

Additional File 3. Putative anhydrobiotic and stress response genes constitutively expressed by an unstressed mixed stage population of *Panagrolaimus superbus*.

ID	Description	Aa = Aphele Num ESTs
Signal Transduction: Protein Kinases and Transcription factors		
PSC00478	Mitogen-activated kinase protein kinase 2	2
PSC01196	MAP-kinase kinase kinase 4 (MAP/ERK kinase kinase 4)	1
PSC01769	Mitogen-activated protein kinase kinase kinase (MAP3K) family member	1
PSC00290	Serine/threonine protein kinase (<i>akt-1</i>)	2
PSC00571	Serine/threonine-protein kinase (NIMA-related kinase)	1
PSC01094	Serine/threonine protein kinase (MELK family)	1
PSC01732	Serine/threonine protein kinase (Pelle/IRAK family)	1
PSC01717	Serine/Threonine protein kinase (polo-like family)	1
PSC04189	Serine/threonine protein kinase (polo-like family)	1
PSC03670	Serine/Threonine kinase (STE20-like) (oxidative stress responsive kinase)	1
PSC04407	Serine/Threonine kinase (STE20-like)	1
PSC00531	Serine/threonine protein kinase	3
PSC03620	Serine/threonine protein kinase	1
PSC04057	Serine/threonine protein kinase	1
PSC01292	Cyclin-dependent serine/threonine kinase	1
PSC00619	Casein kinase (serine/threonine protein kinase)	5
PSC00256	Casein kinase family member	1
PSC00352	Casein kinase family member	1
PSC00703	Casein kinase family member	1
PSC01611	Casein kinase family member	2
PSC02062	Casein kinase family member	1
PSC02346	Casein kinase family member (<i>kin-5</i>)	1
PSC02425	Casein kinase II regulatory subunit	1
PSC02630	Casein kinase family member	1
PSC03823	Casein kinase family member	1
PSC01025	Protein tyrosine kinase (<i>kin-26</i>)	2
PSC01085	Protein tyrosine kinase (<i>kin-5</i>).	1
PSC01406	Protein tyrosine kinase	1
PSC01556	Protein tyrosine kinase	1
PSC01717	Protein tyrosine kinase	1
PSC04481	Protein tyrosine kinase	1
PSC01314	Membrane associated guanylate kinase family protein	1
PSC03667	AMP-activated kinase family member (<i>aak-2</i>)	1
PSC03258	Cyclic AMP-dependent protein kinase	1
PSC01948	Diacylglycerol kinase dgk-5	1
PSC02382	ForKHead transcription factor family member (<i>fkh-7</i>)	3
PSC04534	JuMonJi (JmjC) domain containing protein (<i>jmd-2</i>)	1
PSC04835	JmjC domain containing protein	1
PSC00968	High mobility group protein	2
PSC00428	HMG family member (<i>hmg-4</i>)	1
PSC02085	MNAT (menage a trois) TFIIH subunit family member (<i>mnat-1</i>)	1
Antioxidant Activity		
PSC00113	Manganese superoxide dismutase (<i>sod-2</i>)	2
PSC00206	Glutathione peroxidase	6
PSC02494	Glutathione peroxidase	1
PSC04819	Glutathione peroxidase	1
PSC00992	Peroxiredoxin (2-Cys)	2
PSC03895	Peroxiredoxin (1-Cys)	2
PSC00023	Glutathione S-transferase (sigma class)	3

