

Supplementary Material to “Transcriptome analyses of *Ditylenchus destructor* in responses to cold and desiccation stress”

Table S4 - Genes highly expressed in cold and desiccation treated nematodes. Unigenes tested by qPCR are shown in bold.

Gene ID	CK_6 (FPKM)	D_1G (FPKM)	D_2G (FPKM)	D_1W (FPKM)	D_2W (FPKM)	Nr	KEGG
CL11535	1.8	265.5	154.3	1112.4	789.9	gi 597891109/hypothetical protein Y032_0658g1253 [<i>Ancylostoma ceylanicum</i>]	bta:789503/3e-10/MUC5B, MUC5AC, mucin-5B; oligomeric mucus/gel-forming
Unigene15595	1.1	28.1	3.1	360.2	401.8	gi 557244171 /serine/threonine protein phosphatase, putative [<i>Eimeria necatrix</i>]	NA
Unigene15189	1.0	18.1	1.4	243.4	296.3	gi 557198975/hypothetical protein EMH_0013710 [<i>Eimeria mitis</i>]	NA
Unigene15596	5.5	100.3	4.8	1099.0	1219.3	gi 557234804/hypothetical protein EBH_0049890 [<i>Eimeria brunetti</i>]	NA
CL2646	1.1	1.0	5.1	147.7	159.6	gi 470260102/hypothetical protein DFA_04287 [<i>Dictyostelium fasciculatum</i>]	ame:724159/1e-08/GB10093; uncharacterized LOC724159; K11306 histone acetyltransferase MYST4
Unigene18439	2.1	8.9	23.9	158.9	126.3	NA	NA
Unigene15597	21.4	110.0	27.6	1328.5	1619.6	gi 557169829/myosin heavy chain, putative [<i>Eimeria praecox</i>]	cqu:CpipJ_CPIJ002507/3e-06/nuclear receptor co- repressor 1; K04650 nuclear receptor co-repressor 1
CL7558	1.8	4.2	1.8	111.6	74.6	NA	NA
CL6859	2.2	8.3	5.2	121.7	52.4	gi 341900824/hypothetical protein CAEBREN_18196 [<i>Caenorhabditis brenneri</i>]	fab:101814166/8e-08/HOXD3; homeobox D3
Unigene20352	2.5	6.6	9.2	132.9	102.8	gi 597892762/hypothetical protein Y032_0587g341 [<i>Ancylostoma ceylanicum</i>]	cbr:CBG09373/5e-82/Cbr-ugt-48 C. briggsae; K00699 glucuronosyltransferase

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CL5442	1.0	23.8	13.4	8.9	9.2	gi 541042271/udp-glucuronosyltransferase ugt-48 [<i>Ascaris suum</i>]	bmy:Bm1_13480/3e-53/UDP-glucuronosyl and UDP- glucosyl transferase family protein
CL3923	1.3	6.0	4.2	59.5	39.5	gi 25149822/Protein MIG-6, isoform c [<i>Caenorhabditis elegans</i>]	ocu:100344817/8e-93/ADAMTS18; K08632 a disintegrin and metalloproteinase with thrombospondin motifs 18
Unigene15564	1.9	217.9	5.3	85.5	47.7	gi 187027406/Protein CBG15126 [<i>Caenorhabditis briggsae</i>]	cfr:102511432/1e-13/FAM98B; family with sequence similarity 98, member B
Unigene9153	2.3	5.8	3.0	91.1	109.5	gi 55716698/hypothetical protein EMH_0033040 [<i>Eimeria mitis</i>]	mmu:218695/6e-09/Gm10044; K17299 POTE ankyrin domain family protein
Unigene3174	12.5	32.3	130.8	459.8	337.9	gi 557228633/hypothetical protein EPH_0028000 [<i>Eimeria praecox</i>]	dre:402861/7e-07/rab11fip1b, K12484 Rab11 family- interacting protein 1/2/5
CL2640.Ctig2	43.0	169.7	261.7	1541.3	1656.6	gi 123431955/trichohyalin [<i>Trichomonas vaginalis</i> G3]	dwi:Dwil_GK19899/1e-29/GK19899 gene product from transcript GK19899-RA; K18626 trichohyalin
CL2640	39.2	176.6	256.0	1261.6	1385.6	gi 449709444/trichohyalin, putative [<i>Entamoeba histolytica</i> KU27]	shr:100933589/1e-25/TCHH; trichohyalin
CL7250	19.1	70.0	43.6	613.9	446.3	gi 637345608/PREDICTED: glycine-rich cell wall structural protein [<i>Anolis carolinensis</i>]	cin:100182977/5e-20/heterogeneous nuclear ribonucleoprotein A3 homolog 2-like
CL757	1.5	230.8	14.6	2.8	8.0	NA	NA
CL4446	26.4	1185.3	120.6	30.1	25.0	gi 560135252/GNS1 SUR4 membrane protein domain containing protein [<i>Haemonchus contortus</i>]	xma:102231386/8e-41/elongation of very long chain fatty acids protein 6-like; K10203 [EC:2.3.1.199]
Unigene10683	1.0	40.3	4.6	8.6	1.8	gi 187027406/Protein CBG15126 [<i>Caenorhabditis briggsae</i>]	cin:100185025/7e-10/heterogeneous nuclear ribonucleoprotein D-like; K13044
CL566	1.0	10.7	25.5	0.0	0.0	gi 170591100/GMP synthase [<i>Brugia malayi</i>]	bmy:Bm1_44235/0.0/GMP synthase; K01951

