

Supplementary table 1 Proteins that were most differentially expressed (up/down) in FCP-treated *C. elegans* under 35°C stress.

ID Number ^a	Name of Protein	Accession Number	Fold difference ^b	~Molecular Mass (Da)	~ pI	Coverage (%)	Matched Peaks	Putative Functions
Up regulated proteins due to treatment								
1	IPYR_CAEEL Probable inorganic pyrophosphatase 1 OS= <i>Caenorhabditiselegans</i> GN=pyp/	IPYR	1.32	44,133.7	4.83	20.1	8	Embryo development, egg hatching and growth
2	PSA2_CAEEL Proteasome subunit alpha type-2 OS= <i>Caenorhabditiselegans</i> GN=pas-2 PE	PSA2	1.41	25,318.1	5.85	3.9	1	The proteasome is a multicatalytic proteinase complex which is characterized by its ability to cleave peptides. It has an ATP-dependent proteolytic activity
3	SAR1_CAEEL GTP-binding protein SAR1 OS= <i>Caenorhabditiselegans</i> GN=ZK180.4 PE=2 SV	SAR1	0.15	21,691.4	5.61	9.84	2	Embryo development ending in birth or egg hatching and growth
4	IF5A1_CAEEL Eukaryotic translation initiation factor 5A-1 OS= <i>Caenorhabditiselegans</i>	IF5A1	D	17,849.3	5.23	11.8	2	mRNA-binding protein involved in translation elongation, stress response and maintenance of cell wall integrity.
5	RHO1_CAEEL Ras-like GTP-binding protein rhoA OS= <i>Caenorhabditis elegans</i> GN	RHO1	1.25	21,617.4	4.31	3.12	1	Regulation of acetylcholine secretion and locomotion and involved in small GTPase mediated signal transduction
6	TDX1_CAEEL Probable	TDX1	0.25	24,914.8	6.13	31.9	8	Plays an important role in

	peroxiredoxin prdx-3 OS= <i>Caenorhabditiselegans</i> GN								eliminating peroxides generated during metabolism.
7	NAS16_CAEEL Zinc metalloproteinase nas-16 OS= <i>Caenorhabditis elegans</i> GN	NAS16	2.24	51,491.4	5.61	2.22	1		Hydrolysis the proteins into smaller polypeptides and/or amino acids by cleavage of their peptide bonds.
8	Q9XVT2_CAEEL Protein C15C6.3, partially confirmed by transcript evidence OS=Caen	Q9XVT2	D	77,550.3	5.51	1.14	1		Hermaphrodite genitalia development, mRNA cleavage and positive regulation of growth rate
9	GPX2_CAEEL Probable glutathione peroxidase R05H-10.5 OS= <i>Caenorhabditis elegans</i> GN	O62327	D	18,134.3	6.75	10.4	2		Response to oxidative stress, glutathione peroxidase activity
10	TPIS_CAEEL Triosephosphateisomerase OS= <i>Caenorhabditiselegans</i> GN=tpi-1 PE=1 SV	TPIS	0.29	26,556.4	6.56	4.05	1		Determination of adult lifespan and fatty acid biosynthetic process
11	O62040_CAEEL Putative uncharacterized protein OS= <i>Caenorhabditiselegans</i>	O44751	D	37,708	5.48	2.37	1		Strictosidine synthase (a key enzyme in alkaloid biosynthesis) activity
12	Q9N5D3_CAEEL Drosophila sos homolog protein 1 OS= <i>Caenorhabditis elegans</i> GN=SOS-1	Q9N5D3, Q9NBD3	D	16,902	5.67	0.47	1		DNA binding, Rho guanyl-nucleotide exchange factor activity, calmodulin binding
13	AL7A1_CAEEL Putative aldehyde dehydrogenase family 7 member A1 homolog OS= <i>Caenorhabditiselegans</i>	P46562	D	56,994.8	6.43	4.52	3		Detoxification of aldehydes generated by alcohol metabolism and lipid peroxidation, protects cells from oxidative stress.
14	RSSA_CAEEL 40S	P46769	D	30,685.1	6.12	6.16	2		Assembly and/or stability of the