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PSC00103	Glutathione S-transferase (sigma class)	2
PSC01247	Glutathione S-transferase (sigma class)	1
PSC02624	Glutathione S-transferase (sigma class)	2
PSC03592	Glutathione S-transferase (kappa class)	1
PSC04040	Glutathione S-transferase (kappa class)	1
PSC01767	Glutathione S-transferase family C terminal domain	1
PSC02300	Glutaredoxin	1
PSC01444	Glutaredoxin	1
PSC00712	Thioredoxin	1
PSC01063	Aldehyde dehydrogenase	1
PSC01095	Aldehyde dehydrogenase	3
PSC00896	Aldo/keto reductase family protein	1
PSC02918	Aldo/keto reductase family protein	1
PSC03704	Isocitrate dehydrogenase	1
Late Embryogenesis Abundant Proteins		
PSC00061	Hypothetical protein	10
PSC00416	LEA protein	6
PSC00489	LEA3 protein	2
PSC00514	LEA protein	2
PSC00782	Hypothetical protein	2
PSC01414	LEA protein	1
PSC01455	Hypothetical protein	2
PSC01720	Hypothetical protein	2
PSC01853	Hypothetical protein	1
PSC03871	LEA protein	2
PSC04118	LEA protein	1
PSC04142	LEA-like protein	1
PSC04695	LEA group 3 family member	2
Heat Shock Proteins (HSP)		
PSC00042	HSP90 family member	8
PSC01910	HSP90 family member	1
PSC03614	HSP90 family member	1
PSC00673	HSP70 family member	7
PSC00698	HSP70 family member	2
PSC01451	HSP70 family member	1
PSC02206	HSP70 family member	1
PSC03315	HSP70 family member	1
PSC04333	HSP70 family member	1
PSC02131	HSP60 (mitochondrial-specific chaperone)	1
PSC00160	HSP40 DnaJ domain containing protein	1
PSC00426	HSP40/DNaJ protein family member	1
PSC00581	HSP40/DNaJ protein family member	1
PSC01519	HSP40/DNaJ protein family member	3
PSC02002	HSP40/DNaJ protein family member	1
PSC02842	HSP40/DNaJ protein family member	3
PSC03247	HSP40/DNaJ protein family member	2
PSC02002	HSP40/DNaJ protein family member	1
PSC04179	HSP40/DNaJ protein family member	1
PSC01018	Small heat shock protein/alpha crystallin family member	2
PSC00408	Small heat shock protein/alpha crystallin family member (<i>hsp-17</i>)	1
PSC02762	Small heat shock protein/alpha crystallin family member (<i>hsp-12.1</i>)	1
PSC03116	Small heat shock protein/alpha crystallin family member (<i>hsp-12.1</i>)	2

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HSP co-chaperone proteins

PSC02847	HSP90 co-chaperone Cdc37	1
PSC02470	HSP70 co-chaperone BAG1	2
PSC00168	Tetratricopeptide repeat containing protein	3

Other Chaperone/Chaperonin proteins

PSC03669	Putative mitochondrial chaperone BCS1 family member	1
PSC00547	Mitochondrial prohibitin complex protein 2 (Prohibitin-2) from PsPm	1
PSC0225	Protein disulfide isomerase	2
PSC02974	Protein disulfide isomerase P5 subfamily	1
PSC00740	Protein disulfide isomerase (pdi-2)	6
	Cyclophilin-type peptidyl-prolyl cis-trans isomerase (cyp-5)	1
5	Cyclophilin family member (cyp-7)	1
8	Cyclophilin family member (cyp-13)	1
PSC02549	Cyclophilin family member (cyp-16)	1
PSC02695	Cyclophilin family member (cyp-3)	3
PSC00535	Derlin-2 (Degradation in Endoplasmic Reticulum)	1
PSC02304	DJ-1 family protein	2
PSC03146	Prefoldin subunit 2 (pfd-2)	1
PSC02579	Prefoldin subunit 5	2
PSC0264	Cytosolic T-complex protein 1 (chaperonin), theta subunit	1
PSC01023	Cytosolic T-complex protein 1 (chaperonin), gamma subunit	2
PSC04185	Putative alpha-tubulin folding cofactor B	1

