Table S4. Changed proteins in label-free LC-MS/MS analysis

a. Proteins significantly changed (ANOVA + Tukey, p<0.01) in DMD vs. BMD

Gene names	Protein IDs	Description	Molecular function	Log2 Av. Volumes CTR	Log2 Av. Volumes BMD	Log2 Av. Volumes DMD	Av. Volumes CTR	Av. Volumes BMD	Av. Volumes DMD	Av. Ratio DMD/CTR	Av. Ratio BMD/CTR	Av. Ratio DMD/BMD	% variation DMD/CTR	% variation BMD/CTR	% variation DMD/BMD	N: ANOVA p value	N: ANOVA q-value	C: ANOVA Significant	T: Significant pairs	C: Only identified by site	C: Reverse	C: Contaminant	N: Peptides	N: Razor + unique peptides	N: Unique peptides	N: Sequence coverage [%]	N: Unique + razor sequence coverage [%]	N: Unique sequence coverage [%]	N: Mol. weight [kDa]	N: PEP	N: Intensity
A2M	P01023;F8W7L3;H0YFH1	Alpha-2-macroglobulin	Extracellular matrix	21,49062	23,16003	24,51437	2946600,413	9372678,722	23964076,36	8,133	3,181	2,557	713,3	218,1	155,7	6,873E-05	0,00105263	+	DMD_CTR BMD_CTR DMD_BMD				21	21	21	22,7	22,7	22,7	163,29	0	67604000
COL6A1	P12109;A0A087X0S5	Collagen alpha-1(VI) chain	Extracellular matrix	22,244	23,62645	25,73874	4967195,159	12950011,11	55992878,01	11,273	2,607	4,324	1027,3	160,7	332,4	1,89E-05	0	+	DMD_CTR BMD_CTR DMD_BMD				16	16	16	23,4	23,4	23,4	108,53	0	143710000
COL6A2	P12110;C9JH44;H7C0M5	Collagen alpha-2(VI) chain	Extracellular matrix	22,53744	23,63034	25,34422	6087590,989	12984975,89	42596158,73	6,997	2,133	3,280	599,7	113,3	228,0	5,196E-06	0	+	DMD_CTR BMD_CTR DMD_BMD				10	10	10	13,4	13,4	13,4	108,58	7,7527E-191	133140000
COL6A3	P12111;E7ENL6;C9JNG9;I3L392	Collagen alpha-3(VI) chain	Extracellular matrix	23,84976	25,12892	26,89655	15117958,52	36690926,51	124930457,4	8,264	2,427	3,405	726,4	142,7	240,5	4,061E-07	0	+	DMD_CTR BMD_CTR DMD_BMD				50	50	50	20,8	20,8	20,8	343,67	0	357670000
FGG	C9JC84;P02679;C9JEU5;C9JU00;C9JPQ9	Fibrinogen gamma chain	Extracellular matrix	20,12792	21,92919	23,18751	1145796,972	3993410,639	9552917,667	8,337	3,485	2,392	733,7	248,5	139,2	0,0001147	0,0012549	+	DMD_CTR BMD_CTR DMD_BMD				6	6	6	18,9	18,9	18,9	52,337	3,352E-38	27916000
ASPN	Q9BXN1;Q5TBF2	Asporin	Extracellular matrix	19,89888	19,11032	22,76969	977596,7748	565951,9319	7150883,159	7,315	0,579	12,635	631,5	-42,1	1163,5	0,000267	0,00135065	+	DMD_CTR DMD_BMD				6	6	6	19,7	19,7	19,7	43,417	1,1863E-46	14946000
BGN	P21810;C9JKG1	Biglycan	Extracellular matrix	17,79848	17,42062	20,60187	227969,2956	175440,2199	1591405,434	6,981	0,770	9,071	598,1	-23,0	807,1	0,0004879	0,00118182	+	DMD_CTR DMD_BMD				4	4	4	15,8	15,8	15,8	41,654	1,7432E-10	3559200
CDH13	P55290	Cadherin-13	Extracellular matrix	15,2744	16,10572	18,44144	39632,60015	70518,78512	355980,8234	8,982	1,779	5,048	798,2	77,9	404,8	0,0001866	0,00094118	+	DMD_CTR DMD_BMD				1	1	1	2	2	2	78,286	0,00033905	824870
COL1A1	P02452;I3L3H7	Collagen alpha-1(I) chain	Extracellular matrix	21,30658	22,90347	25,23922	2593699,659	7845695,972	39606118,92	15,270	3,025	5,048	1427,0	202,5	404,8	0,0010397	0,00092857	+	DMD_CTR DMD_BMD				14	14	14	14,1	14,1	14,1	138,94	9,4106E-258	100480000
COL2A1	P02458	Collagen alpha-1(II) chain;Collagen alpha-1(II) chain;Chondrocalcin	Extracellular matrix	24,00779	25,42924	27,45497	16868051,55	45181849,74	183979527,9	10,907	2,679	4,072	990,7	167,9	307,2	0,0008363	0,001	+	DMD_CTR DMD_BMD	+			1	1	1	1,2	1,2	1,2	141,78	0,0040811	480680000
COL1A2	P08123;A0A087WTA8	Collagen alpha-2(I) chain	Extracellular matrix	24,46308	26,30835	28,3301	23127083,39	83100279,87	337450347,9	14,591	3,593	4,061	1359,1	259,3	306,1	0,0008003	0,00100971	+	DMD_CTR DMD_BMD				10	10	10	10,2	10,2	10,2	129,31	1,4142E-200	850970000
DCN	P07585;F8VWU0;F8VUF6;F8VXZ8;F8VX58;F8VNV6;F8VSI3;F8VU58;F8VNW0	Decorin	Extracellular matrix	22,36025	21,75573	24,15746	5384011,273	3541011,258	18711994,41	3,475	0,658	5,284	247,5	-34,2	428,4	0,0001693	0,0009697	+	DMD_CTR DMD_BMD				5	5	5	17	17	17	39,746	8,2658E-24	67635000
FBN1	P35555;H0YND0;P35556;A0A087WYV8;E9PHW4;F6U495	Fibrillin-1	Extracellular matrix	22,17588	22,35933	23,59742	4738109,14	5380579,008	12692034,39	2,679	1,136	2,359	167,9	13,6	135,9	0,0018899	0,00128244	+	DMD_CTR DMD_BMD				16	16	16	7,9	7,9	7,9	312,24	1,5472E-100	50933000
LGALS1	P09382;F8WEI7	Galectin-1	Extracellular matrix	24,55772	24,50821	25,72718	24695074,75	23861973	55546012,03	2,249	0,966	2,328	124,9	-3,4	132,8	0,000928	0,00097196	+	DMD_CTR DMD_BMD				7	7	7	53,3	53,3	53,3	14,716	3,9246E-137	236960000
LUM	P51884;CON__Q05443	Lumican	Extracellular matrix	20,72783	20,18107	23,91296	1736595,115	1188796,218	15794949,62	9,095	0,685	13,287	809,5	-31,5	1228,7	8,226E-06	0	+	DMD_CTR DMD_BMD				7	7	7	28,4	28,4	28,4	38,429	1,9217E-101	38218000
OGN	P20774;Q5TBF5	Mimecan	Extracellular matrix	20,59003	21,27577	24,52528	1578398,435	2538896,231	24145985,31	15,298	1,609	9,510	1429,8	60,9	851,0	7,653E-05	0	+	DMD_CTR DMD_BMD				8	8	8	29,9	29,9	29,9	33,922	3,9471E-64	65387000
PRELP	P51888	Prolargin	Extracellular matrix	19,53767	19,40408	21,58536	761070,1966	693761,3771	3146594,848	4,134	0,912	4,536	313,4	-8,8	353,6	0,00013	0,00114286	+	DMD_CTR DMD_BMD				4	4	4	14,7	14,7	14,7	43,809	2,8065E-12	7253700
ACTC1	P68032	Actin, alpha cardiac muscle 1	Structural/contractile	19,13503	20,20431	22,31191	575728,857	1208101,3	5206599,479	9,043	2,098	4,310	804,3	109,8	331,0	2,163E-05	0	+	DMD_CTR BMD_CTR DMD_BMD				19	2	0	75,1	5,8	0	42,019	0	12057000
MYBPC2	Q14324	Myosin-binding protein C, fast-type	Structural/contractile	25,76984	24,07079	23,63887	57213013,52	17620969,9	13061977,57	0,228	0,308	0,741	-77,2	-69,2	-25,9	9,114E-07	0	+	CTR_DMD CTR_BMD BMD_DMD				34	33	33	41,2	40,2	40,2	128,07	0	281350000
MYH7	P12883;Q9Y2K3;Q494R4	Myosin-7	Structural/contractile	31,15418	31,99621	31,42632	2389696075	4283699105	2885791656	1,208	1,793	0,674	20,8	79,3	-32,6	0,0011691	0,00089655	+	DMD_CTR BMD_CTR BMD_DMD				127	127	43	60,6	60,6	23,7	223,09	0	24269000000
MYOM2	P54296;A0A0J9YVV7	Myomesin-2	Structural/contractile	26,86053	26,95748	26,50007	121849914,7	130319704,8	94910870,62	0,779	1,070	0,728	-22,1	7,0	-27,2	2,301E-06	0	+	CTR_DMD BMD_CTR BMD_DMD				51	51	20	46,3	46,3	17,9	164,89	0	929450000
PDLIM5	Q96HC4;H0Y8Y3;A0A0D9SFR4;H0Y929;D6RGG6;A0A0D9SFW3;D6RAA1	PDZ and LIM domain protein 5	Structural/contractile	25,54106	25,55429	24,71895	48823080,86	49272864,16	27615023,13	0,566	1,009	0,560	-43,4	0,9	-44,0	0,0003411	0,00126829	+	CTR_DMD BMD_CTR BMD_DMD				7	7	2	17,1	17,1	4,7	63,944	2,563E-151	356680000
VIM	P08670;B0YJC4;B0YJC5;A0A1B0GUA0;A0A1B0GTT5;Q5JVS8;A0A1B0GVG8;P41219;H7C5W5;F8W835	Vimentin	Structural/contractile	23,40185	24,11672	26,21193	11083037,53	18190980,87	77727942,93	7,013	1,641	4,273	601,3	64,1	327,3	7,307E-07	0	+	DMD_CTR BMD_CTR DMD_BMD				21	18	18	49,4	43,8	43,8	53,651	9,6217E-250	210020000
ACTN2	P35609;F6THM6	Alpha-actinin-2	Structural/contractile	28,25633	28,6246	28,13858	320629071,5	413869301,3	295499408,2	0,922	1,291	0,714	-7,8	29,1	-28,6	0,0002797	0,00133333	+	BMD_CTR BMD_DMD				49	49	33	63,4	63,4	44,1	103,85	0	2661600000
MYOM1	P52179	Myomesin-1	Structural/contractile	25,31748	25,71434	25,16454	41813921,02	55053845,37	37608097,76	0,899	1,317	0,683	-10,1	31,7	-31,7	0,0013465	0,00104918	+	BMD_CTR BMD_DMD				46	46	7	36,8	36,8	8	187,62	0	353970000
FLNA	P21333;Q60FE5;Q5HY54;A0A087WWY3;H0Y5C6;H0Y5F3	Filamin-A	Structural/contractile	19,38612	19,69162	21,91787	685178,3306	846775,4985	3962199,247	5,783	1,236	4,679	478,3	23,6	367,9	0,0001969	0,00091429	+	DMD_CTR DMD_BMD				15	12	12	10,4	8,9	8,9	280,74	6,9546E-70	9956400
MSN	P26038	Moesin	Structural/contractile	17,35992	15,64657	18,18544	168211,8713	51296,40142	298100,6509	1,772	0,305	5,811	77,2	-69,5	481,1	0,0009675	0,00094546	+	DMD_CTR DMD_BMD				2	2	2	4,7	4,7	4,7	67,819	0,000082088	982570
MYL4	P12829;A0A1C7CYY4;I3L1K6;I3L532;I3L3U1;I3L4B1	Myosin light chain 4	Structural/contractile	19,3346	20,87403	22,8941	661141,7061	1921804,298	7794904,948	11,790	2,907	4,056	1079,0	190,7	305,6	0,0022362	0,00124444	+	DMD_CTR DMD_BMD				6	4	4	33,5	23,4	23,4	21,564	1,2572E-81	17473000
