Supplementary Information

The draft genome of the parasitic nematode *Trichinella spiralis*

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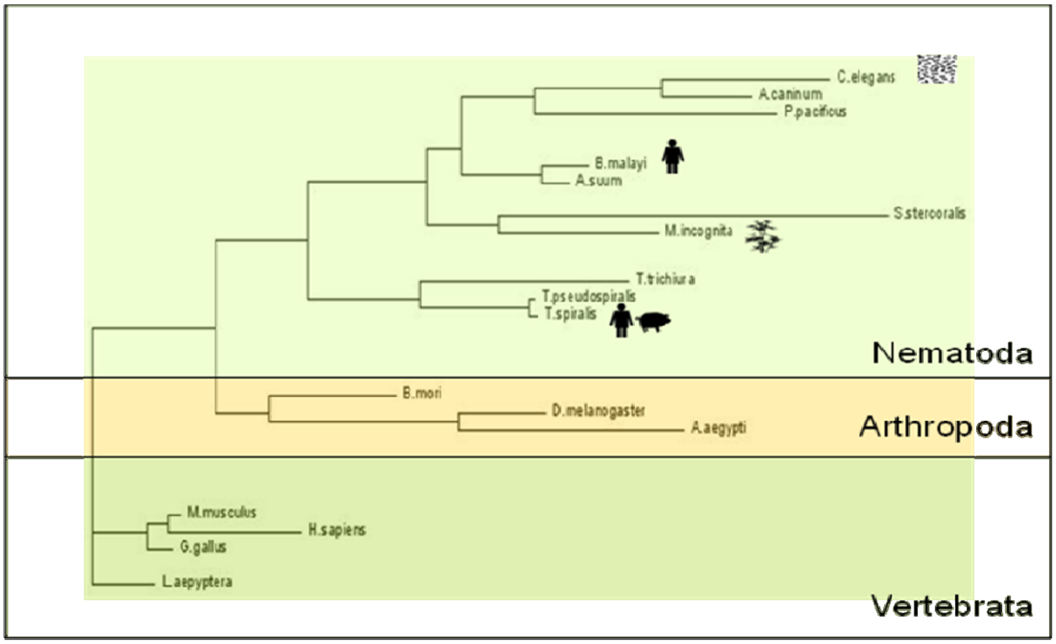
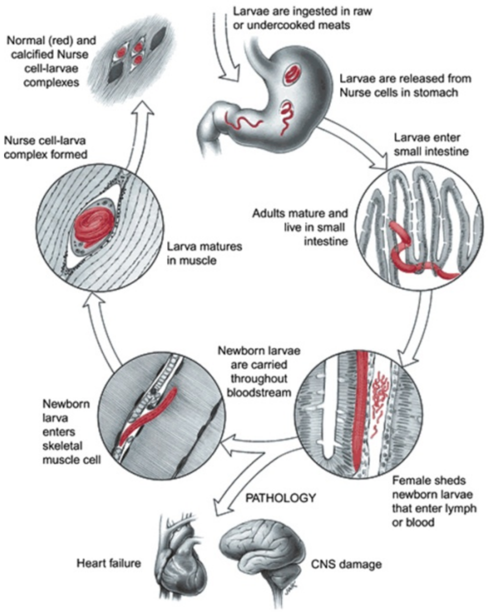
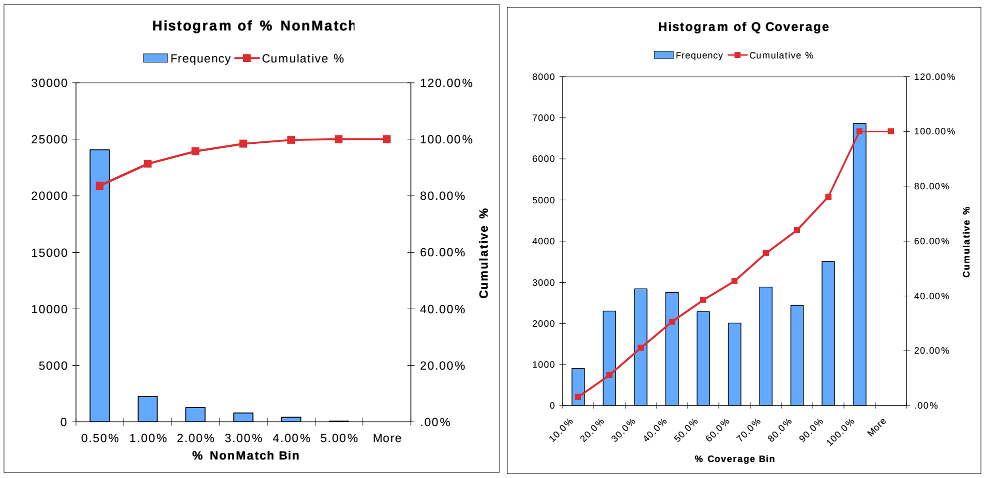
I – Supplementary Figures 1-14



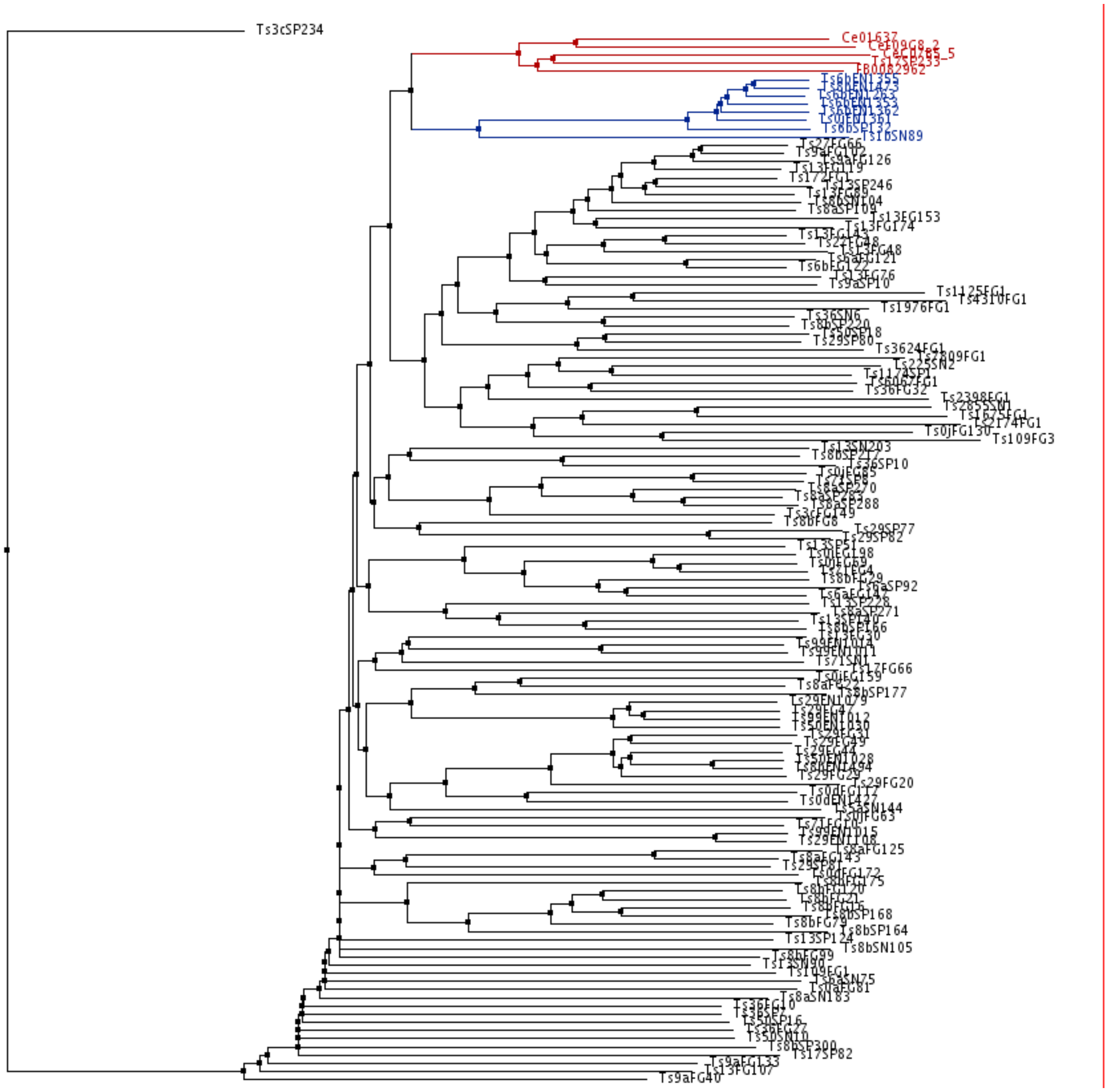
Supplementary Fig.1. The phylogenetic tree based on 18s rRNA sequences of 17 metazoan species. The rRNA sequences were collected from the SILVA database (http://www.arb-silva.de/). Collected sequences were re-aligned using CLUSTALX with manual editing. The phylogeny was reconstructed using DNAML of PHYLIP (ref). The accession numbers are: DQ442665, AF036587, AJ920347, M97573, U60231, AY988440, DQ118536, AX664486, AAQA01004529, X03680, AADN02004142, CABB01000393, AADK01009766, AADB02002333, AC170254, M84229, AY851258. The species with associated trophic ecology were used as representatives that span the phylum and analyzed in this study.



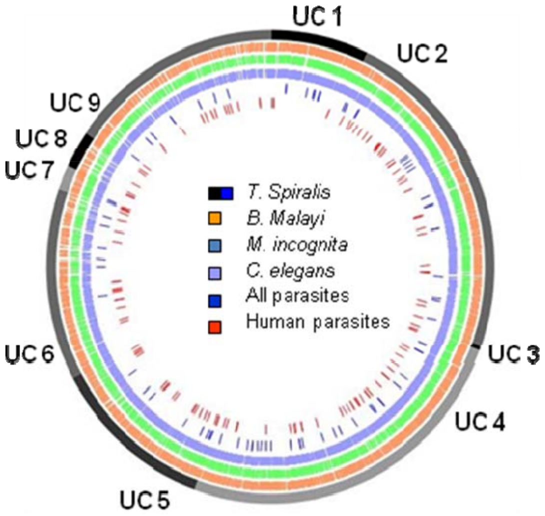
Supplementary Fig.2. Life cycle of *Trichinella spiralis* [1].



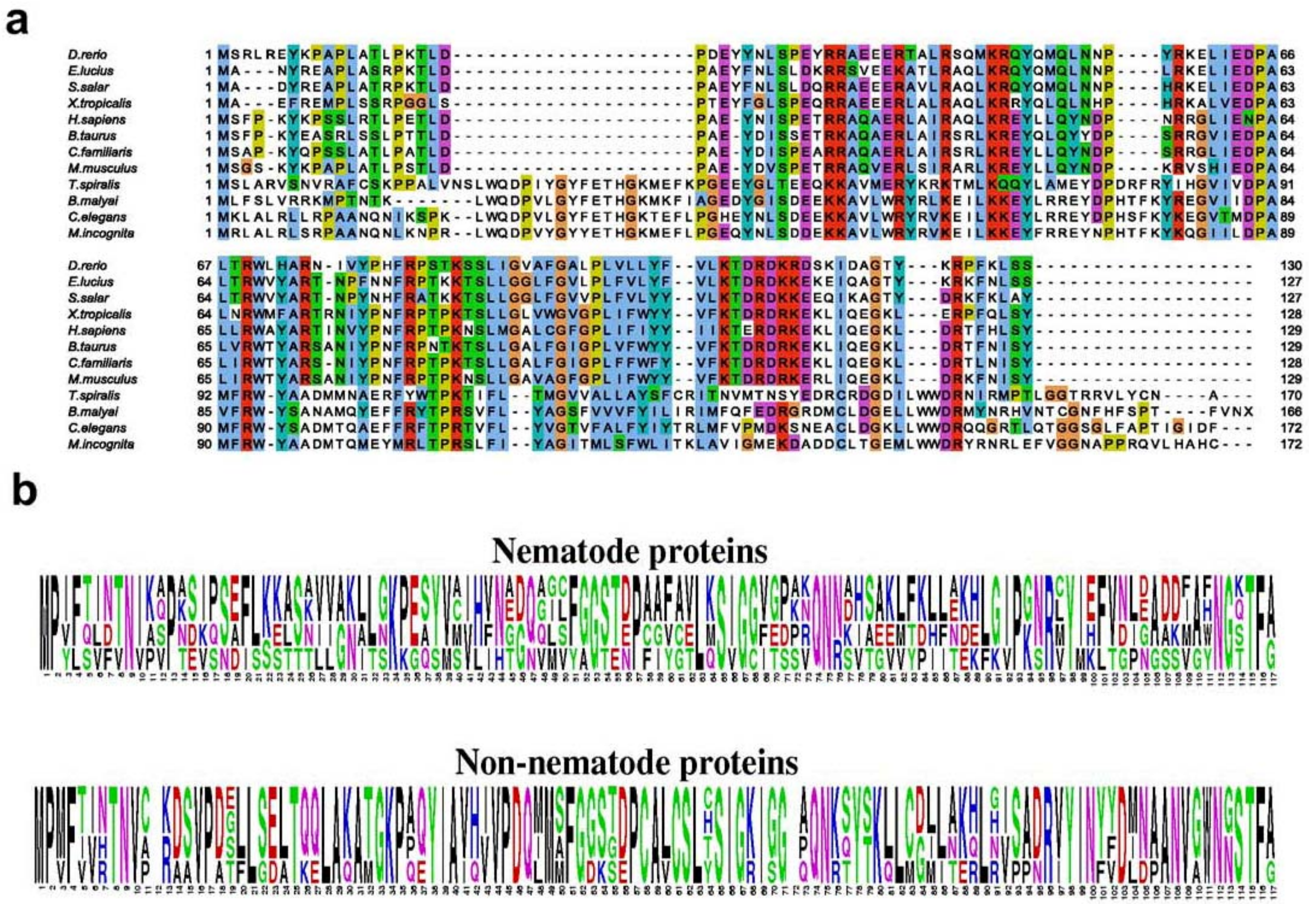
Supplementary Fig. 3. Histograms showing the % nonMatch and % Q Coverage. **“**% NonMatch” indicates that the mappings are indeed high quality, in that 84% of all the EST-cDNA mappings have non-match ratios (defined as non-match bases/total bases of the mapped regions) of less than 0.5%. As expected, the % Query Coverage is more dispersed, as shown in “Histogram of % Q Coverage”.



Supplementary Fig.4. Similarity clustering (neighbor joining unrooted tree) of *T. spiralis* and *C. elegans* DNAse II-like genes.



Supplementary Fig. 5. Distribution of Orthologs on the 9 *T. spiralis* ultracontigs (grey). B. *malayi, M. incognita* and *C. elegans* orthologous genes are in orange, green and violet respectively. Orthologous genes conserved among the three parasites (*M. incognita, B. malayi* and *T. spiralis*) are marked in blue; the orthologous proteins among the two human parasites (*B. malayi* and *T. spiralis*) are marked in red.



Supplementary Fig. 6. Pan-Phylum molecular characteristics. **(a)** Multiple alignment of a family (OrthoMCL5157) associated with K03960 (NADH dehydrogenase 1 beta subcomplex 4) shows nematode-specific insertions. **(b)** Conservation profiling of genes encoding MIF-1 in nematodes (OrthoMCL5321). Nematode-specific conserved residues were observed (e.g. positions 53, 93), despite the higher sequence distance among the nematode (1.202) relative to the vertebrate (0.395) species (human, chicken, frog and zebrafish) spanning approximately the same lengths of time. The overall distance among nematode and vertebrate proteins was 1.1852. Accession numbers and other relevant information are available as Supplementary Note online.

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D.rerio       1 MPMFVVNTNVA-KDSVPAELLSEATQELAKAMGKPQQYIAVQVVPDQMMMFGGKGDPCALCSLTSIG66
H.sapiens     1 MPMFIVNTNVP-RASVPDGFLSELTQQLAQATGKPPQYIAVHVVPDQLMAFGGSSEPCALCSLHSIG66
X.Laevis      1 MPVFTIRTNVC-RDSVPDTLLSDLTKQLAKATGKPAEYIAIHIVPDQIMSFGDSTDPCAVCSLCSIG66
G.gallus      1 MPMFTIHTNVC-KDAVPDSLLGELTQQLAKATGKPAQYIAVHIVPDQMMSFGGSTDPCALCSLYSIG66
M.incognita   1 MPILQVFTNIA-SKSIPSEF-SKATKIIANLTGKKEASVMVLVNAGNVGCFGGSTDPFIYAELQSVG65
C.elegans     1 MPVFSINVNVKVPAEKQNEILKELSTVLGKLLNKPEQYMCIHFHEDQGILYAGTTEPAGFAVLKSIG67
B.malayi      1 MPYFTIDTNIP-QNSISSAFLKKASNVVAKALGKPESYVSIHVNGGQAMVFGGSEDPCAVCVLKSIG66
T.spiralis    1 MPIFTLNTNIK-ATDVPSDFLSSTSALVGNILSKPGSYVAVHINTDQQLSFGGSTNPAAFGTLMSIG66