The Ubiquitin System

PSC00646	Ubiquitin family protein (ubq-1)	4
PSC01689	Ubiquitin family protein (ubq-1)	1
PSC03896	Ubiquitin family protein	1
PSC03347	Ubiquitin/60s ribosomal protein L40 fusion CBR-UBQ-2	1
PSC04895	UBA (human ubiquitin) related family member (uba-1)	1
PSC01404	Polyubiquitin	4
PSC03474	Ubiquitin C (polyubiquitin)	3
PSC00949	Ubiquitin-like domain-containing protein	1
PSC01245	Ubiquitin-activating enzyme E1 CBR-ULA-1	1
PSC03681	Ubiquitin-activating enzyme E1	1
PSC00018	Ubiquitin-conjugating enzyme E2	2
PSC00530	Ubiquitin conjugating enzyme (E2) family member (ubc-3)	1
PSC0105	Ubiquitin conjugating enzyme (E2) family member	1
PSC04120	Ubiquitin conjugating enzyme (E2) family member	1
PSC04454	NEDD8-conjugating enzyme (E2 family member) CBR-UBC-12 protein	1
PSC0099	Ring box protein component of SCF E3 ubiquitin ligase	2
PSC0311	MARCH-VI protein (an E3 ubiquitin ligase)	2
PSC0428	Probable E3 ubiquitin-protein ligase	2
PSC01665	Predicted E3 ubiquitin ligase	2
PSC03058	COP9 signalosome complex subunit 5, a positive regulator of E3 ubiquitin	1
PSC0324	Ubiquitin elongating factor E4	1
PSC0236	Ubiquitin carboxyl-terminal hydrolase family protein (deubiquitinating enz)	1
PSC02861	Ubiquitin carboxyl-terminal hydrolase; deubiquitinating enzyme	1
PSC00475	Ubiquitin fusion degradation protein UFD1	1

The Proteasome

PSC00143	Proteasome subunit alpha type 1	3
PSC04160	Proteasome subunit alpha type 4	1
PSC04237	Proteasome subunit alpha type 4	1

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PSC03688	Proteasome subunit alpha type 7	1
PSC00843	Proteasome subunit beta type 4	2
PSC04388	Proteasome subunit beta type-6	1
PSC00484	Proteasome subunit beta type-7	1
PSC00843	Proteasome subunit beta type 4	2
PSC00315	Proteasome regulatory subunit 4 ATPase	3
PSC01367	Proteasome regulatory subunit 4 ATPase	2
PSC01711	Proteasome regulatory subunit 4 ATPase	2
PSC01771	Proteasome regulatory subunit 4 ATPase	2
PSC00480	Proteasome regulatory subunit 6A ATPase	2