	ribosomal protein SA OS= <i>Caenorhabditis elegans</i> GN=RPS-0 PE=1 SV=3								40S ribosomal subunit and processing of the 20S rRNA-precursor to mature 18S rRNA in a late step of the maturation of 40S ribosomal subunits
15	Q9XW04_CAEEL Protein Y18D10A.21, partially confirmed by transcript evidence OS=C	Q9XW04	D	32,897.3	6.47	2.8	1		Catalytic activity, cation-binding, carbohydrate metabolic process
16	Q94255_CAEEL Saposin-like protein family protein 20	Q94255	D	24,484.9	5.87	2.76	1		Lipid metabolism
17	Q17849_CAEEL Heat shock protein protein 25, isoform a OS= <i>Caenorhabditiselegans</i>	Q17849	D	25,238.6	5.91	4.57	1		Response to heat, protein-binding, Stress response
18	D0LGS3_HALO1 Carbamoyl-phosphate synthase L chain ATP-binding protein OS=Haliang	D0LGS3	1.89	211,022	5.43	0.47	1		ATP-binding, biotin-binding, ligase activity
19	C3JZ86_PSEFS Superoxide dismutase OS	C3JZ86, Q1IE87, Q3K7N1	D	22,743.6	4.52	4.57	1		Superoxide dismutase activity, oxidation reduction, superoxide metabolic process
20	Q18100_CAEEL Sensory axon guidance protein 7	Q18100, Q4PIU9	D	127,605	5.61	0.61	1		Involved in specific pathways by attractive and repulsive cues in the extracellular environment
21	Q6EUT7_CAEEL Protein ZK1151.1g, partially confirmed by transcript evidence OS= <i>Caenorhabditiselegans</i>	Q7K7B6, Q867D9	1.88	561,703	4.41	0.2	1		Cell cycle arrest, Actin-binding and Calcium ion-binding
22	14331_CAEEL 14-3-3-like protein 1 OS= <i>Caenorhabditiselegans</i> GN=PAR-5 PE=1 SV=2 6	Q20655 P41932	1.52	28,173	4.52	10.1	3		Adapter protein involved in regulation of general and specialized signaling pathway

23	MLR1_CAEEL Myosin regulatory light chain 1 OS= <i>Caenorhabditiselegans</i> GN=MLC-1 PE	P19625, P19626	4.9	8,586.4	4.52	31.2	15	Calcium ion-binding, motor activity
24	HSP11_CAEEL Heat shock protein HSP-16.1/HSP-16.11 OS= <i>Caenorhabditiselegans</i> GN=h	P34696	D	16,235.5	6.30	33.8	6	Defense response, determination of adult lifespan, positive regulation of growth rate, response to heat
25	COX5A_CAEEL Cytochrome c oxidase subunit 5A, mitochondrial OS= <i>Caenorhabditis elegans</i>	P55954	D	20,093.3	6.23	13.8	4	Cytochrome-c oxidase activity, metal ion binding
26	O45509_CAEEL Protein F41D3.10, partially confirmed by transcript evidence OS= <i>Caenorhabditiselegans</i>	O45509	D	76,674	6.51	1.19	1	Sequence-specific DNA-binding, steroid hormone receptor activity, zinc ion-binding
27	Q9UAX1_CAEEL Putative uncharacterized protein T12B3.4 OS= <i>Caenorhabditiselegans</i>	Q9UAX1	D	33,698.7	6.71	2.74	2	Protein-binding
28	O18180_CAEEL Protein W09D10.3, confirmed by transcript evidence OS= <i>Caenorhabditiselegans</i>	O18180	2.36	18,421.4	6.63	16.8	5	Determination of adult lifespan, positive regulation of growth rate, structural constituent of ribosome
29	O44751_CAEEL Putative uncharacterized protein OS= <i>Caenorhabditiselegans</i>	O44751	2.02	55,504.4	6.27	1.23	1	ATP-binding, protein kinase activity
30	Q9XUT0_CAEEL Protein K08E3.4, confirmed by transcript evidence OS= <i>Caenorhabditiselegans</i>	Q9XUT0	11.14	71,922.8	6.85	3.11	2	Actin-binding
31	O45177_CAEEL Putative	O45177	10.63	40,387	6.92	2.31	1	RNA-binding

