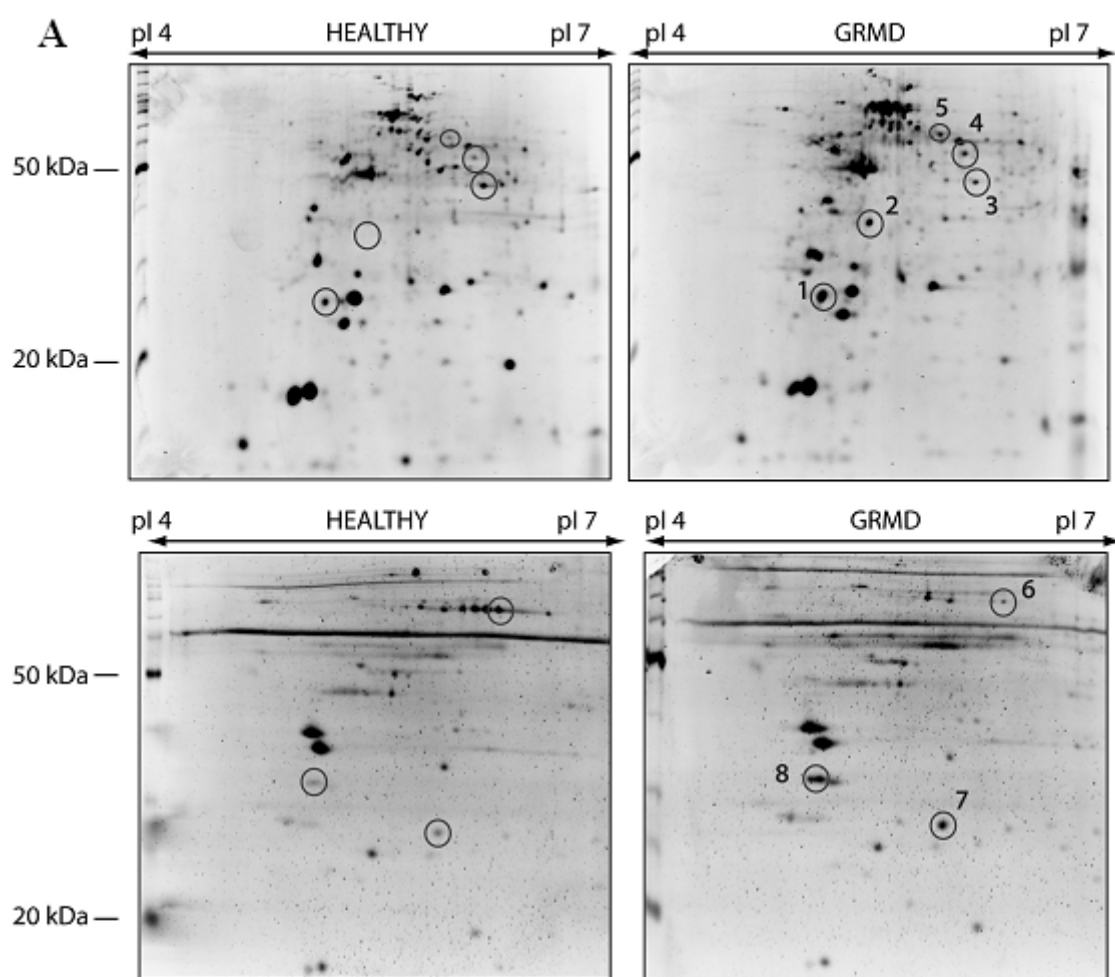
Following the same procedure, 36 protein spots were detected in the phospho-enriched samples, among which 20 showed a differential abundance in dystrophic *vs* healthy dog muscle (Figure 1A-bottom panel). Three spots that showed consistent dysregulation between the 2 experiments and had a great fold-change difference between healthy and GRMD were further processed for identification by mass spectrometry (Figure 1B). This led to the identification of another skeletal muscle marker involved in the contractile function (tropomyosin 4, spot 8), and 2 proteins involved in chaperone functions (heat shock proteins 70 and 27; spots 6 and 7, respectively). Of interest, these 3 proteins (TPM4, HSP70, HSP27) have been described in the literature as phosphoproteins (PhosphoSite database).

### **Figure legend**

#### **Supplemental figure 1: Two-dimensional gel electrophoretic comparison between normal and GRMD dog muscles**

**A-** 2-D gel analysis of cytosolic- and phospho-proteins. Spots excised and identified by MS are encircled. Proteins were detected by Sypro Ruby protein gel staining. Isoelectric focusing was performed over a pH range of 4-7. Healthy and dystrophic samples are represented on the left and right panels, respectively. Top panel: cytosolic-proteins; bottom panel: phospho-proteins.

**B-** MS identification of proteins differentially expressed in dystrophic dog muscle. Stained gels were matched and analyzed with the PDQuest software. Eight proteins detected as differentially expressed in dystrophic dog muscle were then identified by MS. Spectra were analyzed using Mascot and the NCBI non-redundant protein sequence database. MS/MS tolerance was  $\pm 0.8$  Da. \* protein identified by 2D gels and ICAT analysis.



**B**

Spot Identity no.		accession no.	Score/ No.uniq peptides matched	Coverage (%)	Theoretical pI/molecular mass(kDa)	Normalized spot quantitation ratio H/G	ICAT data ratio H/G	ICAT data log2 ratio H/G
1	similar to Tubulin alpha 1 isoform	XP_849601	173/5	13	6.8/20.5	0.42	n.d	
2*	Haptoglobin precursor isoform 2	XP_850996	325/7	25	5.8/38.3	Only in healthy	4.49	6.18
3*	similar to ubiquinol cytochrome reductase	XP_851209	173/7	19	6.04/52.7	1.35	1.49	2.10
4*	Serum albumin	XP_855557	464/11	16	5.51/68.5	0.49	0.36	0.47
5*	Tubulin alpha 2	XP_851095	5443/13	33	5.04/57.4	0.36	0.5	0.48
6	Heat shock 70 kDa protein 1B	Q27965	101/5	9	5.68/70.1	0.2	n.d	
7	Heat shock 27 kDa protein 1	NP_001007519	143/4	16	6.23/22.9	0.71	n.d	
8*	Tropomyosin 4	NP_003281	104/3	14	4.67/28.5	0.19	Only in GRMD	

**Supplementary Table 1:** Quantitative pattern of proteins identified in the ICAT experiment. Relative quantification of proteins (Light-labelled *versus* Heavy-labelled) was performed within the TPP using the ASAP ratio program. Shown here are the ICPL abundance ratio (dystrophic *versus* healthy dog muscle) of the 88 cytosolic proteins (a) and 63 phospho-enriched proteins (b) that were identified. For additional data, see supplementary Tables 2 and 3.\* proteins identified in both experiment (cytosolic and phospho-protein enriched fractions).