PSC00101	Proteasome regulatory subunit 7 ATPase	2
PSC01401	Proteasome regulatory subunit 8	1
PSC00476	Proteasome non-ATPase regulatory subunit Nin1/mts3 family protein	1
PSC02017	Proteasome non-ATPase regulatory subunit 3	1
PSC02933	Proteasome non-ATPase regulatory subunit 6	3
PSC02961	Proteasome non-ATPase regulatory subunit rpn11	1
PSC04653	Adhesion regulating molecule family protein, putative proteasome subu	1
PSC02183	Proteasome non-ATPase regulatory complex subunit protein p97	1
PSC02285	Proteasome non-ATPase regulatory complex PCI domain containing prot	1
PSC02808	Proteasome non-ATPase regulatory complex PCI domain containing prot	1
Autophagy		
PSC02921	Autophagy-related protein 2 B (ATG2)	1
PSC00068	LC3, GABARAP and GATE-16 family member (<i>lgg-1</i>)	1
DNA Damage Response Proteins		
PSC00891	DNA damage inducible protein (DDI1) like	1
PSC02072	Similar to DNA excision repair protein ERCC6	1
PSC04704	Similar to <i>Homo sapiens</i> ERCC6 DNA excision repair protein	1
PSC01193	REX1 (required for excision 1) DNA repair family protein	1
PSC00496	Flap structure-specific endonuclease FEN-1	1
PSC04130	ERCC4 (XPF/Rad1/Mus81-dependent nuclease family) domain containin	1
PSC04614	DeoxyUTPase family member (<i>dut-1</i>)	1
PSC02273	DNA repair protein RAD51 (RecA) homolog	1
PSC04532	SNF2 family N-terminal domain containing protein (putative RAD26 homc	1
PSC03874	DNA mismatch repair protein MutS homolog 6	1
PSC04934	MutS domain family protein	1
PSC02766	Helicase SF2 family member (<i>hel-308</i>)	1
Others		
PSC01029	AquaPorin related family member CBR-AQP-2	1
PSC01205	AquaPorin related family member CBR-AQP-2 _PS_PM	1
PSC02097	Ezrin/Radixin/Moesin family member (<i>erm-1</i>)	1
PSC03641	THaumatIN family member (<i>thn-3</i>)	1
PSC02113	AN1-like Zinc finger family protein	3
PSC01468	RIC1 Putative stress responsive protein T23F2.3 [Caenorhabditis elegans:	1
PSC03821	Mitochondrial ATP-dependent protease PIM1/LON	1
PSC03263	Lon protease homolog, mitochondrial precursor, putative	1