D.rerio      67 KISG-AQNKQYSKLLMGLLNKHLGVSADRIYINFVDMDPANVAWNNSTFG                  115
H.sapiens    67 RIGG-AQNRSYSKQLCGLLAERLRISPDRVYINYYDMNAANVGWNNSTFA                  115
X.Laevis     67 KIGG-PQNKSYTKLLCDILTKQLNIPANRVYINYYDLNAANVGWNGSTFA                  115
G.gallus     67 KIGG-QQNKTYTKLLCDMIAKHLHVSADRVYINYFDINAANVGWNGSTFA                  115
M.incognita  66 GF---TDPNKVTGEMTKLFTEHFGVPGSRVYMKLTGPDADKFAHNGKTFA                  112
C.elegans    68 GVGSAKQNNAISAVVFPIIEKHLGIPGNRLYIEFVNLGAADIAYNGQTFA                  117
B.malayi     67 CVGP-KVNNSHAEKLYKLLADELKIPKNRCYIEFVDIEASSMAFNGSTFG                  115
T.spiralis   67 GIEP-SRNRDHSAKLFDHLNKKLGIPKNRMYIHFVNLNGDDVGWNGTTF-                  114
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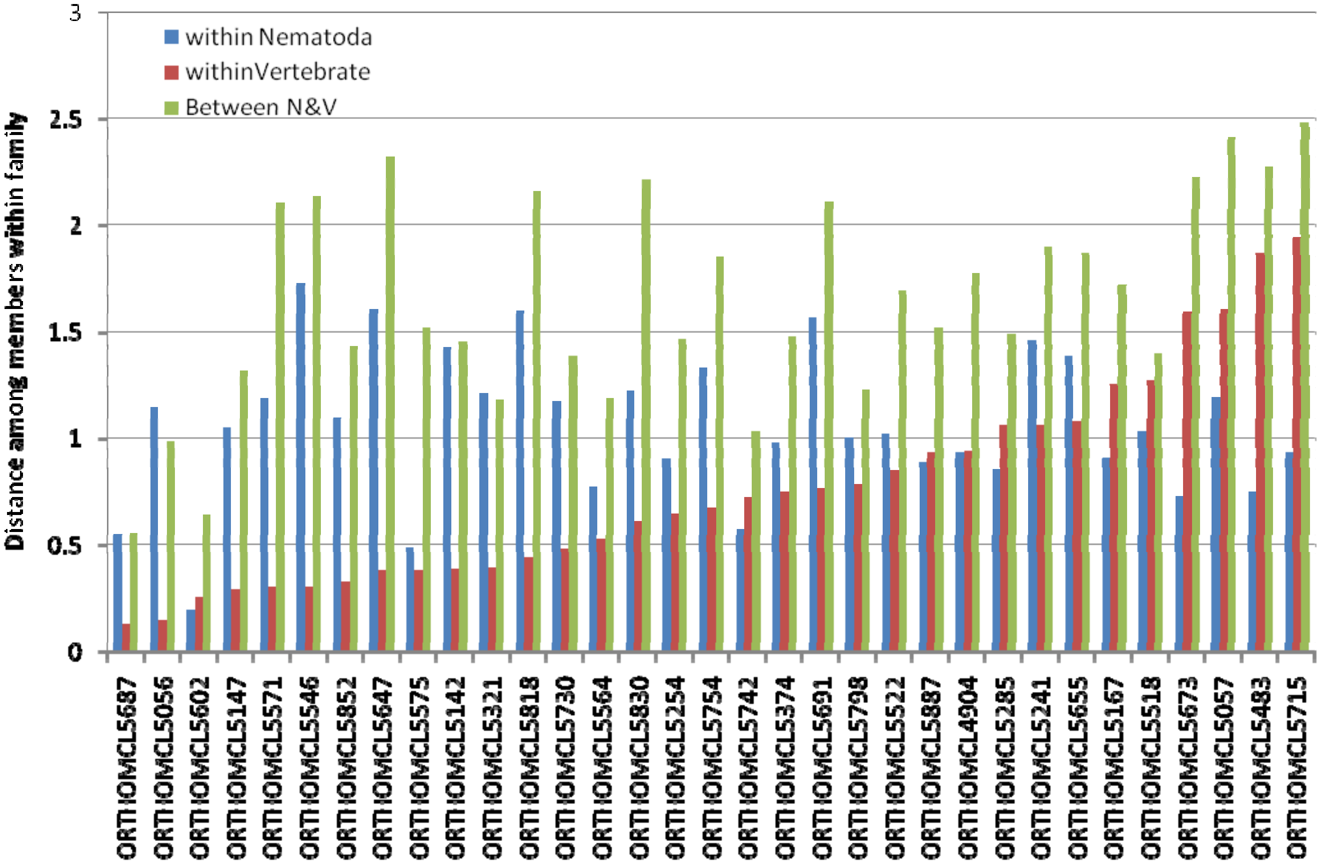
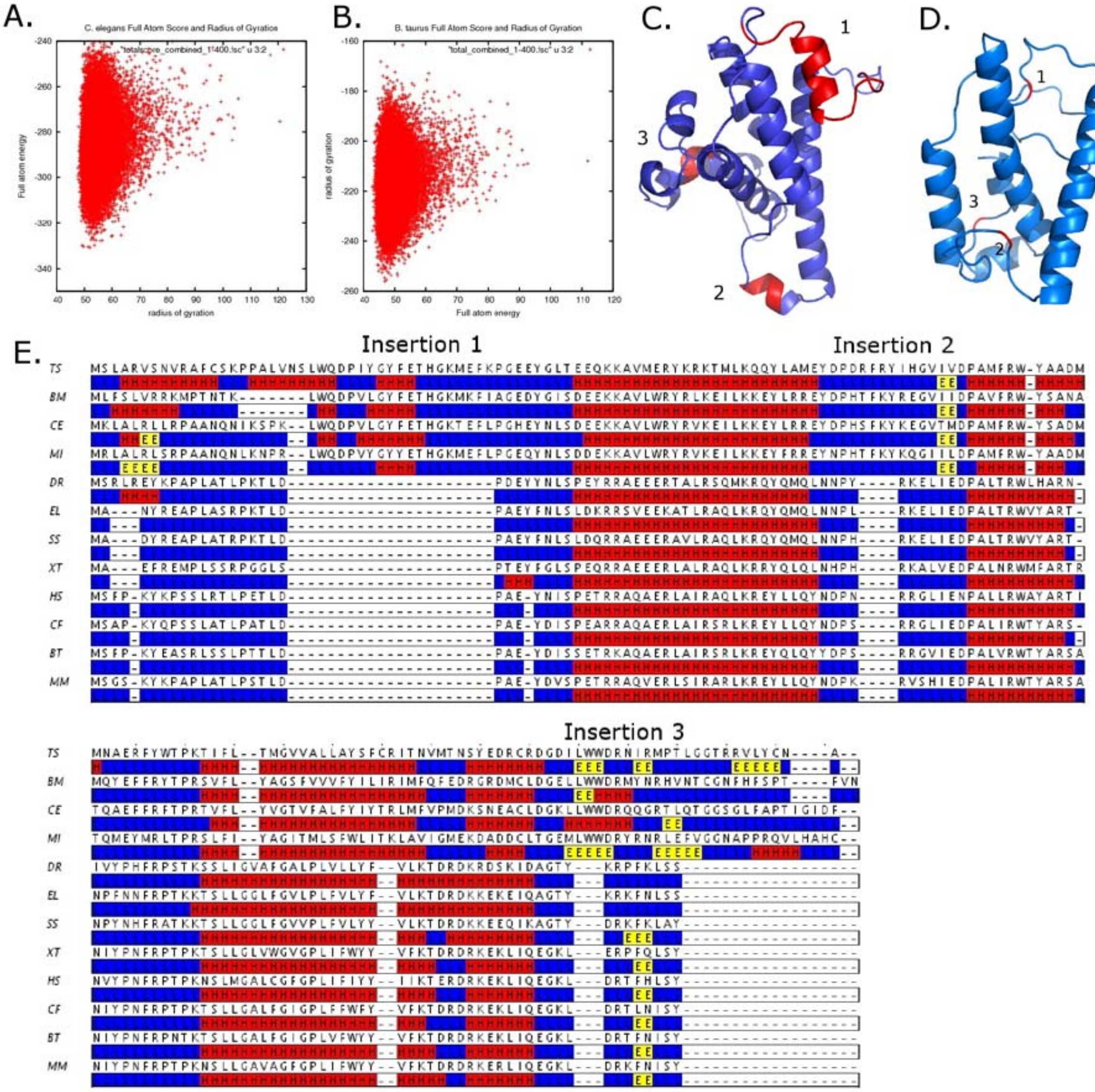
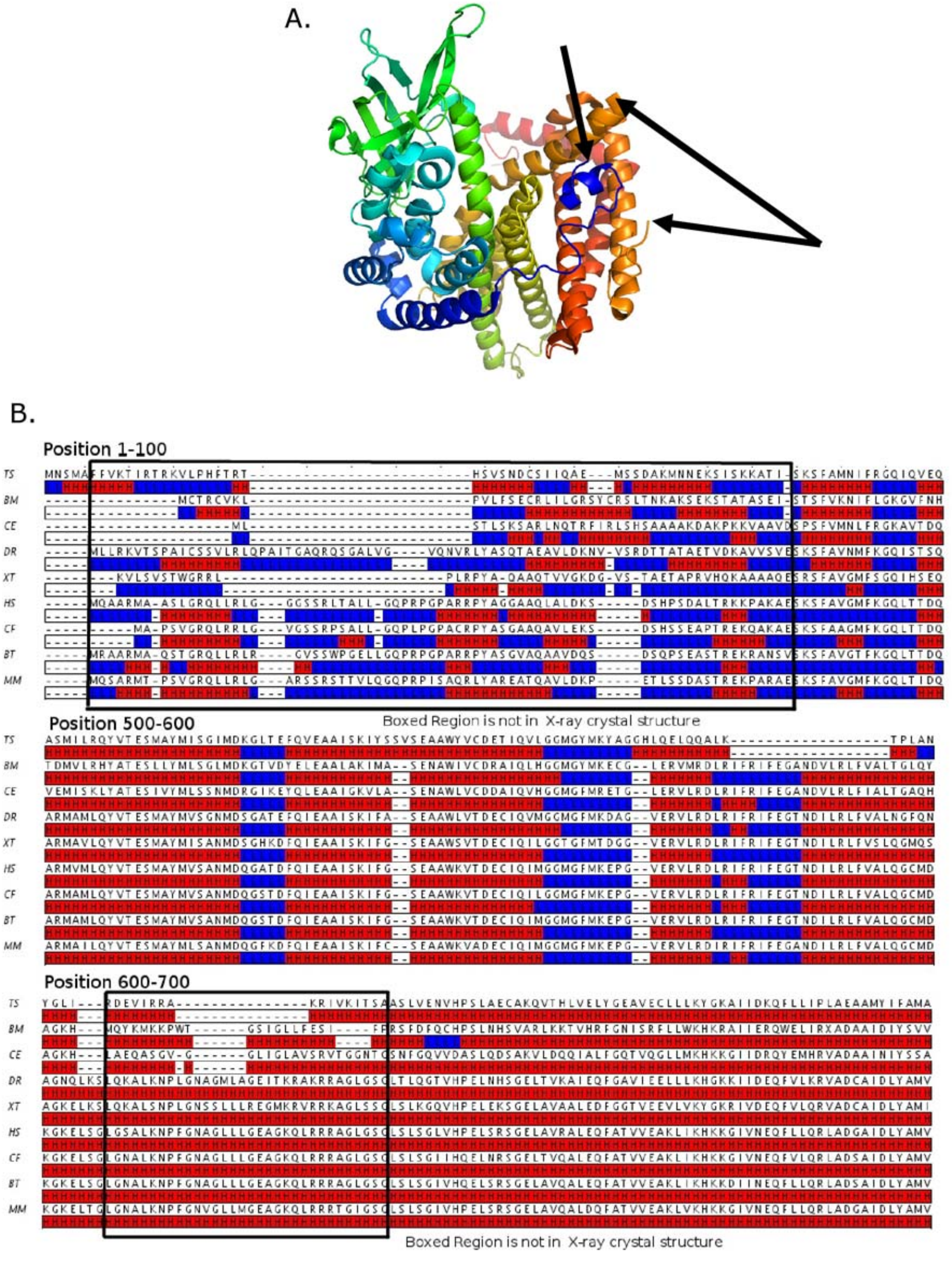
Supplementary Fig. 7. Multiple alignment of a family (ORTHOMCL5321) associated with MIF-1 in nematodes. The sequence distance among nematode members is 1.202 and among vertebrate representatives is 0.395. The overall distance among the nematodes and the vertebrate species is 1.185. Accession numbers or gene IDs of the aligned sequences are: Q02BR7,1, Q6FHV0.1, Q76BK2.1, Q02960.3, Minc15801, Y5613A.3, 14930.m00337, TS_06335.



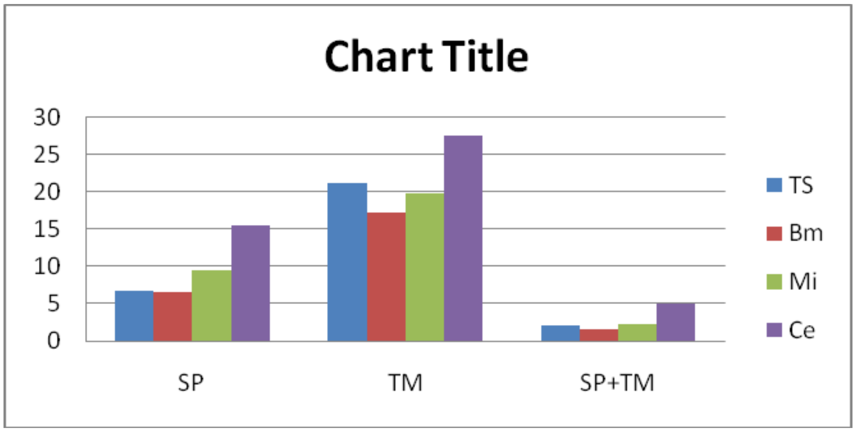
Supplementary Fig. 8. The 33 single copy genes and their inter- and intra-phylum conservation based on distance matrix. The mean distances of each nematode group were compared to that of its corresponding non-nematode group and that of between the members of the two groups (specific example is presented in **Supplementary Fig. 6**).



Supplementary Fig. 9. Structural annotation and comparison of proteins from ORTHOMCL5157. The Rosetta3.0 software suite generated 40,000 decoys, and the full-atom scores were plotted against the radius of gyration for **(A)** *C. elegans* and **(B)** *B. taurus*. The structural prediction for **(C)** *C. elegans* and **(D)** *B. taurus*. The insertions in the *C. elegans* protein are numbered starting at the N terminus and are colored in red. The residues flanking the deletions in the *B. taurus* protein are shown in red and also labeled from the N to C terminus. **(E)** Example of one secondary structure prediction with respect to the sequence alignment for the nematode and non-nematode species. The sequence is shown without coloring and the secondary structure prediction is shown below. Helical regions are colored red and noted by the letter H, beta-sheet regions are colored yellow and noted by the letter E, and loop regions are colored blue and noted by the letter L. The species names are abbreviated as follows: *T. spiralis* (TS), *B. malayi* (BM), *C. elegans* (CE), *M. incognita* (MI), *D. rerio* (DR), *E. lucius* (EL), *S. salar* (SS), *X. tropicalis* (XT), *H. sapiens* (HS), *C. familiaris* (CF), *B. taurus* (BT), *M. musculus* (MM).

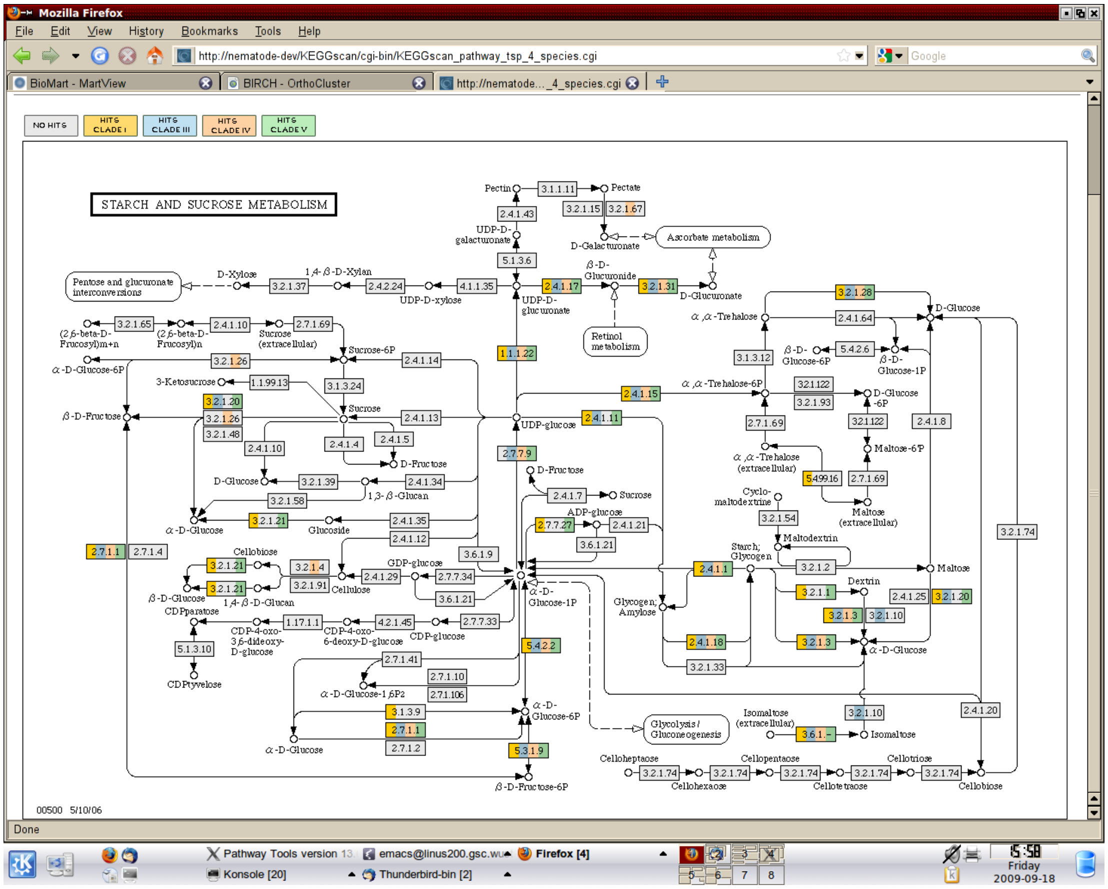


Supplementary Fig. 10. An example of nematode specific indel. Structure and alignments of proteins from **(A)** The X-ray crystal structure of the *H. sapiens* ortholog of P48818 (PDB ID: 3B96). The structure is colored by spectrum such that the N-terminus is shown in blue and the C-terminus is shown in red. **(B)** Sequence alignment of P48818 orthologs. The coloring and species codes are the same as described in **Supplementary Fig. 9.**



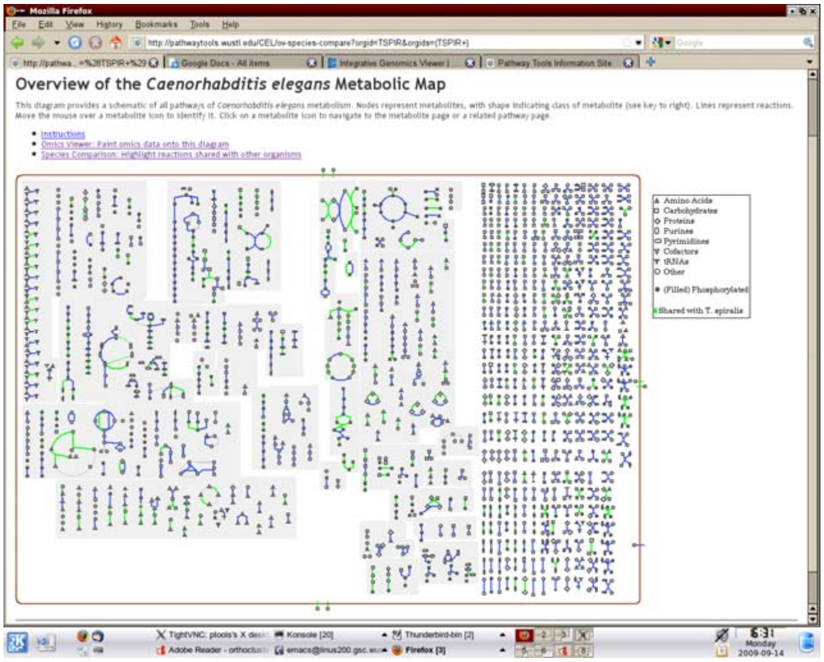
Supplementary Fig. 11. Predicted signal peptides for secretions and transmembrane domains in complete proteomes of four nematode species. TS, *T. spiralis*; BM, *B. malayi*; Mi, *M. incognita*; Ce, *C. elegans.*

Supplementary Fig.12. Enriched and depleted GO categories in orthologous groups with restricted species representation. The heatmap was built based on the GO enrichment and depletion probabilities using R. Specifically, the significance probability values were converted to heatmap temperatures by getting the differences of the two probability values. A significantly enriched term thus had a higher temperature and a significantly depleted term had a lower temperature. The terms that were significantly enriched or depleted in at least one category are displayed.



Supplementary Fig. 13. A screenshot from the NemaPath pathway viewer, here showing all of the associated EC nodes at a specified E-value threshold of 1x10^{-05} or lower in the Starch and Sucrose Metabolism for the four nematode species under study. The NemaPath viewer is available at www.nematode.net.

A.

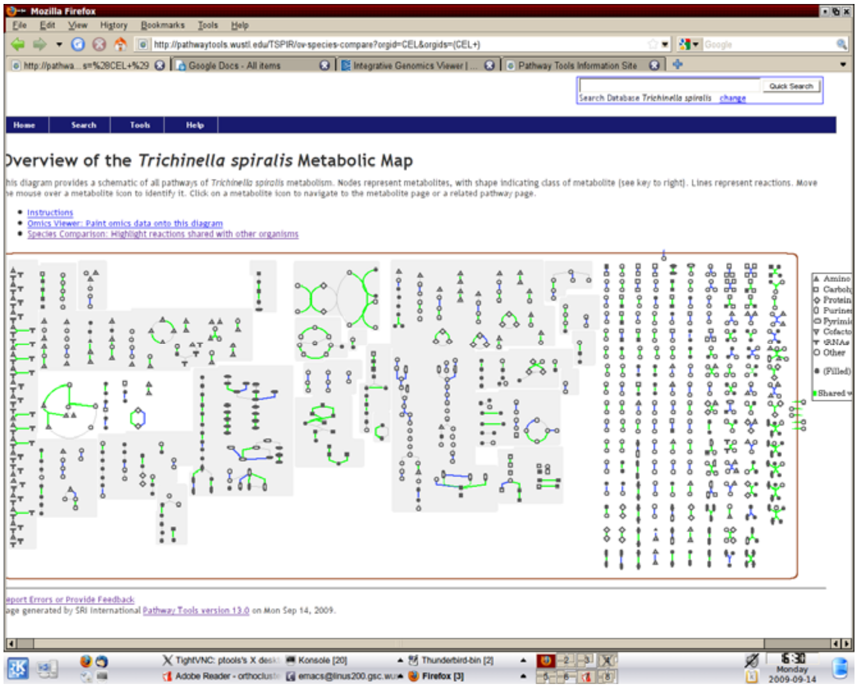


Overview of the *Caenorhabditis elegans* Metabolic Map

This diagram provides a schematic of all pathways of *Caenorhabditis elegans* metabolism. Nodes represent metabolites, with shape indicating class of metabolite (see key to right). Lines represent reactions. Move the mouse over a metabolite icon to identify it. Click on a metabolite icon to navigate to the metabolite page or a related pathway page.

- Instructions
- Omics Viewer: Paint omics data onto this diagram
- Species Comparison: Highlight reactions shared with other organisms

B.



verview of the *Trichinella spiralis* Metabolic Map

his diagram provides a schematic of all pathways of *Trichinella spiralis* metabolism. Nodes represent metabolites, with shape indicating class of metabolite (see key to right). Lines represent reactions. Move he mouse over a metabolite icon to identify it. Click on a metabolite icon to navigate to the metabolite page or a related pathway page.

- Instructions
- Omics Viewer: Paint omics data onto this diagram
- Species Comparison: Highlight reactions shared with other organisms

eport Errors or Provide Feedback
age generated by SRI International Pathway Tools version 13.0 on Mon Sep 14, 2009.

Supplementary Fig. 14. Comparison of metabolic profiling of *C. elegans* and *T. spiralis*. **(A)** .*T. spiralis* painted onto a *C. eleagns* snapshot. **(B).** *C. elegans* painted onto a *T. spiralis* snapshot. Pathway profiling was generated by SRI International Pathway Tools v 13. 0. The *C. elegans* pathway map is based on the complete genome and the *T. spiralisis* based on the 3576 genome contigs that had genes associated with enzyme (EC) numbers. The reactions common among organisms are marked in blue, and the reactions specific to one organism are marked in green. The online metabolic map is interactive resulting in a vast amount of details that can be retrieved by overlaying the nodes. The NemaCyc viewer is available at http://pathwaytools.wustl.edu.

II – Supplementary Supplementary Tables 1-13

Supplementary Table 1. *Trichinella spiralis* genome statistics.

