

Supplementary Table 1. Identification of 81 spots (score >50) from the 2D-gels shown in Figure 3.

Spot ID	Protein	Gene	Accession Nr.	MW	pI	Score	Coverage, %	Matched peptides
1	cytochrome b5	CYB5R1	353818	11130	5.02	250	83.5	19
2	proapolipoprotein lipoprotein G ln I		178775	28944	5.45	901	67.9	43
			229479	28329	5.27	694	52.7	32
3	apolipoprotein A-I	APOA1	90108664	28061	5.27	2282	73.7	92
	lipoprotein G ln I		229479	28329	5.27	1634	56.3	73
	ATP synthase, H ⁺ transporting, gamma polypeptide 1	ATP5C1	16877071	33002	9.23	133	13.1	5
4	NADH dehydrogenase FeS protein	NDUFS	227297	27528	8.28	333	36.1	15
	proapolipoprotein		178775	28944	5.45	269	22.5	9
	lipoprotein G ln I		229479	28329	5.27	219	17.1	7
	peroxiredoxin 3 isoform a precursor	PRDX3	5802974	28017	7.67	115	10.2	2
5	NADH dehydrogenase FeS protein	NDUFS	227297	27528	8.28	245	23.3	10
	enoyl-CoA hydratase	ECHD	1922287	31807	8.34	220	22.1	6
6	NADH dehydrogenase (ubiquinone) Fe-S protein 3	NDUFS3	4758788	30337	6.99	905	59.5	49
	heat shock protein 27	HSP27	662841	22427	7.83	207	30.7	7
	ATP synthase, H ⁺ transporting, gamma polypeptide 1	ATP5C1	16877071	33002	9.23	193	19.1	5
7	prohibitin	PHB	4505773	29843	5.57	930	77.2	56
8	prohibitin	PHB	4505773	29843	5.57	881	63.2	41
9						<50		
10	prohibitin	PHB	4505773	29843	5.57	802	75.7	40
	cathepsin D preproprotein	CTSD	4503143	45037	6.10	318	23.1	9
11	aminoacylase 1	ACY1	4501901	46084	5.77	730	51.7	48
	beta actin	ACTB	4501885	42052	5.29	304	24.0	12
	ATP-specific succinyl-CoA synthetase beta subunit	SUCLA2	3766197	46732	5.84	273	14.1	6
12	aminoacylase 1	ACY1	4501901	46084	5.77	264	23.0	9
	ATP-specific succinyl-CoA synthetase beta subunit	SUCLA2	3766197	46732	5.84	124	9.6	4
13	ATP synthase, H ⁺ transporting, alpha subunit 1	ATP5A1	127798841	59785	9.07	823	34.7	34
	peroxiredoxin 1	PRXD1	4505591	22324	8.27	200	30.7	6
14	ATP synthase, H ⁺ transporting, alpha subunit precursor	ATP5A1	4757810	59828	9.16	631	29.1	29
	peroxiredoxin 1	PRDX1	4505591	22324	8.27	266	41.2	10
	mitochondrial ATP synthase, O subunit precursor	ATP5O	4502303	23377	9.97	146	14.6	3
15	manganese superoxide dismutase	SOD2	34709	24891	8.35	199	21.2	10
16	neuropolyptide h3	HCNP	913159	21027	7.42	502	57.0	25
17	unknown	AF007162.1	2852648	22435	7.18	347	30.4	19
18	beta actin	ACTB	4501885	42052	5.29	295	24.0	11
	alpha actin	ACTA	178027	42480	5.23	265	23.9	10
19	beta actin	ACTB	4501885	42052	5.29	158	15.5	5
20	ribosomal protein P0	RPLP0	4506667	34423	5.71	226	24.6	9
	L-lactate dehydrogenase B	LDHB	4557032	36900	5.71	164	12.6	6
21	L-lactate dehydrogenase B	LDHB	4557032	36900	5.71	245	19.8	11
22	ATP synthase subunit D	ATP5H	O75947	18537	5.21	1636	71.4	90
23	cytochrome c oxidase subunit 5A	COX5A	P20674	16923	6.30	288	22.7	87
24	cytochrome c oxidase subunit 5A	COX5A	P20674	16923	6.30	2671	22.7	104
25	piruvate dehydrogenase E1 component subunit beta	PDHB	P11177	39550	6.20	2416	38.4	108
26	piruvate dehydrogenase E1 component subunit beta	PDHB	P11177	39550	6.20	2361	38.4	109