MYL6	B7Z6Z4;G3V1V0;G8JLA2;J3KND3;P60660;F8W1R7;F8VPF3;G3V1Y7;F8W180;F8VZU9;H0YI43	Myosin light polypeptide 6	Structural/contractile	19,65788	20,23853	21,89826	827201,915	1237099,405	3908706,967	4,725	1,496	3,160	372,5	49,6	216,0	0,0001139	0,00128	+	DMD_CTR DMD_BMD				6	4	4	30,7	20,6	20,6	26,707	2,4947E-45	11425000
MYH3	P11055;A0A087X0T3;A7E2Y1	Myosin-3	Structural/contractile	25,00787	23,22976	26,52193	33737973,88	9836816,095	96359929,35	2,856	0,292	9,796	185,6	-70,8	879,6	0,0063198	0,00343529	+	DMD_CTR DMD_BMD				84	34	34	45,9	23,8	23,8	223,9	0	332040000
MYH8	P13535	Myosin-8	Structural/contractile	20,82081	21,32647	26,35654	1852201,98	2629705,845	85922938,65	46,390	1,420	32,674	4539,0	42,0	3167,4	6,444E-06	0	+	DMD_CTR DMD_BMD				101	32	27	52,9	20,2	16,5	222,76	0	151460000
MYH9	P35579	Myosin-9	Structural/contractile	18,77452	17,80945	20,4109	448428,9829	229709,3412	1394097,468	3,109	0,512	6,069	210,9	-48,8	506,9	0,0162259	0,00602844	+	DMD_CTR DMD_BMD				9	8	6	7,3	6,8	5,2	226,53	5,8958E-37	3869400
NEB	A0A087X1N7;P20929;H0Y786;H7BZD5;H0Y3P5;H7C2Z5;H7C2B3;H7C2D0	Nebulin	Structural/contractile	28,33074	28,43527	27,73421	337600078,8	362968724,1	223269354,1	0,661	1,075	0,615	-33,9	7,5	-38,5	1,467E-05	0	+	CTR_DMD BMD_DMD				213	213	213	42,7	42,7	42,7	990,84	0	2521500000
SPTB	P11277;H0YJE6	Spectrin beta chain, erythrocyte	Structural/contractile	18,88277	18,86924	20,96141	483370,5325	478858,5381	2041799,821	4,224	0,991	4,264	322,4	-0,9	326,4	0,0055763	0,00334545	+	DMD_CTR DMD_BMD				6	6	6	3,8	3,8	3,8	246,47	1,4329E-14	5560500
TTN	A0A0A0MTS7;Q8WZ42;A0A0A0MRA3;H7C1P9;A0A0C4DG59;H7C0U7;A0A0U1RRH3;A0A1B0GXE3;H0Y4J7;REV__H7C1P9	Titin	Structural/contractile	30,68888	30,82858	30,42912	1730905721	1906897300	1445569837	0,835	1,102	0,758	-16,5	10,2	-24,2	0,0006029	0,00108333	+	CTR_DMD BMD_DMD				1023	1023	1022	40,4	40,4	40,4	3994,6	0	13691000000
TUBA1A	Q71U36	Tubulin alpha-1A chain	Structural/contractile	17,01713	17,33276	18,95023	132637,5741	165074,7574	506509,5693	3,819	1,245	3,068	281,9	24,5	206,8	0,002377	0,00123529	+	DMD_CTR DMD_BMD				11	2	1	35	6	3,1	50,135	2,8798E-60	1398100
ENO3	P13929;E5RGZ4;K7EKN2;K7EPM1;E5RG95;E5RI09;P09104;F5H0C8;F5H1C3;U3KQQ1;E5RJH5;K7EP84	Beta-enolase;Enolase	Glycolysis/gluconeogenesis	26,5773	25,45541	24,72468	100130066,3	46008911,85	27724920,74	0,277	0,459	0,603	-72,3	-54,1	-39,7	4,716E-08	0	+	CTR_DMD CTR_BMD BMD_DMD				15	15	13	52,1	52,1	42,9	46,986	0	609970000
ALDOA	P04075;J3KPS3;H3BQN4;H3BPS8;H3BR04;H3BUH7;H3BMQ8;H3BU78;H3BR68;P05062;A0A087WXX2	Fructose-bisphosphate aldolase A;Fructose-bisphosphate aldolase	Glycolysis/gluconeogenesis	28,92671	28,10179	27,62094	510278635,9	288059181,2	206410339,6	0,405	0,565	0,717	-59,5	-43,5	-28,3	0,0001253	0,00118519	+	CTR_DMD CTR_BMD BMD_DMD				21	21	18	79,1	79,1	69,5	39,42	0	2981600000
GPD1	P21695	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic	Glycolysis/gluconeogenesis	23,3927	22,61675	22,20087	11012968,06	6431616,703	4820896,413	0,438	0,584	0,750	-56,2	-41,6	-25,0	2,357E-05	0	+	CTR_DMD CTR_BMD BMD_DMD				10	10	10	41,5	41,5	41,5	37,567	4,7745E-175	75871000
PYGM	P11217;P06737;E9PK47	Glycogen phosphorylase, muscle form	Glycolysis/gluconeogenesis	28,20662	27,38632	26,66533	309769529,6	175429970,7	106430027,5	0,344	0,566	0,607	-65,6	-43,4	-39,3	6,143E-07	0	+	CTR_DMD CTR_BMD BMD_DMD				42	42	35	57	57	47,4	97,091	0	1806800000
LDHB	P07195;A8MW50;C9J7H8;F5H793	L-lactate dehydrogenase B chain;L-lactate dehydrogenase	Glycolysis/gluconeogenesis	21,54269	23,14804	22,25182	3054892,113	9295106,729	4994192,5	1,635	3,043	0,537	63,5	204,3	-46,3	0,0003982	0,00125301	+	DMD_CTR BMD_CTR BMD_DMD				7	6	6	24,3	20,7	20,7	36,638	4,9658E-40	40267000
PGK1	P00558;P07205	Phosphoglycerate kinase 1	Glycolysis/gluconeogenesis	26,22341	24,56197	23,46973	78348917,16	24767930,63	11616966,05	0,148	0,316	0,469	-85,2	-68,4	-53,1	1,112E-05	0	+	CTR_DMD CTR_BMD BMD_DMD				17	17	17	55,6	55,6	55,6	44,614	0	353340000
PKM2	P14618;B4DNK4;H3BQ34;H3BTJ2;H3BUW1;H3BT25;H3BU13;H3BQZ3;H3BN34	Pyruvate kinase isozymes M1/M2;Pyruvate kinase	Glycolysis/gluconeogenesis	27,42974	25,87089	25,53208	180790045,2	61364034,37	48520127,31	0,268	0,339	0,791	-73,2	-66,1	-20,9	2,031E-06	0	+	CTR_DMD CTR_BMD BMD_DMD				24	24	1	54,6	54,6	4,1	57,936	0	936060000
TPI1	P60174;U3KPZ0;U3KQF3;U3KPS5	Triosephosphate isomerase	Glycolysis/gluconeogenesis	26,96807	25,91966	24,88604	131279826,8	63473893,29	31005912,23	0,236	0,484	0,488	-76,4	-51,6	-51,2	6,878E-05	0,00102564	+	CTR_DMD CTR_BMD BMD_DMD				16	16	16	71,3	71,3	71,3	30,791	0	739930000
AGL	P35573	Glycogen debranching enzyme;4-alpha-glucanotransferase;Amylo-alpha-1,6-gluc	Glycolysis/gluconeogenesis	24,18948	23,93292	23,10944	19131942,17	16014994,87	9049709,18	0,473	0,837	0,565	-52,7	-16,3	-43,5	0,0008729	0,00099048	+	CTR_DMD BMD_DMD				27	27	27	21,9	21,9	21,9	174,76	6,9568E-117	121920000
CKM	P06732	Creatine kinase M-type	TCA/Respiratory chain	29,59074	29,0332	28,47429	808537810,1	549368899,9	372919759,3	0,461	0,679	0,679	-53,9	-32,1	-32,1	1,423E-05	0	+	CTR_DMD CTR_BMD BMD_DMD				20	20	18	68	68	65,9	43,101	0	5032700000
ATP5A1	P25705;K7EK77;K7ERX7;K7EJP1;K7EQH4;K7ENJ4;K7ESA0	ATP synthase subunit alpha, mitochondrial	TCA/Respiratory chain	25,34242	25,96818	25,49634	42543046,14	65644918,4	47332900,65	1,113	1,543	0,721	11,3	54,3	-27,9	0,0121612	0,0055102	+	BMD_CTR BMD_DMD				18	18	18	42,5	42,5	42,5	59,75	2,4779E-200	397070000
ATP5C1	P36542	ATP synthase subunit gamma, mitochondrial	TCA/Respiratory chain	21,74919	22,03792	21,78309	3524995,536	4306009,286	3608805,602	1,024	1,222	0,838	2,4	22,2	-16,2	0,0026285	0,00190071	+	BMD_CTR BMD_DMD				4	4	4	15,4	15,4	15,4	32,996	1,1602E-20	30469000
OGDH	E9PCR7;Q02218;E9PDF2;A0A0D9SFS3;E9PFG7;C9J4G7;Q9ULD0	2-oxoglutarate dehydrogenase, mitochondrial	TCA/Respiratory chain	21,20848	21,52688	20,81127	2423196,552	3021597,365	1839994,47	0,759	1,247	0,609	-24,1	24,7	-39,1	0,0128069	0,00552764	+	CTR_DMD BMD_DMD				9	9	9	15,7	15,7	15,7	117,66	8,3983E-40	19140000
ACO2	A2A274;Q99798	Aconitate hydratase, mitochondrial	TCA/Respiratory chain	24,61009	24,60597	23,94154	25607977,88	25534951,8	16110969,76	0,629	0,997	0,631	-37,1	-0,3	-36,9	0,0006269	0,00106122	+	CTR_DMD BMD_DMD				17	17	17	32,4	32,4	32,4	87,819	2,5453E-265	183200000
SLC25A4	P12235;V9GYG0;Q9H0C2	ADP/ATP translocase 1	TCA/Respiratory chain	25,30887	25,63738	24,87938	41565118,82	52193977,05	30863107,64	0,743	1,256	0,591	-25,7	25,6	-40,9	0,0011912	0,00088889	+	CTR_DMD BMD_DMD				11	11	5	38,3	38,3	17,1	33,064	4,1346E-101	331200000
AMPD1	P23109;Q01432;E9PKC5;A0A1B0GTL6	AMP deaminase 1	TCA/Respiratory chain	22,37743	22,48289	21,31667	5448508,79	5861709,335	2611903,201	0,479	1,076	0,446	-52,1	7,6	-55,4	0,0016837	0,00116535	+	CTR_DMD BMD_DMD				11	11	11	22,3	22,3	22,3	90,218	7,272E-94	46093000
ADCK3	Q8NI60	Chaperone activity of bc1 complex-like, mitochondrial	TCA/Respiratory chain	21,36373	21,60553	20,45944	2698507,002	3190895,652	1441800,376	0,534	1,182	0,452	-46,6	18,2	-54,8	0,0012744	0,0008595	+	CTR_DMD BMD_DMD				6	6	6	10,8	10,8	10,8	71,949	1,5202E-16	17386000
UQCRC2	P22695;H3BRG4;H3BSJ9;H3BP04;H3BUI9;H3BUE4;A0A087WVZ4	Cytochrome b-c1 complex subunit 2, mitochondrial	TCA/Respiratory chain	23,53837	23,63976	22,77744	12183032,96	13070038	7189400,283	0,590	1,073	0,550	-41,0	7,3	-45,0	0,0001326	0,00110345	+	CTR_DMD BMD_DMD				8	8	8	28,9	28,9	28,9	48,442	1,5054E-198	97223000
CYC1	P08574	Cytochrome c1, heme protein, mitochondrial	TCA/Respiratory chain	21,02553	21,25471	20,21798	2134593,609	2502103,435	1219602,853	0,571	1,172	0,487	-42,9	17,2	-51,3	0,0173124	0,00597235	+	CTR_DMD BMD_DMD				3	3	3	8	8	8	35,422	7,9474E-06	16136000