***T. spiralis* Genome Assembly v3.7.1**	**Stats**
Genome size estimated by cytometry (Mb)	71.3 +/- 1.2
Total number of reads in database passing QC	4,359,199
WGS reads in database passing QC	3,982,157
BAC end reads in database passing QC	206,713
Fosmid end reads database passing QC	170,329
Total number of reads in the assembly	3,536,878
WGS reads	3,347,411
BAC end reads	40,379
Fosmid end reads	149,088
Total length in assembly (bp)	59,328,746
Total reads in assembly	3,022,749
Total Q20 bases (bp)	
Q20 coverage (X)	33
Total number of contigs	11,146
Average length of contigs (bp)	5,323
Max. length of contigs (bp)	482,167
Number of N50 contigs	230
N50 contig length (bp)	76,634
Number of contigs > 2,000 bp	2,229
Total length of contigs > 2,000 bp (bp)	50,908,998
Total number of supercontigs	8,795
Average length of supercontigs (bp)	6,746
Max. length of supercontigs (bp)	9,739,270
Number of N50 supercontigs	9
N50 supercontig length (bp)	1,738,704
Number of supercontigs > 2,000 bp	1,016
Total length of supercontigs > 2,000 bp (bp)	52,276,751
Total length of all supercontigs (bp)	64,330,920
Total length of non-N/X in supercontigs (bp)	59,325,552
Total A	19,609,992
Total C	10,072,236
Total G	10,056,574
Total T	19,586,750
% A/T	66%
% G/C	34%
CDS	15,808
Total length	15,700,994
Average CDS length (bp)	993
Median CDS length (bp)	603
StDev	1,105

Max CDS length (bp)	37,260
Min length	94
% G/C	43.20%
Protein coding genes	15,808
Total length (aa)	5,218,886
Average length (aa)	330
Median length (aa)	200
StDev	368
Max length (aa)	12,419
Min length	32
rFAM	394
Total length	52,061
Average length (bp)	132
Median length (bp)	109
StDev	143
Max length (bp)	611
Min length	26
tRNA	143
Total length	10,832
Average length (bp)	76
Median length (bp)	73
StDev	7
Max length (bp)	114
Min length	69

Supplementary Table 2. Amino acid composition (%) of complete proteomes of six species.

	Amino Acid	***C. elegans***	***B. malayi***	***T. spiralis***	***D. melanogaster***	***S. cerevisae***
F	Phe	4.84	4.07	4.6	3.56	4.51
S	Ser	8.05	8.11	8.24	8.36	9.05
T	Thr	5.86	5.6	5.43	5.7	5.89
N	Asn	4.9	4.95	4.9	4.68	6.1
K	Lys	6.39	6.19	5.94	5.59	7.28
E	Glu	6.51	6.64	6.07	6.41	6.46
Y	Tyr	3.21	3.16	3.07	2.98	3.37
V	Val	6.21	6.01	6.5	5.9	5.56
Q	Gln	4.07	4.18	4.28	5.18	3.91
M	Met	2.64	2.55	2.41	2.34	2.08
C	Cys	2.07	2.22	2.76	1.91	1.31
L	Leu	8.66	9.17	9.48	9.15	9.58
A	Ala	6.28	6.24	6.52	7.33	5.47
W	Typ	1.11	1.1	1.22	1	1.04
P	Pro	4.85	4.42	4.39	5.5	4.38
H	His	2.28	2.45	2.57	2.64	2.17
D	Asp	5.29	5.42	5.03	5.16	5.78
I	Ile	6.22	6.33	5.62	4.92	6.56
R	Arg	5.12	5.83	5.9	5.57	4.45
G	Gly	5.31	5.25	4.99	6.04	4.94

Supplementary Table 3. Orthologous groups generated by Markov Clustering of 6 complete proteomes. This table lists the number of orthologous groups generated by Orthomcl and the number of genes from each species for a particular combination of species. For example (see line 1), there were 21 orthologous groups with genes only from *C. elegans* and *S. cerevisiae* containing 38 and 28 genes, respectively.

Orthologous groups	**Number of genes per group**					
	C. elegans	***M. incognita***	***B. malayi***	***T. spiralis***	***D. melanogaster***	***S. cerevisiae***
21	38	0	0	0	0	28
1020	5964	0	0	0	0	0
1186	1592	2175	1451	1846	1688	1476
14	0	0	0	17	16	16
22	0	38	24	0	23	0
10	0	88	0	0	0	11
716	0	0	0	0	2972	0
373	0	0	0	0	0	1104
20	0	120	0	0	36	0
27	0	50	33	30	37	0
1407	0	6242	0	0	0	0
189	222	0	202	278	0	0
54	65	102	0	64	74	68
1	0	2	1	0	0	1
4	0	7	4	0	27	23
23	0	46	24	84	0	0
11	35	16	12	0	0	27
629	947	0	684	0	0	0
16	22	29	17	22	0	22
15	0	50	0	43	0	0
54	0	0	55	65	59	0
201	228	346	215	0	245	234
10	15	22	0	0	0	16
122	0	260	141	0	0	0
50	0	0	60	0	64	0
14	0	18	16	20	14	17
36	45	0	0	0	51	42
7	0	0	7	0	19	8
2	3	3	0	3	0	2
343	776	1152	0	0	0	0
4	0	7	0	4	4	0
270	336	0	286	0	350	0
489	537	0	528	653	542	0
2	0	0	2	2	0	2
131	0	0	0	181	181	0
80	118	172	0	0	107	0
27	32	0	0	31	33	33
88	0	0	0	0	164	105
89	114	0	0	261	0	0
5	0	0	72	0	0	7
30	46	43	0	0	39	37
15	24	0	15	0	0	16
355	478	612	390	0	497	0
52	0	0	73	136	0	0
11	0	0	19	28	14	13

308	357	0	329	374	356	350
60	92	118	0	81	0	0
97	116	0	0	117	113	0
271	0	0	822	0	0	0
274	410	511	507	562	0	0
974	0	0	0	4313	0	0
134	221	0	0	0	219	0
543	831	1466	610	0	0	0
8	14	0	0	9	0	8
12	12	0	16	18	0	14
1	0	1	0	0	3	1
85	91	0	87	0	95	98
1041	1278	1844	1213	1322	1417	0
13	0	0	0	48	0	103
97	141	181	0	108	144	0

Supplementary Table 4. Annotation of the 702 protein families born at the Nematoda relative to the two outgroups'corrected to 'proteome size'.

Orthomcl group	**PFAM annotation (#genes with pfam)**
ORTHOMCL8(142 genes,2 taxa):	PF02170(37) PF08699(31) PF02171(70)
ORTHOMCL40(59 genes,4 taxa):	PF00635(59)
ORTHOMCL42(57 genes,3 taxa):	PF03732(3) PF00078(10) PF00552(1) PF00077(3) PF02022(1) PF00665(23) PF00098(2)
ORTHOMCL66(46 genes,3 taxa):	PF05225(1) PF09091(4) PF00024(1)
ORTHOMCL141(28 genes,3 taxa):	PF07801(16)
ORTHOMCL162(25 genes,2 taxa):	
ORTHOMCL180(24 genes,2 taxa):	PF00782(1) PF00097(1) PF04683(1) PF00665(11)
ORTHOMCL195(22 genes,2 taxa):	
ORTHOMCL205(21 genes,2 taxa):	
ORTHOMCL221(20 genes,4 taxa):	PF00026(20) PF07966(3)
ORTHOMCL241(19 genes,4 taxa):	PF06828(16)
ORTHOMCL247(19 genes,2 taxa):	PF00097(18)
ORTHOMCL251(18 genes,2 taxa):	
ORTHOMCL258(18 genes,4 taxa):	PF04870(18)
ORTHOMCL275(17 genes,4 taxa):	PF01484(16) PF01391(17)
ORTHOMCL353(15 genes,2 taxa):	PF00096(12)
ORTHOMCL360(14 genes,4 taxa):	PF00635(13)
ORTHOMCL410(13 genes,4 taxa):	PF00069(11) PF00326(3)
ORTHOMCL453(13 genes,2 taxa):	PF03564(4)
ORTHOMCL481(12 genes,4 taxa):	PF00400(1)
ORTHOMCL482(12 genes,3 taxa):	
ORTHOMCL506(12 genes,2 taxa):	PF06542(10)
ORTHOMCL548(11 genes,4 taxa):	PF00100(11)
ORTHOMCL560(11 genes,4 taxa):	PF00583(4)
ORTHOMCL592(11 genes,4 taxa):	PF00038(11) PF00932(11)
ORTHOMCL601(11 genes,3 taxa):	PF07690(9) PF04928(1)
ORTHOMCL637(10 genes,4 taxa):	PF00397(6)
ORTHOMCL639(10 genes,4 taxa):	PF01549(6) PF03098(10)
ORTHOMCL724(10 genes,4 taxa):	PF00001(1)
ORTHOMCL741(10 genes,4 taxa):	PF04930(1) PF00097(1) PF00643(6)
ORTHOMCL772(10 genes,3 taxa):	PF05422(1) PF03227(6)
ORTHOMCL817(9 genes,4 taxa):	PF00501(6) PF02274(4)
ORTHOMCL827(9 genes,3 taxa):	PF00642(9)
ORTHOMCL840(9 genes,3 taxa):	PF02995(8)
ORTHOMCL886(9 genes,4 taxa):	PF00014(7)
ORTHOMCL896(9 genes,4 taxa):	PF00328(9)
ORTHOMCL930(9 genes,4 taxa):	PF00751(6)
ORTHOMCL934(9 genes,4 taxa):	PF02931(9) PF01852(3) PF02932(6)
ORTHOMCL969(9 genes,4 taxa):	PF01471(2) PF00413(2) PF00041(9)
ORTHOMCL988(9 genes,2 taxa):	PF00059(6)
ORTHOMCL1012(9 genes,3 taxa):	PF01679(9)
ORTHOMCL1016(9 genes,2 taxa):	PF05699(1)
ORTHOMCL1035(8 genes,3 taxa):	PF01683(8) PF00014(8)
ORTHOMCL1085(8 genes,4 taxa):	PF06119(7) PF03782(8) PF08433(1) PF01531(2)
ORTHOMCL1110(8 genes,4 taxa):	PF00008(7) PF01390(5) PF07645(6) PF00092(6) PF00057(1) PF07974(3)
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ORTHOMCL11867(2 genes,2 taxa):	

Supplementary Table 5. Protein families expanded or contracted in *C. elegans* compared to *T. spiralis* when proteome size difference was taken into consideration. All these family changes are significant after bonferroni correction. Only the most abundant domain in this family is presented. In parenthesis is the number of genes associated with this PF id.

Orthologous family ID (#genes, #taxa)	***C. elegans* genes**	***T. spiralis* genes**	**Total genes genes**	**Pfam id§**	**Hypergeometric test P value**
ORTHOMCL1(268 genes,6 taxa):	1	260	261	PF04573(8)	0.000000
ORTHOMCL0(421 genes,4 taxa):	2	201	203	PF05380(100)	0.000000
ORTHOMCL8(142 genes,2 taxa):	2	140	142	PF02171(70)	0.000000
ORTHOMCL24(77 genes,6 taxa):	3	68	71	PF00098(8)	0.000000
ORTHOMCL18(91 genes,6 taxa):	3	57	60	PF00665(24)	0.000000
ORTHOMCL66(46 genes,3 taxa):	1	44	45	PF09091(4)	0.000000
ORTHOMCL266(18 genes,3 taxa):	1	16	17	PF00146(18)	0.000021
ORTHOMCL40(59 genes,4 taxa):	33	5	38	PF00635(59)	0.000033
ORTHOMCL208(21 genes,4 taxa):	2	17	19	PF00300(21)	0.000053
ORTHOMCL353(15 genes,2 taxa):	1	14	15	PF00096(12)	0.000096
ORTHOMCL279(17 genes,4 taxa):	1	14	15	-	0.000096
ORTHOMCL153(26 genes,6 taxa):	20	1	21	PF00097(14)	0.000074
ORTHOMCL32(65 genes,6 taxa):	19	1	20	PF00067(65)	0.000127
ORTHOMCL38(60 genes,6 taxa):	24	3	27	PF00188(59)	0.000194
ORTHOMCL141(28 genes,3 taxa):	18	1	19	PF07801(16)	0.000217

Supplementary Table 6. Genome rearrangements based on OrthoCluster [2]. Ce, *C. elegans*; Cb, *C. briggsae*; Bm, *B. malayi*; Ts, *T. spiralis*.

Genome re-arrangement statistics

		Ce/Cb	**Ce/Bm**	**Ce/Ts**
Number of insertions / deletions		356	9	11
Number of inversions		4454	964	705
Number of reciprocal translocations	total	5991	1031	759
	nested	1328	299	363
	non-nested	4663	732	390
Number of transpositions		389	0	2
The synteny conservation between the two genomes		0.752	0.508	0.28

Supplementary Tables 7. Orthology map created using orthologous genes among three species spanning the phylum (*C. elegans, B. malayi* and *T. spiralis*).

Chr	Start	Stop	Region (bp)		B. malayi	Start	Stop	Region (bp)		T. spiralis
I	8,235,980	8,508,639	272,659	+	bma1.assembly.10416.0	2,997,849	3,218,703	220,854	+	SUPERLINK_TRISPI_SCTG4
I	7,522,515	7,814,546	292,031	+	bma1.assembly.8466.0	35,587	54,918	19,331	+	SUPERLINK_TRISPI_SCTG4
I	5,227,247	5,605,779	378,532	+	bma1.assembly.8116.0	1,393	16,621	15,228	-	SUPERLINK_TRISPI_SCTG4
I	5,605,779	5,648,376	42,597	+	bma1.assembly.7718.0	39,553	54,762	15,209	+	SUPERLINK_TRISPI_SCTG22
I	1,865,315	1,994,537	129,222	+	bma1.assembly.9349.0	4,634	141,102	136,468	+	SUPERLINK_TRISPI_SCTG13
I	7,380,133	7,522,515	142,382	+	bma1.assembly.10045.0	175,503	294,742	119,239	-	SUPERLINK_TRISPI_SCTG12
I	4,319,286	4,476,521	157,235	+	bma1.assembly.10238.0	11,348	15,714	4,366	+	SUPERLINK_TRISPI_SCTG1
I	4,597,037	4,781,793	184,756	+	bma1.assembly.10416.0	904,139	1,394,422	490,283	+	SUPERLINK_TRISPI_SCTG0
I	1,234,457	1,555,692	321,235	+	bma1.assembly.9572.0	2,418,175	3,611,491	1,193,316	-	SUPERLINK_TRISPI_SCTG0
			1,920,649							
I	9,557,441	10,069,569	512,128	+	bma1.assembly.8997.0	7,189	16,834	9,645	-	NA
I	6,047,622	6,609,563	561,941	+	bma1.assembly.8962.0	10,853	30,571	19,718	+	NA
I	9,150,795	9,557,441	406,646	+	bma1.assembly.9943.0	103,371	145,901	42,530	-	NA
I	9,135,536	9,150,795	15,259	+	bma1.assembly.8563.0	4,878	17,034	12,156	+	NA
I	10,069,569	10,289,186	219,617	+	bma1.assembly.6764.0	23,849	32,841	8,992	-	NA
I	10,809,931	11,462,529	652,598	+	bma1.assembly.12171.0	20,528	28,441	7,913	-	NA
I	11,462,529	12,003,354	540,825	+	bma1.assembly.10045.0	294,742	358,402	63,660	-	NA
I	10,289,186	10,539,750	250,564	+	bma1.assembly.10416.0	526,582	904,139	377,557	-	NA
I	10,539,750	10,809,931	270,181	+	bma1.assembly.10244.0	69,725	100,855	31,130	+	NA
I	6,609,563	7,226,081	616,518	+	bma1.assembly.10416.0	2,424,167	2,634,167	210,000	-	NA
I	8,599,105	8,608,706	9,601	+	bma1.assembly.7615.0	12,836	20,678	7,842	+	NA
I	5,648,376	5,777,217	128,841	+	bma1.assembly.10045.0	83,524	175,503	91,979	+	NA
I	5,777,217	5,946,116	168,899	+	bma1.assembly.7792.0	0	7,751	7,751	+	NA
I	5,946,116	6,047,622	101,506	+	bma1.assembly.7283.0	11,077	21,462	10,385	+	NA
I	8,608,706	8,843,966	235,260	+	bma1.assembly.9943.0	49,858	103,371	53,513	-	NA
I	8,843,966	9,135,536	291,570	+	bma1.assembly.10416.0	1,394,422	1,555,878	161,456	-	NA
I	7,226,081	7,380,133	154,052	+	bma1.assembly.10416.0	1,776,901	2,057,417	280,516	+	NA
I	7,814,546	8,235,980	421,434	+	bma1.assembly.10416.0	1,697,709	1,776,901	79,192	+	NA
I	8,508,639	8,599,105	90,466	+	bma1.assembly.8319.0	62,901	76,320	13,419	+	NA
I	1,994,537	2,270,633	276,096	+	bma1.assembly.7316.0	4,968	12,016	7,048	-	NA
I	3,043,739	3,071,190	27,451	+	bma1.assembly.8582.0	21,739	31,315	9,576	+	NA
I	3,071,190	3,281,671	210,481	+	bma1.assembly.10416.0	2,057,417	2,424,167	366,750	-	NA
I	2,270,633	2,750,564	479,931	+	bma1.assembly.10028.0	267,936	278,256	10,320	-	NA
I	2,750,564	3,043,739	293,175	+	bma1.assembly.10045.0	358,402	372,417	14,015	+	NA
I	4,055,158	4,319,286	264,128	+	bma1.assembly.9732.0	330,622	356,073	25,451	+	NA
I	4,476,521	4,597,037	120,516	+	bma1.assembly.10244.0	24,193	69,725	45,532	-	NA
I	3,281,671	3,667,799	386,128	+	bma1.assembly.10416.0	2,634,167	2,784,739	150,572	+	NA
I	4,781,793	5,227,247	445,454	+	bma1.assembly.10244.0	4,027	24,193	20,166	+	NA
I	3,667,799	4,055,158	387,359	+	bma1.assembly.8536.0	2,012	9,593	7,581	-	NA
I	1,053,364	1,234,457	181,093	+	bma1.assembly.10416.0	1,555,878	1,620,995	65,117	-	NA
I	1,555,692	1,767,298	211,606	+	bma1.assembly.8437.0	9,907	18,772	8,865	-	NA
I	1,767,298	1,865,315	98,017	+	bma1.assembly.9554.0	104,939	114,035	9,096	-	NA
			9,029,341							
II	10,992,685	11,210,952	218,267	+	bma1.assembly.6646.0	38,651	83,172	44,521	-	SUPERLINK_TRISPI_SCTG25
II	5,254,196	5,970,119	715,923	+	bma1.assembly.9885.0	362,952	386,979	24,027	-	SUPERLINK_TRISPI_SCTG12
II	14,812,900	15,276,584	463,684	+	bma1.assembly.8500.0	19,865	31,013	11,148	-	SUPERLINK_TRISPI_SCTG10
II	7,798,515	8,240,888	442,373	+	bma1.assembly.9921.0	229,786	411,982	182,196	-	SUPERLINK_TRISPI_SCTG0