a.

entry	Symbol	protein name	Coverage %	ratio mean	ratio stdev	centered log2 ratio	U peps	T peps	precursor ion charge	peptide sequence
1	HINT1	histidine triad nucleotide binding protein 1	21.4	0.56	0.09	-0,43	2	4	3 3	IIFEDDQC[339]LAFHDISPQAPTHFLVIPK IIFEDDQCLAFHDISPQAPTHFLVIPK
2	TPM2	Tropomyosin beta chain	6	0.43	0.04	-0,83	3	5	2 2 3 3	CGDLEELKIVTNNLK C[339]GDLEELKIVTNNLK C[339]GDLEELKIVTNNLK CGDLEELKIVTNNLK
3	HSP90	Heat shock protein HSP 90-alpha A4	12.4	0.32	0.09	-1,28	8	13	3 3 3 3 2 3 2 3	HGLEVIYM[147]IEPIDEYCVQQLKEFEGK HGLEVIYM[147]IEPIDEYC[339]VQQLKEFEGK HSQFIGYPITLFVEKER KHGLEVIYM[147]IEPIDEYC[339]VQQLKEFEGK HSQFIGYPITLFVEK KHGLEVIYM[147]IEPIDEYC[339]VQQLK RVFIM[147]DNC[339]EELIPEYLNfir VFIM[147]DNC[339]EELIPEYLNfirGV
4	TPT1	Translationally-controlled tumor protein	8.7	0.8	0.08	0,12	3	3	2 2 3	IREIADGLCLEVEGK IREIADGLC[339]LEVEGK IREIADGLC[339]LEVEGK
5	ATP5A1	ATP synthase alpha chain	2.3	1.61	0.28	1,19	2	2	3 2	LYCIYVAIGQKR LYC[339]IYVAIGQK
6	LDHA	lactate dehydrogenase A	13	0.67	0.09	-0,15	7	9	2 2 2 3 3 3 3	GLYGIKDDVFLSVPCILGQNGISDVVK GLYGIKDDVFLSVPC[339]ILGQNGISDVVK NVNIFKFIIPNIVKYSPNC[339]K GLYGIKDDVFLSVPCILGQNGISDVVK GLYGIKDDVFLSVPC[339]ILGQNGISDVVK NVNIFKFIIPNIVKYSPNCK NVNIFKFIIPNIVKYSPNC[339]K
7	LDHB	lactate dehydrogenase B	6	0.85	0.05	0,21	4	6	2 2 3 3	GM[147]YGIENEVFLSLPCILNAR GM[147]YGIENEVFLSLPC[339]ILNAR GM[147]YGIENEVFLSLPCILNAR GM[147]YGIENEVFLSLPC[339]ILNAR
8	TUBA2	Tubulin, alpha 2 isoform 2	5.7	0.37	0.06	-1,06	2	2	3 3	AYHEQLSVAEITNACFEPANQM[147]VK AYHEQLSVAEITNAC[339]FEPANQM[147]VK
9	MYLPF	Myosin regulatory light chain 2	20.6	1.64	0.14	1,22	3	4	3 3 3	NICYVITHGDAKDQE QFLEEMLTTCDFRFSPEIR QFLEEM[147]LTTQCDRFSPEIR
10	ACADS	Acyl-Coenzyme A dehydrogenase	6.5	1.11	0.06	0,62	2	2	3 3	IGIAAQALGIAQAALDC[339]AVNYAENRR IGIAAQALGIAQAALDCAVNYAENRR
11	ACO2	Aconitase 2	3.2	1.18	0.17	0,72	2	2	3 3	VAVPSTIHCDHLIEAQLGGEKDLRR VAVPSTIHC[339]DHLIEAQLGGEKDLRR
12	AHSG	Alpha-2-HS-glycoprotein	7	0.31	0.03	-1,33	5	10	2 3 3 3	ELDC[339]DDPETEQAALVAVDYINNHHVLR ELDC[339]DDPETEQAALVAVDYINNHHVLR PETEQAALVAVDYINNHHVLR ELDCDDPETEQAALVAVDYINNHHVLR

									2	C[339]DDPETEQAALVAVDYINNHVLR
13	AK1	Adenylate kinase 1	11	1.39	0.13	0,97	7	11	2	KVNAEGSVDNVFSQVCTHLDALK
									2	VNAEGSVDNVFSQVCTHLDALK
									2	VNAEGSVDNVFSQVC[339]THLDALK
									3	KVNAEGSVDNVFSQVCTHLDALK
									3	KVNAEGSVDNVFSQVC[339]THLDALK
									3	VNAEGSVDNVFSQVCTHLDALK
									3	VNAEGSVDNVFSQVC[339]THLDALK
14	AKR1B1	Aldo-keto reductase family 1, member B1	12.7	0.92	0.06	0,33	2	2	3	HIDCAHVYQNENEVGLAIQEK
									3	VC[339]ALVSC[339]ASHKDYPTTEEF
15	ALB	Serum albumin	46.5	0.36	0.08	-1,10	46	142	2	AFSQYLQQC[339]PFEDHVK
									2	DVFLGTFLEYYSR
									2	GLVLVAFSQYLQQCPFEDHVK
									2	GLVLVAFSQYLQQC[339]PFEDHVK
									2	HPYFYAPELLYYAQQYK
									2	M[147]SCADDFLSVVLNR
									2	M[147]SC[339]ADDFLSVVLNR
									2	SLHTLFGDKLCTVASLR
									2	SLHTLFGDKLC[339]TVASLR
									2	SLHTLFGDKLC[339]TVASLRDK
									2	TNC[339]ELFEKLGEYGFQNALLVR
									3	C[339]C[339]AAENKEGC[339]FSEEGPK
									3	EFNAETTFHADLCTLPEAEK
									3	EFNAETTFHADLC[339]TLPEAEK
									3	EFNAETTFHADLC[339]TLPEAEKQVK
									3	GLVLVAFSQYLQQCPFEDHVK
									3	GLVLVAFSQYLQQC[339]PFEDHVK
									3	HPYFYAPELLYYAQQYK
									3	RHPEYSVSLLLR
									3	SLHTLFGDKLCTVASLR
									3	SLHTLFGDKLC[339]TVASLR
									3	SLHTLFGDKLC[339]TVASLRDK
									3	SQC[339]LAEVERDELPGDLPSLAADFVEDK
									3	TNCELFEKLGEYGFQNALLVR
									3	TNC[339]ELFEKLGEYGFQNALLVR
									3	VHKEC[339]C[339]HGDLLC[339]ADDRADLAK
									2	LVAFSQYLQQC[339]PFEDHVK
									2	PEPDALC[339]AAFQDNEQLFLGK
									3	SLHTLFGDKLCTVASLRDK
									2	FSQYLQQC[339]PFEDHVK
									2	VAFSQYLQQC[339]PFEDHVK
									3	DKSLHTLFGDKLC[339]TVASLR
									3	SQCLAEVERDELPGDLPSLAADFVEDK
									3	LKECCDKPVLEK
									3	HPYFYAPELLYYAQQYKGV
									3	RPC[339]FSGLEVDETYVPK
									3	GVFAEC[339]C[339]QAADKAAC[339]LGPK
									2	PSLAADFVEDKEVC[339]K
									3	CCAAENKEGCFSEEGPK
									3	ANCDKSLHTLFGDKLCTVASLR
									2	EFNAETTFHADLC[339]TLPEAEK
									2	PSLAADFVEDKEVC
									3	RPCFSGLEVDETYVPK
									3	EC[339]C[339]HGDLLC[339]ADDRADLAK
									3	ERDELPGDLPSLAADFVEDKEVC[339]K