MDH2	P40926;G3XAL0	Malate dehydrogenase, mitochondrial;Malate dehydrogenase	TCA/Respiratory chain	23,63677	23,23475	22,83101	13042978,27	9870898,626	7461374,547	0,572	0,757	0,756	-42,8	-24,3	-24,4	0,0025521	0,00147826	+	CTR_DMD BMD_DMD				12	12	12	47,6	47,6	47,6	35,503	1,2407E-144	98633000
NDUFA4	O00483	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	TCA/Respiratory chain	22,47823	22,70197	22,21724	5842806,173	6822977,367	4875909,777	0,835	1,168	0,715	-16,5	16,8	-28,5	0,0040946	0,00299355	+	CTR_DMD BMD_DMD				3	3	3	37	37	37	9,3697	2,7043E-12	46304000
PDHA1	P08559;Q5JPU1;Q5JPT9;Q5JPU0;Q5JPU2;Q5JPU3	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondri	TCA/Respiratory chain	20,55833	20,95319	19,79589	1544094,908	2030199,399	910241,6022	0,589	1,315	0,448	-41,1	31,5	-55,2	0,002494	0,00148905	+	CTR_DMD BMD_DMD				5	5	5	22,8	22,8	22,8	43,295	2,5137E-27	10441000
SLC25A12	O75746;Q9UJS0;B4DGK6;H0YFB2;F8W9J0	Calcium-binding mitochondrial carrier protein Aralar1	Glutamate/glutathione metabolism	22,78718	22,0844	21,66084	7238101,961	4446996,998	3315603,362	0,458	0,614	0,746	-54,2	-38,6	-25,4	0,0001439	0,00106667	+	CTR_DMD CTR_BMD BMD_DMD				8	8	8	15,6	15,6	15,6	74,761	9,7289E-23	39959000
GOT2	P00505	Aspartate aminotransferase, mitochondrial	Glutamate/glutathione metabolism	24,42822	24,36833	22,82415	22574958,5	21656998,89	7425980,005	0,329	0,959	0,343	-67,1	-4,1	-65,7	0,0010085	0,00093694	+	CTR_DMD BMD_DMD				11	11	11	29,8	29,8	29,8	47,517	2,1795E-226	141810000
GSTP1	P09211;A8MX94;A0A087X2E9;A0A087X243	Glutathione S-transferase P	Glutamate/glutathione metabolism	22,29883	21,81174	21,31512	5159607,89	3681188	2609098,536	0,506	0,713	0,709	-49,4	-28,7	-29,1	0,0014204	0,00120325	+	CTR_DMD BMD_DMD				8	8	8	52,4	52,4	52,4	23,356	2,5235E-297	39911000
APM2	Q15847	Adipose most abundant gene transcript 2 protein	Lipid metabolism	16,09015	14,42699	18,17646	69761,81718	22027,07026	296250,8977	4,247	0,316	13,449	324,7	-68,4	1244,9	1,03E-05	0	+	DMD_CTR CTR_BMD DMD_BMD				1	1	1	40,8	40,8	40,8	7,8547	1,3971E-20	754860
ECH1	Q13011;M0R248	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	Lipid metabolism	20,02702	20,95802	20,49872	1068399,666	2037007,696	1481595,304	1,387	1,907	0,727	38,7	90,7	-27,3	9,631E-05	0,00086957	+	DMD_CTR BMD_CTR BMD_DMD				4	4	4	20,4	20,4	20,4	35,816	1,2726E-12	11169000
HADHA	P40939;H0YFD6	Trifunctional enzyme subunit alpha, mitochondrial;Long-chain enoyl-CoA hydrata	Lipid metabolism	23,72817	24,38166	24,1741	13896035,41	21858029,31	18929067,42	1,362	1,573	0,866	36,2	57,3	-13,4	4,953E-05	0	+	DMD_CTR BMD_CTR BMD_DMD				13	13	13	24,9	24,9	24,9	82,999	0	136530000
CRAT	P43155;H0Y4Z7;A6PVN3;B7ZBP5	Carnitine O-acetyltransferase	Lipid metabolism	20,53098	21,38306	20,20479	1515098,33	2734906,347	1208503,315	0,798	1,805	0,442	-20,2	80,5	-55,8	0,0012073	0,00088136	+	BMD_CTR BMD_DMD				5	5	5	9,3	9,3	9,3	70,857	1,6288E-43	13459000
EPHX1	P07099	Epoxide hydrolase 1	Lipid metabolism	16,65536	15,71963	16,92845	103219,7846	53961,02005	124730,0894	1,208	0,523	2,311	20,8	-47,7	131,1	0,0035042	0,00271141	+	CTR_BMD DMD_BMD				1	1	1	4	4	4	52,948	0,00015807	798130
APOA1	P02647;F8W696;CON__P15497	Apolipoprotein A-I;Truncated apolipoprotein A-I	Lipid metabolism	21,97837	21,83592	23,97378	4131888,808	3743405,748	16475055,62	3,987	0,906	4,401	298,7	-9,4	340,1	0,0005075	0,00115556	+	DMD_CTR DMD_BMD				10	10	10	41,2	41,2	41,2	30,777	1,3025E-248	60501000
FABP3	P05413;S4R371;S4R3A2	Fatty acid-binding protein, heart	Lipid metabolism	25,67295	25,96486	24,74324	53496827,1	65494026,81	28083900,77	0,525	1,224	0,429	-47,5	22,4	-57,1	0,0009482	0,00096296	+	CTR_DMD BMD_DMD				7	7	7	48,1	48,1	48,1	14,858	5,5877E-129	421530000
CLU	P10909;H0YC35;H0YLK8;E7ERK6;H0YAS8	Clusterin;Clusterin beta chain;Clusterin alpha chain;Clusterin	Protein/aminoacids metabolism	19,36018	19,0596	21,39456	672968,7557	546400,7734	2756793,931	4,096	0,812	5,045	309,6	-18,8	404,5	4,854E-06	0	+	DMD_CTR DMD_BMD				3	3	3	11,4	11,4	11,4	52,494	1,0473E-22	8683900
AMDHD1	Q96NU7	Probable imidazolonepropionase	Protein/aminoacids metabolism	20,69363	21,7371	22,85681	1695912,141	3495578,977	7596008,03	4,479	2,061	2,173	347,9	106,1	117,3	0,0391427	0,0106462	+	DMD_CTR DMD_BMD	+			1	1	1	4,9	4,9	4,9	46,742	0,038261	20391000
LMNA	P02545;Q3BDU5;Q5TCI8;A0A0C4DGC5;H0YAB0	Prelamin-A/C;Lamin-A/C	Muscle cell development	23,63478	24,4419	25,79783	13024999,67	22790038,09	58333851,68	4,479	1,750	2,560	347,9	75,0	156,0	9,235E-05	0,00088889	+	DMD_CTR BMD_CTR DMD_BMD				14	14	14	27	27	27	74,139	2,5812E-183	219600000
HIST1H2AB	A0A0U1RRH7	Histone H2A type 1-B/E	Transcription/translation regulation	21,40804	21,56155	23,24538	2784409,555	3095090,149	9943897,536	3,571	1,112	3,213	257,1	11,2	221,3	0,0002018	0,00090141	+	DMD_CTR DMD_BMD				4	4	0	37,6	37,6	0	18,552	1,0755E-108	33804000
RPS5	M0R0R2;P46782;M0R0F0;M0QZN2	40S ribosomal protein S5;40S ribosomal protein S5, N-terminally processed	Ribosomes	15,60947	15,29002	16,94031	49994,09216	40064,03202	125759,6864	2,515	0,801	3,139	151,5	-19,9	213,9	0,0100074	0,00487701	+	DMD_CTR DMD_BMD				1	1	1	6,7	6,7	6,7	25,333	0,00064212	523180
RPSA	A0A0C4DG17;P08865;C9J9K3;F8WD59	40S ribosomal protein SA	Ribosomes	18,932	19,0814	20,11667	500149,5448	554719,9169	1136896,902	2,273	1,109	2,049	127,3	10,9	104,9	0,0103939	0,00499471	+	DMD_CTR DMD_BMD				4	4	4	22,3	22,3	22,3	33,313	6,1625E-15	5039900
RPLP1	P05386	60S acidic ribosomal protein P1	Ribosomes	17,64632	17,93255	19,45724	205150,0528	250170,1268	719801,708	3,509	1,219	2,877	250,9	21,9	187,7	0,0016351	0,0011746	+	DMD_CTR DMD_BMD				2	2	2	51,8	51,8	51,8	11,514	2,5343E-13	2714700
RPL30	P62888;E5RI99;A0A0C4DH44;E5RJH3;A0A0B4J213	60S ribosomal protein L30	Ribosomes	17,40075	17,8544	19,13546	173040,4744	236979,0502	575900,4804	3,328	1,370	2,430	232,8	37,0	143,0	0,0106029	0,00494241	+	DMD_CTR DMD_BMD				2	2	2	24,3	24,3	24,3	12,784	7,7963E-06	1830700
YWHAB	P31946	14-3-3 protein beta/alpha;14-3-3 protein beta/alpha, N-terminally processed	Signal transduction	17,7455	18,77574	19,88332	219749,4456	448808,3526	967109,687	4,401	2,042	2,155	340,1	104,2	115,5	0,0010438	0,00092035	+	DMD_CTR DMD_BMD				5	3	3	27,6	20,3	20,3	28,082	1,2865E-108	3236500
YWHAQ	P27348;E9PG15	14-3-3 protein theta	Signal transduction	15,99705	16,65154	18,70087	65402,12994	102946,8385	426111,0681	6,515	1,574	4,139	551,5	57,4	313,9	2,812E-05	0	+	DMD_CTR DMD_BMD				4	2	2	20	12,7	12,7	27,764	1,0115E-18	1175500
YWHAZ	E7EX29;P63104;B0AZS6;E7ESK7;H0YB80;B7Z2E6;E7EVZ2;E9PD24;E5RIR4;E5RGE1	14-3-3 protein zeta/delta	Signal transduction	18,85209	19,41951	20,77451	473199,8202	701221,1572	1793703,499	3,791	1,482	2,558	279,1	48,2	155,8	0,0140747	0,00550244	+	DMD_CTR DMD_BMD				7	5	5	37,8	30,5	30,5	28,036	2,1799E-78	8172100
CALM2	H0Y7A7	Calmodulin	ER/sarcoplasmic reticulum, Calcium handling	21,00251	20,86272	21,99293	2100803,8	1906797,225	4173799,883	1,987	0,908	2,189	98,7	-9,2	118,9	0,0002074	0,00088889	+	DMD_CTR DMD_BMD				4	3	3	23,5	19,8	19,8	20,762	4,4367E-20	19945000
JPH1	Q9HDC5	Junctophilin-1	ER/sarcoplasmic reticulum, Calcium handling	18,60834	18,33682	17,55367	399639,5944	331079,9227	192389,4283	0,481	0,828	0,581	-51,9	-17,2	-41,9	0,0001492	0,00103226	+	CTR_DMD BMD_DMD				1	1	1	2,3	2,3	2,3	71,685	0,00041905	2659000
ANXA1	P04083;Q5T3N1;Q5T3N0	Annexin A1;Annexin	Inflammation/ Immune response	17,50944	17,96533	20,9979	186580,6696	255919,4018	2094101,587	11,224	1,372	8,183	1022,4	37,2	718,3	0,0004467	0,0012093	+	DMD_CTR DMD_BMD				7	7	7	32,1	32,1	32,1	38,714	1,2714E-46	5188300
C3	P01024;M0QYC8;M0QXZ3	Complement C3;Complement C3 beta chain;Complement C3 alpha chain;C3a ana	Inflammation/ Immune response	21,27259	21,86159	23,04403	2533306,138	3810608,597	8648568,927	3,414	1,504	2,270	241,4	50,4	127,0	0,0006135	0,00107216	+	DMD_CTR DMD_BMD				15	15	13	13,2	13,2	11,8	187,15	2,0817E-105	33092000