II	10,866,825	10,992,685	125,860	+	bma1.assembly.6686.0	93,222	103,688	10,466	-	SUPERLINK_TRISPI_SCTG0
			1,966,107							
II	8,583,616	8,738,850	155,234	+	bma1.assembly.8792.0	41,557	64,272	22,715	+	NA
II	8,960,834	9,363,459	402,625	+	bma1.assembly.9885.0	386,979	437,807	50,828	-	NA
II	6,442,012	6,782,814	340,802	+	bma1.assembly.10462.0	65,926	96,396	30,470	+	NA
II	952,395	1,876,525	924,130	+	bma1.assembly.7707.0	2,487	12,892	10,405	+	NA
II	6,782,814	7,317,994	535,180	+	bma1.assembly.7864.0	83,221	102,264	19,043	-	NA
II	7,317,994	7,798,515	480,521	+	bma1.assembly.8973.0	932,932	1,005,315	72,383	-	NA
II	8,738,850	8,960,834	221,984	+	bma1.assembly.8704.0	95,186	103,962	8,776	+	NA
II	8,240,888	8,583,616	342,728	+	bma1.assembly.9885.0	437,807	621,300	183,493	+	NA
II	9,363,459	9,780,550	417,091	+	bma1.assembly.8448.0	4,128	12,122	7,994	-	NA
II	11,409,890	12,129,877	719,987	+	bma1.assembly.6590.0	30,001	35,904	5,903	+	NA
II	11,346,963	11,409,890	62,927	+	bma1.assembly.6646.0	3,161	38,651	35,490	+	NA
II	10,429,489	10,839,820	410,331	+	bma1.assembly.9843.0	39,253	47,150	7,897	+	NA
II	13,467,624	13,547,683	80,059	+	bma1.assembly.9175.0	2,719	15,312	12,593	-	NA
II	13,087,313	13,467,624	380,311	+	bma1.assembly.8091.0	177,957	190,019	12,062	+	NA
II	12,129,877	13,087,313	957,436	+	bma1.assembly.7165.0	11,602	28,256	16,654	+	NA
II	9,999,450	10,429,489	430,039	+	bma1.assembly.8973.0	220,601	487,346	266,745	+	NA
II	9,780,550	9,999,450	218,900	+	bma1.assembly.9126.0	37,661	42,464	4,803	+	NA
II	11,322,741	11,346,963	24,222	+	bma1.assembly.8973.0	487,346	750,164	262,818	+	NA
II	11,210,952	11,322,741	111,789	+	bma1.assembly.9921.0	144,945	229,786	84,841	-	NA
II	10,839,820	10,866,825	27,005	+	bma1.assembly.6449.0	24,109	32,768	8,659	+	NA
II	1,876,525	2,669,570	793,045	+	bma1.assembly.8973.0	750,164	828,693	78,529	-	NA
II	2,669,570	3,501,828	832,258	+	bma1.assembly.8973.0	828,693	932,932	104,239	+	NA
II	13,962,517	14,812,900	850,383	+	bma1.assembly.9950.0	18,916	30,830	11,914	+	NA
II	13,547,683	13,962,517	414,834	+	bma1.assembly.8967.0	1,977	14,673	12,696	-	NA
II	579,619	952,395	372,776	+	bma1.assembly.9885.0	621,300	779,996	158,696	+	NA
II	4,992,192	5,254,196	262,004	+	bma1.assembly.8973.0	1,005,315	1,038,355	33,040	-	NA
II	5,970,119	6,301,594	331,475	+	bma1.assembly.8792.0	27,051	41,557	14,506	-	NA
II	6,301,594	6,442,012	140,418	+	bma1.assembly.9921.0	98,141	144,945	46,804	+	NA
II	3,501,828	4,225,388	723,560	+	bma1.assembly.7212.0	5,552	30,473	24,921	+	NA
II	4,225,388	4,637,879	412,491	+	bma1.assembly.8705.0	8,153	15,911	7,758	+	NA
II	4,637,879	4,992,192	354,313	+	bma1.assembly.9106.0	7,383	14,933	7,550	+	NA
			12,730,858							
III	5,161,741	5,241,610	79,869	+	bma1.assembly.8182.0	20,204	34,844	14,640	+	SUPERLINK_TRISPI_SCTG8
III	4,652,464	4,859,435	206,971	+	bma1.assembly.7976.0	1,664	13,231	11,567	-	SUPERLINK_TRISPI_SCTG8
III	8,126,095	8,194,138	68,043	+	bma1.assembly.9648.0	77,426	376,575	299,149	-	SUPERLINK_TRISPI_SCTG8
III	7,671,403	7,812,830	141,427	+	bma1.assembly.9619.0	1,725	7,199	5,474	-	SUPERLINK_TRISPI_SCTG13
III	10,404,047	10,590,002	185,955	+	bma1.assembly.8611.0	0	11,078	11,078	-	SUPERLINK_TRISPI_SCTG0
III	7,553,346	7,671,403	118,057	+	bma1.assembly.10549.0	10,150	16,914	6,764	+	SUPERLINK_TRISPI_SCTG0
III	13,531,304	13,626,784	95,480	+	bma1.assembly.6852.0	39,444	44,463	5,019	+	SUPERLINK_TRISPI_SCTG0
III	352,862	1,881,597	1,528,735	+	bma1.assembly.10481.0	195,438	210,460	15,022	-	SUPERLINK_TRISPI_SCTG0
III	8,942,944	9,482,619	539,675	+	bma1.assembly.9648.0	376,575	770,829	394,254	-	SUPERLINK_TRISPI_SCTG0
III	187,840	352,862	165,022	+	bma1.assembly.9648.0	905,551	1,030,733	125,182	+	SUPERLINK_TRISPI_SCTG0
			3,129,234							
III	6,337,837	6,813,996	476,159	+	bma1.assembly.9491.0	26,420	37,950	11,530	-	NA
III	4,859,435	4,926,754	67,319	+	bma1.assembly.8837.0	35,312	43,850	8,538	-	NA
III	4,926,754	4,971,191	44,437	+	bma1.assembly.9920.0	7,835	15,096	7,261	-	NA
III	5,353,594	5,619,565	265,971	+	bma1.assembly.8457.0	22,585	32,014	9,429	+	NA
III	2,708,740	2,803,612	94,872	+	bma1.assembly.10494.0	30,463	33,942	3,479	-	NA
III	4,445,770	4,484,528	38,758	+	bma1.assembly.9277.0	29,195	41,145	11,950	+	NA

III	4,484,528	4,652,464	167,936	+	bma1.assembly.10481.0	309,399	404,382	94,983	-	NA
III	5,619,565	5,863,136	243,571	+	bma1.assembly.6959.0	19,706	31,555	11,849	-	NA
III	5,863,136	6,046,506	183,370	+	bma1.assembly.8186.0	8,618	22,137	13,519	+	NA
III	4,971,191	5,081,149	109,958	+	bma1.assembly.7627.0	23,765	37,580	13,815	+	NA
III	5,081,149	5,161,741	80,592	+	bma1.assembly.8931.0	2,541	11,745	9,204	+	NA
III	5,241,610	5,353,594	111,984	+	bma1.assembly.8572.0	120,962	133,844	12,882	-	NA
III	2,803,612	3,065,424	261,812	+	bma1.assembly.7954.0	47,521	59,952	12,431	-	NA
III	4,175,084	4,214,759	39,675	+	bma1.assembly.8294.0	17,554	29,964	12,410	+	NA
III	6,046,506	6,337,837	291,331	+	bma1.assembly.10214.0	87,632	111,815	24,183	+	NA
III	1,881,597	2,490,639	609,042	+	bma1.assembly.8931.0	11,745	22,918	11,173	+	NA
III	2,490,639	2,708,740	218,101	+	bma1.assembly.7627.0	37,580	48,519	10,939	+	NA
III	4,214,759	4,331,606	116,847	+	bma1.assembly.9648.0	770,829	905,551	134,722	+	NA
III	4,331,606	4,445,770	114,164	+	bma1.assembly.10121.0	692,703	980,881	288,178	+	NA
III	3,065,424	3,672,484	607,060	+	bma1.assembly.9838.0	1,015,810	1,218,292	202,482	+	NA
III	3,672,484	4,044,353	371,869	+	bma1.assembly.10651.0	1,590	6,412	4,822	-	NA
III	4,044,353	4,175,084	130,731	+	bma1.assembly.8865.0	6,281	13,627	7,346	+	NA
III	8,440,292	8,942,944	502,652	+	bma1.assembly.8899.0	49,258	56,318	7,060	+	NA
III	8,421,679	8,440,292	18,613	+	bma1.assembly.10214.0	111,815	125,217	13,402	-	NA
III	8,357,760	8,421,679	63,919	+	bma1.assembly.9838.0	351,972	759,620	407,648	+	NA
III	10,003,390	10,278,242	274,852	+	bma1.assembly.7994.0	26,682	35,484	8,802	+	NA
III	9,655,068	10,003,390	348,322	+	bma1.assembly.9838.0	37,165	351,972	314,807	-	NA
III	9,482,619	9,655,068	172,449	+	bma1.assembly.10121.0	226,408	355,901	129,493	+	NA
III	8,059,022	8,126,095	67,073	+	bma1.assembly.10411.0	24,910	34,939	10,029	-	NA
III	7,941,787	8,059,022	117,235	+	bma1.assembly.10121.0	152,373	226,408	74,035	-	NA
III	7,812,830	7,941,787	128,957	+	bma1.assembly.9638.0	3,406	11,872	8,466	+	NA
III	8,277,317	8,357,760	80,443	+	bma1.assembly.8739.0	55,385	60,731	5,346	-	NA
III	8,235,857	8,277,317	41,460	+	bma1.assembly.9555.0	6,133	14,180	8,047	+	NA
III	8,194,138	8,235,857	41,719	+	bma1.assembly.9617.0	194,191	212,649	18,458	-	NA
III	11,819,971	11,926,669	106,698	+	bma1.assembly.9572.0	4,222,832	4,504,605	281,773	+	NA
III	11,702,146	11,819,971	117,825	+	bma1.assembly.7618.0	31,077	38,718	7,641	+	NA
III	11,565,136	11,702,146	137,010	+	bma1.assembly.9429.0	17,922	37,011	19,089	-	NA
III	13,192,250	13,531,304	339,054	+	bma1.assembly.9828.0	13,061	27,431	14,370	-	NA
III	12,440,744	13,192,250	751,506	+	bma1.assembly.7218.0	0	10,490	10,490	-	NA
III	11,926,669	12,440,744	514,075	+	bma1.assembly.7950.0	1,367	24,361	22,994	+	NA
III	10,781,694	10,898,919	117,225	+	bma1.assembly.9707.0	17,072	28,256	11,184	-	NA
III	10,590,002	10,781,694	191,692	+	bma1.assembly.10258.0	66,954	73,627	6,673	-	NA
III	10,278,242	10,404,047	125,805	+	bma1.assembly.9617.0	212,649	228,807	16,158	-	NA
III	11,421,923	11,565,136	143,213	+	bma1.assembly.8628.0	95,289	99,863	4,574	+	NA
III	11,138,756	11,421,923	283,167	+	bma1.assembly.9838.0	759,620	1,015,810	256,190	-	NA
III	6,813,996	7,233,719	419,723	+	bma1.assembly.10481.0	210,460	309,399	98,939	+	NA
III	7,233,719	7,399,296	165,577	+	bma1.assembly.10121.0	355,901	692,703	336,802	-	NA
III	10,898,919	11,138,756	239,837	+	bma1.assembly.9648.0	1,030,733	1,065,129	34,396	+	NA
III	7,399,296	7,553,346	154,050	+	bma1.assembly.8115.0	0	11,795	11,795	-	NA

IV	10,665,070	11,874,980	1,209,910	+	bma1.assembly.7884.0	42,768	50,825	8,057	-	SUPERLINK_TRISPI_SCTG7
IV	13,340,860	13,579,823	238,963	+	bma1.assembly.9114.0	3,029	11,006	7,977	-	SUPERLINK_TRISPI_SCTG5
IV	6,622,809	7,000,288	377,479	+	bma1.assembly.10014.0	891,419	906,810	15,391	+	SUPERLINK_TRISPI_SCTG2
IV	7,000,288	7,565,397	565,109	+	bma1.assembly.9572.0	124,183	286,035	161,852	-	SUPERLINK_TRISPI_SCTG2
IV	16,281,071	17,104,670	823,599	+	bma1.assembly.9016.0	16,861	22,673	5,812	+	SUPERLINK_TRISPI_SCTG11
IV	7,565,397	7,705,389	139,992	+	bma1.assembly.9572.0	6,156,543	6,203,346	46,803	-	SUPERLINK_TRISPI_SCTG1
IV	7,844,648	9,209,915	1,365,267	+	bma1.assembly.9572.0	4,504,605	4,994,848	490,243	+	SUPERLINK_TRISPI_SCTG1
IV	9,209,915	10,138,043	928,128	+	bma1.assembly.10224.0	87,038	210,577	123,539	-	SUPERLINK_TRISPI_SCTG1
IV	13,579,823	13,833,911	254,088	+	bma1.assembly.9572.0	286,035	2,418,175	2,132,140	+	SUPERLINK_TRISPI_SCTG1

			5,902,535							
IV	13,833,911	14,129,053	295,142	+	bma1.assembly.7798.0	10,549	16,105	5,556	-	NA
IV	1,471,996	3,952,396	2,480,400	+	bma1.assembly.7948.0	714	15,767	15,053	-	NA
IV	442,985	1,471,996	1,029,011	+	bma1.assembly.10416.0	1,620,995	1,697,709	76,714	+	NA
IV	14,914,540	16,281,071	1,366,531	+	bma1.assembly.9572.0	3,913,938	4,055,679	141,741	-	NA
IV	14,129,053	14,914,540	785,487	+	bma1.assembly.10224.0	210,577	237,294	26,717	-	NA
IV	10,138,043	10,665,070	527,027	+	bma1.assembly.9572.0	3,611,491	3,756,286	144,795	-	NA
IV	7,705,389	7,844,648	139,259	+	bma1.assembly.8924.0	61,546	70,219	8,673	-	NA
IV	5,855,264	6,622,809	767,545	+	bma1.assembly.10014.0	906,810	924,948	18,138	+	NA
IV	12,933,990	13,340,860	406,870	+	bma1.assembly.6760.0	6,211	16,459	10,248	-	NA
IV	3,952,396	5,855,264	1,902,868	+	bma1.assembly.6680.0	17,252	26,069	8,817	-	NA
IV	11,874,980	12,933,990	1,059,010	+	bma1.assembly.8656.0	11,309	18,496	7,187	+	NA
V	7,060,568	7,487,394	426,826	+	bma1.assembly.10301.0	256,345	966,176	709,831	-	SUPERLINK_TRISPI_SCTG7
V	6,883,841	7,060,568	176,727	+	bma1.assembly.10301.0	3,222,859	3,437,935	215,076	-	SUPERLINK_TRISPI_SCTG1
			603,553							
V	7,487,394	8,120,600	633,206	+	bma1.assembly.7797.0	20,147	25,399	5,252	+	NA
V	6,378,926	6,883,841	504,915	+	bma1.assembly.10365.0	271,629	284,822	13,193	-	NA
V	10,386,403	10,747,052	360,649	+	bma1.assembly.10301.0	1,634,955	2,474,572	839,617	-	NA
V	9,973,623	10,386,403	412,780	+	bma1.assembly.10301.0	2,925,039	3,222,859	297,820	-	NA
V	9,122,430	9,973,623	851,193	+	bma1.assembly.8228.0	3,975	18,717	14,742	-	NA
V	8,120,600	9,122,430	1,001,830	+	bma1.assembly.10365.0	284,822	349,980	65,158	+	NA
V	1,968,505	3,134,236	1,165,731	+	bma1.assembly.10301.0	2,474,572	2,925,039	450,467	-	NA
V	1,108,165	1,968,505	860,340	+	bma1.assembly.6685.0	4,289	25,407	21,118	-	NA
V	233,441	1,108,165	874,724	+	bma1.assembly.8230.0	15,362	28,436	13,074	-	NA
V	103,830	233,441	129,611	+	bma1.assembly.10416.0	2,784,739	2,997,849	213,110	+	NA
V	5,920,293	6,378,926	458,633	+	bma1.assembly.8921.0	24,646	36,482	11,836	+	NA
V	5,241,384	5,920,293	678,909	+	bma1.assembly.8560.0	35,831	43,665	7,834	-	NA
V	4,445,322	5,241,384	796,062	+	bma1.assembly.10301.0	966,176	1,634,955	668,779	-	NA
V	3,134,236	4,445,322	1,311,086	+	bma1.assembly.8789.0	34,128	42,363	8,235	-	NA
V	12,647,113	15,342,895	2,695,782	+	bma1.assembly.7697.0	12,493	19,096	6,603	-	NA
V	15,342,895	18,806,609	3,463,714	+	bma1.assembly.9435.0	11,113	29,504	18,391	+	NA
V	18,806,609	19,937,327	1,130,718	+	bma1.assembly.9528.0	71,969	77,350	5,381	+	NA
V	10,747,052	11,105,988	358,936	+	bma1.assembly.10365.0	349,980	413,930	63,950	+	NA
V	11,105,988	11,943,816	837,828	+	bma1.assembly.9744.0	717	7,360	6,643	-	NA
V	19,937,327	20,245,848	308,521	+	bma1.assembly.8584.0	15,821	27,744	11,923	-	NA
V	11,943,816	12,647,113	703,297	+	bma1.assembly.9648.0	29,562	77,426	47,864	+	NA
X	2,591,517	3,485,878	894,361	+	bma1.assembly.8833.0	22,613	178,244	155,631	-	SUPERLINK_TRISPI_SCTG7
X	8,307,397	10,998,987	2,691,590	+	bma1.assembly.9572.0	4,994,848	5,715,336	720,488	-	SUPERLINK_TRISPI_SCTG3
			3,585,951					876,119		
X	15,063,332	15,750,959	687,627	+	bma1.assembly.8408.0	17,872	29,164	11,292	-	NA
X	10,998,987	14,497,650	3,498,663	+	bma1.assembly.9533.0	829,410	1,279,534	450,124	-	NA
X	15,750,959	16,147,850	396,891	+	bma1.assembly.9572.0	5,715,336	6,156,543	441,207	-	NA
X	14,712,584	15,063,332	350,748	+	bma1.assembly.6757.0	506	8,305	7,799	-	NA
X	14,497,650	14,712,584	214,934	+	bma1.assembly.9572.0	4,055,679	4,222,832	167,153	+	NA
X	7,880,441	8,307,397	426,956	+	bma1.assembly.9533.0	817,021	829,410	12,389	-	NA
X	2,442,557	2,591,517	148,960	+	bma1.assembly.7867.0	139,585	151,311	11,726	+	NA
X	2,394,499	2,442,557	48,058	+	bma1.assembly.9537.0	439,273	447,066	7,793	-	NA

X	5,899,841	7,880,441	1,980,600	+	bma1.assembly.9533.0	1,279,534	1,689,560	410,026	-	NA
X	3,485,878	5,899,841	2,413,963	+	bma1.assembly.9572.0	3,756,286	3,913,938	157,652	+	NA
NA	NA	NA		NA	bma1.assembly.10547.0	3,631	14,422	10,791	+	SUPERLINK_TRISPI_SCTG45
NA	NA	NA		NA	bma1.assembly.11742.0	0	8,306	8,306	+	SUPERLINK_TRISPI_SCTG12
NA	NA	NA		NA	bma1.assembly.6264.0	9,055	25,509	16,454	+	SUPERLINK_TRISPI_SCTG10
NA	NA	NA		NA	bma1.assembly.7787.0	10,543	25,506	14,963	+	SUPERLINK_TRISPI_SCTG10
NA	NA	NA		NA	bma1.assembly.7821.0	33,176	41,134	7,958	+	SUPERLINK_TRISPI_SCTG1

Supplementary Table 8. *C. elegans* based annotation of the 328 single-copy orthologous groups.

Orthologous group ID	**C. elegans RNAi phenotype**	**Genes in this group**
ORTHOMCL2309		12492.m00173 F21H11.2a FBpp0076146 Minc11585 Tsp_00555 YIL129C
ORTHOMCL2311	Prl Lvl Unc Adl Gro	12496.m00293 FBpp0073410 Minc13993 Tsp_00183 Y76A2A.2 YDR270W
ORTHOMCL2314		12508.m00092 FBpp0071077 Minc17248a Tsp_02642 YML059C ZK370.4b
ORTHOMCL2318	WT	12565.m00052 C52E12.1 FBpp0072214 Minc04726 Tsp_05996 YDR266C
ORTHOMCL2319	Clr Lva Sck Emb Lon Gro	12568.m00015 F09E5.2 FBpp0072887 Minc11061 Tsp_11653 YGL065C
ORTHOMCL2320	Bli Ocs Emb Pvl Ste Unc Stp	12575.m00211 FBpp0079641 Minc17985 T05G5.3 Tsp_11762 YBR160W
ORTHOMCL2321	Emb	12575.m00213 FBpp0070317 Minc02178 Tsp_02600 W02B12.10 YDL201W
ORTHOMCL2324		12598.m00175 FBpp0079628 Minc01093 Tsp_02039 Y51H7C.6a YPR105C
ORTHOMCL2326	WT	12616.m00132 FBpp0077419 Minc15908 T03F1.3 Tsp_04645 YCR012W
ORTHOMCL2330	Lva Pch Emb	12724.m00019 C30B5.4 FBpp0080829 Minc10250 Tsp_08389 YIR005W
ORTHOMCL2332		12737.m00157 FBpp0086845 Minc09159 T04A8.7a Tsp_10647 YEL011W
ORTHOMCL2333	fat_content_reduced	12778.m00055 FBpp0079575 Minc07331 Tsp_04516 Y50D7A.9 YGR021W
ORTHOMCL2341	early_larval_arrest	12903.m00106 C16C10.8 FBpp0087437 Minc06710 Tsp_02224 YCR087C-A
ORTHOMCL2345	Ced	12971.m00013 C41D11.8 FBpp0087120 Minc17633 Tsp_09257 YJL208C
ORTHOMCL2346	Lva Bli Prl Emb Lvl transgene_subcellular_localization_abnormal	13001.m00046 FBpp0080495 Minc16482a T14F9.1 Tsp_02924 YPR036W
ORTHOMCL2351	Lva Emb	13073.m00116 FBpp0074075 Minc01303 Tsp_07802 Y37E3.10 YJR007W
ORTHOMCL2352	Emb	13073.m00117 FBpp0080708 Minc08978a Tsp_08590 Y37E3.9 YGR132C
ORTHOMCL2353		13073.m00118 FBpp0077142 Minc08977 Tsp_02079 Y37E3.8a YGL103W
ORTHOMCL2360	Emb	13154.m00136 FBpp0079294 Minc16258 T22C1.3 Tsp_05206 YLR459W
ORTHOMCL2371	Emb Lvl Ste Unc Gro	13227.m00137 FBpp0072693 Minc03403 Tsp_10268 Y71F9AL.17 YDL145C
ORTHOMCL2376	WT	13249.m00079 F40F4.7 FBpp0087227 Minc04692 Tsp_01637 YOR253W
ORTHOMCL2383		13260.m00100 FBpp0086973 Minc11005 Tsp_00702 Y65B4BR.5b YHR193C
ORTHOMCL2385	Dpy Bmd Slu Pvl Unc Gro	13261.m00259 C08H9.2 FBpp0089202 Minc01407 Tsp_10795 YJL080C
ORTHOMCL2389	failure_to_hatch nuclear_appearance_abnormal Emb Mul	13276.m00051 F10C2.4 FBpp0075277 Minc14417 Tsp_06599 YDL102W
ORTHOMCL2391	Lva spontaneous_mutation_rate_increased Emb Gro	13293.m00126 C54G10.2 FBpp0099511 Minc03446 Tsp_06737 YOR217W
ORTHOMCL2392		13294.m00107 F43D9.3a FBpp0089084 Minc14003 Tsp_07033 YDR189W
ORTHOMCL2393	Let Clr Prl Ric Unc Gro	13298.m00052 FBpp0088945 Minc15811a T20B5.1 Tsp_06362 YBL037W
ORTHOMCL2402	Clr thin Emb Stp Gro	13325.m00226 FBpp0072117 Minc00301 T06D8.5 Tsp_08197 YER141W
ORTHOMCL2404	Cyk Lva distal_tip_cell_migration_abnormal chromosome_segregation_abnormal Emb Pvl Mul	13345.m00128 F35G12.8 FBpp0080489 Minc15914a Tsp_07237 YLR086W
ORTHOMCL2409	WT	13355.m00154 F36D4.2 FBpp0079332 Minc16750 Tsp_04134 YDR246W
ORTHOMCL2410		13356.m00240 C37C3.8b FBpp0082187 Minc12175 Tsp_08382 YJR008W
ORTHOMCL2420	WT	13401.m00093 C04G6.3 FBpp0112984 Minc16940 Tsp_10708 YKR031C
ORTHOMCL2423	WT	13411.m00123 B0035.16 FBpp0070168 Minc06524a Tsp_04039 YDL033C
ORTHOMCL2425	Emb	13415.m00444 C09G12.9 FBpp0075088 Minc17375 Tsp_03768 YCL008C
ORTHOMCL2426	WT	13415.m00454 FBpp0080827 Minc17878 Tsp_06063 W10D9.4 YBL021C
ORTHOMCL2433	WT	13480.m00173 C14A4.3 FBpp0084183 Minc16180 Tsp_09458 YNL219C
ORTHOMCL2435	Lva Emb Stp	13486.m00112 F54A3.3 FBpp0082788 Minc14304a Tsp_09755 YJL014W
ORTHOMCL2436		13499.m00137 F59A2.1b FBpp0084188 Minc16751a Tsp_00378 YDR002W
ORTHOMCL2448	WT	13586.m00156 B0334.4 FBpp0087591 Minc17976 Tsp_07093 YLR193C
ORTHOMCL2454	Emb Mei Ste	13644.m00291 FBpp0073893 Minc15359 Tsp_11031 W10C6.1 YNL172W
ORTHOMCL2455	WT	13658.m00036 F08F8.7 FBpp0088028 Minc11587 Tsp_12251 YJL121C
ORTHOMCL2456	Lva Emb Ste Stp	13662.m00127 FBpp0089163 Minc17194 Tsp_05366 Y76B12C.7 YDR301W
ORTHOMCL2458	Emb Pvl Ste Mul	13674.m00035 C25D7.6 FBpp0070729 Minc19113 Tsp_04051 YEL032W
ORTHOMCL2466	Ocs Emb Lvl Ste transgene_subcellular_localization_abnormal	13736.m00400 F56H1.4 FBpp0083843 Minc14887a Tsp_07392 YOR117W