									3	ANC[339]DKSLHTLFGDKLC[339]TVASLR
									3	LVAFSQYLQQC[339]PFEDHVK
16	ANXA6	Annexin A6	3.4	0.55	0.11	-0,45	2	3	3	EIKDAISGIGTDEKC[339]LIEILASR
									2	DAISGIGTDEKC[339]LIEILASR
17	APOBEC2	Apolipoprotein B	6.3	0.54	0.05	-0,48	4	4	2	NKTFLC[339]YVVEAQGK
									3	NKTFLCYVVEAQGK
									2	TFLCYVVEAQGK
									3	NKTFLC[339]YVVEAQGK
18	ATP2A2	SERCA2	5.2	1.58	0.18	1,16	2	2	3	CLALATHDNPLRREEM[147]NLEDSANFIK
									3	YETNLTFVGCVGM[147]LDPPRIEVASSVK
19	CA3	Carbonic anhydrase III	11.9	1.3	0.07	0,86	6	16	2	EAPFTKFDPSCLPACR
									2	EAPFTKFDPSC[339]LFPAC[339]R
									3	EAPFTKFDPSCLPACR
									3	EAPFTKFDPSC[339]LFPAC[339]R
									3	GKEAPFTKFDPSCLPACR
									3	GKEAPFTKFDPSC[339]LFPAC[339]R
									2	GKEAPFTKFD
									2	EAPFTKFDPSC[339]LFPAC
									2	ILLKEPM[147]TVSSDQM[147]AK
20	CALR	Calreticulin	6.3	0.37	0.01	-1,06	2	3	3	CKDDEFTHLYTLIVRPDNTYEVK
									3	C[339]KDDEFTHLYTLIVRPDNTYEVK
21	CKMT2	Creatine kinase, mitochondrial 2	10.5	0.1	0.01	-3,06	4	5	2	SEVELVQIVIDGVNYLVDC[339]EK
									3	LIDDHFLFDKPVSPLLTC[339]AGM[147]AR
									3	SEVELVQIVIDGVNYLVDC[339]EK
									2	LIDDHFLFDKPVSPLLTC[339]AGMAR
22	CSRP3	Cysteine and glycine-rich protein 3	25.3	0.24	0.05	-1,72	4	8	3	GIGYGQGAGCLSTDTEHGLGLQFQQSPKPAR
									3	GIGYGQGAGC[339]LSTDTEHGLGLQFQQSPKPAR
									3	KALDSTTVAAHESEIYCK
									3	KALDSTTVAAHESEIYC[339]K
23	ENO3	Enolase 3	17.5	1.17	0.06	0,70	7	7	2	SGETEDTFIADLVVGLCTGQIK
									2	SGETEDTFIADLVVGLC[339]TGQIK
									3	SGETEDTFIADLVVGLCTGQIK
									3	SGETEDTFIADLVVGLC[339]TGQIK
									3	TAIQAAAGYPDKVVIGM[147]DVAASEFYR
									3	IGAEVYHHLKGVK
									2	FGANAILGVSLAVCK
									2	FGANAILGVSLAVC[339]K
24	FABP3	Fatty acid binding protein 3	10.5	1.35	0.1	0,92	9	23	2	LILTLTHGSAVCTR
									2	LILTLTHGSAVC[339]TR
									2	ILTLTHGSAVCTR
									2	LTLTHGSAVCTR
									3	LILTLTHGSAVCTR
									3	LILTLTHGSAVC[339]TR
									2	LTLTHGSAVC[339]TR
									2	TLTHGSAVCTR
									2	TLTHGSAVC[339]TR
25	FABP4	Fatty acid binding protein 4	10.6	1.31	0.13	0,88	2	2	3	KRVDDKLVVECIM[147]K
									3	RVDDKLVVEC[339]IM[147]K