C4B	P0C0L5;A0A0G2JL54;A0A140TA29;F5GXS0	Complement C4-B;Complement C4 beta chain;Complement C4-B alpha chain;C4a	Inflammation/ Immune response	17,22355	17,73388	19,59116	153040,0792	217986,611	789817,6049	5,161	1,424	3,623	416,1	42,4	262,3	0,0008909	0,00098113	+	DMD_CTR DMD_BMD				5	5	1	5,6	5,6	1,5	192,75	2,1417E-13	2346300
IGKC	A0A075B6H6;P01834	Ig kappa chain C region	Inflammation/ Immune response	24,94056	24,90044	26,12262	32200059,09	31316941,8	73062105,8	2,269	0,973	2,333	126,9	-2,7	133,3	0,0017555	0,00114729	+	DMD_CTR DMD_BMD				5	5	5	79,4	79,4	79,4	11,609	0	316600000
IGLC6	A0A075B6K9	Ig lambda-6 chain C region	Inflammation/ Immune response	19,88523	20,83892	22,09979	968390,9022	1875599,02	4494689,422	4,641	1,937	2,396	364,1	93,7	139,6	0,0004714	0,0011954	+	DMD_CTR DMD_BMD				3	3	1	46,2	46,2	17,9	11,236	7,542E-27	14275000
IGLL5	A0A0B4J231	Immunoglobulin lambda-like polypeptide 5	Inflammation/ Immune response	17,27794	17,39899	18,88426	158919,8708	172829,5043	483870,0103	3,045	1,088	2,800	204,5	8,8	180,0	0,0005125	0,00114286	+	DMD_CTR DMD_BMD				3	1	1	22,8	8,8	8,8	23,15	1,2665E-26	1895700
ANXA2	P07355	Annexin A2;Annexin	Stress response	22,76107	23,3415	25,10737	7108284,53	10628981,32	36146935,34	5,085	1,495	3,401	408,5	49,5	240,1	6,929E-06	0	+	DMD_CTR DMD_BMD				14	14	14	47,2	47,2	47,2	38,604	3,7914E-175	104840000
ANXA5	P08758;D6RBL5;D6RBE9;E9PHT9	Annexin A5;Annexin	Blood coagulation	20,85734	20,80727	22,37207	1899699,768	1834899,988	5428303,672	2,857	0,966	2,958	185,7	-3,4	195,8	8,068E-05	0,00095238	+	DMD_CTR DMD_BMD				7	7	7	33,4	33,4	33,4	35,936	1,3051E-74	20994000
APOH	P02749;J3QRN2;J3QLI0	Beta-2-glycoprotein 1	Blood coagulation	17,83775	18,08945	20,26488	234259,82	278911,907	1259901,922	5,378	1,191	4,517	437,8	19,1	351,7	0,0056361	0,0033253	+	DMD_CTR DMD_BMD				3	3	3	13,6	13,6	13,6	38,298	5,2265E-23	2614900
HP	P00738;H0Y300;J3QR68;J3QLC9;A0A0C4DGL8;A0A087WU08;H3BS21;P00739;J3KRH2;A0A0A0MRD9;J3KTC3;H3BMJ7;J3QQI8;J3KSV1	Haptoglobin;Haptoglobin alpha chain;Haptoglobin beta chain	Transport	21,01447	21,0745	22,96979	2118291,936	2208292,735	8214777,106	3,878	1,042	3,720	287,8	4,2	272,0	0,0025571	0,00146763	+	DMD_CTR DMD_BMD				11	11	11	35,7	35,7	35,7	45,205	1,7746E-31	25611000
HPX	P02790;Q9BS19	Hemopexin	Transport	20,94378	21,52588	23,0163	2017000,485	3019503,679	8483922,433	4,206	1,497	2,810	320,6	49,7	181,0	6,675E-05	0,00108108	+	DMD_CTR DMD_BMD				7	7	7	23,6	23,6	23,6	51,676	1,6991E-53	29831000
IFIT2	A0A087X279;P09913	Interferon-induced protein with tetratricopeptide repeats 2	Other proteins	24,83408	23,41002	22,62487	29909075,89	11145978,96	6467918,189	0,216	0,373	0,580	-78,4	-62,7	-42,0	0,0001289	0,00116364	+	CTR_DMD CTR_BMD BMD_DMD				1	1	1	2,5	2,5	2,5	55,984	0,00095248	151850000
AHNAK	Q09666	Neuroblast differentiation-associated protein AHNAK	Other proteins	19,66154	21,63028	23,6309	829303,1232	3246108,969	12990017,15	15,664	3,914	4,002	1466,4	291,4	300,2	9,758E-05	0,00085106	+	DMD_CTR BMD_CTR DMD_BMD				23	23	23	14,4	14,4	14,4	629,09	2,9998E-55	31387000
ACAT1	P24752;E9PRQ6;H0YEL7;E9PKF3	Acetyl-CoA acetyltransferase, mitochondrial	Other proteins	22,86782	23,01262	22,52071	7654199,111	8462309,377	6017404,877	0,786	1,106	0,711	-21,4	10,6	-28,9	0,0046366	0,00305	+	CTR_DMD BMD_DMD				8	8	8	25,5	25,5	25,5	45,199	3,4287E-223	61770000
AKR1A1	P14550	Alcohol dehydrogenase [NADP(+)]	Other proteins	13,60247	14,20747	15,81593	12438,02671	18917,97436	57685,85571	4,638	1,521	3,049	363,8	52,1	204,9	0,0027564	0,00198601	+	DMD_CTR DMD_BMD				1	1	1	5,8	5,8	5,8	36,573	0,0029075	195970
ADH1B	P00325	Alcohol dehydrogenase 1B	Other proteins	18,81997	18,15485	19,75228	462780,9652	291846,4512	883138,3876	1,908	0,631	3,026	90,8	-36,9	202,6	0,0011591	0,00090435	+	DMD_CTR DMD_BMD				2	2	2	9,1	9,1	9,1	39,854	9,6779E-06	2864700
AKR1B1	P15121;E9PCX2;E9PEF9;C9JRZ8	Aldose reductase	Other proteins	21,99769	21,52157	20,17804	4187593,58	3010496,48	1186302,085	0,283	0,719	0,394	-71,7	-28,1	-60,6	0,0101683	0,00502128	+	CTR_DMD BMD_DMD				4	4	4	14,2	14,2	14,2	35,853	1,5313E-93	26734000
SERPINA3	P01011;G3V3A0	Alpha-1-antichymotrypsin;Alpha-1-antichymotrypsin His-Pro-less	Other proteins	16,86436	17,29983	18,78931	119310,3769	161349,5468	453049,7633	3,797	1,352	2,808	279,7	35,2	180,8	0,0091872	0,00421739	+	DMD_CTR DMD_BMD				1	1	1	4,5	4,5	4,5	47,65	5,9591E-15	1814300
SERPINA1	P01009	Alpha-1-antitrypsin;Short peptide from AAT	Other proteins	23,38824	23,5981	25,70047	10978974,74	12698018,07	54527096,5	4,967	1,157	4,294	396,7	15,7	329,4	2,672E-07	0	+	DMD_CTR DMD_BMD				7	7	1	26,6	26,6	3,8	46,736	0	164010000
ANXA11	P50995	Annexin A11	Other proteins	17,08763	16,84431	18,37241	139280,1368	117663,7177	339348,9444	2,436	0,845	2,884	143,6	-15,5	188,4	0,0134053	0,00558416	+	DMD_CTR DMD_BMD				2	2	2	4,8	4,8	4,8	54,389	0,00011286	1309900
CMBL	Q96DG6	Carboxymethylenebutenolidase homolog	Other proteins	21,55628	20,78077	19,14925	3083804,763	1801503,47	581431,6175	0,189	0,584	0,323	-81,1	-41,6	-67,7	0,0001063	0,00083333	+	CTR_DMD BMD_DMD				4	4	4	18,4	18,4	18,4	28,048	3,3211E-43	17315000
PXMP2	F5GZF7	Peroxisomal membrane protein 2 (Fragment)	Other proteins	18,47646	19,09272	20,74205	364727,6376	559089,6065	1753796,591	4,809	1,533	3,137	380,9	53,3	213,7	0,0038416	0,00284211	+	DMD_CTR DMD_BMD	+			1	1	1	34,7	34,7	34,7	5,227	0,031642	4774300
PEBP1	P30086	Phosphatidylethanolamine-binding protein 1;Hippocampal cholinergic neurostimula	Other proteins	23,40808	23,0459	22,52869	11131000,98	8659786,342	6050781,258	0,544	0,778	0,699	-45,6	-22,2	-30,1	0,000259	0,00105263	+	CTR_DMD BMD_DMD				8	8	8	67,4	67,4	67,4	21,057	1,8185E-169	71062000
HHATL	Q9HCP6;C9JJ25;C9JHL0	Protein-cysteine N-palmitoyltransferase HHAT-like protein	Other proteins	19,75595	18,63147	18,1819	885387,8192	406098,4513	297370,0858	0,336	0,459	0,732	-66,4	-54,1	-26,8	0,005062	0,00306748	+	CTR_DMD BMD_DMD				3	3	3	8,9	8,9	8,9	56,703	6,8734E-10	8122500
SELENBP1	Q13228;A6PVX1;F8WCR4;F2Z2W8;H0Y532;C9JVL0	Selenium-binding protein 1	Other proteins	20,55131	20,30919	19,46868	1536599,757	1299198,103	725532,1403	0,472	0,846	0,558	-52,8	-15,4	-44,2	0,012595	0,00555556	+	CTR_DMD BMD_DMD				5	5	5	15,3	15,3	15,3	52,39	4,0222E-33	10607000
VDAC1	P21796;C9JI87	Voltage-dependent anion-selective channel protein 1	Other proteins	24,32656	25,0239	24,02369	21038959,2	34114931,89	17054983,22	0,811	1,622	0,500	-18,9	62,2	-50,0	0,0106332	0,00491667	+	CTR_DMD BMD_DMD				13	13	13	64	64	64	30,772	0	198850000

b. Other proteins significantly changed vs. CTR, but not in DMD vs. BMD

Gene names	Protein IDs	Description	Molecular function	Log2 Av. Volumes CTR	Log2 Av. Volumes BMD	Log2 Av. Volumes DMD	Av. Volumes CTR	Av. Volumes BMD	Av. Volumes DMD	Av. Ratio DMD/CTR	Av. Ratio BMD/CTR	Av. Ratio DMD/BMD	% variation DMD/CTR	% variation BMD/CTR	% variation DMD/BMD	N: ANOVA p value	N: ANOVA q-value	C: ANOVA Significant	T: Significant pairs	C: Only identified by site	C: Reverse	C: Contaminant	N: Peptides	N: Razor + unique peptides	N: Unique peptides	N: Sequence coverage [%]	N: Unique + razor sequence coverage [%]	N: Unique sequence coverage [%]	N: Mol. weight [kDa]	N: PEP	N: Intensity
FGB	P02675;D6REL8;CON__P02676	Fibrinogen beta chain;Fibrinopeptide B;Fibrinogen beta chain	Extracellular matrix	20,63795	22,9865	23,83094	1631706,333	8310477,831	14922025,06	9,145	5,093	1,796	814,5	409,3	79,6	2,003E-07	0	+	DMD_CTR BMD_CTR				9	9	9	26,9	26,9	26,9	55,928	3,9262E-74	47847000
HSPG2	P98160;A0A0U1RQT3	Basement membrane-specific heparan sulfate proteoglycan core protein;Endorep	Extracellular matrix	20,94928	21,51797	22,40569	2024704,591	3002993,663	5556288,192	2,744	1,483	1,850	174,4	48,3	85,0	8,698E-05	0,00093023	+	DMD_CTR BMD_CTR				13	13	13	4,7	4,7	4,7	468,83	1,5817E-58	24490000
