

Supplemental table 1. Spot map table (6 gels).

Total number of detected spots = 3181±141; Matched spots = 2456±475

No.	Status	Image	Label	No.of Spots	Matched	Group
1	Matched	80067 STANDARD CY2.gel	Cy2	3171	2344	Standard
2	Matched	80067 Cy3.gel	Cy3	3171	2344	HF
3	Matched	80067 Cy5.gel	Cy5	3171	2344	Control
4	Matched	80068 STANDARD CY2.gel	Cy2	3126	2294	Standard
5	Matched	80068 Cy3.gel	Cy3	3126	2294	Control
6	Matched	80068 Cy5.gel	Cy5	3126	2294	HS
7	Matched	80069 STANDARD CY2.gel	Cy2	3409	3409	Standard
8	Matched	80069 Cy3.gel	Cy3	3409	3409	HS
9	Matched	80069 Cy5.gel	Cy5	3409	3409	HFS
10	Matched	80070 STANDARD CY2.gel	Cy2	3269	2298	Standard
11	Matched	80070 Cy3.gel	Cy3	3269	2298	HFS
12	Matched	80070 Cy5.gel	Cy5	3269	2298	HS
13	Matched	80071 STANDARD CY2.gel	Cy2	3004	2297	Standard
14	Matched	80071 Cy3.gel	Cy3	3004	2297	HF
15	Matched	80071 Cy5.gel	Cy5	3004	2297	HFS
16	Matched	81979 STANDARD CY2.gel	Cy2	3106	2096	Standard
17	Matched	81979 Cy3.gel	Cy3	3106	2096	Control
18	Matched	81979 Cy5.gel	Cy5	3106	2096	HF

Supplementary table 2. Details of the sequenced peptides for the analyzed proteins

Spot	Acc. Number	protein name	pI	Pm (Da)	score	cov. (%)	peptides
853	Q9ER34	Aconitate hydratase, mitochondrial (Aconitase)	7,40	82.461,90	24,1	6%	4
sequenced peptides			z	m/z	dm/z	z-score	p-value
R.ADIANLAEEFK.D			2	610,819	-0,008	5,599004	1,07E-05
K.DINQEVYNFLATAGAK.Y			2	877,466	-0,025	5,347003	2,16E-05
R.EHAALPR.H			2	461,741	0,0007	6,605289	2,78E-08
R.VDVSPTSQR.L			2	494,763	0,0068	6,567498	2,5E-08
Spot	Acc. Number	protein name	pI	Pm (Da)	score	cov. (%)	peptides
980	P48721	Stress-70 protein, mitochondrial (GRP-75) (PBP74)	6,08	73.857,72	43,3	10%	5
sequenced peptides			z	m/z	dm/z	z-score	p-value
R.AQFEGIVTDLIK.R			2	667,381	0,0093	12,5874	4,07E-34
R.QAASSLQQASLK.L			2	616,339	0,0037	5,969511	7,48E-07
R.TTPSVVAFTPDGER.L			2	738,386	0,4837	8,645423	2,38E-15
R.VINEPTAAALAYGLDK.S			2	823,451	0,0073	9,263805	3,51E-18
K.VQQTVQDLFGR.A			2	645,851	-0,007	6,849408	2,8E-09
Spot	Acc. Number	protein name	pI	Pm (Da)	score	cov. (%)	peptides
995	P63018	Heat shock cognate 71 kDa protein	5,37	70871,07	62,5	13%	7
sequenced peptides			z	m/z	dm/z	z-score	p-value
K.DAGTIAGLNVL.R			2	600,347	0,0066	7,663696	5,03E-12
R.FEELNADLFR.G			2	627,322	0,0104	8,899032	2,83E-16
R.IINEPTAAAIAYGLDK.K			2	830,465	0,0142	7,8936	1,03E-12

K.LLQDFFNGK.E	2	541,293	0,0058	6,500576	2,71E-08
K.NQVAMNPTNTVFDK.R	2	833,412	0,0132	10,35768	1,7E-22
R.TTPSYVAFTDTER.L	2	744,377	-0,023	11,79777	2,24E-29
K.VEIIANDQGNR.T	2	614,825	0,0072	9,426937	1,78E-18

Spot	Acc. Number	protein name	pl	Pm (Da)	score	cov. (%)	peptides
1057	P04762	catalase	7,45	59.626,03	87,8	22%	10
sequenced peptides			z	m/z	dm/z	z-score	p-value

R.DAMLFPSFIHSQK.R	2	768,891	0,0119	6,355475	5,64E-08
K.DAQLFIQR.K	2	495,779	0,0073	9,082751	4,65E-17
K.DYPLIPVGK.L	2	501,296	-0,009	9,941385	1E-20
K.EAETFPFNPFDLTK.V	2	828,414	0,0128	7,747397	2,23E-12
R.FNSANEDNVTQVR.T	2	747,368	-0,015	12,80388	5,93E-35
R.FSTVAGESGSADTVR.D	2	742,373	0,0179	8,125962	1,39E-13
R.LAQEDPDYGLR.D	2	638,825	0,0128	9,105353	3,96E-17
R.LGPNYLQIPVNCPYR.A	2	902,478	0,0142	6,574384	1,08E-08
K.LNIMTAGPR.G	2	494,776	0,0103	9,982775	8,37E-21
K.VLNEEER.K	2	444,729	0,0042	7,759361	5,26E-12