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CL2521	2.3	103.7	53.6	12.8	11.4	gi 556759154/PREDICTED: uncharacterized protein YIR042C-like [<i>Pantholops hodgsonii</i>]	NA
CL1727	2.2	26.0	34.3	5.3	5.7	gi 597896822/hypothetical protein Y032_0446g1597 [<i>Ancylostoma ceylanicum</i>]	cel:CELE_T22H6.2/2e-99/alh-13; ALdehyde deHydrogenase; K12657 delta-1-pyrroline- 5- carboxylate synthetase [EC:2.7.2.11 1.2.1.41]
CL3801	1.3	18.5	20.0	0.0	0.0	gi 393907986/CBR-NURF-1 protein [<i>Loa loa</i>]	bmy:Bm1_11520/3e-46/PHD-finger family protein; K11728 nucleosome-remodeling factor subunit BPTF
Unigene15619	2.8	27.4	40.0	15.6	17.4	gi 341879718/hypothetical protein CAEBREN_32771 [<i>Caenorhabditis brenneri</i>]	loa:LOAG_06978/8e-29/ubiquitin C II; K08770 ubiquitin C
Unigene15620	1.78	15.72	16.88	1.68	3.71	gi 542249255 PREDICTED: polyubiquitin-C-like [<i>Oreochromis niloticus</i>]	fab:101807900/3e-16/UBC; ubiquitin C; K08770
CL5442	1.0	23.8	13.4	8.9	9.2	gi 541042271/udp-glucuronosyltransferase ugt-48 [<i>Ascaris suum</i>]	bmy:Bm1_13480/3e-53/UDP-glucuronosyl and UDP- glucosyl transferase family protein; K00699 glucuronosyltransferase [EC:2.4.1.17]
CL757	1.5	230.8	14.6	2.8	8.0	NA	NA
CL10164	2.0	43.1	17.1	13.9	3.7	gi 3085018790/CRE-GPDH-2 protein [<i>Caenorhabditis remanei</i>]	cel:CELE_K11H3.1/5e-149/gpdh-2; Glycerol-3- Phosphate DeHydrogenase; K00006 [EC:1.1.1.8]
CL583	16.9	381.5	142.2	10.3	10.2	gi 597833081/hypothetical protein Y032_0351g3245 [<i>Ancylostoma ceylanicum</i>]	cel:CELE_K09H11.7/2e-121/K09H11.7; K19269 phosphoglycolate phosphatase [EC:3.1.3.18 3.1.3.48]
CL6083	77.5	1750.9	571.6	35.6	58.4	gi 225712408/Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial precursor [<i>Lepeophtheirus salmonis</i>]	aqu:100637276/2e-81/hydroxyacyl-coenzyme A dehydrogenase, mitochondrial-like; K00022 3- hydroxyacyl-CoA dehydrogenase [EC:1.1.1.35]
CL2302	3.5	45.0	25.5	30.7	33.4	gi 597836309/hypothetical protein Y032_0287g1432 [<i>Ancylostoma ceylanicum</i>]	crg:105332293/5e-43/WW domain-containing oxidoreductase-like