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nchus avenae; Da = *Ditylenchus africanus*; Pm = *Plectus murrayi*; Ps = *Panagrolaimus superbus*.

Best Blast Hit **E value (Blastx)** **Distribution of Homologs.** Aa = *Aphelenchus avenae*

NP_001022238 [<i>Caenorhabditis elegans</i>]	2.00E-09 Ps
XP_001901903.1 [<i>Brugia malayi</i>]	1.00E-43 Aa:Da:Pm:Ps
XP_001898512 [<i>Brugia malayi</i>]	2.00E-55 Aa:Pm:Ps
XP_001901834 [<i>Brugia malayi</i>]	4.00E-72 Aa:Ps
XP_001626746 [<i>Nematostella vectensis</i>]	9.00E-51 Aa:Da:Pm:Ps
AAL06641.1 [<i>Ancylostoma caninum</i>]	1.00E-24 Ps
NP_502587 [<i>Caenorhabditis elegans</i>]	6.00E-48 Aa:Da:Pm:Ps
XP_001898212 [<i>Brugia malayi</i>]	7.00E-44 Da:Ps
XP_001894280 [<i>Brugia malayi</i>]	9.00E-42 Ps
XP_001893839 [<i>Brugia malayi</i>]	2.00E-52 Aa:Da:Pm:Ps
XP_974490.2 [<i>Tribolium castaneum</i>]	3.00E-44 Aa:Da:Pm:Ps
XP_001893635 [<i>Brugia malayi</i>]	2.00E-09 Aa:Da:Pm:Ps
XP_001895074.1 [<i>Brugia malayi</i>]	8.00E-46 Aa:Da:Pm:Ps
XP_001900648.1 [<i>Brugia malayi</i>]	1.00E-12 Ps
ACM08574.1 [<i>Salmo salar</i>]	1.00E-18 Ps
XP_001894030 [<i>Brugia malayi</i>]	2.00E-111 Da:Ps
XP_001900145 [<i>Brugia malayi</i>]	4.00E-40 Da:Ps
XP_001897369 [<i>Brugia malayi</i>]	1.00E-41 Da:Ps
XP_001898636 [<i>Brugia malayi</i>]	6.00E-63 Da:Ps
NP_495788 [<i>Caenorhabditis elegans</i>]	9.00E-81 Da:Ps
XP_001901784 [<i>Brugia malayi</i>]	4.00E-59 Aa:Pm:Ps
NP_492694 [<i>Caenorhabditis elegans</i>]	1.00E-30 Aa:Da:Pm:Ps
XP_001901236 [<i>Brugia malayi</i>]	2.00E-50 Ps
NP_496952.1 [<i>Caenorhabditis elegans</i>]	8.00E-17 Da:Ps
XP_001894031 [<i>Brugia malayi</i>]	3.00E-40 Da:Ps
NP_501309 [<i>Caenorhabditis elegans</i>]	6.00E-37 Aa:Da:Pm:Ps
XP_002639291 [<i>Caenorhabditis brigantiae</i>]	1.00E-08 Ps
XP_003112081 [<i>Caenorhabditis remanei</i>]	7.00E-22 Ps
hypothetical protein CRE_29498 [Caenorhabditis elegans]	8.00E-66 Ps
XP_001898212 [<i>Brugia malayi</i>]	7.00E-44 Da:Ps
XP_002639142 [<i>Caenorhabditis brigantiae</i>]	8.00E-32 Aa:Da:Pm:Ps
XP_001897858 [<i>Brugia malayi</i>]	6.00E-17 Ps
NP_510711 [<i>Caenorhabditis elegans</i>]	2.00E-67 Aa:Ps
NP_508671 [<i>Caenorhabditis elegans</i>]	3.00E-41 Aa:Pm:Ps
XP_001899947 [<i>Brugia malayi</i>]	2.00E-53 Ps
XP_001899999 [<i>Brugia malayi</i>]	3.00E-57 Aa:Ps
XP_001899999 [<i>Brugia malayi</i>]	1.00E-20 Ps
XP_001893320 [<i>Brugia malayi</i>]	7.00E-21 Ps
XP_001893362 [<i>Brugia malayi</i>]	9.00E-11 Aa:Da:Ps
NP_498633 [<i>Caenorhabditis elegans</i>]	1.00E-18 Aa:Da:Ps
NP_494280 [<i>Caenorhabditis elegans</i>]	3.00E-22 Aa:Da:Ps
NP_492290 [<i>Caenorhabditis elegans</i>]	1.00E-64 Da:Pm:Ps
AAT28332 [<i>Haemonchus contortus</i>]	3.00E-99 Aa:Pm:Ps
ACX55058 [<i>Haemonchus contortus</i>]	3.00E-69 Aa:Pm:Ps
AAT28332 [<i>Haemonchus contortus</i>]	4.00E-80 Aa:Pm:Ps
ACZ67203 [<i>Meloidogyne incognita</i>]	1.00E-41 Aa:Da:Ps
AAF21097 [<i>Dirofilaria immitis</i>]	1.00E-50 Aa:Da:Ps
XP_002630606 [<i>Caenorhabditis brigantiae</i>]	3.00E-36 Aa:Da:Pm:Ps