CAPNS1	A0A0C4DGQ5;K7ELJ7;P04632;K7EM73;A0A075B7C0;K7EIV0;K7EKD8;U3KQE2;K7EMQ1;K7ES78	Calpain small subunit 1	Extracellular matrix	17,27349	17,44952	17,72939	158430,4369	178990,0667	217309,2409	1,372	1,130	1,214	37,2	13,0	21,4	0,0263159	0,00808439	+	DMD_CTR				3	3	3	14,9	14,9	14,9	33,786	1,4715E-08	1869400
LAMC1	P11047	Laminin subunit gamma-1	Extracellular matrix	22,15304	22,5306	23,46936	4663688,501	6058797,26	11613987,09	2,490	1,299	1,917	149,0	29,9	91,7	0,0002506	0,00085333	+	DMD_CTR				10	10	10	9	9	9	177,6	1,8567E-156	48362000
ACTN3	Q08043;A0A087WSZ2;K7EP19;D6RH00	Alpha-actinin-3	Structural/contractile	25,43867	23,39192	23,49984	45478142,67	11007015,45	11861967,6	0,261	0,242	1,078	-73,9	-75,8	7,8	6,671E-06	0	+	CTR_DMD CTR_BMD				35	24	23	51,5	37,3	36,4	103,24	0	248600000
FLNC	Q14315;O75369;E7EN95;F8WE98	Filamin-C	Structural/contractile	26,76471	27,18679	27,17035	114019868,4	152770421,1	151039431,6	1,325	1,340	0,989	32,5	34,0	-1,1	0,0045139	0,00295541	+	DMD_CTR BMD_CTR				76	76	73	40,6	40,6	39,4	291,02	0	1090600000
MYH1	P12882	Myosin-1	Structural/contractile	31,42612	30,33682	30,4349	2885391628	1356103363	1451502590	0,503	0,470	1,070	-49,7	-53,0	7,0	0,0001918	0,00092754	+	CTR_DMD CTR_BMD				127	96	23	60,1	49,8	13,1	223,14	0	15891000000
MYH4	Q9Y623	Myosin-4	Structural/contractile	25,89414	24,84158	25,19257	62360968,57	30064966,18	38345926,71	0,615	0,482	1,275	-38,5	-51,8	27,5	0,0001448	0,00104918	+	CTR_DMD CTR_BMD				80	8	8	39,1	3,9	3,9	223,07	0	479670000
MYOM3	Q5VTT5	Myomesin-3	Structural/contractile	23,4768	24,31451	24,11442	11674035,3	20863964,73	18162003,21	1,556	1,787	0,870	55,6	78,7	-13,0	0,0001577	0,00101587	+	DMD_CTR BMD_CTR				27	27	27	26	26	26	162,19	0	124340000
MYOT	A0A0C4DFM5;Q9UBF9;B4DT68	Myotilin	Structural/contractile	24,39395	25,22689	24,86759	22045028,4	39269067,4	30611915,78	1,389	1,781	0,780	38,9	78,1	-22,0	0,0050455	0,00310559	+	DMD_CTR BMD_CTR				17	17	17	56,2	56,2	56,2	55,394	2,8252E-125	228860000
TNNC1	P63316;C9JDI3	Troponin C, slow skeletal and cardiac muscles	Structural/contractile	24,95007	26,19009	26,55056	32413017,52	76560132,99	98291273,43	3,032	2,362	1,284	203,2	136,2	28,4	3,424E-05	0	+	DMD_CTR BMD_CTR				5	5	5	34,2	34,2	34,2	18,402	9,6715E-157	473580000
TNNC2	P02585;C9J7T9	Troponin C, skeletal muscle	Structural/contractile	25,62979	24,31555	24,67901	51920106,25	20879010,42	26861005,96	0,517	0,402	1,287	-48,3	-59,8	28,7	5,874E-05	0	+	CTR_DMD CTR_BMD				9	9	8	60	60	55,6	18,122	8,5465E-276	296520000
TNNT3	P45378;F8WA37;H9KVA2;C9JCA5	Troponin T, fast skeletal muscle	Structural/contractile	27,14715	25,17573	26,18888	148629989,4	37900932,28	76495948,3	0,515	0,255	2,018	-48,5	-74,5	101,8	8,936E-05	0,00090909	+	CTR_DMD CTR_BMD				13	13	2	36,1	36,1	3,3	31,824	9,6167E-111	754390000
TPM1	P09493;H0YL52;Q6ZN40;H0YKP3;H0YK48;H0YNC7;H0YKX5;B7Z596;H7BYY1;F5H7S3;A0A087WTJ7;H0YL42;H0YKZ6;H0YK20;K7ELP0;H0YLS7	Tropomyosin alpha-1 chain	Structural/contractile	28,44118	27,14258	27,52768	364458675,1	148159921,7	193489495	0,531	0,407	1,306	-46,9	-59,3	30,6	6,939E-06	0	+	CTR_DMD CTR_BMD				19	10	7	49,3	29,6	21,5	32,708	0	2236000000
MYL1	P05976	Myosin light chain 1/3, skeletal muscle isoform	Structural/contractile	29,12532	28,22647	29,07903	585591755	314061095,8	567100819,4	0,968	0,536	1,806	-3,2	-46,4	80,6	0,0045337	0,00293671	+	CTR_BMD				15	15	12	82,5	82,5	69,6	21,145	0	4625600000
FHOD1	Q9Y613	FH1/FH2 domain-containing protein 1	Structural/contractile	16,11742	15,21747	14,78637	71093,00518	38099,11855	28257,96592	0,397	0,536	0,742	-60,3	-46,4	-25,8	0,0027361	0,002	+	CTR_DMD				1	1	1	1,3	1,3	1,3	126,55	0,0023502	400600
MYPN	Q86TC9;A0A087WX60	Myopalladin	Structural/contractile	12,63479	13,70617	14,51712	6359,907203	13364,97946	23447,0695	3,687	2,101	1,754	268,7	110,1	75,4	0,0207827	0,0064	+	DMD_CTR	+			2	2	2	3,2	3,2	3,2	145,26	0,00052957	94299
MYL2	P10916;G3V1V8;Q9BUA6	Myosin regulatory light chain 2, ventricular/cardiac muscle isoform	Structural/contractile	25,81071	26,60145	26,69299	58856972,55	101820301,4	108490238,5	1,843	1,730	1,066	84,3	73,0	6,6	0,009674	0,00470968	+	DMD_CTR				11	11	11	73,5	73,5	73,5	18,789	1,2786E-206	836930000
MYOZ1	Q9NP98	Myozenin-1	Structural/contractile	24,62478	24,03624	23,74067	25870058,85	17203991,65	14016958,49	0,542	0,665	0,815	-45,8	-33,5	-18,5	0,0050501	0,00308642	+	CTR_DMD				12	12	12	64,5	64,5	64,5	31,744	1,3502E-296	186550000
MYOZ2	Q9NPC6	Myozenin-2	Structural/contractile	20,89948	22,03772	22,15261	1956006,861	4305412,388	4662298,68	2,384	2,201	1,083	138,4	120,1	8,3	0,0064463	0,00355814	+	DMD_CTR				3	3	3	14,4	14,4	14,4	29,898	7,1072E-20	22787000
OBSCN	A6NGQ3;Q5VST9;A0A0A0MRI8;H3BQA7;A0A1B0GTS2	Obscurin	Structural/contractile	22,2717	22,85628	23,30911	5063487,643	7593218,013	10393008,49	2,053	1,500	1,369	105,3	50,0	36,9	0,0012738	0,00086667	+	DMD_CTR				26	26	26	5,7	5,7	5,7	972,99	0	57583000
PDLIM7	Q9NR12;D6RH06;H7BYK4;D6RF83;D6RAN1	PDZ and LIM domain protein 7	Structural/contractile	20,54727	19,8334	19,72637	1532302,814	934218,1833	867419,2893	0,566	0,610	0,928	-43,4	-39,0	-7,2	0,0133028	0,00564	+	CTR_DMD				2	2	2	4,8	4,8	4,8	49,844	3,6006E-06	9588400
PLEC	Q15149;E9PMV1;H0YDN1;E9PKG0;E9PIA2;P58107;A0A087X1U6;A0A075B730;E9PQ28	Plectin	Structural/contractile	23,60026	23,79986	24,23213	12717043,75	14603997,59	19705977,78	1,550	1,148	1,349	55,0	14,8	34,9	0,0166348	0,00605607	+	DMD_CTR				55	55	55	15,9	15,9	15,9	531,78	6,6296E-202	125060000
TUBB	P07437	Tubulin beta chain	Structural/contractile	21,24771	21,45076	22,32553	2489992,558	2866303,604	5255985,992	2,111	1,151	1,834	111,1	15,1	83,4	1,277E-05	0	+	DMD_CTR				14	14	2	48,2	48,2	9,5	49,67	2,1503E-112	22957000
TUBB4B	P68371	Tubulin beta-4B chain	Structural/contractile	19,25207	18,27699	18,35052	624382,2503	317630,5162	334238,8713	0,535	0,509	1,052	-46,5	-49,1	5,2	0,0228635	0,00710917	+	CTR_DMD				13	2	1	42,5	7,2	3,8	49,83	0	2196600
TUBB8	Q3ZCM7	Tubulin beta-8 chain	Structural/contractile	16,44179	17,0477	17,11174	89016,79884	135478,0875	141627,3178	1,591	1,522	1,045	59,1	52,2	4,5	0,0318014	0,00876494	+	DMD_CTR				5	1	1	16,9	7,2	7,2	49,775	7,8621E-11	696640
MYO1A	Q9UBC5;G3V342	Unconventional myosin-Ia	Structural/contractile	20,6248	20,32915	18,36286	1616901,093	1317297,709	337110,0237	0,208	0,815	0,256	-79,2	-18,5	-74,4	0,0460589	0,0116889	+	CTR_DMD	+			1	1	1	1,4	1,4	1,4	118,4	0,0086315	10310000
WDR1	O75083;D6RD66	WD repeat-containing protein 1	Structural/contractile	18,81934	19,71637	19,81275	462578,9208	861427,5866	920941,5058	1,991	1,862	1,069	99,1	86,2	6,9	0,0551784	0,014227	+	DMD_CTR				4	4	4	13,4	13,4	13,4	66,193	3,2124E-50	5542400
FBP2	O00757;P09467	Fructose-1,6-bisphosphatase isozyme 2	Glycolysis/gluconeogenesis	23,32017	20,94314	20,24342	10472989,64	2016105,913	1241299,655	0,119	0,193	0,616	-88,1	-80,7	-38,4	3,101E-05	0	+	CTR_DMD CTR_BMD				8	8	8	32,2	32,2	32,2	36,743	7,1932E-32	51611000
GYS1	P13807;M0QYU1	Glycogen [starch] synthase, muscle	Glycolysis/gluconeogenesis	20,23163	21,00696	20,95234	1231196,832	2107293,743	2029003,608	1,648	1,712	0,963	64,8	71,2	-3,7	0,0005853	0,00109474	+	DMD_CTR BMD_CTR				8	8	8	17,9	17,9	17,9	83,785	2,1044E-24	12519000
LDHA	P00338;F5GXY2;F5GYU2;F5GXH2;F5H6W8;F5H5J4;A0A087WUM2;F5GZQ4;P07864;F5H245;G3XAP5;F5H155;F5H5G7;F5GXU1;F5GWW2;F5GXC7;F5H8H6	L-lactate dehydrogenase A chain	Glycolysis/gluconeogenesis	25,60261	23,8349	23,62645	50951101,49	14963040,23	12950011,11	0,254	0,294	0,865	-74,6	-70,6	-13,5	7,806E-05	0,00097561	+	CTR_DMD CTR_BMD				12	12	11	43,4	43,4	39,8	36,688	7,389E-169	262830000
PFKM	P08237;F8VP00;F8VZQ1;F8VNX2;F8VX13;F8VSL1;F8VZI0;F8VTQ3;F8VYK8;F8VUB8;F8VW30;F8VSF7;F8W1J8;F8VVE3;H0YHB8	6-phosphofructokinase, muscle type	Glycolysis/gluconeogenesis	24,61526	23,1966	22,65139	25699910,51	9613297,83	6587912,67	0,256	0,374	0,685	-74,4	-62,6	-31,5	2,279E-05	0	+	CTR_DMD CTR_BMD				19	19	19	33,7	33,7	33,7	85,182	2,8501E-302	127240000