ORTHOMCL2467		13736.m00405 FBpp0082816 Minc11069 R06C7.5a Tsp_06112 YLR359W
ORTHOMCL2470	Dpy small Emb Pvl Ste Lva transgene_expression_increased transgene_subcellular_localization_abnormal Stp	13780.m00058 FBpp0075700 K04G2.1 Minc07301 Tsp_05772 YPL237W
ORTHOMCL2472	WT	13786.m00077 FBpp0085393 Minc03680 Tsp_03383 Y67H2A.7 YKL134C
ORTHOMCL2474	WT	13792.m00111 FBpp0080148 Minc11668 Tsp_05486 Y57A10A.15 YOR330C
ORTHOMCL2475	Emb Lvl Ste embryonic_terminal_arrest_variable_emb unclassified	13818.m00236 F46F11.5 FBpp0083214 Minc16114 Tsp_10702 YHR039C-A
ORTHOMCL2478	Emb Ste Lva Gro	13818.m00242 F58B3.5 FBpp0085809 Minc16706 Tsp_00605 YGR264C
ORTHOMCL2480		13824.m00056 C03D6.3a FBpp0073739 Minc13946 Tsp_02609 YGL130W
ORTHOMCL2482	WT	13834.m00091 C28G1.3 FBpp0083436 Minc14675 Tsp_03288 YGL233W
ORTHOMCL2483		13842.m00014 F48F5.5 FBpp0076791 Minc11588 Tsp_08637 YMR274C
ORTHOMCL2485	WT	13847.m00043 F10E7.5 FBpp0087511 Minc16058 Tsp_13341 YKL009W
ORTHOMCL2487	WT	13889.m00011 F32H2.4 FBpp0081350 Minc08958 Tsp_00088 YNL253W
ORTHOMCL2488	WT	13906.m00035 FBpp0076827 Minc03753 Tsp_10838 W08E12.7 YDR101C
ORTHOMCL2491		13924.m00036 F28B12.2a FBpp0111738 Minc08587 Tsp_09605 YBR083W
ORTHOMCL2493	WT	13943.m00028 F07A11.3 FBpp0079710 Minc16624 Tsp_10556 YDL116W
ORTHOMCL2497	WT	13970.m00032 F13B12.1 FBpp0111905 Minc04974 Tsp_06200 YPR133C
ORTHOMCL2500		13985.m00052 FBpp0084907 Minc16467 Tsp_07528 Y69A2AR.18b YBR039W
ORTHOMCL2502	Dpy Age Emb Pvl Ste Unc embryonic_terminal_arrest_variable_emb transposon_silencing_abnormal Gro	13994.m00022 F43G9.1 FBpp0074550 Minc15213 Tsp_10049 YOR136W
ORTHOMCL2506	Emb Cyk Mul Stp Gro	14037.m00192 F31E3.3 FBpp0074246 Minc04219 Tsp_04544 YJR068W
ORTHOMCL2507	WT	14038.m00032 FBpp0087958 Minc05871 Tsp_03561 Y71G12B.24 YHR024C
ORTHOMCL2509		14040.m00262 F27D4.4a FBpp0087806 Minc08580 Tsp_05049 YOR091W
ORTHOMCL2511	Emb	14052.m00195 FBpp0070723 Minc08973 Tsp_00314 Y39G10AL.3 YDL108W
ORTHOMCL2513	Emb	14058.m00556 F36F2.6 FBpp0072249 Minc11167 Tsp_10222 YMR277W
ORTHOMCL2515	Emb late_larval_arrest Lva sterile_F1 reduced_brood_size	14058.m00577 FBpp0074227 Minc14187 Tsp_07169 Y23H5B.6 YJL033W
ORTHOMCL2518	WT	14077.m00081 FBpp0111804 Minc14479 Tsp_11836 Y71A12B.4 YMR068W
ORTHOMCL2528	WT	14134.m00016 FBpp0084843 Minc08927 Tsp_08308 W07G4.3 YOR112W
ORTHOMCL2531	WT	14170.m00174 C24H11.6 FBpp0073876 Minc12333 Tsp_00798 YMR150C
ORTHOMCL2534	WT	14208.m00920 FBpp0077576 Minc16977 T09F3.2 Tsp_10570 YBR192W
ORTHOMCL2538	WT	14224.m00314 FBpp0081606 Minc05175 Tsp_03046 Y39B6A.2 YGR123C
ORTHOMCL2539	WT	14230.m00217 FBpp0076247 Minc10492 Tsp_04600 Y39A1C.2 YGL141W
ORTHOMCL2540	Emb Unc Ste Lva reduced_brood_size	14230.m00219 FBpp0079182 Minc00813 Tsp_04321 Y49E10.15 YOR159C
ORTHOMCL2541	Emb Ste Lva transgene_expression_increased transgene_subcellular_localization_abnormal Stp	14237.m00397 F22B5.9 FBpp0084021 Minc11060 Tsp_09583 YLR060W
ORTHOMCL2543	Pch late_larval_arrest Lva reduced_brood_size Gro	14237.m00402 FBpp0077735 Minc09546a Tsp_06445 W07E6.2 YCR072C
ORTHOMCL2545	Emb	14237.m00409 FBpp0076418 Minc09541a Tsp_06824 Y17G7B.4 YHR068W
ORTHOMCL2546	WT	14239.m00344 FBpp0079949 Minc12214 Tsp_02445 YDR120C ZC376.5
ORTHOMCL2547	WT	14241.m00049 FBpp0081004 Minc12073 Tsp_13222 Y47D3A.28 YIL150C
ORTHOMCL2548		14246.m00080 FBpp0071302 Minc18537 T02G5.9b Tsp_06904 YDR037W
ORTHOMCL2549	Dpy Emb Unc Bmd Lva Stp Gro	14246.m00081 C27F2.10 FBpp0075833 Minc16293 Tsp_07191 YJR084W
ORTHOMCL2555		14262.m00042 FBpp0087645 H20J04.4b Minc14482 Tsp_01918 YHR169W
ORTHOMCL2561	Lvl Ste	14317.m00276 F21D5.7 FBpp0076872 Minc18122 Tsp_07809 YPR088C
ORTHOMCL2562	Pch Emb Ste Rup Bmd Lva transgene_expression_increased transgene_subcellular_localization_abnormal Stp	14324.m00042 FBpp0079992 K01C8.10 Minc00918 Tsp_08448 YDL143W
ORTHOMCL2564	Emb Lvl Lva early_larval_arrest Gro	14330.m00199 FBpp0078633 H43I07.2 Minc13966a Tsp_06988 YPR110C
ORTHOMCL2565	WT	14330.m00201 FBpp0079234 H43I07.3 Minc13965 Tsp_09221 YPL227C
ORTHOMCL2566	WT	14336.m00025 FBpp0079597 Minc01734 Tsp_06532 Y57G11C.34 YJR113C

ORTHOMCL2567	WT	14347.m00047 FBpp0076607 H06I04.2 Minc15100 Tsp_05828 YGR112W
ORTHOMCL2568		14348.m00099 C08F8.2a FBpp0078544 Minc00373 Tsp_02850 YPL029W
ORTHOMCL2578	Emb Ste	14372.m00207 F28C6.6 FBpp0112455 Minc08155 Tsp_09513 YMR061W
ORTHOMCL2582	Emb	14387.m00338 F28B3.1 FBpp0072420 Minc01228 Tsp_08740 YOR093C
ORTHOMCL2584	Emb Ste Lva reduced_brood_size	14389.m00197 C16A3.9 FBpp0099990 Minc02205 Tsp_02639 YDR064W
ORTHOMCL2585		14389.m00203 FBpp0075680 Minc13389 Tsp_01793 YNL243W ZK370.3a
ORTHOMCL2586	WT	14393.m00059 FBpp0112564 Minc00320 Tsp_00542 Y54G11A.11 YKL160W
ORTHOMCL2587	Emb	14393.m00060 FBpp0071526 Minc14052 R06A4.8 Tsp_07883 YPR184W
ORTHOMCL2591	Emb Pvl Ste Sck transgene_expression_increased transgene_subcellular_localization_abnormal	14424.m00385 FBpp0072494 K02F2.3 Minc17259 Tsp_05143 YML049C
ORTHOMCL2592	cell_stress_response_abnormal	14424.m00394 FBpp0077357 Minc04216 Tsp_09697 W06D4.6 YGL163C
ORTHOMCL2593	WT	14437.m00024 FBpp0081434 Minc17870 T07A5.2 Tsp_04856 YKR030W
ORTHOMCL2594	Emb Unc Bmd Lva Stp Gro	14442.m00128 FBpp0083861 Minc11070 T06D8.8 Tsp_00727 YDR427W
ORTHOMCL2597		14469.m00103 FBpp0086063 Minc16881 T19A6.2a Tsp_11679 YNR053C
ORTHOMCL2599	spontaneous_mutation_rate_increased	14479.m00131 FBpp0087867 Minc01921 T28A8.7 Tsp_09579 YMR167W
ORTHOMCL2607		14529.m00214 C10C5.6b FBpp0070850 Minc14103 Tsp_04303 YHR186C
ORTHOMCL2609	Emb	14538.m00478 FBpp0075982 Minc11797 Tsp_07390 Y66D12A.15 YIL143C
ORTHOMCL2610	Emb Unc Lva Gro	14540.m00056 C36B1.3 FBpp0080121 Minc08381 Tsp_09380 YIL021W
ORTHOMCL2612	Emb Lva	14546.m00096 B0464.2 FBpp0072562 Minc15997 Tsp_02172 YOL145C
ORTHOMCL2613	thin Emb Lon Unc Gro	14554.m00235 FBpp0074237 Minc02899 T12D8.7 Tsp_01650 YMR236W
ORTHOMCL2615	distal_tip_cell_migration_abnormal Emb Pvl Ste Bmd transgene_expression_increased Stp transgene_subcellular_localization_abnormal	14563.m00108 FBpp0078400 Minc17075 T13H5.4 Tsp_00418 YDL030W
ORTHOMCL2616		14563.m00109 C05C10.6b FBpp0077645 Minc13225 Tsp_00624 YKL213C
ORTHOMCL2617	small Emb Pvl Unc reduced_brood_size Gro	14567.m00026 D2021.1 FBpp0079664 Minc02745 Tsp_03329 YBR112C
ORTHOMCL2618		14569.m00222 F20B6.8b FBpp0072450 Minc07852 Tsp_07484 YJL141C
ORTHOMCL2619	Pvl Lvl Ste Lva Gro	14575.m00066 FBpp0079305 Minc17135 Tsp_00911 Y75B8A.7 YJR002W
ORTHOMCL2621	glp Emb fat_content_reduced Him unclassified	14589.m00213 FBpp0079802 Minc08564 Tsp_12012 YMR224C ZC302.1
ORTHOMCL2622	Emb Lva	14590.m00348 FBpp0085724 Minc04828 Tsp_10723 Y82E9BR.15 YPL046C
ORTHOMCL2624	Emb Lva Sck	14599.m00271 FBpp0070861 Minc08980 T04A8.14 Tsp_02371 YGR116W
ORTHOMCL2626	Dpy Pch Sle Emb Ste Bmd Lva Stp Gro	14608.m00265 D2013.5 FBpp0086700 Minc07059 Tsp_02116 YOR211C
ORTHOMCL2630	WT	14612.m00129 C04F12.10 FBpp0086207 Minc07573 Tsp_03936 YJR117W
ORTHOMCL2633	Emb Lvl Ste spontaneous_mutation_rate_increased Mul transgene_subcellular_localization_abnormal	14616.m00147 D1081.8 FBpp0072468 Minc05493 Tsp_07418 YMR213W
ORTHOMCL2635	Emb Lvl Ste fat_content_reduced Bmd Sck	14631.m00037 F20D12.2 FBpp0074178 Minc01024 Tsp_05363 YDR159W
ORTHOMCL2638	Emb reduced_brood_size	14634.m00550 F35F11.1 FBpp0081448 Minc10352 Tsp_04052 YLR418C
ORTHOMCL2640	Clr Emb Lvl Unc Rup Lva Ced Gro	14643.m00078 FBpp0078483 M57.2 Minc09555 Tsp_09299 YJL031C
ORTHOMCL2642		14648.m00054 FBpp0076451 Minc11460 T17E9.2b Tsp_00547 YLR195C
ORTHOMCL2647	thin Emb Unc Stp Gro	14659.m00191 C55B7.8 FBpp0076409 Minc09985 Tsp_09915 YKL149C
ORTHOMCL2650	Egl Emb Lvl Unc Rup cell_division_abnormal Vul Mul	14673.m00023 F26E4.1 FBpp0081665 Minc02539 Tsp_07431 YGL190C
ORTHOMCL2654	Age Emb	14686.m00197 FBpp0085326 K07H8.1 Minc14656 Tsp_02571 YER007W
ORTHOMCL2655		14687.m00366 F33H1.1b FBpp0111808 Minc08233 Tsp_07936 YLR176C
ORTHOMCL2660	WT	14704.m00450 D2023.6 FBpp0072227 Minc11994 Tsp_03160 YLR253W
ORTHOMCL2662	small Emb Unc Ste Lva Sck transgene_subcellular_localization_abnormal Gro	14704.m00456 FBpp0079951 H19N07.1 Minc16006 Tsp_08936 YDR172W
ORTHOMCL2664		14712.m00227 FBpp0085627 K07A1.9a Minc05028 Tsp_00010 YGL017W
ORTHOMCL2665		14713.m00192 FBpp0077654 Minc03015 Tsp_06428 Y105E8A.23b YFL036W
ORTHOMCL2666	Emb unclassified Mul	14713.m00193 FBpp0081756 Minc09242 R10E4.4 Tsp_07749 YLR274W

ORTHOMCL2667		14715.m01236 FBpp0079278 Minc13151 Tsp_03075 YGR218W ZK742.1a
ORTHOMCL2671	Egl Emb Pvl Unc Rup Bmd	14719.m00183 FBpp0077106 Minc14874 R02D3.5 Tsp_01343 YKL019W
ORTHOMCL2677	Dpy Emb Pvl Lvl Ste Lva Stp Gro	14744.m00190 FBpp0080997 Minc17447 T26G10.1 Tsp_02129 YHR065C
ORTHOMCL2678	Emb Lvl Ste Bmd Lva transgene_expression_increased reduced_brood_size Gro	14749.m00216 FBpp0077251 Minc12165 R74.1 Tsp_00765 YPL160W
ORTHOMCL2683	late_larval_arrest Lva Stp	14763.m00261 F45E12.2 FBpp0082893 Minc07241 Tsp_00909 YGR246C
ORTHOMCL2686	Sle Emb oogenesis_abnormal Lva reduced_brood_size	14765.m00816 C08B6.9 FBpp0082065 Minc07033 Tsp_00060 YPR180W
ORTHOMCL2687	WT	14768.m00188 FBpp0079711 Minc01163 Tsp_06818 Y62E10A.10 YKL207W
ORTHOMCL2694	WT	14773.m00915 F46C5.8 FBpp0084189 Minc08793 Tsp_09092 YCL001W
ORTHOMCL2696	Emb transgene_subcellular_localization_abnormal	14775.m00061 F55A3.3 FBpp0072743 Minc13731a Tsp_05443 YGL207W
ORTHOMCL2698	Emb Lvl Ric Unc Lva transgene_subcellular_localization_abnormal Gro	14776.m00033 F23C8.6 FBpp0074859 Minc02714 Tsp_11192 YKR035W-A
ORTHOMCL2700	WT	14788.m00090 F46F6.2 FBpp0111810 Minc12074 Tsp_04112 YBL105C
ORTHOMCL2702	Emb Lva reduced_brood_size	14794.m00099 FBpp0074906 LLC1.3 Minc06711 Tsp_03154 YFL018C
ORTHOMCL2704	WT	14819.m00068 FBpp0082110 Minc17002 Tsp_10246 W06D4.5 YOR357C
ORTHOMCL2707		14855.m00193 C29A12.3a FBpp0072041 Minc02244 Tsp_04168 YDL164C
ORTHOMCL2709	Age	14857.m00322 C54G4.6 FBpp0079391 Minc12738 Tsp_11052 YOR111W
ORTHOMCL2710	distal_tip_cell_migration_abnormal Emb Pvl Lva reduced_brood_size	14873.m00236 F26F4.11 FBpp0078086 Minc05981 Tsp_00326 YOR224C
ORTHOMCL2712	WT	14896.m00034 FBpp0071982 Minc13730 T23D8.8 Tsp_05684 YMR176W
ORTHOMCL2718	small Emb Lvl Ste embryonic_terminal_arrest_variable_emb Lva	14916.m00491 FBpp0083371 Minc11713 Tsp_03116 Y105E8A.16 YHL015W
ORTHOMCL2719	distal_tip_cell_migration_abnormal Emb Pvl Ste Unc Lva Pna Sck reduced_brood_size transgene_subcellular_localization_abnormal Gro	14916.m00497 FBpp0080484 Minc06523 Tsp_08627 Y48G1A.5 YGL238W
ORTHOMCL2726	Clr Emb Lvl Ste Unc Lva Sck	14922.m00062 F55A11.2 FBpp0080390 Minc13657 Tsp_03009 YLR026C
ORTHOMCL2727		14923.m00297 FBpp0084955 Minc05268 Tsp_02540 Y43C5A.6a YER095W
ORTHOMCL2731	Clr Emb Lon early_larval_arrest Gro	14929.m00395 FBpp0073806 Minc02945 Tsp_00437 Y49E10.2 YPL059W
ORTHOMCL2734	thin Emb Gro	14930.m00335 F43G9.3 FBpp0088485 Minc15217 Tsp_10011 YHR002W
ORTHOMCL2736	Ste Lva	14930.m00349 FBpp0084959 Minc01679 T24B8.1 Tsp_09338 YBL092W
ORTHOMCL2737		14931.m00314 C23H3.4a FBpp0086842 Minc05450 Tsp_08839 YMR296C
ORTHOMCL2740	Emb Lvl Ste Lva transgene_subcellular_localization_abnormal	14933.m00221 D1054.15 FBpp0073459 Minc06925 Tsp_06269 YPL151C
ORTHOMCL2750	distal_tip_cell_migration_abnormal Pch Sle Emb Lon Ste Lva early_larval_arrest Stp Gro	14943.m00197 FBpp0087045 Minc10930 Tsp_05558 W07E6.1 YNL061W
ORTHOMCL2752		14946.m00538 FBpp0074691 Minc04376a R11G1.4a Tsp_06293 YNL161W
ORTHOMCL2754	Emb Lvl Ste Unc Bmd Gro	14950.m01850 FBpp0078205 Minc07625 T16H12.4 Tsp_04726 YLR005W
ORTHOMCL2756	Emb	14950.m01860 FBpp0080890 Minc03454 Tsp_00175 Y6D11A.2 YNR035C
ORTHOMCL2761		14952.m01380 FBpp0080114 Minc02769 Tsp_09497 Y6B3A.1a YDR170C
ORTHOMCL2781	Emb Ste Lva transgene_subcellular_localization_abnormal	14955.m00257 F25H2.10 FBpp0078134 Minc02151 Tsp_06972 YLR340W
ORTHOMCL2783		14956.m00503 FBpp0077424 Minc15982 T12E12.4b Tsp_06787 YLL001W
ORTHOMCL2784	WT	14956.m00507 FBpp0085657 Minc08367 T05E11.4 Tsp_10437 YHL022C
ORTHOMCL2786	WT	14956.m00534 FBpp0072481 Minc07771 Tsp_10889 Y54G2A.18 YDL072C
ORTHOMCL2791	WT	14958.m00349 F17E5.2 FBpp0075714 Minc15201 Tsp_03773 YNL083W
ORTHOMCL2799	WT	14961.m04940 C52D10.12 FBpp0112509 Minc11072 Tsp_07063 YOL060C
ORTHOMCL2805	WT	14961.m05002 C01G5.6 FBpp0074054 Minc05030 Tsp_05024 YER143W
ORTHOMCL2806	WT	14961.m05031 B0285.4 FBpp0080320 Minc12793 Tsp_08223 YDR435C
ORTHOMCL2807		14961.m05052 C44C1.4a FBpp0081548 Minc06525 Tsp_08612 YGL095C
ORTHOMCL2812	Emb Ste Lva	14961.m05136 FBpp0080723 Minc04840 Tsp_03388 Y106G6H.3 YGL030W