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CL11535	1.8	265.5	154.3	1112.4	789.9	gi 597891109/hypothetical protein Y032_0658g1253 [<i>Ancylostoma ceylanicum</i>]	bta:789503/3e-10/MUC5B, MUC5AC, mucin-5B; oligomeric mucus/gel-forming;
Unigene3174	12.5	32.3	130.8	459.8	337.9	gi 557228633/hypothetical protein EPH_0028000 [<i>Eimeria praecox</i>]	dre:402861/7e-07/rab11fip1b, si:ch211-187d7.3; RAB11 family interacting protein 1 (class I) b;
Unigene15189	1.0	18.1	1.4	243.4	296.3	gi 557198975/hypothetical protein EMH_0013710 [<i>Eimeria mitis</i>]	NA
CL2554	13.7	266.0	67.5	114.1	99.4	gi 560120930/Protein F55H12.4 [<i>Haemonchus contortus</i>]	NA
Unigene15564	1.9	217.9	5.3	85.5	47.7	gi 187027406/Protein CBG15126 [<i>Caenorhabditis briggsae</i>]	cfr:102511432/1e-13/FAM98B; family with sequence similarity 98, member B; K15434 protein FAM98B cin:100179166/6e-83/probable pyridoxine biosynthesis
Unigene20945	4.3	77.0	24.2	73.7	110.3	gi 170317959/PLP synthase [<i>Heterodera glycines</i>]	SNZERR; K06215 pyridoxal 5'-phosphate synthase pdxS subunit [EC:4.3.3.6]
CL2302	6.1	114.3	53.3	66.5	85.0	gi 17532791/Protein DHS-7 [<i>Caenorhabditis elegans</i>]	crg:105332293/7e-51/WW domain-containing oxidoreductase-like; K19329
CL5833	4.0	10.3	2.9	52.3	57.7	gi 541041775/putative oxidoreductase dhs-27 [<i>Ascaris suum</i>]	NA
Unigene15628	1.5	27.9	5.2	39.6	25.1	gi 541044223/gut esterase 1 [<i>Ascaris suum</i>]	cel:CELE_R12A1.4/9e-84/ges-1; Gut esterase 1; K01044 carboxylesterase 1 [EC:3.1.1.1]
Unigene6241	2.7	49.3	16.1	28.8	31.5	gi 341879600/hypothetical protein CAEBREN_00122 [<i>Caenorhabditis brenneri</i>]	cbr:CBG13096/7e-12/Hypothetical protein CBG13096; K19329 WW domain-containing oxidoreductase
CL4901	1.2	25.5	7.6	15.4	8.3	NA	NA
CL11742	1.1	18.7	5.7	13.0	12.7	gi 322789360/hypothetical protein SINV_11101 [<i>Solenopsis invicta</i>]	bmor:101737103/7e-29/L-xylulose reductase-like; K03331 L-xylulose reductase [EC:1.1.1.10]