27	enoyl-CoA hydratase	HADHA	P30084	31823	8.34	158	11.7	10
28	3,2-trans-enoyl-CoA isomerase	EHHADH	P42126	33080	8.80	354	22.8	53
	ATP synthase, subunit gamma	ATP5C1	P36542	33032	9.23	197	21.1	11
29	thioredoxin-dependent peroxide reductase	PRDX3	P30048	28017	7.67	69	7.0	6
30	voltage-dependent anion-selective channel protein 2	VDAC2	P45880	32060	7.49	283	20.1	35
31	delta(3,5)-delta(2,4)-dienoyl-CoA isomerase	ECH1	Q13011	36136	8.16	581	35.1	92
	voltage-dependent anion-selective channel protein 2	VDAC2	P45880	32060	7.49	282	20.1	28
32	voltage-dependent anion-selective channel protein 1	VDAC1	P21796	30868	8.62	453	23.0	61
	voltage-dependent anion-selective channel protein 2	VDAC2	P45880	32060	7.49	317	20.4	29
33	voltage-dependent anion-selective channel protein 1	VDAC1	P21796	30868	8.62	414	30.0	48
	voltage-dependent anion-selective channel protein 2	VDAC2	P45880	32060	7.49	336	26.9	49
34	electron transfer flavoprotein, subunit alpha	ETF A	P13804	35400	8.62	100	12.3	8
35						<50		
36	voltage-dependent anion-selective channel protein 1	VDAC1	P21796	30868	8.62	173	11.7	9
	ESI protein homolog	ESI	P30042	28495	8.50	171	14.2	21
37	ESI protein homolog	ESI	P30042	24495	8.50	82	10.4	4
38	superoxide dismutase	SOD2	P04179	24878	8.35	123	14.0	11
39	superoxide dismutase	SOD2	P04179	24878	8.35	271	27.9	32
40	unknown							
41	enoyl-CoA hydratase domain-containing protein 3	ECHDC3	Q96DC8	33015	8.9	1031	31.4	53
	adenylate kinase 2	AK2	P54819	26689	7.67	447	18.8	31
42						<50		
43	voltage-dependent anion-selective channel protein 1	VDAC1	P21796	30868	8.62	4098	52.3	161
	voltage-dependent anion-selective channel protein 3	VDAC3	Q9Y277	30981	8.85	818	<5.0	21
	hydroxyacyl-coenzyme A dehydrogenase	HADH	Q16836	34313	8.88	341	23.9	20
44	electron transfer flavoprotein, subunit beta	ETF B	P38117	28054	8.24	542	42.0	64

Supplementary Table 1 (continued).

Spot ID	Proteins identified	Gene	Accession Nr.	MW	pI	Score	Coverage, %	Matched peptides
45	(coiled-coil-helix) domain-containing protein 3	CHCHD3	Q9NX63	26421	8.48	326	25.1	29
	protein NipSnap homolog 2	GBAS	O75323	33949	9.42	194	15.7	14
46	(coiled-coil-helix) domain-containing protein 3	CHCHD3	Q9NX63	26421	8.48	475	47.6	45
	protein NipSnap homolog 2	GBAS	O75323	33949	9.42	309	18.5	54
47	cytochrome b-c1 complex subunit 7	UQCRB	P14927	13522	8.73	123	38.7	30
	haemoglobin subunit alpha	HBA2	P69905	15305	8.72	114	24.6	11
48	cytochrome c oxydase subunit 5B	COX5B	P10606	13915	9.07	802	40.3	49
49	heat shock protein HSP 90 alpha	HSP90AA1	P07900	85006	4.94	432	11.2	50
	heat shock protein HSP 90 beta	HSP90AB1	P08238	83554	4.97	312	7.6	41
50	myosin regulatory light chain MRLC2	MYLC2B	O14950	19824	4.71	376	57.0	40
51	V-type proton ATPase subunit F	VATF	Q16864	13362	5.29	99	18.5	24
52	adseverin	ADSV	Q9Y6U3	80895	5.50	525	5.6	26
	apoptosis-inducing factor 1	AIFM1	O95831	67144	9.04	120	<5.0	5
53	keratin, type II cytoskeletal 1	KRT1	P04264	66149	8.16	151	8.7	17