Spot	Acc. Number	protein name	pl	Pm (Da)	score	cov. (%)	peptides
1425	Q63081	Protein disulfide-isomerase A6 (CaBP1)	4,99	46.192,99	45,6	17%	5
sequenced peptides			z	m/z	dm/z	z-score	p-value

K.DVVELTDDTFDK.N	2	698,834	0,0066	7,282629	1,09E-10
K.GSFSEQGINEFLR.E	2	742,371	-0,009	8,747707	6,63E-16

R.GSTAPVGGGSFPNITPR.E	2	807,927	0,0114	8,871881	1,89E-16
K.LAAVDATVNQVLASR.Y	2	764,435	0,0065	10,24565	2,4E-22
R.TGEAIVDAALSALR.Q	2	693,893	0,0101	10,47676	1,88E-23

Spot	Acc. Number	protein name	pl	Pm (Da)	score	cov. (%)	peptides
2167	P13803	Electron transfer flavoprotein subunit alpha, mitochondrial (Alpha-ETF)	8,77	34.951,37	15,4	9%	2

sequenced peptides	z	m/z	dm/z	z-score	p-value
--------------------	---	-----	------	---------	---------

K.GLLPEELTPLILETQK.Q	2	897,528	0,0115	8,607963	3,64E-16
K.LNVAPVSDIIEIK.S	2	705,924	0,0099	6,769409	1,34E-09

Spot	Acc. Number	protein name	pl	Pm (Da)	score	cov. (%)	peptides
2284	P14141	Carbonic anhydrase 3 (CA-III)	7,36	29.300,21	30,2	15%	4

sequenced peptides	z	m/z	dm/z	z-score	p-value
--------------------	---	-----	------	---------	---------

K.EPMTVSSDQMAK.L	2	678,302	0,0071	6,737836	3,52E-09
R.GGPLSGPYR.L	2	452,243	0,0056	8,015848	6,79E-13
R.VVFDDTFDR.S	2	557,274	0,0103	8,915527	1,57E-16
K.YNTFGEALK.Q	2	521,772	0,0083	6,562605	1,74E-08

Spot	Acc. Number	protein name	pl	Pm (Da)	score	cov. (%)	peptides
2379	P08010	Glutathione S-transferase Mu 2 (GST Yb2)	8,07	25.571,44	43,2	24%	5

sequenced peptides	z	m/z	dm/z	z-score	p-value
--------------------	---	-----	------	---------	---------

K.ITQSNAILR.Y	2	508,308	0,0093	5,9924	4,75E-07
R.LFLEYTDTSYEDK.K	2	812,393	0,0185	11,23985	8,44E-27
K.LYSEFLGK.Q	2	478,767	0,0092	5,720673	2,68E-06

R.VDVLENQAMDTR.L 2 703,848 0,0154 11,71685 4,74E-29

K.YSMGDAPDYDR.S 2 653,269 0,0127 8,518105 1,43E-15

Spot	Acc. Number	protein name	pl	Pm (Da)	score	cov. (%)	peptides
------	-------------	--------------	----	---------	-------	----------	----------

2495 Q78JT3 3-hydroxyanthranilate 3,4-dioxygenase (HAD) (3-HAO) 6,27 32.804,31 18,4 7% 2

sequenced peptides	z	m/z	dm/z	z-score	p-value
--------------------	---	-----	------	---------	---------

R.FANTMGLVIER.R 2 633,336 0,4933 5,630227 5,52E-06

R.QGEIFLLPAR.V 2 572,335 0,0054 7,43183 2,97E-11

Spot	Acc. Number	protein name	pl	Pm (Da)	score	cov. (%)	peptides
------	-------------	--------------	----	---------	-------	----------	----------

2542 Q63716 Peroxiredoxin-1 8,59 22.109,42 66,0 37% 7

sequenced peptides	z	m/z	dm/z	z-score	p-value
--------------------	---	-----	------	---------	---------

K.ADEGISFR.G 2 447,727 0,0074 8,125233 2,99E-13

K.ATAVMPDGQFK.D 2 590,798 0,0105 8,929016 1,75E-16

R.GLFIIDDK.G 2 460,765 0,0068 8,347874 2,11E-14

R.LVQAFQFTDK.H 2 598,837 0,0176 8,263024 3,41E-14

K.QGGLGPMNIPLVSDPK.R 2 819,949 0,0194 9,683683 8,53E-20

R.QITINDLPVGR.S 2 613,37 -0,021 12,38245 5,32E-33

R.TIAQDYGVLK.A 2,00 554,321 0,0149 8,061819 1,7E-13