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XP_003097116 [Caenorhabditis rer	8.00E-26 Aa:Da:Pm:Ps
ABN64198 [<i>Meloidogyne incognita</i>]	9.00E-18 Aa:Da:Pm:Ps
CAA53218 [<i>Ascaris suum</i>]	7.00E-45 Aa:Da:Pm:Ps
AAH87819 [<i>Xenopus tropicalis</i>]	1.00E-09 Ps
XP_416525 [<i>Gallus gallus</i>]	4.00E-39 Ps
XP_002647889 [<i>Caenorhabditis brig</i>	6.00E-12 Aa:Ps
XP_001896673 [<i>Brugia malayi</i>]	2.00E-25 Aa:Pm:Ps
XP_002638831 [<i>Caenorhabditis brig</i>	9.00E-23 Aa:Pm:Ps
XP_002629673 [<i>Caenorhabditis brig</i>	9.00E-15 Da:Ps
XP_002722699 [<i>Oryctolagus cunicu</i>	3.00E-72 Aa:Ps
AF522285 [<i>Steinernema feltiae</i>]	1.00E-127 Ps
EDP34082 [<i>Brugia malayi</i>]	5.00E-64 Aa:Da:Ps
XP_002636304 [<i>Caenorhabditis brig</i>	2.00E-51 Aa:Da:Ps
CAP38507 [<i>Caenorhabditis briggsae</i>	4.00E-80 Aa:Ps
ZP_02181127 [Flavobacteriales bact	6.00E-13 Ps
NP_001024042 [<i>Caenorhabditis ele</i>	1.00E-07 Da:Ps
CAA80491 CAA80491.1 [<i>Glycine me</i>	2.00E-10 Ps
CAA80491 [<i>Glycine max</i>]	4.00E-12 Ps
XP_002638006 [<i>Caenorhabditis brig</i>	7.00E-12 Aa:Da:Ps
XP_002637990 [<i>Caenorhabditis brig</i>	4.00E-15 Ps
XP_965543 [<i>Neurospora crassa</i>]	6.00E-08 ~Z
ZP_04776234 [<i>Gemella haemolysan</i>	1.00E-13 Aa:Da:Ps
ZP_01786547 [<i>Haemophilus influen</i>	1.00E-09 Aa:Da:Ps
XP_002637990 [<i>Caenorhabditis brig</i>	5.00E-06 Ps
NP_199244.1 [<i>Arabidopsis thaliana</i>]	1.00E-05 Aa:Da:Ps
XP_002637990 [<i>Caenorhabditis brig</i>	5.00E-06 Ps
NP_001024044 [<i>Caenorhabditis ele</i>	9.00E-11 Ps
ACZ13352 [<i>Bursaphelenchus xyloph</i>	1.00E-115 Aa:Da:Pm:Ps
NP_50662 [<i>Caenorhabditis elegans</i>	2.00E-21 Aa:Da:Pm:Ps
XP_002637777 [<i>Caenorhabditis brig</i>	1.00E-25 Aa:Da:Pm:Ps
AAAD13154 [<i>Setaria digitata</i>]	1.00E-127 Aa:Pm:Ps
AF278536 [<i>Parastromyloides trichos</i>	3.00E-81 Aa:Pm:Ps
ABG74349 [<i>Bursaphelenchus xylopt</i>	3.00E-23 Aa:Da:Pm:Ps
YP_498583 [<i>Novosphingobium aron</i>	3.00E-09 Ps
XP_001741942 [<i>Entamoeba dispar</i>]	1.00E-05 Aa:Pm:Ps
XP_002635521 [<i>Caenorhabditis brig</i>	4.00E-37 Aa:Da:Pm:Ps
AF121264 [<i>Onchocerca volvulus</i>]	6.00E-15 Da:Pm:Ps
XP_001894590 [<i>Brugia malayi</i>]	2.00E-19 Aa:Pm:Ps
NP_504452 [<i>Caenorhabditis elegans</i>	1.00E-12 Aa:Pm:Ps
XP_001893892 [<i>Brugia malayi</i>]	2.00E-28 Aa:Da:Ps
XP_002635348 [<i>Caenorhabditis brig</i>	2.00E-08 Aa:Pm:Ps
XP_001900052 [<i>Brugia malayi</i>]	1.00E-36 Aa:Pm:Ps
NP_491662 [<i>Caenorhabditis elegans</i>	6.00E-28 Ps
XP_001894786 [<i>Brugia malayi</i>]	3.00E-14 Aa:Pm:Ps
XP_001900052 [<i>Brugia malayi</i>]	1.00E-36 Aa:Pm:Ps
XP_001898046 [<i>Brugia malayi</i>]	6.00E-33 Da:Ps
ACZ13350 [<i>Bursaphelenchus xyloph</i>	2.00E-15 Aa:Da:Pm:Ps
XP_002635059 [<i>Caenorhabditis brig</i>	2.00E-18 Aa:Da:Pm:Ps
XP_002641973 [<i>Caenorhabditis brig</i>	1.00E-05 Aa:Da:Ps
XP_002641973 [<i>Caenorhabditis brig</i>	5.00E-06 Aa:Da:Pm:Ps