26	FHL1	Four and a half LIM domains 1	45.3	0.82	0.08	0,16	22	35	2	C[339]LHPLANETFVAK
									2	FTAVEDQYYC[339]VDC[339]YK
									2	FVFHEEQVYCPDCAK
									2	FVFHEEQVYC[339]PDC[339]AK
									3	CFDKFCANTCVECR
									3	CLHPLANETFVAKDNK
									3	FTAVEDQYYCVDCYKNFVAK
									3	GCFKPIVAGDQNVEYKK
									3	GC[339]FKPIVAGDQNVEYKK
									3	QVIGTGSFFPKGEDFYCVTCHETK
									3	QVIGTGSFFPKGEDFYC[339]VTC[339]HETK
									3	VGTM[147]TEKFDCHYCR
									3	VGTM[147]TEKFDC[339]HYC[339]R
									2	CLHPLANETFVAK
									3	FVFHEEQVYCPDCAK
									3	FVFHEEQVYC[339]PDC[339]AK
									2	C[339]AGC[339]KNPITGFGK
									3	GEDFYC[339]VTC[339]HETK
									3	GC[339]FKPIVAGDQNVEYK
									3	KC[339]AGC[339]KNPITGFGK
									2	HDTC[339]FR
									3	C[339]LHPLANETFVAK
27	FLNC	Filamin C, gamma	1.4	0.59	0.16	-0,35	2	2	3	IEC[339]DDKGDGSC[339]DVR
									3	VHTPSGAVEEC[339]YVSELDSDKHTIR
28	GOT2	Glutamic-oxaloacetic transaminase 2	12.6	1.82	0.11	1,38	6	8	2	NLDKEYLPIAGLAEFCK
									2	NLDKEYLPIAGLAEFC[339]K
									3	HFIEQGINVCLCQSYAK
									3	NLDKEYLPIAGLAEFCK
									3	NLDKEYLPIAGLAEFC[339]K
									3	THVEM[147]GPPDPILGVTEAFKR
29	HMGB1	High mobility group protein B1	7.4	0.92	0.07	0,33	2	2	3	RPPSAFFLFC[339]SEYRPK
									3	RPPSAFFLFCSEYRPK
30	HP	Haptoglobin	6.3	4.49	0.42	2,76	2	2	2	SC[339]TVAEYGVYVK
									2	YAAGILSFDK
31	HSPB6	Heat shock protein B6	14.8	1.53	0.16	1,11	3	9	2	FGEGLEAELAALCPAALAPYYLR
									2	FGEGLEAELAALC[339]PAALAPYYLR
									3	FGEGLEAELAALCPAALAPYYLR
32	CKM	Creatine kinase M-type	20.2	2.83	0.15	2,05	7	9	3	TVGCVAGDEESYQVFKDLFDPIIQDR
									3	IM[147]TVGC[339]VAGDEESYQVFKDLFDPIIQDR
									2	TFLVWVNEEDHLR
									3	IM[147]TVGCVAGDEESYQVFKDLFDPIIQDR
									2	LRDKETPSGFTLD
									2	LFDPIIQDR
									3	LRDKETPSGFTLDDVIQTGVD
									3	SIKGYTLPPHCSRGE
33	LGALS1	Lectin, galactoside-binding, soluble, 1	25.9	0.43	0.05	-0,83	2	5	3	SFVLNLGKDGDNLCCLHFNPR
									3	FEAHGDVNTIVC[339]NSK
35	MYH2	Myosin heavy chain 2	3.8	1.22	0.1	0,77	3	8	2	KLEDECSELKKDIDDLELTLAK
									2	KLEDEC[339]SELKKDIDDLELTLAK



									3	EKNDLQLQVQAEAEGLADAEERCDQLIK
									3	HDCDLLREQYEEEQESKAELQR
									3	KLEDECSELKKDIDDLELTLAK
									3	KLEDEC[339]SELKKDIDDLELTLAK
									3	LEDECSELKKDIDDLELTLAK
									3	LEDEC[339]SELKKDIDDLELTLAK
									3	NDLQLQVQAEAEGLADAEERCDQLIKT
36	MYH7	Myosin heavy chain 7	3.8	1.22	0.1	0,77	6	8	2	KLEDECSELKKDIDDLELTLAK
									2	KLEDEC[339]SELKKDIDDLELTLAK
									3	HDCDLLREQYEEETEAK
									3	HDC[339]DLLREQYEEETEAK
									3	KLEDECSELKKDIDDLELTLAK
									3	KLEDEC[339]SELKKDIDDLELTLAK
									3	LEDECSELKKDIDDLELTLAK
									3	LEDEC[339]SELKKDIDDLELTLAK
									2	LPVYNAEVVAAYR
									3	M[147]VTRINATLETQPR
									3	HDC[339]DLLREQYEEETEA
									2	GLCHPR
37	MYH8	Myosin heavy chain 8	5	1.22	0.1	0,77	2	2	2	KLEDECSELKKDIDDLELTLAK
									2	KLEDEC[339]SELKKDIDDLELTLAK
									3	EKNDLQLQVQSEADALADAEERC[339]EQLIK
									3	HDC[339]DLLREQYEEEQEGKAELQR
									3	KLEDECSELKKDIDDLELTLAK
									3	KLEDEC[339]SELKKDIDDLELTLAK
									3	LEDECSELKKDIDDLELTLAK
									3	QVEQEK[339]DIQAALAEAEASLEHEEGK
									3	LEDEC[339]SELKKDIDDLELTLAK
38	MYL1	Myosin, light chain 1	18.1	0.45	0.03	-0,76	6	18	2	M[147]KEEEVEALM[147]AGQEDSNGC[339]INYEAFVK
									3	M[147]KEEEVEALM[147]AGQEDSNGCINYEAFVK
									3	M[147]KEEEVEALM[147]AGQEDSNGC[339]INYEAFVK
									3	MKEEEVEALM[147]AGQEDSNGCINYEAFVK
									3	MKEEEVEALM[147]AGQEDSNGC[339]INYEAFVK
									3	M[147]KEEEVEALMAGQEDSNGC[339]INYEAFVK
39	OBSCN	Obscurin	1.5	0.76	0.08	0,04	2	2	3	HHHIDQLGDGTC[339]SLLVTGLGR
									3	VSLRQDGAVC[339]JELQIR
40	PARK7	Parkinson disease 7-DJ-1	15.5	1.48	0.38	1,06	5	6	3	GLIAAICAGPTALLAHEIGFGSK
									3	GLIAAIC[339]AGPTALLAHEIGFGSK
									3	KGLIAAICAGPTALLAHEIGFGSK
									3	KGLIAAIC[339]AGPTALLAHEIGFGSK
									2	AAICAGPTALLAHEIGFGSK
41	PDLIM3	PDZ and LIM domain 3	5.7	0.38	0.05	-1,02	4	5	3	QKGYFFVEGELYC[339]ETHAR
									3	GYFFVEGELYCETHAR
									3	GYFFVEGELYC[339]ETHAR
									2	EGELYC[339]ETHAR
42	PGAM2	Phosphoglycerate mutase 2	13.8	0.51	0.07	-0,57	5	10	2	M[147]EFDICYTSVLKR
									2	M[147]EFDIC[339]YTSVLKR
									3	RYAGLKPGLPTC[339]ESLKDTIAR
									3	M[147]EFDICYTSVLKR
									3	M[147]EFDIC[339]YTSVLKR