	uncharacterized protein OS= <i>Caenorhabditiselegans</i> GN=K07H8								
32	C5I WV5_PIG Trypsinogen OS= <i>Sus scrofa</i> PE=2 SV=1	C5I WV5, P00761	1.0	21,959.7	5.61	4.55	1	Proteolysis, serine-type endopeptidase activity	
33	ATPB_CAEEL ATP synthase subunit beta, mitochondrial OS= <i>Caenorhabditiselegans</i> GN	P46561	1.59	57,509.3	4.73	1.86	1	ATP-binding, hydrogen ion transporting ATP synthase activity	
34	Q21057_CAEEL Galectin OS= <i>Caenorhabditis elegans</i> PE=2 SV=1 6239	Q21057, Q9N384	3.79	15,911.4	4.42	26	4	Sugar-binding	
35	Q20804_CAEEL CNB-1 OS= <i>Caenorhabditis elegans</i> GN=CNB-1 PE=2 SV=3 6239	Q20804	1.01	19,654.9	5.10	5.85	1	Calcium ion-binding	
36	HSP17_CAEEL Heat shock protein HSP-16.48/HSP- 16.49 OS= <i>Caenorhabditiselegans</i> GN	P02513	8.43	16,282	5.83	11.2	2	Determination of adult lifespan, endoplasmic reticulum unfolded protein response to heat	
Down regulated proteins due to treatment									
37	MLE_CAEEL Myosin, essential light chain OS= <i>Caenorhabditiselegans</i> GN=mlc-3 PE=1	P19625, P19626	0.75	17,127.1	5.27	76.5	14	Locomotion and all cellular and reproductive activity	
38	Q22066_CAEEL Aspartate aminotransferase OS= <i>Caenorhabditis elegans</i> GN=T01Cf8.4 PE	Q22066	0.37	15,266.2	4.42	2.24	1	Biosynthetic process and cellular amino acid metabolic process	

39	Q20644_CAEEL Protein F52B5.3, partially confirmed by transcript evidence OS= <i>Caenorhabditiselegans</i>	Q20644	D	162,454	6.53	0.7	1	Inorganic anion exchanger activity
40	EIF3C_CAEEL Eukaryotic translation initiation factor 3 subunit C OS= <i>Caenorhabditiselegans</i>	P34563	D	103,827	6.45	0.67	1	Protein synthesis, translation initiation factor activity
41	RL18_CAEEL 60S ribosomal protein L18 OS= <i>Caenorhabditis elegans</i> GN=RPL-18 PE=3 SV	O45946	0.30	51,385.2	6.73	3.72	1	RNA-binding, Structural constituent of ribosome
42	Q23440_CAEEL Protein ZK1307.8, confirmed by transcript evidence OS= <i>Caenorhabditiselegans</i>	A8DYR6, Q8IG31	0.46	58,045.8	4.81	1.38	1	Calcium ion-binding, protein-binding,
43	A8DYR6_CAEEL Peroxiredoxin protein 2, isoform b OS= <i>Caenorhabditis elegans</i> GN	A8DYR6, Q8IG31	0.80	21,767	5.45	14.9	3	Thioredoxin peroxidase activity, determination of adult lifespan, hydrogen peroxide catabolic process

D –Differential protein. These specified differential proteins were found to be expressed due to FCP treatment under stressed conditions, includes both up/down regulation; a) ID number indicates the excised differential protein spot from the 2-DE master reference gel; b) The mean (n = 6) factor of increase/decrease in protein spot due to FCP treatment compared to control *C. elegans* worm proteome, obtained from the 6 replicate gels (3 biological and 3 technical replicates). The ‘P’ value of each differential spot was ≤ 0.05 .