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XP_001898527 [<i>Brugia malayi</i>]	6.00E-48 Aa:Ps
NP_491893 [<i>Caenorhabditis elegans</i>]	3.00E-18 Ps
XP_001902724 [<i>Brugia malayi</i>]	2.00E-38 Aa:Ps
XP_502366 [<i>Yarrowia lipolytica</i>]	1.00E-11 Da:Ps
AAA68353.2 [<i>Caenorhabditis elegans</i> <i>briggsae</i>]	6.00E-31 Aa:Da:Ps
remanei]	1.00E-26 Ps
AAS84455] [<i>Ancylostoma caninum</i>]	3.00E-20 Aa:Pm:Ps
XP_001896264 [<i>Brugia malayi</i>]	3.00E-90 Aa:Pm:Ps
	1.00E-07 Aa:Da:Ps
	1.00E-54 Aa:Da:Ps
<i>contortus</i>]	6.00E-77 Aa:Da:Ps
XP_001950714 [<i>Acyrtosiphon pisum</i>]	3.00E-13 Aa:Da:Ps
ABI18377 [<i>Steinernema carpocapsa</i>]	1.00E-54 Aa:Da:Ps
XP_003141396 [<i>Loa loa</i>]	1.00E-17 Ps
ACO10402 [<i>Caligus rogercresseyi</i>]	1.00E-13 Ps
NP_494764 [<i>Caenorhabditis elegans</i>]	2.00E-11 Ps
ACO51647 [<i>Rana catesbeiana</i>]	4.00E-12 Ps
XP_002634608 [<i>Brugia malayi</i>]	1.00E-50 Da:Pm:Ps
XP_001893392 [<i>Brugia malayi</i>]	1.00E-142 Da:Pm:Ps
NP_506367 [<i>Caenorhabditis elegans</i>]	1.00E-19 Aa:Ps
NP_741157 [<i>Caenorhabditis elegans</i>]	3.00E-36 Aa:Da:Pm:Ps
NP_741157 [<i>Caenorhabditis elegans</i>]	2.00E-87 Aa:Da:Pm:Ps
EEY21912.1 [<i>Verticillium albo-atrum</i>]	2.00E-07 Ps
XP_002640882 [<i>Caenorhabditis brig</i>]	2.00E-18 Aa:Da:Pm:Ps
XP_001901573 [<i>Brugia malayi</i>]	4.00E-88 Ps
AAA28154 [<i>Caenorhabditis elegans</i>]	1.00E-140 Aa:Da:Pm:Ps
CAX79672 [<i>Schistosoma japonicum</i>]	4.00E-42 Aa:Da:Pm:Ps
XP_001900515 [<i>Brugia malayi</i>]	1.00E-13 Da:Ps
XP_002642216 [<i>Caenorhabditis brig</i>]	1.00E-42 Aa:Ps
XP_001901573 [<i>Brugia malayi</i>]	4.00E-58 Da:Ps
ABI98680 [<i>Litopenaeus vannamei</i>]	1.00E-43 Aa:Da:Pm:Ps
NP_490882 [<i>Caenorhabditis elegans</i>]	3.00E-24 Aa:Da:Pm:Ps
XP_001893040 [<i>Brugia malayi</i>]	5.00E-30 Ps
XP_001901439 [<i>Brugia malayi</i>]	2.00E-07 Ps
XP_002640529 [<i>Caenorhabditis brig</i>]	2.00E-35 Aa:Da:Pm:Ps
XP_001629958 [<i>Nematostella vectis</i>]	2.00E-51 Aa:Da:Pm:Ps
XP_001902550 [<i>Brugia malayi</i>]	3.00E-42 Ps
XP_001896220 [<i>Brugia malayi</i>]	7.00E-25 Ps
NP_491091 [<i>Caenorhabditis elegans</i>]	2.00E-22 Aa:Da:Pm:Ps
XP_003137030 [<i>Loa loa</i>]	2.00E-37 Aa:Da:Ps
XP_001896629 [<i>Brugia malayi</i>]	1.00E-15 Ps
XP_001898078 [<i>Brugia malayi</i>]	1.00E-43 Aa:Ps
XP_969056 [<i>Tribolium castaneum</i>]	4.00E-55 Ps
XP_001902965 [<i>Brugia malayi</i>]	1.00E-08 Ps
XP_001895018 [<i>Brugia malayi</i>]	7.00E-81 Aa:Da:Pm:Ps
XP_002639985 [<i>Caenorhabditis brig</i>]	5.00E-82 Aa:Da:Pm:Ps
XP_001894874 [<i>Brugia malayi</i>]	4.00E-09 Ps