ENO1	P06733;K7EM90	Alpha-enolase	Glycolysis/gluconeogenesis/glycogen metabolism	25,04614	24,41667	24,36386	34644908,26	22394948,3	21590001,38	0,623	0,646	0,964	-37,7	-35,4	-3,6	0,0333788	0,00921739	+	CTR_DMD				7	5	5	25,3	16,1	16,1	47,168	3,3479E-125	219240000
ALDOC	P09972;A8MVZ9;J3QKP5;J3KSV6;C9J8F3;K7EKH5	Fructose-bisphosphate aldolase C;Fructose-bisphosphate aldolase	Glycolysis/gluconeogenesis/glycogen metabolism	24,42611	23,47308	23,77485	22541965,84	11643972,49	14353010,16	0,637	0,517	1,233	-36,3	-48,3	23,3	0,0303339	0,00853878	+	CTR_DMD				4	1	1	15,9	6,3	6,3	39,455	3,7677E-199	166120000
GPD1L	Q8N335;C9JM46;C9JFA7;C9K0P5	Glycerol-3-phosphate dehydrogenase 1-like protein	Glycolysis/gluconeogenesis/glycogen metabolism	20,38163	19,39693	18,93128	1366098,425	690331,6001	499899,9995	0,366	0,505	0,724	-63,4	-49,5	-27,6	0,0052775	0,00304878	+	CTR_DMD				4	4	4	14,5	14,5	14,5	38,418	3,0083E-12	9635400
GYG1	P46976;C9JQ42;G5E9W8	Glycogenin-1	Glycolysis/gluconeogenesis/glycogen metabolism	21,01168	20,39513	19,74236	2114199,371	1378941,669	877086,7398	0,415	0,652	0,636	-58,5	-34,8	-36,4	0,0481877	0,0117226	+	CTR_DMD				4	4	4	14,6	14,6	14,6	39,383	1,379E-08	11904000
PGAM2	P15259;Q8N0Y7	Phosphoglycerate mutase 2	Glycolysis/gluconeogenesis/glycogen metabolism	24,97561	23,79778	22,89015	32991933,64	14582957,5	7773592,223	0,236	0,442	0,533	-76,4	-55,8	-46,7	0,0020951	0,00127273	+	CTR_DMD				11	11	7	55,3	55,3	41,5	28,766	4,2281E-89	167140000
IDH3A	P50213;H0YL72;H0YMU3;H0YLI6;H0YKD0	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	TCA/Respiratory chain	18,37645	19,04244	19,24848	340300,56	539940,1597	622830,4701	1,830	1,587	1,154	83,0	58,7	15,4	0,0015318	0,001184	+	DMD_CTR BMD_CTR				2	2	2	9,6	9,6	9,6	39,591	0,000034631	3520100
UQCR10	Q9UDW1	Cytochrome b-c1 complex subunit 9	TCA/Respiratory chain	18,85303	19,65412	19,43961	473508,238	825048,8407	711059,1249	1,502	1,742	0,862	50,2	74,2	-13,8	0,0005421	0,00111828	+	DMD_CTR BMD_CTR				2	2	2	38,1	38,1	38,1	7,3084	1,8161E-07	4641900
ETFB	P38117;M0QY67	Electron transfer flavoprotein subunit beta	TCA/Respiratory chain	20,76887	21,40036	20,8254	1786704,972	2767899,25	1858104,229	1,040	1,549	0,671	4,0	54,9	-32,9	0,0601107	0,0156655	+	BMD_CTR				5	5	5	22,4	22,4	22,4	27,843	1,7083E-124	15880000
NDUFS4	O43181;H0Y9M8	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial	TCA/Respiratory chain	18,56871	17,5816	17,55615	388811,1321	196150,2978	192720,4311	0,496	0,504	0,983	-50,4	-49,6	-1,7	0,0773658	0,0216933	+	CTR_BMD				1	1	1	8,6	8,6	8,6	20,108	5,2533E-07	2316600
COX5A	H3BNX8;P20674;H3BV69;H3BRM5	Cytochrome c oxidase subunit 5A, mitochondrial	TCA/Respiratory chain	19,61405	19,28736	18,60028	802448,9007	639843,6985	397413,1265	0,495	0,797	0,621	-50,5	-20,3	-37,9	0,0268018	0,00833613	+	CTR_DMD				2	2	2	14,4	14,4	14,4	17,235	2,3987E-11	5167400
COX6B1	P14854	Cytochrome c oxidase subunit 6B1	TCA/Respiratory chain	20,61782	20,85285	21,13345	1609097,148	1893796,655	2300394,719	1,430	1,177	1,215	43,0	17,7	21,5	0,138575	0,0399763	+	DMD_CTR				2	2	2	33,7	33,7	33,7	10,192	2,7201E-39	15219000
SLC25A11	Q02978;I3L1P8	Mitochondrial 2-oxoglutarate/malate carrier protein	TCA/Respiratory chain	21,29098	20,85628	20,3738	2565804,823	1898304,503	1358704,224	0,530	0,740	0,716	-47,0	-26,0	-28,4	0,0786225	0,0221518	+	CTR_DMD				7	7	7	22,9	22,9	22,9	34,061	4,5479E-150	20464000
AK1	Q5T9B7;P00568;H0Y4J6;H0YID2;Q9Y6K8	Adenylate kinase isoenzyme 1	Energy transfer	24,68966	23,71377	23,72806	27060028,07	13758024,56	13894975,93	0,513	0,508	1,010	-48,7	-49,2	1,0	0,0004098	0,0012381	+	CTR_DMD CTR_BMD				10	10	10	57,6	57,6	57,6	23,411	6,5784E-148	176880000
CKB	P12277;G3V4N7;H0YJG0;G3V461	Creatine kinase B-type	Energy transfer	19,40208	20,80002	21,5956	692800,286	1825702,164	3169008,283	4,574	2,635	1,736	357,4	163,5	73,6	4,875E-07	0	+	DMD_CTR BMD_CTR				7	5	5	25,7	20,2	20,2	42,644	1,3043E-56	12239000
CKMT2	P17540;P12532;D6R998;D6RHV3;F8WCN3;C9JSQ1;C9JT96	Creatine kinase S-type, mitochondrial	Energy transfer	25,00028	24,24016	23,80912	33560944,92	19815966,51	14698035,44	0,438	0,590	0,742	-56,2	-41,0	-25,8	0,0002166	0,00087671	+	CTR_DMD CTR_BMD				12	12	12	42,2	42,2	42,2	47,504	0	204110000
CAP2	P40123;E9PDI2;A0A087WZ15;A0A087X0J3;B7Z385	Adenylyl cyclase-associated protein 2;Adenylyl cyclase-associated protein	Energy transfer	19,78764	19,39594	18,8613	905051,2726	689858,0462	476230,3366	0,526	0,762	0,690	-47,4	-23,8	-31,0	0,0007412	0,0010297	+	CTR_DMD				2	2	2	7,5	7,5	7,5	52,823	9,3647E-06	5714300
GSTM2	F6XZQ7;P28161;E9PHN6;E9PHN7;E9PLF1;E7EWW9;A0A0A0MR85;P09488;Q03013;B9ZVX7;E9PGV1;H3BQT3	Glutathione S-transferase Mu 2	Glutamate/glutathione metabolism	21,33952	19,89745	19,8527	2653600,944	976628,2605	946799,8815	0,357	0,368	0,969	-64,3	-63,2	-3,1	0,0148314	0,00567308	+	CTR_DMD CTR_BMD				4	4	4	28,2	28,2	28,2	26,097	7,63E-14	14652000
ARL6IP5	O75915;F8WF33;C9JQU6;F8WF90	PRA1 family protein 3	Glutamate/glutathione metabolism	18,77188	19,2408	19,60277	447609,1492	619523,7221	796199,2572	1,779	1,384	1,285	77,9	38,4	28,5	0,0157427	0,00576077	+	DMD_CTR				2	2	2	16	16	16	21,614	0,000022298	3982300
GLRX	P35754	Glutaredoxin-1	Glutamate/glutathione metabolism	18,89478	17,81716	17,46387	487411,2416	230940,2319	180779,3041	0,371	0,474	0,783	-62,9	-52,6	-21,7	0,0164377	0,00597183	+	CTR_DMD				2	2	2	11,3	11,3	11,3	11,776	6,3132E-06	2880200
GPT	P24298	Alanine aminotransferase 1	Glutamate/glutathione metabolism	18,10886	18,11868	17,19104	282689,7406	284620,4899	149630,0071	0,529	1,007	0,526	-47,1	0,7	-47,4	0,0413704	0,0108897	+	CTR_DMD				1	1	1	3,4	3,4	3,4	54,636	2,4772E-07	2177600
GSTO1	P78417;Q5TA02;Q5TA01	Glutathione S-transferase omega-1	Glutamate/glutathione metabolism	19,34453	18,81856	18,17777	665708,0092	462328,8929	296520,0224	0,445	0,694	0,641	-55,5	-30,6	-35,9	0,030353	0,00850407	+	CTR_DMD				2	2	2	9,5	9,5	9,5	27,566	0,000037997	4742400
HAGH	Q16775;H3BPQ4;H3BPK3;H3BQW8	Hydroxyacylglutathione hydrolase, mitochondrial	Glutamate/glutathione metabolism	19,80865	19,16273	18,43669	918327,9944	586889,7556	354810,702	0,386	0,639	0,605	-61,4	-36,1	-39,5	0,0260575	0,00815319	+	CTR_DMD				4	4	4	18,5	18,5	18,5	33,805	2,1731E-10	6079900
ACAA2	P42765;A0A0B4J2A4;K7EME0;K7EJ68;K7EJB1;K7ER88	3-ketoacyl-CoA thiolase, mitochondrial	Lipid metabolism	19,25813	20,1447	20,13458	627010,4664	1159201,551	1151098,612	1,836	1,849	0,993	83,6	84,9	-0,7	0,0039618	0,00301299	+	DMD_CTR BMD_CTR				3	3	3	10,8	10,8	10,8	41,924	1,3842E-85	7327100
CYB5R1	Q9UHQ9;H7C0R7	NADH-cytochrome b5 reductase 1	Lipid metabolism	21,50969	22,34684	22,29317	2985808,069	5334198,198	5139405,305	1,721	1,787	0,963	72,1	78,7	-3,7	0,0017089	0,00115625	+	DMD_CTR BMD_CTR				3	3	3	15,7	15,7	15,7	34,094	2,7309E-36	31951000
PLIN4	A0A0J9YXN7;Q96Q06	Perilipin-4	Lipid metabolism	19,39739	19,92316	19,96804	690551,7459	994188,5759	1025602,32	1,485	1,440	1,032	48,5	44,0	3,2	0,008866	0,00426374	+	DMD_CTR BMD_CTR				4	4	4	7,7	7,7	7,7	136,02	4,5243E-60	6350900
CYB5R3	P00387;B1AHF3	NADH-cytochrome b5 reductase 3;NADH-cytochrome b5 reductase 3 membrane-	Lipid metabolism	19,02655	19,6489	20,56328	534025,8304	822069,0197	1549401,918	2,901	1,539	1,885	190,1	53,9	88,5	0,0133633	0,00561194	+	DMD_CTR				2	2	2	8	8	8	34,234	1,7046E-07	5504000
ECHS1	P30084	Enoyl-CoA hydratase, mitochondrial	Lipid metabolism	18,85221	19,08439	19,68854	473239,1815	555870,7717	844969,6515	1,786	1,175	1,520	78,6	17,5	52,0	0,0588813	0,0152028	+	DMD_CTR				3	3	3	19,3	19,3	19,3	31,387	1,4112E-39	4315500
CAND2	O75155	Cullin-associated NEDD8-dissociated protein 2	Protein/aminoacids metabolism	16,0436	15,04781	15,22132	67546,80919	33872,10438	38200,92628	0,566	0,501	1,128	-43,4	-49,9	12,8	0,0069045	0,00411494	+	CTR_DMD				2	2	2	2,1	2,1	2,1	135,25	2,1362E-06	414560
PREP	P48147	Prolyl endopeptidase	Protein/aminoacids metabolism	18,52818	17,81635	17,4829	378040,1659	230810,6071	183179,6864	0,485	0,611	0,794	-51,5	-38,9	-20,6	0,040676	0,0107176	+	CTR_DMD				6	6	6	13,1	13,1	13,1	80,699	1,2335E-15	2820400