	adservin	ADSV	Q9Y6U3	80895	5.5	129	<5.0	15
54						<50		
55	cytochrome b-c1 complex subunit 1	QCR1	P31930	53297	5.94	157	<5.0	5
	actin, cytoplasmic 1	ACTB	P60709	42052	5.29	143	9.9	9
	tubulin alpha-1C chain	TBA1C	Q9BQE3	50548	4.96	76	11.6	9
56	pyruvate kinase isozymes M1/M2	PKM2	P14618	58470	7.96	534	22.4	31
	L-lactate dehydrogenase B chain	LDHB	P07195	36900	5.71	57	5.4	3
57	guanine nucleotide-binding protein, subunit beta-1	GNB1	P62873	38151	5.60	360	11.8	19
	guanine nucleotide-binding protein, subunit beta-2	GNB2	P62879	38048	5.60	377	11.8	20
	heat shock protein beta-1	HSPB1	P04792	22826	5.98	124	13.2	5
	L-lactate dehydrogenase B chain	LDHB	P07195	36900	5.71	76	5.4	4
58	annexin A4	ANXA4	P09525	36088	5.84	1199	69.0	113
59	prohibitin	PHB	P35232	29843	5.57	1016	46.3	59
	cathepsin	CATD	P07339	45037	6.10	2515	33.0	117
60	prohibitin	PHB	P35232	29843	5.57	2392	60.7	90
61	cathepsin	CATD	P07339	45037	6.10	1473	23.3	76
62	cathepsin	CATD	P07339	45037	6.10	3407	33.0	161
	prohibitin	PHB	P35232	29843	5.57	930	44.9	77
63	heat shock protein beta-1	HSPB1	P04792	22826	5.98	1199	59.5	57
64	heat shock protein beta-1	HSPB1	P04792	22826	5.98	3773	68.3	156
	NADH dehydrogenase (ubiquinone) Fe-S protein 3	NDUS3	O75489	30337	6.99	429	36.7	19
65	heat shock protein beta-1	HSPB1	P04792	22826	5.98	656	42.0	33
66	dihydropyridyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex	DLST	P36857	49041	9.11	660	28.3	104
67	heat shock protein beta-1	HSPB1	P04792	22826	5.98	4994	72.2	205
68	keratin, type II cytoskeletal 1	KRT1	P04264	66149	8.16	123	6.5	6
69	keratin, type II cytoskeletal 1	KRT1	P04264	66149	8.16	126	7.9	8
70	heat shock protein beta-1	HSPB1	P04792	22826	5.98	157	22.0	8
71	V-type proton ATPase subunit E1	ATP6V0E1	P36543	26186	7.71	300	26.1	26
72						<50		
73	peroxiredoxin 6	PRDX6	P30041	25133	6.00	1688	81.7	79
74	cytochrome b-c1 complex subunit Rieske	UQCRCF1	P47985	29934	8.55	355	37.2	55
	methylmalonate-semialdehyde dehydrogenase (acylating)	ALDH6A1	Q02252	58259	8.72	182	9.3	16
75	voltage-dependent anion-selective channel protein 2	VDAC2	P45880	32060	7.49	410	33.3	60
	voltage-dependent anion-selective channel protein 1	VDAC1	P21796	30868	8.62	141	13.8	9
	keratin, type II cytoskeletal 1	KRT1	P04264	66149	8.16	137	12.0	8
76	glyceraldehyde-3-phosphate dehydrogenase	GAPDH	P04406	36201	8.57	2004	37.0	64
	electron transfer flavoprotein subunit alpha	ETF A	P13804	35400	8.62	1905	59.5	83
77	triosephosphate isomerase	TPI1	P60174	26938	6.45	3315	69.5	119
78	abhydrolase domain-containing protein 11	ABHD11	Q8NFV4	34725	9.50	376	35.2	49
	carbonic anhydrase 2	CA2	P00918	29285	6.87	360	29.6	46
	hemoglobin subunit beta	HBB	P68871	16102	6.75	358	57.8	32
	trifunctional enzyme subunit beta	HADHB	P55084	51547	9.45	180	7.4	14
79	hemoglobin subunit beta	HBB	P68871	16102	6.75	617	95.2	68
80	superoxide dismutase	SOD2	P04179	24878	8.35	129	14.4	13
81	ATP synthase subunit alpha	ATP5A1	P25705	59828	9.16	671	19.0	67