43	PGK1	Phosphoglycerate kinase 1	4.8	1.1	0.37	0,61	2	11	3 3	SLLGKDVFLKDCVQGEVEK SLLGKDVFLKDC[339]VGQGEVEK
44	PGM1	Phosphoglucomutase 1	7.9	1.24	0.14	0,79	4	4	2 3 3 3	HGFFVNPSDSVAVIAANIFSIPYFQQTGVR LSLC[339]GEESFGTGSDBIR LSLCGEESFGTGSDBIR HGFFVNPSDSVAVIAANIFSIPYFQQTGVR
45	PRDX3	Peroxisdoxid 3	9.7	1.42	0.19	1,00	2	2	3 3	YLVLFYPLDFTFVCPTFVAFSDK YLVLFYPLDFTFVC[339]PTEVAFSDK
46	MYH3	Myosin heavy chain embryonic	5.2	1.18	0.06	0,72	3	3	2 2 3 3 3 3 3 3 3 3 3 3	KLEDECSELKKDIDDLTLAK KLEDEC[339]SELKKDIDDLTLAK HDC[339]DLLREQYEEEQEGKAEQR KLEDECSELKKDIDDLTLAK KLEDEC[339]SELKKDIDDLTLAK LEDECSELKKDIDDLTLAK TKC[339]EESQAELEASLKESR TYC[339]FVVDSSKEEYAK LEDEC[339]SELKKDIDDLTLAK NDLQLQVQAESENLLDAEERCQLIK NDLQLQVQAESENLLDAEERC[339]DQLIK
47	MDH2	Malate dehydrogenase	14.2	1.38	0.18	0,95	4	9	3 3 3 3	FVFSLV DAM[147]NGKEGVVECSFVK FVFSLV DAM[147]NGKEGVVEC[339]SFVK GYLGPEQLPDC[339]LKGK[339]DVVVIPAGVPR GYLGPEQLPDC[339]LKGCDVVVIPAGVPR
48	ALDOA	Aldolase A	25.8	1.2	0.13	0,74	11	38	3 3 3 3 3 3 3 2 3 3 2 3	ALSDHHIYLEGTLLKPNM[147]VTPGHACTHK ALSDHHIYLEGTLLKPNM[147]VTPGHAC[339]THK QLLLTADDRVNPCIGGVILFHETLYQK QLLLTADDRVNPC[339]IGGVILFHETLYQK YASICQQNGIVPIVEPEILPDGDHDLKR YASIC[339]QQNGIVPIVEPEILPDGDHDLKR PIVEPEILPDGDHDLKR TADDRVNPC[339]IGGVILFHETLYQK LTADDRVNPCIGGVILFHETLYQK ALANSLACQK ADDRVNPC[339]IGGVILFHETLYQK
49	TTN	Cardiac titin	0.1	0.49	0.04	-0,63	4	4	3 3 3 3	KLKDVHETLGFPVAFECR KLKDVHETLGFPVAFEC[339]R FRVPDLLEGK[339]QYEFK IPC[339]AEM[147]SDKGLYSFEVK
50	GSTP1	Glutathione S-transferase PI isozyme	13.3	0.33	0.03	-1,24	2	2	3 3	SLGLYGKDDQEAALLDVNDGVEDLRCK SLGLYGKDDQEAALLDVNDGVEDLRCK[339]K
51	TF	Transferrin	4.4	0.63	0.08	-0,25	3	4	3 3 3	CLVEKGDVAFVKDQTVLQNTGGK C[339]LVEKGDVAFVKDQTVLQNTGGK GTDKCK[339]AC[339]SNHEPYFGYSGAFK
52	TPI1	Triosephosphate isomerase	15.7	0.81	0.05	0,14	10	24	2 2 2 2 3 3	VAHALAEGLGVIACIGEK VAHALAEGLGVIACIGEKLDER VAHALAEGLGVIAC[339]IGEK VAHALAEGLGVIAC[339]IGEKLDER VAHALAEGLGVIACIGEK VAHALAEGLGVIACIGEKLDER

									3	VAHALAEGLGVIACIGEKLDEREAGITEK
									3	VAHALAEGLGVIAC[339]IGEKLDER
									3	VAHALAEGLGVIAC[339]IGEKLDEREAGITEK
									3	VAHALAEGLGVIAC[339]IGEK
									3	GESDELIGQKVAHALAEGLGVIAC[339]IGEK
53	TUBB2C	Tubulin, beta 2C	9.9	0.52	0.09	-0,54	3	4	2	LTTPTYGDLNHLVSATM[147]SGVTTTC[339]LR
									3	LTTPTYGDLNHLVSATM[147]SGVTTCLR
									3	M[147]REIVHLQAGQC[339]GNQIGAK
54	UQCRH	Ubiquinol-cytochrome c reductase	19.8	1.49	0.22	1,07	3	4	2	SQTEEDCTEELFDLHAR
									3	SQTEEDCTEELFDLHAR
									3	SQTEEDC[339]TEELFDLHAR
55a	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	21.8	1.17	0.12	0,70	6	7	3	FNSDTHSSTFDAGAGIALNDHFVK
								7	3	THSSTFDAGAGIALNDHFVK
								7	3	VPTPNVSVVDLTC[339]RLEK
								7	3	LTGM[147]AFRVPTPNVSVVDLTCRLEK
								7	3	VIHDHFGIVEGLM[147]TTVHAITATQK
								7	3	LTGM[147]AFRVPTPNVSVVDLTC[339]RLEK
56	VCP	Valosin-containing protein	5	0.7	0.03	-0,08	2	2	2	QAAPC[339]VLFFDELDSIAK
									2	ETHGHVGADLAALC[339]SEAALQAIR
									2	QAAPCVLFFDELDSIAK
57	no descripton	ENSCAFG00000014139	14.7	0.62	0.1	-0,27	2	2	3	SHSSFSC[339]LVTHEGSTVEK
									3	SHSSFSC[339]LVTHEGSTVEKK
58	SYPL2	Synaptophysin-like 2	9.6	0.74	0.08	0,00	2	2	3	C[339]NNEAKDVSSIIVLFGYPFR
									3	CNNEAKDVSSIIVLFGYPFR
59a	ACTC	Cardiac actin	16.4	0.41	0.06	-0,90	2	3	2	PSFIGM[147]ESAGIHETTYNSIM[147]K
									3	C[339]PETLFQPSFIGM[147]ESAGIHETTYNSIM[147]K
									3	EKLC[339]YVALDFENEM[147]ATAASSSSLEK
									2	QPSFIGMESAGIHETTYNSIM[147]K
									3	EKLCYVALDFENEM[147]ATAASSSSLEK
									2	HHTFYNELR
60	CLIC4	Chloride intracellular channel 4	7.1	0.25	0.03	-1,66	2	2	2	TDVNKIEEFLEEVL[339]PPK
									3	TDVNKIEEFLEEVL[339]PPK
61	VDAC1	voltage-dependent anion channel 1	6.5	1.98	0.3	1,51	1	1	2	EHINLGCDVDFDIAGPSIR
62	A1AG1	similar to Alpha-1 acid glycoprotein	11.2	0.17	0.02	-2,25	1	1	3	KPEVTQEQM[147]TVFHEALAC[339]M[147]DLHK
63	HSPA8	Heat shock cognate 71 kDa protein	3.4	0.61	0.08	-0,30	1	2	3	GPAVGIDLGTTYSC[339]VGVFQHGK
64	EEF2	Elongation factor 2	3.5	0.65	0.1	-0,20	1	1	3	LM[147]EPIYLVEIQC[339]PEQVVGGIYGVNLRK
65	A1BG	Alpha-1-B glycoprotein	3.6	0.29	0.02	-1,43	1	2	3	RVHHVLSPEGTEAC[339]FQLR
66	AKR1A1	Aldo-keto reductase family 1	8.6	0.55	0.06	-0,45	1	1	3	QIDDVLSVASVRPAVLQVEC[339]HPYLAQK
67	ANXA2	Annexin A2	8	0.48	0.06	-0,66	1	1	3	EVKGDLENAFLNLVQC[339]IQNKPLYFADR
68	CAMK2D	Calcium/calmodulin-dependent protein kinase	5.9	2.71	0.27	1,99	1	1	3	SNKPIHTIILNPHVHLVGDDAAC[339]IAYIR