PSMB2	P49721;A0A087WVV1	Proteasome subunit beta type-2	Protein/aminoacids metabolism	15,81896	15,67265	16,7349	57807,13693	52232,13301	109070,3921	1,887	0,904	2,088	88,7	-9,6	108,8	0,0086147	0,00415642	+	DMD_CTR				1	1	1	5,5	5,5	5,5	22,836	0,00038516	585090
CSRP3	P50461	Cysteine and glycine-rich protein 3	Muscle cell development	23,68859	25,33139	25,63589	13519982,98	42219027,17	52140099,49	3,857	3,123	1,235	285,7	212,3	23,5	0,0001137	0,00130612	+	DMD_CTR BMD_CTR				6	6	6	47,9	47,9	47,9	20,969	1,0879E-182	230130000
KBTBD10	O60662;E9PBE3	Kelch repeat and BTB domain-containing protein 10	Muscle cell development	23,80843	24,2	24,18374	14691007,27	19271960,42	19055973,81	1,297	1,312	0,989	29,7	31,2	-1,1	0,0018551	0,00129231	+	DMD_CTR BMD_CTR				14	14	14	29,4	29,4	29,4	68,036	5,2939E-212	132940000
CSDA	P16989;A0A0D9SEI8;H0Y449;Q9Y2T7;P67809	DNA-binding protein A	Transcription/translation regulation	19,62487	19,99175	20,60612	808489,7736	1040596,868	1596100,429	1,974	1,290	1,531	97,4	29,0	53,1	0,0094578	0,00473514	+	DMD_CTR				4	4	4	21,8	21,8	21,8	40,089	5,9853E-33	7871100
HIST1H2BK	U3KQK0	Histone H2B type 1-K	Transcription/translation regulation	20,52717	21,50019	22,14799	1511102,403	2966211,419	4647392,295	3,075	1,963	1,567	207,5	96,3	56,7	0,0162469	0,006	+	DMD_CTR				3	3	3	19,9	19,9	19,9	18,804	2,1888E-07	21220000
ZEB1	P37275	Zinc finger E-box-binding homeobox 1	Transcription/translation regulation	16,89818	17,82505	17,1803	122140,3196	232206,6881	148520,2373	1,216	1,901	0,640	21,6	90,1	-36,0	0,01227	0,00548223	+	DMD_CTR	+			1	1	1	1,9	1,9	1,9	124,07	0,043559	993550
EEF1A2	Q05639	Elongation factor 1-alpha 2	Ribosomes	23,78935	24,20784	24,69853	14497994,39	19376974,61	27226911,44	1,878	1,337	1,405	87,8	33,7	40,5	0,0057424	0,00330539	+	DMD_CTR				10	10	10	22	22	22	50,47	7,1864E-60	141880000
EEF1D	E9PRY8;P29692;A0A087X1X7;E9PK01;E9PQZ1;H0YCK7;E9PI39;E9PQ49;E9PL12;E9PPR1;H0YE72;E9PIZ1;E9PMW7;H0YE58	Elongation factor 1-delta	Ribosomes	20,08602	20,46054	20,99328	1112998,332	1442900,113	2087406,288	1,875	1,296	1,447	87,5	29,6	44,7	0,0230992	0,00707826	+	DMD_CTR				2	2	2	6,7	6,7	6,7	76,569	0,000056875	9510100
EEF1G	P26641	Elongation factor 1-gamma	Ribosomes	21,05808	21,049	21,48158	2183301,59	2169603,53	2928194,592	1,341	0,994	1,350	34,1	-0,6	35,0	0,0371427	0,0101395	+	DMD_CTR				5	5	5	14	14	14	50,118	6,8116E-23	15939000
CD36	P16671;E7EU05;E9PLT1	Platelet glycoprotein 4	Signal transduction	17,39657	18,45671	18,92992	172539,8403	359768,6622	499428,9757	2,895	2,085	1,388	189,5	108,5	38,8	0,0007049	0,00105051	+	DMD_CTR BMD_CTR				1	1	1	3,8	3,8	3,8	53,053	4,6584E-08	2225100
PACSIN3	Q9UKS6;A0A0C4DGG1;E9PIY1;E9PNM9;E9PJ75;E9PJ33;H0YDM6	Protein kinase C and casein kinase substrate in neurons protein 3	Signal transduction	19,38129	20,78109	21,95837	682888,2571	1801903,101	4075003,873	5,967	2,639	2,262	496,7	163,9	126,2	0,0003008	0,00128395	+	DMD_CTR BMD_CTR				7	7	7	21,7	21,7	21,7	48,486	1,7875E-19	13672000
YWHAE	P62258;K7EM20;K7EIT4;I3L3T1;B4DJF2;P31947;I3L0W5;A0A0J9YWE8;Q4VY19;A0A0J9YWZ2;Q4VY20	14-3-3 protein epsilon	Signal transduction	23,1281	23,21371	23,64317	9167519,506	9727987,875	13100967,3	1,429	1,061	1,347	42,9	6,1	34,7	0,0105849	0,00496842	+	DMD_CTR				8	8	6	35,7	35,7	28,6	29,174	3,2232E-92	77723000
ATP2A1	O14983;H3BTW4;H3BVB2;H3BTF1;H3BUT9	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1	ER/sarcoplasmic reticulum, Calcium handling	26,75557	26,23688	25,9455	113299794,2	79083862,55	64621011,62	0,570	0,698	0,817	-43,0	-30,2	-18,3	0,0001759	0,00095522	+	CTR_DMD CTR_BMD				30	30	19	40,5	40,5	25,9	110,25	0	753120000
CASQ2	O14958	Calsequestrin-2	ER/sarcoplasmic reticulum, Calcium handling	21,63112	23,56883	23,76769	3247999,546	12442991,16	14281953,6	4,397	3,831	1,148	339,7	283,1	14,8	0,0001321	0,00112281	+	DMD_CTR BMD_CTR				5	5	5	13,8	13,8	13,8	46,435	1,7217E-25	66128000
RTN4	Q9NQC3;F8W914;H7C106;A0A0U1RQR6	Reticulon-4	ER/sarcoplasmic reticulum, Calcium handling	21,28116	22,33775	22,99759	2548399,449	5300694,632	8374606,656	3,286	2,080	1,580	228,6	108,0	58,0	0,0022083	0,00125373	+	DMD_CTR BMD_CTR				2	2	2	2,2	2,2	2,2	129,93	8,4648E-15	35529000
CASQ1	P31415;C9JAC8	Calsequestrin-1	ER/sarcoplasmic reticulum, Calcium handling	25,28284	24,67217	24,48855	40821900,1	26733955,95	23539004,95	0,577	0,655	0,880	-42,3	-34,5	-12,0	0,0115036	0,00536082	+	CTR_DMD				8	8	8	41,4	41,4	41,4	45,16	2,092E-279	258670000
DYSF	O75923;Q9NZM1	Dysferlin	ER/sarcoplasmic reticulum, Calcium handling	18,75071	19,28157	20,2986	441088,9214	637280,9456	1289696,348	2,924	1,445	2,024	192,4	44,5	102,4	0,0032114	0,00236735	+	DMD_CTR				9	9	9	6,2	6,2	6,2	237,29	2,2431E-18	5517200
HRC	P23327;M0QZ43	Sarcoplasmic reticulum histidine-rich calcium-binding protein	ER/sarcoplasmic reticulum, Calcium handling	19,40416	19,96097	20,86514	693799,8485	1020588,599	1909998,401	2,753	1,471	1,871	175,3	47,1	87,1	0,0173728	0,00594495	+	DMD_CTR				3	3	3	8,3	8,3	8,3	80,243	1,2601E-18	7168400
NSFL1C	Q9UNZ2;F2Z2K0;R4GNE6;R4GMY2;G3V4V8	NSFL1 cofactor p47	ER/sarcoplasmic reticulum, Calcium handling	19,15642	19,59802	20,09275	584328,4468	793582,1225	1118202,465	1,914	1,358	1,409	91,4	35,8	40,9	0,105365	0,0299012	+	DMD_CTR				3	3	3	11,9	11,9	11,9	40,572	4,2794E-38	5162400
PDIA3	P30101	Protein disulfide-isomerase A3	ER/sarcoplasmic reticulum, Calcium handling	17,77831	18,2041	19,36941	224804,2835	301981,3651	677288,0426	3,013	1,343	2,243	201,3	34,3	124,3	0,0136083	0,00555665	+	DMD_CTR				3	3	3	10,1	10,1	10,1	56,782	1,3332E-07	1781700
SRL	Q86TD4;B4DYT9	Sarcalumenin	ER/sarcoplasmic reticulum, Calcium handling	21,81944	22,40383	22,52805	3700887,884	5181110,779	6048097,641	1,634	1,400	1,167	63,4	40,0	16,7	0,0416048	0,0110758	+	DMD_CTR				9	9	9	12	12	12	100,79	1,9017E-88	36959000
VCP	P55072	Transitional endoplasmic reticulum ATPase	ER/sarcoplasmic reticulum, Calcium handling	19,52394	19,7956	20,64262	753861,5161	910058,6505	1636996,719	2,171	1,207	1,799	117,1	20,7	79,9	0,0035269	0,00269333	+	DMD_CTR				7	7	7	14,8	14,8	14,8	89,321	1,9354E-30	7652500
IGHM	A0A1B0GUU9;A0A075B6N9;A0A087WYJ9;P01871;P04220	Ig mu chain C region;Ig mu heavy chain disease protein	Inflammation/ Immune response	19,06424	19,84847	22,26648	548160,9381	944027,9181	5045199,893	9,204	1,722	5,344	820,4	72,2	434,4	0,0058976	0,00328571	+	DMD_CTR				5	5	5	13,1	13,1	13,1	51,923	4,7748E-24	12175000
MIF	P14174	Macrophage migration inhibitory factor	Inflammation/ Immune response	19,09187	19,43345	19,47868	558760,3019	708029,5266	730578,6154	1,307	1,267	1,032	30,7	26,7	3,2	0,104639	0,0297709	+	DMD_CTR				1	1	1	7,8	7,8	7,8	12,476	3,6608E-06	5253800
HSPA9	P38646;H0Y8S0	Stress-70 protein, mitochondrial	Stress response	20,3444	21,06677	21,41483	1331296,051	2196492,283	2795800,525	2,100	1,650	1,273	110,0	65,0	27,3	0,000961	0,00095413	+	DMD_CTR BMD_CTR				4	4	4	9,7	9,7	9,7	73,68	5,4327E-15	13520000
HSPB6	O14558;K7EP04	Heat shock protein beta-6	Stress response	22,95817	24,22052	24,49479	8148877,994	19548031,52	23641037,26	2,901	2,399	1,209	190,1	139,9	20,9	0,0007942	0,00101961	+	DMD_CTR BMD_CTR				6	6	6	63,1	63,1	63,1	17,135	1,3328E-46	154020000
HSPA1B	A0A0G2JIW1;P0DMV8;P0DMV9;V9GZ37	Heat shock 70 kDa protein 1B	Stress response	23,87764	23,8532	23,53124	15412953,61	15154049,19	12122971,25	0,787	0,983	0,800	-21,3	-1,7	-20,0	0,107292	0,0298773	+	CTR_DMD				11	10	7	28,3	26,3	16,5	70,108	1,6632E-197	125080000
HSPB2	A8KAH6;Q16082;E9PN16	Heat shock protein beta-2	Stress response	21,49614	22,51965	23,03688	2957896,211	6012985,296	8605812,637	2,909	2,033	1,431	190,9	103,3	43,1	0,0508775	0,0125797	+	DMD_CTR				4	4	4	31,3	31,3	31,3	20,232	6,6535E-32	36604000
