

Supplemental Table 1. Differentially abundant or nitrosylated proteins in skeletal muscle biopsy samples.

No.	Protein name	Accession [#]	Gel Spot No.	pI	MW (kD)	MS ID Expectation Value	Protein Score	Abundance Ratio	p-Value		Ratio of Ratios
									Asc-	Asc+	
1	Aconitate hydratase, mitochondrial	Q99798	2006	7.44	86	6.29E-05	85	1.03	0.01612	0.99352	-1.54
2	Actin, alpha cardiac muscle 1	P68032	1043	5.63	300	1.58E-15	191	1.4	0.01977	0.25189	1.54
3	Actin, alpha skeletal muscle	P68133	1081	5.68	200	5.00E-41	446	2.11	0.97017	0.01293	-2.22
4	Actin, aortic smooth muscle	P62736	1047	5.94	300	1.99E-05	90	1.91	0.53328	0.00717	-1.66
5	Actin, gamma-enteric smooth muscle	E9PG30	383	3.23	18	1.26E-04	88	2.33	0.29908	0.00774	-1.49
6	ATP synthase subunit alpha	A8K092	1037	5.97	300	1.99E-42	466	1.53	0.68164	0.03628	-1.31
7	ATP synthase subunit beta, mitochondrial	P06576	199	4.43	50	1.26E-56	602	-1.52	0.5741	0.03756	1.82
8	Beta-enolase	P13929	1328	6.19	47	1.26E-05	92	1.59	0.86688	0.03349	-1.61
9	Carbonic anhydrase 3	P07451	307	5.23	26	3.15E-01	48	1.04	0.0485	0.67605	-2.74
10	Carbonic anhydrase 3	P07451	1911	5.96	39	1.99E-18	226	-2.32	0.22228	0.04024	1.48
11	Cofilin 2 (Muscle), isoform CRA_d	G3V5P4	1396	6.57	40	3.97E-12	163	1.65	0.45021	0.04577	-1.3
12	Creatine kinase M-type	P06732	232	5.2	43	6.29E-12	155	1.1	0.02917	0.84146	-2.09
13	Creatine kinase M-type	P06732	1281	6.65	56	5.00E-37	412	-2.09	0.31114	0.04904	1.36
14	Cytochrome b-c1 complex subunit Rieske, mitochondrial	P47985	1280	6.47	56	1.26E-04	82	-1.17	0.03556	0.53098	1.5
15	DEAH (Asp-Glu-Ala-His) box polypeptide 35 (Fragment)	Q5THQ9	1919	6.64	25	6.29E+00	44	-1.81	0.64737	0.049	1.32
16	Desmin	P17661	194	4.9	52	2.51E-85	889	1.07	0.03127	0.60351	1.57
17	Desmin	P17661	190	5.09	52	3.97E-06	97	-2.98	0.67297	0.0126	5.38
18	Desmin	P17661	161	4.94	58	6.29E-29	325	1.07	0.02834	0.47118	-1.83
19	DnaJ homolog subfamily C member 3	Q13217	1778	6.16	12	6.29E+00	35	-1.6	0.97308	0.04322	1.55
20	EV15-like protein	Q96CN4	2392	8.65	16	1.99E+00	40	1.05	0.03606	0.68538	-1.56
21	Fructose-bisphosphate aldolase A	P04075	2173	9.58	41	6.29E-29	325	-1	0.0297	0.92406	1.78
22	Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic	P21695	1460	6.12	34	5.00E-02	56	1.35	0.39966	0.02285	-1.51
23	Glycolipid transfer protein domain-containing protein 2	A6NH11	2060	9.17	60	5.00E+00	36	-1.01	0.00039	0.82194	-1.68
24	Heat shock cognate 71 kDa protein	P11142	129	5.06	70	1.99E-13	170	-1.87	0.98016	0.03882	1.65

25	Histidine protein methyltransferase 1 homolog	O95568	253	3.63	35	7.92E-01	44	-1.45	0.24894	0.04389	1.8
26	Histidine protein methyltransferase 1 homolog	O95568	1517	5.66	27	3.97E-01	47	1.7	0.08884	0.02778	-2.15
27	Histidine protein methyltransferase 1 homolog	O95568	1647	5.89	18	3.97E-01	47	2.22	0.80181	0.04677	-3.4
28	Histidine protein methyltransferase 1 homolog	O95568	66	5.07	130	7.92E-01	44	-2.1	0.63497	0.01079	2.53
29	Histidine protein methyltransferase 1 homolog	O95568	70	3.72	129	7.92E-01	44	-1.63	0.51677	0.01018	2
30	Histidine protein methyltransferase 1 homolog	O95568	149	5.1	65	9.98E+00	33	-2.98	0.69976	0.00185	4.44
31	Keratin, type II cytoskeletal 1	P04264	62	5.19	135	2.51E-02	59	-1.1	0.02247	0.64301	-2.62
32	Keratin, type II cytoskeletal 1	P04264	2281	9.91	25	2.51E-04	79	1.5	0.18722	0.03796	-2.55
33	LIM domain-binding protein 3	O75112	2527	9.64	31	2.51E-03	69	-1.2	0.02037	0.60566	2.21
34	Myoglobin	P02144	1708	6.36	16	3.15E-01	48	1.7	0.83927	0.01625	-1.56
35	Myoglobin	P02144	2494	8.4	16	7.92E-02	54	1.1	0.02386	0.45031	-1.59
36	Myosin regulatory light chain 2, ventricular/cardiac muscle isoform	P10916	370	3.25	19	3.97E-02	57	2.64	0.42875	0.0379	-4.6
37	Myosin-1	P12882	1122	5.47	150	3.97E-02	57	-3.42	0.3205	0.02464	1.81
38	Phosphoglucosylase-1	P36871	151	5.16	62	3.97E-02	57	1.7	0.04417	0.79217	-3.21
39	Protein ALEX	P84996	2121	8.87	47	9.98E+01	23	-1.05	0.04195	0.73628	-1.55
40	Retinal dehydrogenase 1	P00352	1865	6.49	58	6.29E-03	65	-2.22	0.87484	0.00736	2.32
41	Serum albumin	P02768	1053	6.12	300	7.92E-06	94	1.36	0.93935	0.03639	-1.5
42	TNNT1 protein	Q3B759	1669	6.14	17	9.98E-04	79	-1.59	0.45014	0.04551	1.36
43	Tropomyosin alpha-3 chain	P06753	92	4.03	98	6.29E-12	155	1.82	0.04149	0.34539	1.89
44	Tropomyosin alpha-3 chain	P06753	101	4.03	86	9.98E-27	303	1.19	0.03941	0.78602	3.47
45	Tropomyosin beta chain	P07951	1126	5.51	139	5.00E-20	236	2.45	0.29052	0.01466	-3.7
46	Troponin T, slow skeletal muscle	P13805	1456	6.23	34	5.00E-01	46	1.61	0.63826	0.03874	-1.67
47	Voltage-dependent anion-selective channel protein 2	P45880	2266	7.37	29	1.58E-01	51	-1.09	0.02353	0.77362	2.47
48	WD repeat-containing and planar cell polarity effector protein fritz homolog	O95876	2371	7.17	17	7.92E+00	34	-1.76	0.63391	0.03279	3.09
49	Zinc finger protein 394	Q53G13	1875	6.74	85	6.29E+00	35	-1.01	0.01539	0.89004	-2.11
NUMBERS OF SPOTS <= Boundary								14	19	30	23
NUMBERS OF SPOTS >= Boundary								14			19

#When multiple gel spots identify as one protein (as judged by accession number), each is included in the table because of the possibility that these could be isoforms.