70	GNAS	GNAS complex locus	1.9	0.79	0.07	0,10	1	1	3	SNEYQLIDC[339]AQYFLDKIDVIK
71	GOT1	Glutamic-oxaloacetic transaminase 1	4.1	0.45	0.03	-0,76	1	1	2	YFVSEGFELFCAQSFSK
72	GRHPR	Glyoxylate reductase/hydroxypyruvate reductase	5.8	0.7	0.08	-0,08	1	1	3	GVAGAHGLLC[339]LLSDHVDKR
73	HPX	Hemopexin	5.2	0.41	0.03	-0,90	1	6	3	EFGSPHGINLETVDAAFTC[339]PGTSR
75	MTPN	Myotrophin	17.8	0	0	NA	1	1	3	KPLHYAADC[339]GQLEILEFLLK
78	PKM2	Pyruvate kinase M	3	0.92	0.07	0,33	1	1	3	AGKPVICATQM[147]LESM[147]IK
81	PFN1	profilin 1	19.4	0.49	0.06	-0,63	1	2	3	C[339]SVIRDSLLQDGEFTM[147]DLR
83	ANXA1	Annexin I	5.8	0.4	0.02	-0,94	1	1	3	LYGVSLC[339]QAILDETKGDYEK
86	TPM4	Tropomyosin 4	9.3	0	0	NA	1	1	3	AEVSELKC[339]GDLEELKNVTNNLK
87	ANP32A	Acidic leucine-rich nuclear phosphoprotein 32	8.4	0.34	0.03	-1,19	1	1	2	SLDLFNC[339]EVTNLNDYRENVFK
89	PLIN4	perilipin 4	2	0.45	0.03	-0,76	1	1	3	QTILRPLEALSSGVASAPD TLCAGLDLAR
90	HMGB2	High-mobility group box 2	7.6	0.89	0.08	0,28	1	1	3	RPPSAFFLFC[339]SEHRPK
91	UQCRC1	Ubiquinol-cytochrome c reductase I	4.4	1.2	0.19	0,74	1	1	3	HFSSVSETYTEDTVPTLAPCR
93	FETUB	Fetuin B	6.2	0.37	0.05	-1,06	1	1	3	QVAM[147]GSLFYLTLDVLETDC[339]HVL SR
95	KBTBD10	Kelch repeat and BTB	3	0.89	0.07	0,28	1	2	3	C[339]LFGLGEVDDKIYVVAGK
96	PPP1CB	protein phosphatase PP1-beta catalytic subunit	3.7	0.5	0.05	-0,60	1	1	3	FLNRHDLDLICR
100	NDUFAB1	NADH dehydrogenase 1	12.3	1.04	0.06	0,52	1	1	3	LM[147]C[339]PQEIVDYADKKDVYE
102	ACADVL	Acyl-Coenzyme A dehydrogenase	3.3	1.22	0.21	0,77	1	1	3	VTDECIQILGGM[147]GFM[147]KEPGVER
103	YWHAG	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase	7.7	0.7	0.07	-0,08	2	2	3	ELEAVC[339]QDVLSLLDNYLIK
105	CCT7	CCT7 chaperonin containing TCP1	5.1	0.75	0.12	0,02	1	1	3	ELEAVC[339]QDVLSLLDNYLIK
111	PFKM	6-phosphofructokinase	2.9	999	0	NA	1	1	3	INALTAASEAAC[339]LIVSVDETIKNPR
									3	CNENYTTDFIFNLYSEEGKGIFDSR

b.

entry	Symbol	protein name	Coverage %	ratio mean	ratio stdev	centered log2 ratio	U peps	T peps	precursor ion charge	peptide sequence
1	MYOT	Myotilin	4.2	3.3	0.28	1,85	3	3	3	KVFEGDSVKLEQCISAVPPPK
									3	KVFEGDSVKLEC[339]QISAVPPPK
									3	VFEGDSVKLEQCISAVPPPK
2	TPM2	Tropomyosin-2	12.8	0.54	0.1	-0,76	8	17	2	CKQLEEEQQALQKK
									2	C[339]KQLEEEQQALQK
									2	C[339]KQLEEEQQALQKK
									3	CKQLEEEQQALQKK
									3	C[339]KQLEEEQQALQKK

[illegible]