HSPD1	P10809;E7ESH4;E7EXB4;C9JL25;C9JCQ4;C9JL19	60 kDa heat shock protein, mitochondrial	Stress response	21,21869	22,01488	21,93912	2440406,419	4237788,04	4020991,902	1,648	1,737	0,949	64,8	73,7	-5,1	0,0507745	0,0126255	+	DMD_CTR				8	8	8	20,8	20,8	20,8	61,054	1,5594E-31	25621000
HSPE1	S4R3N1;P61604;B8ZZL8	10 kDa heat shock protein, mitochondrial	Stress response	20,77298	21,3208	22,03782	1791802,257	2619391,003	4305710,826	2,403	1,462	1,644	140,3	46,2	64,4	0,0045529	0,00291824	+	DMD_CTR				1	1	1	5,4	5,4	5,4	29,736	6,1239E-33	20678000
PRDX5	P30044	Peroxiredoxin-5, mitochondrial	Stress response	15,87203	16,15516	17,16162	59973,18618	72977,29216	146609,5951	2,445	1,217	2,009	144,5	21,7	100,9	0,0174638	0,00591781	+	DMD_CTR				3	3	3	18,2	18,2	18,2	22,086	3,374E-09	1064600
SOD1	P00441;H7BYH4	Superoxide dismutase [Cu-Zn]	Stress response	21,16907	20,77724	20,6664	2357898,197	1797100,922	1664203,007	0,706	0,762	0,926	-29,4	-23,8	-7,4	0,0734417	0,0195152	+	CTR_DMD				4	4	4	53,9	53,9	53,9	15,936	4,3199E-23	15852000
HBG2	P69892	Hemoglobin subunit gamma-2	Transport proteins	21,88632	23,27427	23,27625	3876491,31	10145031,44	10158964,36	2,621	2,617	1,001	162,1	161,7	0,1	0,0005012	0,00116854	+	DMD_CTR BMD_CTR				7	6	6	57,8	51	51	16,126	1,0935E-108	51165000
TF	P02787;H7C5E8;C9JVG0;F8WCI6;F8WEK9;C9JB55;F8WC57	Serotransferrin	Transport proteins	24,27021	25,25933	26,19227	20233043,31	40162061,83	76675907,45	3,790	1,985	1,909	279,0	98,5	90,9	0,0004241	0,00122353	+	DMD_CTR BMD_CTR				23	23	23	39	39	39	77,063	1,5807E-277	268910000

HBB	P68871;F8W6P5;A0A087WK4	Hemoglobin subunit beta;LVV-hemorphin-7	Transport	30.06458	30.39754	31.01119	1122898204	1414397026	2166204976	1,327	1,260	1,530	26,7	26,0	53,0	0,0005293	0,00113043	+	DMD_CTR	14	14	8	93,9	93,9	67,3	15,998	0	11813000000
HBD	P02042;E9PF78;E9PEW8;C9JRG2;A8MUF7	Hemoglobin subunit delta	Transport	25,05796	25,78472	26,22319	34829819.93	67890435.88	76359975.45	2,243	1,655	1,365	124,3	65,5	38,5	0,0027911	0,00169562	+	DMD_CTR	12	6	6	91,2	53,1	53,1	16,055	0	369710000
HBE1	P02100	Hemoglobin subunit epsilon	Transport	19,02071	19,81774	20,87085	531868.4742	924132.3775	1917307.093	3,605	1,738	2,075	203,7	73,8	107,5	0,0005483	0,00110638	+	DMD_CTR	3	2	2	20,4	13,6	13,6	16,203	7,3006E-20	7479000
ORM1	P02763;P19652	Alpha-1-acid glycoprotein 1	Transport	17,21004	17,93168	19,02221	5545510.09	250019.1032	533421.7904	3,456	1,623	2,135	246,7	62,3	111,0	0,0013489	0,00087395	+	DMD_CTR	3	3	3	15,4	15,4	15,4	23,511	7,9347E-06	2051000
TTR	P02766;A0A087WV95;A0A087WT59	Transthyretin	Transport	20,21845	19,63574	21,72764	1220000.239	923492.0397	3496887.615	2,866	0,757	3,767	186,7	-24,3	278,7	0,0117342	0,00533033	+	DMD_CTR	2	2	2	30,6	30,6	30,6	15,887	1,7245E-20	12278000
EPN2	Q96N46;A0A0U1RRI7;Q96N46;Q9H4M9;C9JCB3;C9JFH1;C9JJ13	Epsin 2	Cytoskeleton	19,54379	19,67592	20,8247	831921.4166	958832.3752	1867302.89	2,267	1,171	1,927	126,7	17,1	93,7	0,0053144	0,00134152	+	DMD_CTR	4	4	4	9,9	9,9	9,9	61,191	7,0379E-11	8034000
PTBP	Q9UIJ7	Polypyrimidine tract binding protein 2	Cytoskeleton	20,89645	21,29851	22,20735	1891903.096	2930762.561	4844513.022	2,492	1,365	1,672	149,3	34,1	93,1	6,19E-05	0	+	DMD_CTR	4	4	4	20,8	20,8	20,8	43,476	7,2756E-10	23045000
CNDP2	Q96KP4;A0A087WXK4;Q96BF1	Cytosolic nonspecific dipeptidase	Other proteins	20,61963	20,96455	21,57146	1622000.121	1000000.000	2000000.000	1,233	0,955	1,667	23,3	-4,7	28,0	0,0259415	0,00509902	+	CTR_DMD CTR_BMD	4	4	4	23,8	23,8	23,8	52,204	2,1103E-15	10500000
CA2	P00918;E9PK37;E9PER5	Carbonic anhydrase 2	Other proteins	20,62943	18,9655	20,74585	1622008.903	1023758.24	8792717.1487	0,542	0,631	0,855	-45,8	209,3	-14,3	0,0259415	0,03849562	+	CTR_DMD CTR_BMD	4	4	4	23,8	23,8	23,8	29,246	2,5425E-16	10500000
HIST1H4A	P62805	Histone H4	Other proteins	21,32619	24,08877	24,6329	26291695.518	17841950.44	26016075.26	9,895	6,786	1,468	886,7	574,3	45,8	4,67E-05	0	+	DMD_CTR BMD_CTR	6	6	6	57,3	57,3	57,3	11,367	1,8823E-17	89581000
IGHG1	A0A0A0MS08;P01857;A0A0A0MS07	Ig gamma-1 chain C region	Other proteins	24,18055	25,17486	26,15833	19014016.74	37878051.45	76945357.38	3,942	1,992	1,979	294,7	95,2	97,9	1,66E-05	0	+	DMD_CTR BMD_CTR	11	11	6	40,4	40,4	22,1	42,911	1,8252E-186	297500000
METTL7A	H0YI09;Q8H8H0;F8VQK6	Methyltransferase-like protein 7A	Other proteins	19,90707	20,64373	20,98503	983162.2522	1638256.699	2075503.595	2,111	1,666	1,265	111,3	-55,0	26,7	0,0041807	0,00297436	+	DMD_CTR BMD_CTR	2	2	2	11,1	11,1	11,1	28,188	2,2986E-13	10238000
MCM3AP	O60318;A0A0A0MUE7	80 kDa MCM3-associated protein	Other proteins	19,73858	21,23922	19,49257	8687450.0983	2475362.433	732601.5421	0,843	2,669	0,256	-65,3	155,0	-70,6	0,0097671	0,00413333	+	BMD_CTR	1	1	1	1,4	1,4	1,4	218,4	0,005647	7635200
NAP1L1	H0YKC3	Nucleosome assembly protein 1-like 1 (Fragment)	Other proteins	19,58536	18,05925	18,54272	779816.5866	273134.1159	381869.4548	0,492	0,352	1,398	-50,8	-53,1	38,8	0,0979767	0,027175	+	CTR_BMD	1	1	1	8,6	8,6	8,6	22,417	0,023383	4528800
VDAC3	Q9Y277;E5RK28;E5RJN6;E5RFP6;E5RK27;E5RHE1	Voltage-dependent anion-selective channel protein 3	Other proteins	21,38558	21,93863	23,5748	11054974.81	14953594.22	12537966.11	1,136	1,331	0,853	13,4	-16,0	-14,7	0,0142819	0,00547573	+	BMD_CTR	8	8	8	45,9	45,9	45,9	30,959	6,4438E-22	98035000
APOB	O95445	Apolipoprotein-B mRNA-editing enzyme APOBEC-2	Other proteins	20,62212	19,28531	18,92088	1613680.27	630138.1748	496359.3127	0,308	0,397	0,788	-61,0	-21,3	-19,5	0,0050952	0,00334627	+	CTR_DMD	4	4	4	8,3	8,3	8,3	69,9	4,9844E-11	8057400
ESRRG;ESRRG2	P62508;Q9Y5Y7	Estrogen receptor	Other proteins	20,62212	19,28531	18,92088	1613680.27	630138.1748	496359.3127	0,308	0,397	0,788	-61,0	-21,3	-19,5	0,0050952	0,00334627	+	CTR_DMD	4	4	4	8,3	8,3	8,3	69,9	4,9844E-11	8057400
CA1	P00915;E9HP7;E9HB1;E9FF67;H0YBE2;E9RG4;E9RF9;E9RJ8;E9RG81;E9RFL2;E9RGJ8;E9RFL6;E9RI2	Carbonic anhydrase 1	Other proteins	22,87951	23,41326	23,33583	7716472.203	11171038.7	10588923.75	1,372	1,448	0,948	20,4	44,8	-5,2	0,0036656	0,0073133	+	DMD_CTR	7	7	7	33,7	33,7	33,7	28,87	4,5158E-43	75095000
CRIP2	P52943;H0YFA4	Cysteine-rich protein 2	Other proteins	16,54234	17,10729	18,48976	95442.22131	141191.1367	368110.6592	3,857	1,479	2,605	280,3	47,9	160,7	0,0038624	0,00303268	+	DMD_CTR	1	1	1	15,4	15,4	15,4	22,492	6,1138E-33	1146700
HINT1	P49773;C9JE4D;D6RE99;D6REP8	Histidine triad nucleotide-binding protein 1	Other proteins	18,67497	16,857	15,44236	618526.5612	103337.1876	44541.42359	0,166	0,247	0,431	-83,3	-75,3	-58,9	0,0033858	0,00239135	+	CTR_DMD	1	1	1	15,9	15,9	15,9	13,802	7,6588E-17	2399100
NRDC1	F8W1Q5	Nuclear receptor subfamily 2 group C member 1 (Fragment)	Other proteins	18,32316	19,07466	18,91887	327959.9227	552134.4139	495618.3232	1,511	1,684	0,898	51,3	68,4	-10,2	0,0063463	0,00989038	+	DMD_CTR	1	1	1	100	100	100	1,8852	0,0092874	2850600
PADI2	Q9Y2J8	Protein-arginine deiminase type-2	Other proteins	20,96466	21,53488	21,63854	2046404.626	3038394.2	3267011.369	1,596	1,485	1,075	59,8	48,5	7,5	0,0145444	0,00556522	+	DMD_CTR	9	9	9	18,6	18,6	18,6	75,563	1,3946E-71	21978000
PPIA	P62937;C9JS57;F8W6E5;A0A075B759;A0A075B767;A0A0B4J2A2;A0A0H2UHG8;F5H3B4;F5H2B4;F5DN28;F5DN37;Q9Y536	Peptidyl-prolyl cis-trans isomerase A;Peptidyl-prolyl cis-trans isomerase	Other proteins	21,36994	21,67116	22,68001	2767590.572	3330405.838	9627392.806	2,395	1,207	1,995	139,3	20,7	98,5	0,0002913	0,0013	+	DMD_CTR	6	6	6	38,2	38,2	38,2	18,012	1,1893E-27	24502000
SLC4A1	P02730;A0A0A0MS98	Band 3 anion transport protein	Other proteins	19,60351	20,53839	21,33859	984426.7968	1522650.221	3031890.913	2,887	1,531	1,732	188,3	53,1	74,1	0,0169173	0,00418544	+	DMD_CTR	6	6	6	9,8	9,8	9,8	101,79	1,2537E-28	12413000

Legend:

- **Significant Increment in protein abundance (Tukey HSD, p<0.01)**
- **Significant Decrement in protein abundance (Tukey HSD, p<0.01)**
- **Tendential Increment in protein abundance (Tukey HSD, p>0.01)**
- **Tendential Decrement in protein abundance (Tukey HSD, p>0.01)**