ORTHOMCL2819	Emb Bmd	14961.m05187 FBpp0077363 Minc08957 Tsp_03568 Y110A7A.4 YOR074C
ORTHOMCL2824	late_larval_arrest	14961.m05276 FBpp0072020 Minc13544 Tsp_06741 Y73B6BL.3 YHR069C
ORTHOMCL2827	Emb Lvl Ste Cyk Lva Mul transgene_subcellular_localization_abnormal Gro	14961.m05290 C50F2.3 FBpp0086749 Minc14510 Tsp_03302 YDR416W
ORTHOMCL2831		14963.m01769 F46B6.6a FBpp0084662 Minc07199 Tsp_07892 YOL023W
ORTHOMCL2834	Emb Lva	14963.m01791 FBpp0083105 Minc12411 Tsp_06065 Y67H2A.1 YLR277C
ORTHOMCL2835		14963.m01815 F32D8.14 FBpp0080011 Minc10490 Tsp_06588 YGR172C
ORTHOMCL2837		14965.m00422 C38C10.5b FBpp0072453 Minc03690 Tsp_03799 YLR071C
ORTHOMCL2838	Emb Pvl Ste Cyk Lva Sck transgene_expression_increased Stp Gro Mul	14965.m00425 FBpp0074756 Minc12788 T22D1.10 Tsp_01893 YPL235W
ORTHOMCL2843	Emb Ste Cyk Mul	14968.m01448 FBpp0085619 Minc11093 Tsp_05750 W03D2.4 YBR088C
ORTHOMCL2844	Unc Lva Gro	14968.m01475 FBpp0078362 Minc10954 R06A4.9 Tsp_10488 YNL317W
ORTHOMCL2845	Emb Unc	14968.m01479 F11H8.1 FBpp0086711 Minc05186 Tsp_09278 YPR066W
ORTHOMCL2846	WT	14968.m01493 F45H10.1 FBpp0100026 Minc11518 Tsp_07602 YBR006W
ORTHOMCL2848		14971.m02793 FBpp0076600 Minc14752 Tsp_10065 Y110A7A.17a YBL084C
ORTHOMCL2849	WT	14971.m02795 FBpp0082457 Minc00590 Tsp_10027 Y71F9B.2 YGR046W
ORTHOMCL2855	Pch Emb Pvl Ste Lva Sck Gro	14971.m02877 FBpp0088519 Minc04224 Tsp_07475 Y48B6A.1 YMR049C
ORTHOMCL2856	WT	14971.m02879 FBpp0081368 Minc04225 T03F1.12 Tsp_03394 YJL004C
ORTHOMCL2863	Rup	14972.m07020 FBpp0088843 Minc00816 T07A9.6 Tsp_07635 YNL128W
ORTHOMCL2864	WT	14972.m07024 FBpp0083416 Minc00315 Tsp_01354 YNL168C ZK688.3
ORTHOMCL2867	Clr Emb pale Gro	14972.m07042 B0035.5 FBpp0074517 Minc03039 Tsp_02567 YNL241C
ORTHOMCL2868	WT	14972.m07043 B0035.4 FBpp0076858 Minc10439 Tsp_11074 YNL153C
ORTHOMCL2869	WT	14972.m07048 FBpp0086975 Minc09338a Tsp_06712 YPR140W ZK809.2
ORTHOMCL2872	Ste Lva	14972.m07055 FBpp0089284 Minc01136 Tsp_09334 YPL218W ZK180.4
ORTHOMCL2873	small Prl Muv intestinal_morphology_abnormal Emb Pvl Ste Unc germ_cell_morphology_abnormal Lva fertility_abnormal unclassified Ced Gro	14972.m07056 FBpp0083975 Minc09035 T19E7.3 Tsp_00471 YPL120W
ORTHOMCL2874		14972.m07058 FBpp0083801 Minc14657 Tsp_08209 Y77E11A.13a YLR208W
ORTHOMCL2876	WT	14972.m07114 FBpp0080854 K07A3.1 Minc04259 Tsp_00778 YLR377C
ORTHOMCL2883	Emb Lvl Ste Unc Lva Ocs	14972.m07172 F25H2.9 FBpp0086066 Minc15898 Tsp_05973 YGR253C
ORTHOMCL2885		14972.m07201 FBpp0083954 Minc12863 Tsp_06709 YAL021C ZC518.3b
ORTHOMCL2886		14972.m07206 F32B6.8b FBpp0083411 Minc00302 Tsp_06919 YOR070C
ORTHOMCL2893	Egl Emb Ste Lva early_larval_arrest Stp Gro	14972.m07291 F32E10.1 FBpp0080211 Minc08030 Tsp_04317 YGR145W
ORTHOMCL2896	WT	14972.m07317 C33F10.2 FBpp0070698 Minc04220a Tsp_01646 YMR055C
ORTHOMCL2900	WT	14972.m07357 C18B12.6 FBpp0070085 Minc03018 Tsp_11066 YML067C
ORTHOMCL2911	spontaneous_mutation_rate_increased	14972.m07472 F29C4.6 FBpp0087712 Minc15382 Tsp_06711 YGL211W
ORTHOMCL2913		14972.m07494 FBpp0083646 Minc15848 R160.1a Tsp_09623 YOL062C
ORTHOMCL2914		14972.m07496 FBpp0087637 Minc17969 T07A9.9a Tsp_00145 YPL093W
ORTHOMCL2917		14972.m07515 C27B7.1b FBpp0082521 Minc16586 Tsp_05766 YNL246W
ORTHOMCL2919		14972.m07521 FBpp0086318 Minc11087 Tsp_09296 Y38F2AL.3a YKL080W
ORTHOMCL2922	Unc	14972.m07554 F46H6.1 FBpp0074665 Minc07867 Tsp_05197 YDL135C
ORTHOMCL2926	WT	14972.m07595 FBpp0070249 Minc09525 Tsp_06067 YDR313C ZK632.12
ORTHOMCL2929	Pvl	14972.m07600 F42G8.6 FBpp0079295 Minc09523 Tsp_04285 YHR111W
ORTHOMCL2933	fat_content_reduced	14972.m07651 FBpp0083132 Minc12088 Tsp_08794 Y41D4A.6 YMR293C
ORTHOMCL2934	WT	14972.m07689 FBpp0075151 H21P03.1 Minc15628 Tsp_11560 YOR298C-A
ORTHOMCL2936		14972.m07699 F44A6.1b FBpp0074937 Minc04257 Tsp_01138 YLR250W
ORTHOMCL2945		14972.m07767 C10G11.5a FBpp0077845 Minc13899 Tsp_01576 YDR531W
ORTHOMCL2955	spontaneous_mutation_rate_increased	14972.m07885 FBpp0080203 H26D21.2 Minc15984 Tsp_09659 YOL090W
ORTHOMCL2960	WT	14972.m07948 F39C12.1 FBpp0077507 Minc15225 Tsp_05070 YBL104C
ORTHOMCL2963	Emb Unc Ste Rup Lva Sck transgene_expression_increased Adl transgene_subcellular_localization_abnormal	14973.m02632 F57B9.2 FBpp0111584 Minc13530 Tsp_05273 YCR093W

ORTHOMCL2964	Emb Lvl Ste Sck Ocs	14973.m02646 F49C12.8 FBpp0083687 Minc02773 Tsp_03448 YPR108W
ORTHOMCL2965		14973.m02649 FBpp0082504 Minc03831 Tsp_01372 Y54F10AL.1a YBR187W
ORTHOMCL2968	Emb Unc oogenesis_abnormal Lva Gro	14973.m02695 FBpp0078880 K10D2.6 Minc08943 Tsp_02446 YHR042W
ORTHOMCL2971	Clr Emb Pvl Ste transgene_subcellular_localization_abnormal	14973.m02705 C50C3.6 FBpp0087124 Minc14825 Tsp_01598 YHR165C
ORTHOMCL2976		14974.m00825 FBpp0073204 Minc09341 Tsp_08736 YLR382C ZK524.3a
ORTHOMCL2977	Dpy Unc	14974.m00828 FBpp0078052 Minc09240 Tsp_11355 Y65B4A.1 YNL286W
ORTHOMCL2978	WT	14974.m00829 FBpp0076826 Minc08389 Tsp_08941 Y65B4A.8 YGR277C
ORTHOMCL2979	Emb Ste Unc Lva transgene_subcellular_localization_abnormal Gro	14974.m00831 F28H1.3 FBpp0089366 Minc09243 Tsp_10224 YOR335C
ORTHOMCL2980	Emb Pvl Unc Rup Nmo Stp	14974.m00843 F33H2.5 FBpp0083800 Minc01164 Tsp_07270 YNL262W
ORTHOMCL2984	WT	14975.m04343 FBpp0080551 Minc16065 Tsp_00413 YDR221W ZK1307.8
ORTHOMCL2985	Egl early_larval_arrest	14975.m04348 FBpp0076918 Minc07697 Tsp_05519 YDR496C ZK945.3
ORTHOMCL2988	WT	14975.m04383 FBpp0077750 Minc14486 T13H5.7 Tsp_01350 YNL072W
ORTHOMCL2990	Him	14975.m04403 D2085.6 FBpp0086042 Minc11542 Tsp_10141 YPL175W
ORTHOMCL2993	WT	14975.m04453 C15F1.6 FBpp0073017 Minc16185 Tsp_07269 YDL015C
ORTHOMCL2994	WT	14975.m04463 FBpp0082929 Minc08799 Tsp_10309 Y110A2AM.3 YER100W
ORTHOMCL3004	Emb Unc	14977.m04860 F59G1.5 FBpp0070363 Minc14380 Tsp_10590 YER075C
ORTHOMCL3007		14977.m04879 FBpp0086640 Minc16448 Tsp_06110 Y48E1A.1a YOR341W
ORTHOMCL3009	Emb Gro	14977.m04906 F56D1.3 FBpp0086704 Minc03489 Tsp_04008 YPL013C
ORTHOMCL3010	Lva early_larval_arrest Gro	14977.m04928 F44G4.1 FBpp0079946 Minc00314 Tsp_02353 YHR088W
ORTHOMCL3011		14977.m04933 E04A4.4a FBpp0087449 Minc17950 Tsp_05739 YKR079C
ORTHOMCL3012		14977.m04967 FBpp0081906 Minc04290 Tsp_00229 YOR143C ZK637.9b
ORTHOMCL3013	Clr distal_tip_cell_migration_abnormal Emb Pvl Ste Lva Sck transgene_subcellular_localization_abnormal Gro	14977.m04984 FBpp0083684 Minc16484 T05C12.7 Tsp_04075 YDR212W
ORTHOMCL3017		14977.m05014 C47D12.1a FBpp0085431 Minc18017 Tsp_10464 YHR099W
ORTHOMCL3018	Emb	14977.m05017 F53G2.6 FBpp0077399 Minc12053 Tsp_08210 YOR160W
ORTHOMCL3020	Pch Emb Unc Rup Bmd Gro	14977.m05034 FBpp0075839 Minc01765 Tsp_03661 YKL028W ZK550.4
ORTHOMCL3025	Pch Emb	14977.m05069 F33A8.1 FBpp0080638 Minc02744 Tsp_05710 YGR278W
ORTHOMCL3027	WT	14977.m05106 C08B11.8 FBpp0079595 Minc07767 Tsp_07541 YOR002W
ORTHOMCL3031	Emb Lva reduced_brood_size	14979.m04376 F37C12.1 FBpp0086387 Minc07695 Tsp_05442 YKL095W
ORTHOMCL3035	WT	14979.m04412 FBpp0112471 Minc07622 Tsp_00228 Y48G9A.1 YGL195W
ORTHOMCL3037		14979.m04452 FBpp0085527 Minc15808a R01H10.3c Tsp_01713 YLR429W
ORTHOMCL3045	WT	14979.m04523 FBpp0083167 Minc01703 Tsp_10032 Y71H2AM.6 YIL083C
ORTHOMCL3052	Pvl Unc Gro	14979.m04604 FBpp0070643 Minc00400 Tsp_06359 W02D7.7 YGL200C
ORTHOMCL3057	Emb	14979.m04656 FBpp0071503 Minc07330 Tsp_03297 Y50D7A.2 YER171W
ORTHOMCL3062	WT	14980.m02684 FBpp0071817 M03C11.5 Minc19020 Tsp_00240 YPR024W
ORTHOMCL3064	Emb Ste Lva	14980.m02695 FBpp0073003 Minc01440a Tsp_01788 Y54F10BM.2 YAL035W
ORTHOMCL3072	Dpy Emb Lvl Unc Bmd Lva transgene_expression_increased Gro	14980.m02764 B0285.1 FBpp0078014 Minc03854 Tsp_01670 YKL139W
ORTHOMCL3078	Emb Pvl Ste Unc Lva Sck Stp Gro	14980.m02812 FBpp0074918 Minc17656 T20B12.1 Tsp_05597 YNL313C
ORTHOMCL3092	WT	14981.m02416 FBpp0074822 Minc00804 Tsp_05916 Y55F3AM.4 YNR007C
ORTHOMCL3093		14981.m02419 FBpp0081262 H17B01.4a Minc11519 Tsp_05809 YCL045C
ORTHOMCL3095	Emb unclassified	14981.m02426 C47D12.8 FBpp0070624 Minc12332 Tsp_10891 YPL022W
ORTHOMCL3096	WT	14981.m02430 FBpp0110549 Minc11505 Tsp_08058 Y54E2A.12 YFL027C
ORTHOMCL3097	Dpy Emb Lvl Ric Unc Bmd Lva Gro	14981.m02432 F08D12.1 FBpp0083319 Minc11506 Tsp_08515 YPL210C
ORTHOMCL3098		14981.m02447 FBpp0081317 Minc17521 Tsp_00580 Y17G7B.5a YBL023C
ORTHOMCL3101	Dpy small Slu Emb Pvl Lva Stp Gro	14981.m02456 FBpp0079590 Minc16915 Tsp_05534 YOL141W ZK970.2
ORTHOMCL3102	lipid_depleted Lva reduced_brood_size	14982.m02207 FBpp0089153 Minc17605 Tsp_09896 Y48C3A.7 YLL034C
ORTHOMCL3107		14982.m02242 F37C12.13a FBpp0074129 Minc00386 Tsp_00006 YDR280W
ORTHOMCL3109	Emb Sck	14982.m02265 FBpp0074660 M03C11.7 Minc11621 Tsp_07851 YDR473C

ORTHOMCL3114	WT	14990.m07668 FBpp0082215 K11G12.5 Minc03312 Tsp_02240 YLR348C
ORTHOMCL3115	Ste	14990.m07677 FBpp0083629 Minc16804 Tsp_00416 W09C3.4 YNR003C
ORTHOMCL3116	WT	14990.m07684 FBpp0087865 Minc08963 Tsp_08777 Y71G12B.8 YLL008W
ORTHOMCL3120		14990.m07719 FBpp0073073 Minc16016 Tsp_10095 Y105E8B.8a YML130C
ORTHOMCL3122	distal_tip_cell_migration_abnormal Pch Emb Pvl Unc Ste Lva Sck transgene_expression_increased Gro	14990.m07752 FBpp0087764 Minc00339 Tsp_03480 Y55F3AR.3 YJL008C
ORTHOMCL3123	Emb Lvl Lon Unc Bmd Lva Sck early_larval_arrest transgene_subcellular_localization_abnormal	14990.m07753 FBpp0073847 K02F2.2 Minc17349a Tsp_04769 YER043C
ORTHOMCL3124	Emb Lvl Ste Lva transgene_subcellular_localization_abnormal Gro	14990.m07762 F36A2.6 FBpp0086269 Minc18053 Tsp_02186 YOL040C
ORTHOMCL3125	Emb Lvl Ste Lva	14990.m07764 C30F8.2 FBpp0070584 Minc18052 Tsp_05300 YLR447C
ORTHOMCL3127	Emb	14990.m07815 FBpp0083514 Minc18245 Tsp_09727 Y47D3A.29 YNL102W
ORTHOMCL3130	Emb Ste Lva Sck	14990.m07831 FBpp0082591 Minc17095 Tsp_11644 Y54E10BR.6 YDR404C
ORTHOMCL3132	Emb Ste reduced_brood_size	14990.m07835 FBpp0071248 Minc05202 Tsp_10801 Y54E10BL.6 YJL128C
ORTHOMCL3135	Prl Emb Mlt Lvl Ric Ste Unc Lva Gro transgene_subcellular_localization_abnormal	14990.m07862 FBpp0074278 Minc16917 Tsp_05353 Y34D9A.10 YPR173C
ORTHOMCL3144	WT	14990.m07967 FBpp0079327 M01E5.2 Minc06136b Tsp_05365 YHR168W
ORTHOMCL3149		14990.m07989 FBpp0075866 M01B12.5a Minc11010 Tsp_08684 YOR119C
ORTHOMCL3150	thin Lva Gro	14990.m08001 C10H11.8 FBpp0071303 Minc04061 Tsp_00266 YNL006W
ORTHOMCL3153	Emb	14990.m08017 FBpp0088408 Minc16206 Tsp_10364 W08E3.3 YBR025C
ORTHOMCL3155	Emb Pvl Ste Unc Rup Gro	14990.m08048 FBpp0086223 Minc17683 Tsp_05685 Y47G6A.8 YKL113C
ORTHOMCL3162	Emb Lva reduced_brood_size	14990.m08091 B0205.6 FBpp0079874 Minc04068 Tsp_02416 YCL017C
ORTHOMCL3164	Emb Mlt Lvl Lon Unc Ste Lva unclassified Gro	14990.m08097 FBpp0078973 Minc11011 Tsp_08094 Y48B6A.3 YOR048C
ORTHOMCL3168		14990.m08127 F02E9.4b FBpp0087003 Minc11800 Tsp_00655 YOL004W
ORTHOMCL3169		14990.m08143 FBpp0087984 Minc13935b T08G11.1a Tsp_05552 YLL040C
ORTHOMCL3170		14990.m08144 FBpp0077497 Minc11006 Tsp_08848 Y65B4BR.4a YER125W
ORTHOMCL3175	Emb	14992.m10836 F26F2.7 FBpp0083043 Minc10353 Tsp_04290 YER140W
ORTHOMCL3179	embryonic_morphology_abnormal gastrulation_abnormal Emb Ste Mig cell_proliferation_increased Ced Stp Gro	14992.m10856 FBpp0087110 Minc09753 T21H3.3 Tsp_03217 YBR109C
ORTHOMCL3181		14992.m10877 C47E12.5a FBpp0087583 Minc17080 Tsp_02492 YKL210W
ORTHOMCL3182	Emb Ste Sck transgene_subcellular_localization_abnormal	14992.m10882 FBpp0070402 M03F8.3 Minc02375 Tsp_09327 YLR117C
ORTHOMCL3188		14992.m10913 C37H5.6a FBpp0083395 Minc06952 Tsp_02901 YNL220W
ORTHOMCL3191	WT	14992.m10931 FBpp0086720 Minc17033 Tsp_10866 Y60A3A.13 YPR047W
ORTHOMCL3195	WT	14992.m10962 F53F4.3 FBpp0085690 Minc16973 Tsp_03184 YNL148C
ORTHOMCL3199	Emb Mei Pvl Lvl Unc Ste protein_subcellular_localization_abnormal chromosome_segregation_abnormal unclassified	14992.m10991 F18E2.3 FBpp0078977 Minc15566 Tsp_06183 YIL026C
ORTHOMCL3200	Pvl Ste early_larval_arrest	14992.m10995 FBpp0079607 Minc02738 Tsp_08939 W09C5.1 YER126C
ORTHOMCL3208	Clr Pch Gro	14992.m11113 C24G6.8 FBpp0081196 Minc18255 Tsp_02906 YBL057C
ORTHOMCL3209		14992.m11127 FBpp0071740 Minc11746 T04H1.4b Tsp_00253 YNL250W
ORTHOMCL3221	late_larval_arrest Lva Gro	14992.m11287 FBpp0087709 Minc02974a Tsp_03427 Y39B6A.14 YGR245C
ORTHOMCL3222	germ_cell_development_abnormal Emb gonad_development_abnormal	14992.m11312 FBpp0081640 Minc13153 Tsp_00410 Y57E12AL.5 YHR058C
ORTHOMCL3225		14992.m11326 FBpp0078583 Minc00785 Tsp_02484 YLR239C ZC410.7b
ORTHOMCL3226	Emb Lvl Unc Bmd Lva transgene_expression_increased Stp Gro	14992.m11328 B0035.11 FBpp0078353 Minc17189 Tsp_05978 YOR123C
ORTHOMCL3228	WT	14992.m11360 C01G10.10 FBpp0074583 Minc13298 Tsp_05524 YDL104C
ORTHOMCL3230		14992.m11367 F41E6.4a FBpp0082285 Minc12906 Tsp_02930 YNL201C