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CL4572	1.3	28.9	23.1	12.5	6.3	gi 340375388/PREDICTED: trans-1,2-dihydrobenzene-1,2-diol dehydrogenase-like [<i>Amphimedon queenslandica</i>]	xtr:100145807/1e-28/dhdh; K00078 dihydrodiol dehydrogenase / D-xylose 1-dehydrogenase (NADP) [EC:1.3.1.20 1.1.1.179]
Unigene10683	1.0	40.3	4.6	8.6	1.8	gi 187027406/Protein CBG15126 [<i>Caenorhabditis briggsae</i>]	cin:100185025/7e-10/heterogeneous nuclear ribonucleoprotein D-like
CL9198	33.5	64.6	113.6	57.1	90.4	gi 74776553/RecName: alpha-trehalose-phosphate synthase [UDP-forming] 2;	bmor:101741435/6e-43/alpha-trehalose-phosphate synthase [UDP-forming]
CL3586	445.2	262.3	1641.8	1425.6	1125.7	gi 392920154/Protein LEA-1, isoform a [<i>Caenorhabditis elegans</i>]	NA
CL10174	285.5	1501.3	1269.1	471.0	1052.8	gi 24418520/RecName: Full= Protein LEA-1	NA
4783	499.1	57.6	36.9	122.2	24.7	gi 541039287/heat shock protein [<i>Ascaris suum</i>]	dvi:Dvir_GJ21096/7e-16/GJ21096 gene product from transcript GJ21096-RA; K09542 crystallin, alpha B
CL3560	2	3.8	20.4	30.8	23.8	gi 312065685 calreticulin family protein [<i>Loa loa</i>]	loa:LOAG_00322/0.0/calreticulin family protein; K08054 calnexin
CL8617	2.2	14.4	18.3	21.8	23.9	gi 597870679 hypothetical protein Y032_0023g847 [<i>Ancylostoma ceylanicum</i>]	loa:LOAG_00382/1e-77/oxidoreductase; K00011 aldehyde reductase [EC:1.1.1.21]
CL6038	1.66	9.1	6.8	40.5	35.8	gi 541045808 neurocalcin delta [<i>Ascaris suum</i>]	NA
U5578	0.98	0	0	42.1	35.3	gi 17557246 Protein NLP-29 [<i>Caenorhabditis elegans</i>]	spu:594428/3e-11/peroxisomal membrane protein; K13344
CL10174	285.5	1501.3	471.0	1269.1	1052.8	gi 24418520 LEA1 protein [<i>Aphelenchus avenae</i>]	NA
CL8223	3.2	4.2	9.5	22.4	32.6	gi 24418520 LEA1 protein [<i>Aphelenchus avenae</i>]	ptg:102962717/7e-07/SRRM2; serine/arginine repetitive matrix 2; K13172
CL1306	459.0	496.4	1822.0	3630.2	2894.2	gi 392920154 Protein LEA-1, isoform a [<i>Caenorhabditis elegans</i>]	nvi:100122475/3e-19/microtubule-associated protein futsch-like; K10380

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CL2422	0.25	1.76	8.14	6.68	4.67	gi 90959527 PvLEA1 protein [<i>Polypedilum vanderplanki</i>]	sp Q95V77 LEA1_APHAV
CL4616	3644.4	1731.6	15608.3	5381.9	12046.3	gi 146331045 LEA5 protein [<i>Steinernema carpocapsae</i>]	NA
49558	8.8	25.4	19.6	28	30.6	gu 130157.1 small HSP21-like protein [<i>Bursaphelenchus xylophilus</i>]	NA
CL653	724.5	1189.4	1033.9	297.7	389.6	gi 573006128 hsp 70A [<i>Ditylenchus destructor</i>]	bmy:Bm1_43675/0.0/heat shock 70 kDa protein
CL9628	1.9	4.1	4	4.9	4.0	gi 221706451 hsp 90 [<i>Steinernema feltiae</i>]	loa:LOAG_00073/8e-07/heat shock protein 90
U11847	1.7	2	1	46.7	49.9	gi 170591664 small heat shock protein 12.6, [<i>Brugia malayi</i>]	tgu:100230097/7e-13/CRYAB; crystallin, alpha B
CL9687	4.2	55.0	39.4	1.4	0.5	gi 328925282 heat shock protein 20 [<i>Bursaphelenchus doui</i>]	NA
CL9198	33.5	64.6	57.1	113.6	90.4	gi 74776553 Trehalose-6-phosphate synthase 2	bmor:101741435/6e-43/alpha, alpha-trehalose-phosphate synthase [UDP-forming];
Unigene13345	0.37	2.15	1.41	0.7	2.05	gi 74776556 Trehalose-6-phosphate synthase 1;	sp Q5K2C4 TPS1_APHAV/0.0/Alpha, alpha-trehalose-phosphate synthase [UDP-forming] 1
CL1469	0	1.39	0	8.11	12.56	gi 541048301 serine threonine-protein phosphatase 5 [<i>Ascaris suum</i>]	bmy:Bm1_15955/0.0/serine/threonine protein phosphatase 5
CL1053	285	173.1	633.2	2256.3	1547.9	gi 514684442 response regulator receiver protein [<i>Salpingoeca rosetta</i>]	dre:402861/8e-23/ RAB11 family interacting protein 1 (class I) b