									3	GEDFYCVTCHETK
									3	C[339]LHPLANETFVAK
12	FLNC	* Filamin C, gamma	3.1	1.39	0.17	0,60	4	4	3	ECPEGHVVTYTPM[147]APGNYLIAIK
									3	RPIPCKVEPGGAETQAVR
									3	SPFPVHVAEAC[339]NPNAC[339]JR
									3	AFGPGLEPTGCIVDKPAEFTIDAR
13	HSPB7	Heat shock 27kDa protein family, member 7	10.9	1.18	0.11	0,37	2	2	3	C[339]QLPEDVDPTSVTSALREDGSLTIR
									3	CQLPEDVDPTSVTSALREDGSLTIR
14	PFKM	* 6-phosphofructokinase, muscle type	8.3	1.85	0.17	1,02	4	6	2	CNENYTDFIFNLYSEEGK
									3	M[147]GVEAVM[147]ALLEGTPDTPACVVSLSGNQAVR
									3	RGITNLC[339]VIGGDGSLTGADTFR
									3	M[147]GVEAVM[147]ALLEGTPDTPAC[339]VVSLSGNQAVR
15	LGALS1	* Lectin, galactoside-binding 1	8.9	0.35	0.03	-1,39	2	2	2	DGDNLC[339]LHFNP
									3	DGDNLCLHFNP
16	MYBPC1	Myosin binding protein C, slow type	5	0.74	0.25	-0,31	6	9	2	M[147]FSNQGVCTLEIR
									2	TNATISELVIGNEYFR
									3	LNFDLCKETTFEPK
									2	C[339]STELFVR
									2	CSTELFVR
									2	LNFDLCK
17	MYH2	* Myosin-2	3.1	2.12	0.89	1,21	3	4	2	C[339]NGVLEGIR
									2	CNGVLEGIR
									2	HDC[339]DLLR
									3	NDLQLQVQAEAGLADAEERCDQLIK
									2	TNAACAALDKK
									2	CIIPNETK
18	MYH7	* Myosin-7	2.6	1	0.11	0,13	3	4	2	C[339]NGVLEGIR
									2	VIQYFAVIAAIGDR
									3	HDCDLLREQYEEETAK
									2	CNGVLEGIR
									2	HDC[339]DLLR
									2	LQDLVDKLQLK
19	MYL1	* Myosin, light chain 1	18.1	0.87	0.62	-0,07	3	3	3	M[147]KEEEVEALM[147]AGQEDSNGCINYEAFVK
									3	M[147]KEEEVEALM[147]AGQEDSNGC[339]INYEAFVK
									3	M[147]KEEEVEALMAGQEDSNGC[339]INYEAFVK
20			2.8	-1	0		2	2	2	GAFHRPVLGGFR
									3	GAFHRPVLGGFR
21	PDHA1	Pyruvate dehydrogenase alpha 1	10.5	1.28	0.11	0,48	3	3	3	NFYGGNGIVGAQVPLGAGIALACK
									2	VDGM[147]DILCVR
									2	FAAAYCR
22	PRKAR1A	Protein kinase, cAMP-dependent type I	2.9	2.03	0.16	1,15	2	2	2	VLGPCSDILKR
									2	VLGPC[339]SDILKR
23	MYH3	Developmental myosin heavy chain embryonic	4.2	0.47	0.19	-0,96	3	3	2	C[339]NGVLEGIR
									3	NDLQLQVQAESENLLDAEERC[339]DQLIK
									3	TKC[339]JESQAELEASLKESR
									2	CNGVLEGIR

									2	HDC[339]DLLR
									3	TYC[339]FVVDSKEEYAK
									2	CIIPNETK
24	ACTC	* Cardiac actin	9.6	1.21	0.07	0,40	2	2	3	TTGIVLDSGDGVTHNVPIYEGYALPHAIM[147]R
									2	C[339]DIDIR
25	RPS6KA1	Ribosomal protein S6 kinase	3.2	1.27	0.06	0,47	2	2	3	AENGLLM[147]TPCYTANFVAPEVLKR
									3	AENGLLM[147]TPC[339]YTANFVAPEVLKR
26	TNNI1	Troponin I type 1	5.7	0.81	0.03	-0,18	2	2	2	GLSLSALQDLCR
									2	GLSLSALQDLC[339]R
27	TUBB2C	* Tubulin, beta 2C	11.9	0.32	0.2	-1,52	6	11	2	EIVHLQAGQC[339]GNQIGAK
									2	M[147]REIVHLQAGQCGNQIGAK
									3	MREIVHLQAGQC[339]GNQIGAK
									3	M[147]REIVHIQAGQCGNQIGAK
									3	M[147]REIVHIQAGQC[339]GNQIGAK
									3	LTTPTYGDLNHLVSATM[147]SGVTTC[339]LR
									2	YLTVAAVFR
28a	LOC488411	hypothetical gene supported by NM_001003142	20.2	0.81	0.05	-0,18	3	5	2	VPTPNVSVVDLTCRLEK
									2	VPTPNVSVVDLTC[339]RLEK
									3	VPTPNVSVVDLTCRLEK
29	MYBPC2	Myosin binding protein C	2.6	0.81	0.15	-0,18	2	2	3	AVNELGEALAECKLEVR
									3	RPSPFDA GTYSCR
30	TUBB6	Tubulin, beta 6	7.6	0.29	0.02	-1,66	1	1	3	M[147]REIVHIQAGQC[339]GNQIGTK
									2	YLTVAAVFR
									2	YLTVAAVFRGPMS[167]M[147]K
31	PSMA3	Proteasome subunit, alpha type, 3	4.3	1.35	0.28	0,56	2	2	2	C[339]KDG VVFGVEK
									3	C[339]KDG VVFGVEK
32	EIF2S3	eukaryotic translation initiation factor 2 gamma	5.3	0.79	0.07	-0,21	1	1	3	SFDVNKPGC[339]EVDDLKGGVAGGSILK
33	C1QBP	Complement component 1	10	1.08	0.06	0,24	1	1	3	ALVLDC[339]HYPEDEVGQEEDESDIFSIR
34	CA3	* Carbonic anhydrase III, muscle specific	6.5	1.41	0.13	0,62	1	1	3	GKEAPFTKFDPSCLFPACR
35	CYC1	Cytochrome c-1	4	1.4	0.15	0,61	1	1	2	HLVGVCYTEDEAK
36	EEF1B2	Eukaryotic translation elongation factor 1 beta 2	8.9	0.57	0.08	-0,68	1	2	3	LQIQC[339]VVEDDKVGTDM[147]LEER
37	FGG	Fibrinogen gamma chain	4.1	1.3	0.12	0,51	1	1	3	CHAGHLNGVYYQGGVYSK
39	MYL6B	Myosin, light chain 6B, alkali	12.8	0.58	0.04	-0,66	1	1	3	M[147]TEEEVETVLAGHEDSNGC[339]INYEAFK
40	MYPN	Myopalladin	1.7	0.51	0.07	-0,84	1	1	3	CQSPTNYLQGLDGKPII AAPVFTK
41	NDRG2	NDRG family member 2	4.7	1.13	0.12	0,30	1	1	3	YFLQGM[147]GYM[147]ASSCM[147]TR
42	PCYT1A	Phosphate cytidylyltransferase 1	6.8	0.42	0.04	-1,12	1	2	3	C[339]AIGLQQPAPFSDEIEVDFSKPYVR
43	PRKAR2A	Protein kinase, cAMP-dependent, type II, alpha	3.9	1.58	0.47	0,79	1	2	2	CLVM[147]DVQAFER
44	PSMD1	Proteasome 26S subunit, non-ATPase	2.2	0.74	0.05	-0,31	1	1	3	TPEQC[339]PSVVSLSESYNPHVR