ORTHOMCL3232	Emo Emb Lvl ovulation_abnormal Ste Lva unclassified reduced_brood_size transgene_subcellular_localization_abnormal Gro Stp	14992.m11391 C17H12.14 FBpp0078349 Minc12533 Tsp_00958 YOR332W
ORTHOMCL3234	reduced_brood_size developmental_delay_postembryonic	14992.m11407 FBpp0071277 Minc16223 Tsp_00811 W03F9.1 YGR211W
ORTHOMCL3235	WT	14992.m11412 F41E6.9 FBpp0074964 Minc12903 Tsp_06047 YDR486C
ORTHOMCL3236	WT	14992.m11418 C01G10.8 FBpp0085258 Minc18254a Tsp_02541 YDR214W
ORTHOMCL3237	Spn Emb Cyk unclassified	14992.m11420 F26E4.10 FBpp0087926 Minc14843 Tsp_06192 YMR239C
ORTHOMCL3238	WT	14992.m11424 FBpp0082570 K08H10.9 Minc14484 Tsp_08307 YOR115C
ORTHOMCL3239		15009.m00160 FBpp0073900 Minc14666 Tsp_03047 Y39B6A.3b YLL027W
ORTHOMCL3241	Lvl late_larval_arrest Lva	15032.m00057 F55B12.4 FBpp0078373 Minc13960a Tsp_04511 YER168C
ORTHOMCL3244	Emb Ste Lva early_larval_arrest Gro	15083.m00074 C47E12.7 FBpp0080052 Minc10026 Tsp_07494 YDR087C
ORTHOMCL3245	Egl distal_tip_cell_migration_abnormal ectopic_expression_transgene Emb Pvl Unc Ste Lva ray_ectopic Vul Stp Gro	15097.m00070 FBpp0076457 Minc15474 Tsp_09908 W02A11.4 YDR390C
ORTHOMCL3248	distal_tip_cell_migration_abnormal Emb Unc Bmd Lva	15131.m00095 F49D11.1 FBpp0083581 Minc10024 Tsp_12048 YDR364C
ORTHOMCL3250	Emb Lva sterile_F1 reduced_brood_size Stp Gro	15133.m00188 E02H1.1 FBpp0084729 Minc18613 Tsp_00414 YPL266W
ORTHOMCL3254	Emb Sck Stp	15158.m00054 FBpp0082356 Minc06361 Tsp_06875 Y105E8A.20 YGR171C
ORTHOMCL3256	Sle Emb Ste Lva early_larval_arrest Gro	15158.m00057 C15H11.9 FBpp0076738 Minc13549 Tsp_00837 YOR294W
ORTHOMCL3270	Sle Emb Lvl Ste Lva Sck Stp Gro	15233.m00028 FBpp0071892 Minc09547 T01C3.7 Tsp_01344 YDL014W
ORTHOMCL3271		15242.m00013 FBpp0086097 Minc08196 Tsp_02250 Y54E2A.11a YOR361C
ORTHOMCL3272	Dpy Slu Emb Ste Lva Sck transgene_subcellular_localization_abnormal	15258.m00017 F54E7.2 FBpp0075614 Minc07126 Tsp_07028 YOR369C
ORTHOMCL3273	WT	15263.m00046 F55A3.1 FBpp0072779 Minc07559 Tsp_10121 YIL030C
ORTHOMCL3274	WT	15276.m00013 FBpp0077790 Minc18075 R09E12.3 Tsp_03199 YOR027W
ORTHOMCL3281		15304.m00117 C47B2.6b FBpp0072455 Minc18399 Tsp_10020 YBR019C
ORTHOMCL3287	small Emb Mlt Lvl Unc fat_content_reduced Lva Adl Gro	15410.m00008 FBpp0078598 Minc12641 T27F7.1 Tsp_01988 YKL041W
ORTHOMCL3289	Emb	15432.m00013 FBpp0081087 Minc15246 Tsp_03194 Y75B8A.14 YLR243W
ORTHOMCL3290	Slu Pvl Unc Stp Gro	15434.m00030 FBpp0072976 Minc06101 T27A3.2 Tsp_11048 YBR058C
ORTHOMCL3296	Stp	15508.m00009 C10C6.1 FBpp0075315 Minc13998 Tsp_09405 YFL033C
ORTHOMCL3300		15544.m00027 F19B6.2a FBpp0075952 Minc05176 Tsp_00718 YGR048W

Supplementary Table 9. Gene counts of the 274 Nematode Orthologous Groups (including the 85 nematode-specific single-copy genes).

Orthologous group	**Number of genes**			
ID	***C. elegans***	***M. incognita***	***B. malayi***	***T. spiralis***
ORTHOMCL0(421_genes,4_taxa):	*2*	*24*	*194*	*201*
ORTHOMCL40(59_genes,4_taxa):	33	19	2	5
ORTHOMCL221(20_genes,4_taxa):	14	4	1	1
ORTHOMCL241(19_genes,4_taxa):	9	8	1	1
ORTHOMCL258(18_genes,4_taxa):	9	5	1	3
ORTHOMCL275(17_genes,4_taxa):	9	6	1	1
ORTHOMCL360(14_genes,4_taxa):	6	4	2	2
ORTHOMCL410(13_genes,4_taxa):	3	1	1	8
ORTHOMCL481(12_genes,4_taxa):	1	1	1	9
ORTHOMCL548(11_genes,4_taxa):	2	6	2	1
ORTHOMCL560(11_genes,4_taxa):	6	1	3	1
ORTHOMCL592(11_genes,4_taxa):	5	4	1	1
ORTHOMCL637(10_genes,4_taxa):	1	2	6	1
ORTHOMCL639(10_genes,4_taxa):	3	4	1	2
ORTHOMCL724(10_genes,4_taxa):	4	3	2	1
ORTHOMCL741(10_genes,4_taxa):	2	4	3	1
ORTHOMCL817(9_genes,4_taxa):	2	3	1	3
ORTHOMCL886(9_genes,4_taxa):	1	2	2	4
ORTHOMCL896(9_genes,4_taxa):	3	1	2	3
ORTHOMCL930(9_genes,4_taxa):	1	6	1	1
ORTHOMCL934(9_genes,4_taxa):	3	3	1	2
ORTHOMCL969(9_genes,4_taxa):	1	5	2	1
ORTHOMCL1085(8_genes,4_taxa):	2	4	1	1
ORTHOMCL1110(8_genes,4_taxa):	2	1	2	3
ORTHOMCL1140(8_genes,4_taxa):	2	3	2	1
ORTHOMCL1168(8_genes,4_taxa):	1	3	2	2
ORTHOMCL1268(8_genes,4_taxa):	2	1	1	4
ORTHOMCL1289(8_genes,4_taxa):	1	2	2	3
ORTHOMCL1295(8_genes,4_taxa):	4	1	2	1
ORTHOMCL1567(7_genes,4_taxa):	1	2	2	2
ORTHOMCL1596(7_genes,4_taxa):	2	2	1	2
ORTHOMCL1646(7_genes,4_taxa):	1	3	1	2
ORTHOMCL1674(7_genes,4_taxa):	3	2	1	1
ORTHOMCL1692(7_genes,4_taxa):	1	4	1	1
ORTHOMCL1713(7_genes,4_taxa):	1	3	1	2
ORTHOMCL1808(7_genes,4_taxa):	2	2	2	1
ORTHOMCL1816(7_genes,4_taxa):	2	2	1	2
ORTHOMCL1820(7_genes,4_taxa):	1	4	1	1
ORTHOMCL1840(7_genes,4_taxa):	4	1	1	1
ORTHOMCL1939(7_genes,4_taxa):	2	1	2	2
ORTHOMCL1943(7_genes,4_taxa):	1	4	1	1
ORTHOMCL2010(7_genes,4_taxa):	2	2	2	1
ORTHOMCL2040(7_genes,4_taxa):	3	2	1	1
ORTHOMCL2141(7_genes,4_taxa):	1	1	1	4
ORTHOMCL2299(6_genes,4_taxa):	1	2	2	1
ORTHOMCL2380(6_genes,4_taxa):	1	1	2	2
ORTHOMCL2432(6_genes,4_taxa):	1	2	2	1
ORTHOMCL2464(6_genes,4_taxa):	1	3	1	1
ORTHOMCL2496(6_genes,4_taxa):	2	2	1	1

ORTHOMCL2499(6_genes,4_taxa):	1	3	1	1
ORTHOMCL2520(6_genes,4_taxa):	1	2	2	1
ORTHOMCL2524(6_genes,4_taxa):	1	1	1	3
ORTHOMCL2644(6_genes,4_taxa):	1	3	1	1
ORTHOMCL2669(6_genes,4_taxa):	1	2	2	1
ORTHOMCL2675(6_genes,4_taxa):	2	1	2	1
ORTHOMCL2681(6_genes,4_taxa):	1	2	1	2
ORTHOMCL2695(6_genes,4_taxa):	1	2	1	2
ORTHOMCL2732(6_genes,4_taxa):	1	3	1	1
ORTHOMCL2753(6_genes,4_taxa):	1	3	1	1
ORTHOMCL2759(6_genes,4_taxa):	1	2	2	1
ORTHOMCL2785(6_genes,4_taxa):	2	2	1	1
ORTHOMCL2787(6_genes,4_taxa):	2	1	2	1
ORTHOMCL2790(6_genes,4_taxa):	2	2	1	1
ORTHOMCL2817(6_genes,4_taxa):	1	2	2	1
ORTHOMCL2821(6_genes,4_taxa):	1	3	1	1
ORTHOMCL2842(6_genes,4_taxa):	1	2	2	1
ORTHOMCL2860(6_genes,4_taxa):	1	1	1	3
ORTHOMCL2870(6_genes,4_taxa):	2	2	1	1
ORTHOMCL2901(6_genes,4_taxa):	1	2	1	2
ORTHOMCL2946(6_genes,4_taxa):	1	2	1	2
ORTHOMCL2970(6_genes,4_taxa):	1	2	2	1
ORTHOMCL2991(6_genes,4_taxa):	1	3	1	1
ORTHOMCL3006(6_genes,4_taxa):	2	2	1	1
ORTHOMCL3028(6_genes,4_taxa):	1	2	1	2
ORTHOMCL3050(6_genes,4_taxa):	2	1	1	2
ORTHOMCL3051(6_genes,4_taxa):	1	2	1	2
ORTHOMCL3053(6_genes,4_taxa):	1	3	1	1
ORTHOMCL3069(6_genes,4_taxa):	1	2	1	2
ORTHOMCL3091(6_genes,4_taxa):	1	2	1	2
ORTHOMCL3100(6_genes,4_taxa):	1	1	1	3
ORTHOMCL3108(6_genes,4_taxa):	1	2	1	2
ORTHOMCL3112(6_genes,4_taxa):	1	2	1	2
ORTHOMCL3172(6_genes,4_taxa):	1	2	1	2
ORTHOMCL3185(6_genes,4_taxa):	1	3	1	1
ORTHOMCL3190(6_genes,4_taxa):	1	1	1	3
ORTHOMCL3216(6_genes,4_taxa):	2	2	1	1
ORTHOMCL3219(6_genes,4_taxa):	1	2	1	2
ORTHOMCL3286(6_genes,4_taxa):	3	1	1	1
ORTHOMCL3515(5_genes,4_taxa):	1	2	1	1
ORTHOMCL3530(5_genes,4_taxa):	1	1	1	2
ORTHOMCL3539(5_genes,4_taxa):	1	2	1	1
ORTHOMCL3540(5_genes,4_taxa):	1	2	1	1
ORTHOMCL3552(5_genes,4_taxa):	1	2	1	1
ORTHOMCL3585(5_genes,4_taxa):	1	2	1	1
ORTHOMCL3588(5_genes,4_taxa):	1	1	2	1
ORTHOMCL3590(5_genes,4_taxa):	2	1	1	1
ORTHOMCL3599(5_genes,4_taxa):	1	1	1	2
ORTHOMCL3612(5_genes,4_taxa):	1	1	1	2
ORTHOMCL3624(5_genes,4_taxa):	1	2	1	1
ORTHOMCL3656(5_genes,4_taxa):	1	1	2	1
ORTHOMCL3657(5_genes,4_taxa):	1	2	1	1
ORTHOMCL3658(5_genes,4_taxa):	1	2	1	1
ORTHOMCL3665(5_genes,4_taxa):	1	2	1	1

ORTHOMCL3713(5_genes,4_taxa):	1	2	1	1
ORTHOMCL3718(5_genes,4_taxa):	1	2	1	1
ORTHOMCL3728(5_genes,4_taxa):	1	2	1	1
ORTHOMCL3737(5_genes,4_taxa):	1	2	1	1
ORTHOMCL3740(5_genes,4_taxa):	1	1	1	2
ORTHOMCL3796(5_genes,4_taxa):	1	1	1	2
ORTHOMCL3799(5_genes,4_taxa):	1	2	1	1
ORTHOMCL3815(5_genes,4_taxa):	1	2	1	1
ORTHOMCL3822(5_genes,4_taxa):	1	2	1	1
ORTHOMCL3825(5_genes,4_taxa):	1	2	1	1
ORTHOMCL3833(5_genes,4_taxa):	1	2	1	1
ORTHOMCL3859(5_genes,4_taxa):	1	2	1	1
ORTHOMCL3870(5_genes,4_taxa):	1	2	1	1
ORTHOMCL3923(5_genes,4_taxa):	2	1	1	1
ORTHOMCL3926(5_genes,4_taxa):	1	2	1	1
ORTHOMCL3943(5_genes,4_taxa):	1	2	1	1
ORTHOMCL3958(5_genes,4_taxa):	1	1	1	2
ORTHOMCL3960(5_genes,4_taxa):	2	1	1	1
ORTHOMCL3978(5_genes,4_taxa):	1	1	1	2
ORTHOMCL3980(5_genes,4_taxa):	1	1	2	1
ORTHOMCL4002(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4006(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4009(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4012(5_genes,4_taxa):	1	1	2	1
ORTHOMCL4016(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4027(5_genes,4_taxa):	2	1	1	1
ORTHOMCL4028(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4036(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4040(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4043(5_genes,4_taxa):	2	1	1	1
ORTHOMCL4049(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4050(5_genes,4_taxa):	1	1	1	2
ORTHOMCL4083(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4089(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4095(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4103(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4114(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4121(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4131(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4141(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4142(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4148(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4150(5_genes,4_taxa):	2	1	1	1
ORTHOMCL4151(5_genes,4_taxa):	1	1	1	2
ORTHOMCL4155(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4160(5_genes,4_taxa):	1	1	1	2
ORTHOMCL4162(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4164(5_genes,4_taxa):	1	1	1	2
ORTHOMCL4165(5_genes,4_taxa):	1	1	1	2
ORTHOMCL4179(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4181(5_genes,4_taxa):	1	1	1	2
ORTHOMCL4185(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4205(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4219(5_genes,4_taxa):	1	2	1	1

ORTHOMCL4225(5_genes,4_taxa):	1	1	1	2
ORTHOMCL4232(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4242(5_genes,4_taxa):	2	1	1	1
ORTHOMCL4252(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4260(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4261(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4283(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4287(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4288(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4310(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4323(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4327(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4337(5_genes,4_taxa):	1	1	1	2
ORTHOMCL4347(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4349(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4361(5_genes,4_taxa):	2	1	1	1
ORTHOMCL4373(5_genes,4_taxa):	1	1	1	2
ORTHOMCL4375(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4379(5_genes,4_taxa):	1	1	1	2
ORTHOMCL4406(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4416(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4417(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4419(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4427(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4441(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4443(5_genes,4_taxa):	1	1	1	2
ORTHOMCL4451(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4459(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4493(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4512(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4525(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4560(5_genes,4_taxa):	1	2	1	1
ORTHOMCL4887(4_genes,4_taxa):	1	1	1	1
ORTHOMCL4904(4_genes,4_taxa):	1	1	1	1
ORTHOMCL4953(4_genes,4_taxa):	1	1	1	1
ORTHOMCL4963(4_genes,4_taxa):	1	1	1	1
ORTHOMCL4982(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5007(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5011(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5013(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5044(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5045(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5056(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5057(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5058(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5067(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5084(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5111(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5142(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5147(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5148(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5155(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5157(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5160(4_genes,4_taxa):	1	1	1	1

ORTHOMCL5167(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5211(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5213(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5241(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5254(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5261(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5275(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5285(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5321(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5330(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5367(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5374(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5396(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5414(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5417(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5418(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5436(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5443(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5453(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5475(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5483(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5484(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5489(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5518(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5522(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5527(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5528(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5540(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5546(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5564(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5571(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5575(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5585(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5586(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5595(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5602(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5632(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5647(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5652(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5655(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5673(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5687(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5689(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5691(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5707(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5715(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5730(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5737(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5742(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5754(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5769(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5772(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5798(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5803(4_genes,4_taxa):	1	1	1	1

ORTHOMCL5805(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5818(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5830(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5837(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5840(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5852(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5864(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5886(4_genes,4_taxa):	1	1	1	1
ORTHOMCL5887(4_genes,4_taxa):	1	1	1	1

Supplementary Table 10. Gene Onthology functions significantly enriched (at P<0.01) or depleted when intra- or inter-specific orthologous groups were compared to the complete repertoire of GO terms for *T. spiralis*.