Additional File 3. Putative anhydrobiotic and stress response genes constitutively expressed by an unstressed mixed stage population of *Panagrolaimus superbus*.

XP_001901359 [<i>Brugia malayi</i>]	4.00E-21 Aa:Da:Pm:Ps
XP_001901133 [<i>Brugia malayi</i>]	1.00E-69 Aa:Ps
NP_500125 [<i>Caenorhabditis elegans</i>]	3.00E-41 Da:Ps
XP_002646072 [<i>Caenorhabditis brig</i>]	1.00E-77 Ps
XP_001901133 [<i>Brugia malayi</i>]	1.00E-69 Aa:Ps
XP_002636822 [<i>Caenorhabditis brig</i>]	5.00E-66 Da:Ps
XP_002632145 [<i>Caenorhabditis brig</i>]	2.00E-67 Da:Ps
XP_002636822 [<i>Caenorhabditis brig</i>]	1.00E-101 Da:Ps
XP_002636822 [<i>Caenorhabditis brig</i>]	1.00E-101 Da:Ps
XP_001893780 [<i>Brugia malayi</i>]	1.00E-122 Da:Ps
NP_506005 [<i>Caenorhabditis elegans</i>]	5.00E-62 Da:Ps
XP_001895811 [<i>Brugia malayi</i>]	1.00E-114 Da:Ps
XP_001900412 [<i>Brugia malayi</i>]	1.00E-37 Aa:Da:Pm:Ps
XP_001896092 [<i>Brugia malayi</i>]	1.00E-50 Ps
XP_001899710 [<i>Brugia malayi</i>]	9.00E-85 Ps
XP_001895575 [<i>Brugia malayi</i>]	1.00E-117 Aa:Da:Ps
EDP30417 [<i>Brugia malayi</i>]	4.00E-50 Aa:Ps
XP_001897611 [<i>Brugia malayi</i>]	5.00E-82 Aa:Ps
XP_001895373 [<i>Brugia malayi</i>]	6.00E-28 Ps
XP_001894001 [<i>Brugia malayi</i>]	3.00E-43 Da:Ps
	2.00E-07 Da:Ps
EFN63197 [<i>Ascaris suum</i>]	1.00E-12 Ps
NP_495277 [<i>C. elegans</i>]	1.00E-08 Ps
EFN73309 [<i>Camponotus floridanus</i>]	5.00E-07 Ps
XP_001901347 [<i>Brugia malayi</i>]	5.00E-06 Ps
XP_001901347 [<i>Brugia malayi</i>]	1.00E-66 Ps
XP_001895844	3.00E-11 Ps
NP_594972 [<i>Schizosaccharomyces</i>]	9.00E-05 Ps
XP_001898641 [<i>Brugia malayi</i>]	9.00E-13 Ps
AAB57697 [<i>Caenorhabditis elegans</i>]	4.00E-25 Aa:Ps
EDP30027 [<i>Brugia malayi</i>]	6.00E-86 Ps
XP_001899059 [<i>Brugia malayi</i>]	2.00E-12 Ps
NP_491163 [<i>Caenorhabditis elegans</i>]	1.00E-47 Ps
NP_001154964 [<i>Nasonia vitripennis</i>]	8.00E-06 Ps
NP_001022911 [<i>Caenorhabditis elec</i>]	2.00E-22 Ps
XP_002629697 [<i>Caenorhabditis brig</i>]	3.00E-58 Aa:Ps
XP_002629697 [<i>Caenorhabditis brig</i>]	3.00E-10 Aa:Ps
NP_491560 [<i>Caenorhabditis elegans</i>]	8.00E-18 Ps
NP_502361 [<i>Caenorhabditis elegans</i>]	3.00E-43 Aa:Ps
XP_002646596 [<i>Caenorhabditis brig</i>]	6.00E-31 Ps
NP_508934 [<i>Caenorhabditis elegans</i>]	1.00E-18 Aa:Da:Pm:Ps
NP_492796 [<i>Caenorhabditis elegans</i>]	3.00E-19 Ps
XP_001895229 [<i>Brugia malayi</i>]	6.00E-63 Ps

Additional File 3. Putative anhydrobiotic and stress response genes constitutively expressed by an unstressed mixed stage population of *Panagrolaimus superbus*.

ae; Da = *Ditylenchus africanus*; Pm = *Plectus murrayi*.