45	PTGES3	Prostaglandin E synthase 3	9.4	0.51	0.07	-0,84	1	1	2	SKLTFSC[339]LGGSDNFK
46	RANBP5	RAN binding protein 5	1.9	0.98	0.12	0,10	1	1	3	YAAC[339]NAVGM[147]ATDFAPGFQKK
47	TPM3	Tropomyosin 3	5.6	0.76	0.06	-0,27	1	1	3	C[339]SEEEEEELKNVTNNLK
48	TPM4	* Tropomyosin 4	10.1	0	0	NA	1	1	3	LAQAKEENVGLHQTLNQTLNELNC[339]I
49	UQCRC1	* Ubiquinol-cytochrome c reductase core protein I	4.8	2.75	0.35	1,59	1	1	3	AVELLADIVQNCSLEDSQIEKER
50	VCP	* Valosin-containing protein	2	0.65	0.05	-0,49	1	1	2	VHLGDVISIQPC[339]PDVK
51	AMPD2	adenosine monophosphate deaminase 2	1.6	999	0	NA	1	1	2	C[339]GVPFTDLLDAK
52	CKM	* Creatine kinase M-type	2.6	2.53	0.13	1,47	1	1	2	GYTLPPHCSR
53a	VIM	Vimentin-like protein	4.5	0.02	0.02	-2,06	1	1	3	QVQSLTC[339]EVDALKGTNESLER
55	ENO1	ENO1 enolase 1	3.5	2.35	0.34	1,36	1	4	2	FGANAILGVSLAVCK
56	LDB3	LIM domain binding 3	1.7	0.74	0.27	-0,31	1	2	3	TPLCGHCNNVIR
57	CFL2	Cofilin 2	6.6	5.71	0.73	2,64	1	1	2	AVLFCLSDDKR
58	UQCRH	* Ubiquinol-cytochrome c reductase hinge protein	9.9	0.74	0.19	-0,31	2	2	2 2	ERLELC[339]DQR ERLELCDQR
59	PDHB	Pyruvate dehydrogenasebeta	3.1	2.67	0.3	1,54	1	1	2	EGIECEVINM[147]R
60	TPM1	Tropomyosin	5.8	0.77	0.08	-0,25	1	1	3	C[339]AELEEEELKTVTNNLK
61	MYOM3	Myomesin-3	0.7	3.23	0.48	1,82	1	1	2	TGKEYEFC[339]VK
62	KBTD10	* Kelch repeat and BTB (POZ) domain	1.3	1.1	0.07	0,27	1	1	2	KFIDCTLK
63	ANXA6	* Annexin A6	1.2	1.1	0.05	0,27	1	1	2	FM[147]TILCTR
64	MYL3	Myosin, light chain 3	13.8	0.13	0.01	-2,82	1	1	3	LTEDEVEKLM[147]AGQEDSNGC[339]INYEGVLS[167]
65	TOMM70A	Translocase of outer mitochondrial membrane 70	1	1.42	0.08	0,63	1	1	2	C[339]FALYR
66	MYBPH	Myosin binding protein H	2.5	0.46	0.05	-0,99	1	1	2	LGLQGYVLELC[339]R

\* protein identified in both experiment (cytosolic and phospho-enriched fraction)



**Supplementary Table 4:** List of non-changing proteins in dystrophic vs healthy dog muscle

- a. cytosolic protein sample
- b. phospho-enriched protein sample

\* proteins identified in both experiment (cytosolic and phospho-protein enriched fractions).

**Supplementary Table 4:****a. Cytosolic protein sample**

<b>Symbol</b>	<b>Protein name</b>	<b>Log 2 ratio Healthy/GRMD</b>
APOBEC2	Apolipoprotein B	-0.48
AKR1A1	Aldo-keto reductase family ,. member A1	-0.45
ANXA6	Annexin A6	-0.45
HINT1	Histidine triad nucleotide binding protein 1	-0.43
FLNC	Filamin C, gamma (actin binding protein 280)	-0.35
HSPA8	Heat shock cognate 71 kDa protein	-0.30
TF	Transferrin	-0.25
EEF2	Elongation factor 2	-0.20
LDHA	Lactate dehydrogenase A	-0.15
GRHPR	Glyoxylate reductase/hydroxypyruvate reductase	-0.08
YWHAG	Tyrosine 3-monooxygenase activation protein	-0.08
VCP	Valosin-containing protein	-0.08
SYPL2	Synaptophysin-like 2	0.00
CCT7	CCT7 chaperonin containing TCP1, subunit 7	0.02
OBSCN	Obscurin	0.04
GNAS	GNAS complex locus	0.10
TPT1	Translationally-controlled tumor protein (TCTP)	0.12
TPI1	Triosephosphate isomerase (TIM)	0.14
FHL1	Four and a half LIM domains 1	0.16
LDHB	Lactate dehydrogenase B	0.21
HMGB2	High-mobility group box 2	0.28
KBTBD10	Kelch repeat and BTB (POZ) domain containing 10	0.28
HMGB1	High mobility group protein B1 (High mobility group protein 1)	0.33
PKM2	Pyruvate kinase M	0.33
AKR1B1	Aldo-keto reductase family 1, member B1	0.33
NDUFAB1	NADH dehydrogenase 1	0.52

**b. phospho-enriched protein sample**

<b>Symbol</b>	<b>Protein name</b>	<b>Log 2 ratio Healthy/GRMD</b>
VCP	* Valosin-containing protein	-0.49
MYBPC1	Myosin binding protein C. slow type	-0.31
PSMD1	Proteasome 26S subunit. non-ATPase. 1	-0.31
LDB3	LIM domain binding 3	-0.31
UQCRH	* Ubiquinol-cytochrome c reductase hinge protein	-0.31
EHD2	EH-domain containing 2	-0.29
TPM3	Tropomyosin 3	-0.27
TPM1	Tropomyosin 1	-0.25
EIF2S3	Eukaryotic translation initiation factor 2, subunit 3 gamma	-0.21
TNNI1	Troponin I type 1	-0.18
MYBPC2	Myosin binding protein C, fast type	-0.18
GAPDH	hypothetical gene supported by NM_001003142	-0.18
HSP90AA4P	* putative heat shock protein HSP 90-alpha A4	-0.14
MYL1	* Myosin, light chain 1, alkali; skeletal, fast	-0.07
APOBEC2	* Apolipoprotein B	-0.02
FHL1	* Four and a half LIM domains 1	0.04
RANBP5	RAN binding protein 5	0.10
MYH7	* Myosin-7 (Myosin heavy chain 7)	0.13
C1QBP	Complement component 1, q subcomponent binding protein	0.24
KBTBD10	* Kelch repeat and BTB (POZ) domain containing 10	0.27
ANXA6	* Annexin A6	0.27
NDRG2	NDRG family member 2	0.30
HSPB7	Heat shock 27kDa protein family, member 7 (cardiovascular)	0.37
ACTC	* Cardiac actin	0.40
RPS6KA1	Ribosomal protein S6 kinase, 90kDa, polypeptide 1	0.47
PDHA1	Pyruvate dehydrogenase (lipoamide) alpha 1	0.48
FGG	Fibrinogen gamma chain	0.51