		P-value							
GI id	**GO Descriptor**	***T. spiralis* only**		**Ts/Ce**		**Ts/Bm**		**Ts/Mi**	
		Depleted	**Enriched**	**Depleted**	**Enriched**	**Depleted**	**Enriched**	**Depleted**	**Enriched**
Biological process (1052 GO terms total)									
GO:0006412	translation	5.74E-006	0.999998	0.0610811	0.989314	0.064482	1	0.3187	1
GO:0006508	proteolysis	0.999649	0.000545	0.16136	0.92158	0.546561	0.655336	0.1425	1
GO:0006886	intracellular protein transport	1.66E-005	0.999996	0.239829	0.937822	0.267562	1	0.577	1
GO:0016043	cellular component organization and biogenesis	8.28E-008	1	0.13137	0.972021	0.132946	1	0.2914	1
GO:0006189	de novo' IMP biosynthetic process	0.508145	1	1	0.0005968	0.976663	1	0.9902	1
GO:0006259	DNA metabolic process	1	2.03E-056	0.0199741	1	0.730211	0.54585	0.2164	1
GO:0006278	RNA-dependent DNA replication	1	1.36E-006	0.332593	1	0.593024	1	0.8041	1
GO:0006334	nucleosome assembly	1	2.38E-012	0.140746	1	0.394286	1	0.6783	1
GO:0016192	vesicle-mediated transport	0.0002398	0.999971	0.538304	0.794105	0.46109	1	0.724	1
GO:0035023	regulation of Rho protein signal transduction	0.0008004	1	0.907303	0.407687	0.998271	0.024533	0.9015	1
GO:0043170	macromolecule metabolic process	1	8.00E-012	0.290718	0.849286	0.194753	1	0.2961	1
GO:0007186	G-protein coupled receptor protein signaling pathway	0.143298	0.906975	0.999995	2.99E-005	0.332912	1	0.632	1
GO:0009060	aerobic respiration	8.59E-007	1	0.285933	1	0.551967	1	0.7804	1
GO:0009086	methionine biosynthetic process	0.508145	1	1	0.0005968	0.976663	1	0.9902	1
GO:0015074	DNA integration	0.589959	0.490799	0.198434	0.951905	0.23686	1	1	3.43E-011
Molecular Function (1542 GO terms total)									
GO:0005506	iron ion binding	2.36E-005	0.999995	0.202813	0.950421	0.812837	0.551408	0.7056	1
GO:0003677	DNA binding	0.93298	0.082455	0.0001925	0.999954	0.648266	0.536156	1	1.55E-005
GO:0003676	nucleic acid binding	0.0105466	0.992024	1	7.53E-026	0.245441	0.854829	0.7515	0.478907
GO:0003682	chromatin binding	0.0250016	1	0.660605	1	0.895258	1	1	0.0009696
GO:0005524	ATP binding	0.0066239	0.994901	0.0009113	0.99963	0.23432	0.878243	0.1482	0.96872
GO:0020037	heme binding	0.0001398	0.999954	0.121085	0.974723	0.747966	0.625207	0.6525	1
GO:0001584	rhodopsin-like receptor activity	0.169999	0.891805	0.999951	0.0002459	0.485202	1	0.7301	1
GO:0005515	protein binding	3.52E-010	1	0.132674	0.916501	0.933749	0.131785	0.696	0.541992
GO:0030414	protease inhibitor activity	1	7.38E-008	0.544904	0.677594	0.760249	0.612344	0.6622	1
GO:0031419	cobalamin binding	0.330977	1	1	6.59E-005	0.967375	1	0.9857	1
GO:0004531	deoxyribonuclease II activity	1	1.06E-063	0.0052771	1	0.246771	1	0.5441	1
GO:0004252	serine-type endopeptidase activity	1	7.17E-011	0.684065	0.545557	0.458766	1	0.7125	1
GO:0005496	steroid binding	0.330977	1	0.883123	1	0.999999	0.000354	0.9857	1
GO:0005089	Rho guanyl-nucleotide exchange factor activity	0.0004278	1	0.791292	0.581734	0.998546	0.021802	0.9038	1
GO:0003964	RNA-directed DNA polymerase activity	0.999998	6.67E-006	0.160317	1	0.613545	1	0.8086	1
GO:0003924	GTPase activity	4.27E-005	0.999993	0.11002	1	0.554904	1	0.774	1
GO:0003735	structural constituent of ribosome	5.12E-008	1	0.0205093	0.997092	0.210503	1	0.5077	1

GO:0008270	zinc ion binding	1.35E-005	0.999991	0.842932	0.214575	0.981719	0.042023	0.9529	0.128274
GO:0008565	protein transporter activity	0.0001723	0.99998	0.449074	0.846246	0.60674	1	0.8046	1
Cellular Component (645 GO terms total)									
GO:0005840	ribosome	2.53E-005	0.999992	0.0088291	1	0.189683	1	0.5335	1
GO:0016021	integral to membrane	0.003021	0.998034	0.999778	0.0005712	0.042838	0.993434	0.4608	0.850262
GO:0000786	nucleosome	1	1.91E-014	0.0684267	1	0.417637	1	0.7189	1
GO:0005576	extracellular region	1	2.07E-007	0.921581	0.181419	0.651432	0.716067	0.6214	1
GO:0005622	intracellular	0.0056329	0.996132	0.999981	5.29E-005	0.673445	0.518371	0.525	0.753943
GO:0005634	nucleus	0.999908	0.000141	2.24E-005	0.999996	0.953418	0.101527	0.9956	0.0222729

Supplementary Table 11. Gene Onthology functions significantly enriched (at P<0.01) or depleted when the 2,517 nematode orthologous groups (NOGs). The NOGS were compared to the complete proteomes of the four nematode species. Of the total of 20,208 GO ids in Biological processes 4,918 are associated with the 2,157 NOGs, and of the 27,935 Molecular Function GO ids 6,444 were associated with the 2,517 NOGS. FDR, false discovery rate. Biological Processes GOs are in blue, Molecular Function GOs are in red.

GO Id	GO in all 4 species	Go in NOGs	FDR depleted	FDR enriched	P value depleted	P value enriched
GO:0006096	105	41	1	0.002223	0.999873	0.0002809
GO:0006099	48	25	1	0.000388	0.999991	3.11E-05
GO:0006259	1044	303	1	0.001276	0.0002621	0.999881
GO:0006260	459	110	1	1	7.08E-05	0.999963
GO:0006265	37	19	1	0.001672	0.999903	0.0003489
GO:0006269	11	8	1	0.004223	0.9999	0.0009768
GO:0006270	43	23	1	0.000369	0.99999	3.68E-05
GO:0006304	32	17	1	0.001849	0.999988	0.0003174
GO:0006334	234	107	1	0	1	6.20E-13
GO:0006355	1787	288	0	1	7.53E-18	1
GO:0006396	421	163	1	0	0.999891	0.0002225
GO:0006397	95	38	1	0.002102	0.999986	4.01E-05
GO:0006412	1055	387	1	0	1	4.83E-17
GO:0006457	299	126	1	0	1	9.79E-11
GO:0006461	214	116	1	0	1	1.98E-18
GO:0006468	1554	316	0.000213	1	2.77E-05	0.999979
GO:0006754	206	73	1	0.00125	5.71E-05	1
GO:0006813	282	34	0	1	1.57E-07	1
GO:0006814	115	14	0.004691	1	0.0008716	0.999648
GO:0006817	348	47	0	1	3.31E-07	1
GO:0006836	66	5	0.002129	1	0.0009077	0.999773
GO:0006869	54	8	0.30343	1	0.0004038	1
GO:0006886	484	184	1	0	1	1.54E-11
GO:0006904	38	19	1	0.002224	0.999842	0.0005396
GO:0006913	135	52	1	0.000841	0.999719	0.0005992
GO:0007186	954	95	0	1	1.22E-30	1
GO:0007606	136	0	0	1	2.91E-17	1
GO:0009060	92	25	1	1	4.62E-06	1
GO:0015031	671	257	1	0	0.999985	3.00E-05
GO:0015074	215	97	1	0	1	1.91E-11
GO:0015986	171	73	1	0	1	9.44E-08
GO:0016042	116	6	0	1	5.56E-06	0.999999
GO:0016043	1639	577	1	0	1	6.76E-19
GO:0016070	2662	633	1	1	0.999955	0.0001856
GO:0016071	167	79	1	0	1	3.94E-12
GO:0016192	302	128	1	0	1	3.43E-07
GO:0019538	5765	1618	1	0	1	1.07E-13
GO:0043170	10151	2743	1	0	1	1.13E-11
GO:0043687	2230	497	0.04649	1	0.999615	0.0006433
GO:0044267	5610	1538	1	0	1	1.34E-06
GO:0045941	19	13	1	0.000519	0.999992	6.12E-05
GO:0051246	108	15	0.031657	1	3.99E-06	1
GO:0051258	75	39	1	0	1	1.45E-06

GO:0055114	**146**	**12**	**0**	**1**	**4.08E-13**	**1**
GO:0000104	7	6	1	0.004813	0.999965	0.0008448
GO:0001509	7	6	1	0.004813	0.999965	0.0008448
GO:0001584	631	60	0	1	1.41E-17	1
GO:0003676	6322	1653	1	0	1	2.89E-07
GO:0003677	3223	769	1	0.336103	1	1.70E-18
GO:0003700	1514	212	0	1	8.08E-20	1
GO:0003707	506	10	0	1	1.28E-43	1
GO:0003723	743	230	1	0	0.999797	0.0002855
GO:0003735	635	245	1	0	1	5.92E-19
GO:0003755	70	35	1	0	1	7.94E-07
GO:0003887	199	20	0	1	1.58E-06	0.999999
GO:0003899	114	51	1	0	0.999998	5.67E-06
GO:0003918	21	12	1	0.004167	0.999844	0.0007829
GO:0003924	273	112	1	0	1	2.53E-11
GO:0004190	227	87	1	0	0.999871	0.0002332
GO:0004194	28	19	1	0	1	5.84E-07
GO:0004219	7	6	1	0.004813	0.999965	0.0008448
GO:0004252	207	34	0.04989	1	0.0007225	0.999675
GO:0004298	71	35	1	0	1	1.22E-06
GO:0004386	435	181	1	0	0.999967	7.74E-05
GO:0004518	538	91	0.000819	1	0.999834	0.0005776
GO:0004531	134	0	0	1	4.97E-16	1
GO:0004605	7	6	1	0.004813	0.999965	0.0008448
GO:0004623	55	2	0.000287	1	8.13E-05	0.999991
GO:0004672	1571	324	0.040236	1	1.02E-09	1
GO:0004722	33	17	1	0.001748	0.999911	0.0003477
GO:0004725	240	34	0.001416	1	0.0003776	0.999801
GO:0004730	15	10	1	0.001935	0.999948	0.0003958
GO:0004888	1186	123	0	1	6.97E-20	1
GO:0005097	88	34	1	0.003947	0.999665	0.0007515
GO:0005179	85	4	0	1	4.00E-06	1
GO:0005215	2446	577	1	1	4.54E-05	0.999972
GO:0005230	277	38	0.00021	1	0.000469	0.999762
GO:0005267	275	34	0	1	2.21E-05	0.999995
GO:0005272	67	2	0	1	5.05E-06	1
GO:0005351	56	27	1	0.000258	0.99999	3.27E-05
GO:0005516	32	0	0.000832	1	0.0002255	1
GO:0005524	3542	1029	1	0	1	5.59E-19
GO:0005525	653	215	1	0	1	3.92E-09
GO:0005529	453	22	0	1	6.84E-27	1
GO:0008026	313	133	1	0	1	7.97E-15
GO:0008094	90	42	1	0	1	4.10E-07
GO:0008137	62	27	1	0.00151	0.999898	0.000282
GO:0008235	132	43	1	0.029493	0.999989	7.52E-05
GO:0008270	3672	739	0	1	2.34E-06	0.999998
GO:0008312	32	16	1	0.004167	0.999786	0.0007925
GO:0008375	63	6	0.019766	1	0.0005791	0.999953
GO:0008378	47	1	0.000205	1	6.63E-05	0.999996
GO:0008408	201	16	0	1	5.72E-14	1
GO:0008450	6	6	1	0.000746	1	0.0001504
GO:0008553	9	7	1	0.004403	0.999943	0.0007963
GO:0008565	187	103	1	0	1	1.27E-16
GO:0015077	254	99	1	0	0.999965	0.0008448

GO:0015450	26	16	1	0.000276	0.999995	2.96E-05
GO:0016298	173	18	0	1	0.0003812	1
GO:0016651	99	46	1	0	1	2.83E-06
GO:0016747	291	59	1	1	8.93E-08	1
GO:0016758	437	46	0	1	1.17E-11	1
GO:0016773	1810	385	0.14273	1	0.0009827	0.999726
GO:0016844	8	7	1	0.001248	0.999992	0.0002214
GO:0016986	18	11	1	0.002733	0.9999	0.0005978
GO:0017111	1291	514	1	0	0.999998	5.12E-06
GO:0030414	308	58	0.188443	1	0.0002825	0.999979
GO:0042302	323	27	0	1	2.34E-12	1
GO:0043565	1215	153	0	1	2.64E-21	1
GO:0046933	136	70	1	0	1	5.22E-13
GO:0046961	140	70	1	0	1	3.15E-12
GO:0046983	221	27	0	1	5.77E-06	0.999998
GO:0050661	29	17	1	0.000313	0.999992	4.06E-05
GO:0051082	187	71	1	3.70E-05	0.999998	3.18E-06
GO:0051536	116	44	1	0.001215	0.999573	0.0009976

Supplementary Table 12. Gene Onthology functions significantly enriched (at P<0.01) or depleted when the 64 orthologous groups conserved among the three parasitic nematodes were compared to their complete proteomes. Of the total of 20,208 GO ids in Biological processes 81 are associated with this group, and of the 27,935 Molecular Function GO ids 101 are associated with this group. FDR, false discovery rate. Biological Processes GOs are in blue, Molecular Function GOs are in red.

GO Id	GO in all 4 species	Go in NOGs	FDR depleted	FDR enriched	P value depleted	P value enriched
GO:0000059	23	3	1	0.001844	0.999998	0.000104
GO:0006278	67	10	1	0	1	1.24E-13
GO:0006508	1651	22	1	0	0.999998	9.86E-06
GO:0007179	29	4	1	0.000237	1	5.27E-06
GO:0009439	4	2	1	0.001756	1	9.47E-05
GO:0015074	215	18	1	0	1	3.76E-19
GO:0003677	3223	29	1	0.0001	1	1.03E-07
GO:0003723	743	20	1	0	1	2.16E-12
GO:0003964	67	10	1	0	1	5.05E-14
GO:0004190	227	16	1	0	1	1.84E-16
GO:0004287	4	2	1	0.00261	1	7.73E-05
GO:0004462	3	2	1	0.001145	1	3.87E-05
GO:0004525	16	3	1	0.000987	1	2.48E-05
GO:0005524	3542	2	0.000146	1	0.000135	0.999983
GO:0008824	4	2	1	0.00261	1	7.73E-05

Supplementary Table 13. KEGG pathways mapping for the four nematodes under study (Kegg v.46 was used and the top hit better than 1e-010 was considered).

				# Genes			
Pathway name	**KO in pathway**	**Represented KO in nemas**	**Conserved KO in all nemas**	**Ce**	**Mi**	**Bm**	**Ts**
1. Metabolism	2258	785	337	2480	1822	1132	1069
1.1 Carbohydrate Metabolism	550	192	92	626	499	294	252
Glycolysis / Gluconeogenesis	55	25	17	78	66	57	34
Citrate cycle (TCA cycle)	50	25	16	50	42	42	31
Pentose phosphate pathway	42	18	12	28	28	19	20
Pentose and glucuronate interconversions	41	10	4	104	101	14	9
Fructose and mannose metabolism	52	21	14	97	64	44	37
Galactose metabolism	38	14	6	38	33	24	18
Ascorbate and aldarate metabolism	24	4	2	10	7	2	3
Starch and sucrose metabolism	68	28	15	193	164	56	37
Aminosugars metabolism	38	15	10	78	45	35	28
Nucleotide sugars metabolism	20	6	3	17	14	10	3
Pyruvate metabolism	67	23	12	62	45	41	26
Glyoxylate and dicarboxylate metabolism	57	17	3	21	22	8	8
Propanoate metabolism	59	22	6	54	31	19	30
Butanoate metabolism	66	21	7	67	45	34	28
Inositol metabolism	9	3	1	3	3	1	12
Inositol phosphate metabolism	39	24	12	60	44	44	60
1.2 Energy Metabolism	408	131	71	235	210	144	123
Oxidative phosphorylation	202	96	52	138	117	91	70
Reductive carboxylate cycle (CO2 fixation)	32	9	6	17	15	13	8
Methane metabolism	49	6	2	25	20	11	13
Nitrogen metabolism	107	16	10	41	54	27	27
Sulfur metabolism	27	5	1	14	4	3	5
1.3 Lipid Metabolism	325	144	52	710	380	218	199
Fatty acid biosynthesis	26	7	3	32	11	10	10
Fatty acid elongation in mitochondria	8	8	4	19	17	11	8
Fatty acid metabolism	32	21	10	152	71	30	26
Synthesis and degradation of ketone bodies	7	6	1	6	8	3	4
Biosynthesis of steroids	47	16	4	18	14	9	7
Bile acid biosynthesis	22	10	5	54	32	16	21
Androgen and estrogen metabolism	19	7	2	109	72	19	22
Glycerolipid metabolism	41	15	6	84	60	32	34
Glycerophospholipid metabolism	58	32	15	185	85	69	64
Ether lipid metabolism	12	10	5	51	38	24	26
Sphingolipid metabolism	31	19	8	55	44	23	19
Arachidonic acid metabolism	28	11	3	57	28	12	13
Linoleic acid metabolism	12	6	2	45	24	12	23
alpha-Linolenic acid metabolism	14	3	2	23	14	7	11
Biosynthesis of unsaturated fatty acids	28	12	4	59	17	18	13
1.4 Nucleotide Metabolism	174	78	35	306	294	182	182
Purine metabolism	134	54	26	278	260	158	165
Pyrimidine metabolism	76	35	16	56	69	36	42
1.5 Amino Acid Metabolism	484	188	75	607	430	250	266
Glutamate metabolism	39	22	13	46	47	29	35
Alanine and aspartate metabolism	42	19	9	37	37	18	14
Glycine, serine and threonine metabolism	64	33	10	92	51	36	38
Methionine metabolism	38	14	7	31	21	15	18

Cysteine metabolism	21	6	2	27	7	5	5
Valine, leucine and isoleucine degradation	51	30	8	71	51	19	32
Valine, leucine and isoleucine biosynthesis	20	8	3	21	11	16	15
Lysine degradation	45	17	8	76	57	39	30
Arginine and proline metabolism	53	14	10	46	36	19	38
Histidine metabolism	35	11	4	47	37	20	23
Tyrosine metabolism	54	22	10	154	94	63	53
Phenylalanine metabolism	38	11	7	120	59	43	33
Tryptophan metabolism	52	27	9	111	76	24	29
Phenylalanine, tyrosine and tryptophan biosynthesis	49	7	4	16	18	6	7
1.6 Metabolism of Other Amino Acids	126	55	26	222	119	73	76
beta-Alanine metabolism	24	15	4	39	32	12	10
Taurine and hypotaurine metabolism	15	4	2	12	9	4	3
Aminophosphonate metabolism	13	5	2	32	23	19	21
Selenoamino acid metabolism	23	12	5	64	28	28	31
Cyanoamino acid metabolism	13	6	4	20	14	6	6
D-Glutamine and D-glutamate metabolism	6	2	2	4	5	3	9
D-Arginine and D-ornithine metabolism	2	1	0	4	1	0	0
Glutathione metabolism	38	16	13	98	45	26	20
1.7 Glycan Biosynthesis and Metabolism	160	83	30	163	153	95	89
N-Glycan biosynthesis	34	27	11	44	70	34	33
N-Glycan degradation	8	7	4	12	15	10	9
O-Glycan biosynthesis	13	7	2	48	23	13	12
Chondroitin sulfate biosynthesis	19	7	2	13	5	5	5
Heparan sulfate biosynthesis	18	10	3	6	8	9	10
Keratan sulfate biosynthesis	13	5	2	11	28	5	3
Glycosaminoglycan degradation	14	6	1	10	10	5	3
Peptidoglycan biosynthesis	24	1	1	7	9	5	4
Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	24	17	6	18	15	14	15
1.8 Biosynthesis of Polyketides and Nonribosomal Peptides	4	2	1	5	6	4	1
Polyketide sugar unit biosynthesis	4	2	1	5	6	4	1
1.9 Metabolism of Cofactors and Vitamins	301	91	31	392	298	174	185
Thiamine metabolism	20	5	4	26	17	16	15
Riboflavin metabolism	18	7	4	55	56	29	21
Vitamin B6 metabolism	14	4	0	5	1	3	3
Nicotinate and nicotinamide metabolism	30	15	3	29	16	11	17
Pantothenate and CoA biosynthesis	24	13	6	20	22	11	8
Biotin metabolism	11	6	1	27	23	17	8
Lipoic acid metabolism	4	3	2	5	6	4	3
Folate biosynthesis	53	8	4	108	83	60	84
One carbon pool by folate	22	14	4	19	19	8	13
Retinol metabolism	29	10	3	104	61	14	8
Porphyrin and chlorophyll metabolism	83	11	5	91	63	17	13
1.10 Biosynthesis of Secondary Metabolites	55	25	13	234	115	59	47
Terpenoid biosynthesis	8	5	3	10	5	5	2
Limonene and pinene degradation	21	11	5	140	43	34	32
Alkaloid biosynthesis I	13	5	3	20	38	10	4
Alkaloid biosynthesis II	8	3	3	63	30	12	10
Caffeine metabolism	6	2	0	2	0	0	1
1.11 Xenobiotics Biodegradation and Metabolism	178	61	27	548	249	125	119
Caprolactam degradation	13	6	2	22	12	12	8

gamma-Hexachlorocyclohexane degradation	23	9	4	128	57	20	21
3-Chloroacrylic acid degradation	4	2	2	16	7	5	4
Styrene degradation	19	5	2	9	11	3	3
Naphthalene and anthracene degradation	12	4	3	54	29	18	23
Benzoate degradation via CoA ligation	67	13	6	119	40	36	34
Atrazine degradation	12	1	1	3	1	3	1
Bisphenol A degradation	7	4	2	40	14	10	15
1- and 2-Methylnaphthalene degradation	13	7	4	106	32	34	25
Geraniol degradation	7	5	3	27	16	13	5
Metabolism of xenobiotics by cytochrome P450	15	9	3	154	66	11	9
Drug metabolism - cytochrome P450	14	9	4	160	66	12	9
Drug metabolism - other enzymes	22	18	9	151	89	22	21

III – Supplementary Note

Phylogenetic relationship among *T. spiralis*, other nematodes and non-nematode species.

Nematodes are believed to have originated from an ecdysozoan ancestor on the order of 650-1200 million years ago [3],[4] as free-living marine species and subsequently adapted independently to terrestrial environments at least sixteen times [5] and to parasitism at least eleven times [4]. Within the nested Nematoda phylogeny (**Supplementary Fig.1**; the trophic ecology of each of the 4 nematode species used in this study for pan-phylum analysis is indicated), the majority of intensively studied nematodes belong to three major crown clades; Rhabditina (e.g. *Caenorhabditis* spp., hookworms, strongylid parasites of livestock, *Heterorhabditis* spp.), Tylenchina (e.g. *Strongyloides* spp., and plant parasites such as root knot, cyst, and lesion nematodes), and Spirurina (e.g. parasites of vertebrates, such as ascarids, and filarial nematodes) [6-7]. Each of these clades is represented by one or more annotated genomes: Rhabditina – *Caenorhabditis elegans* [8], *C. briggsae* [9], and *Pristionchus pacificus* [10]; Tylenchina – *Meloidogyne incognita* [11] and *M. hapla* [12]; and Spirurina – *Brugia malayi* [13]. These major crown clades together form a monophyletic group, the terrestrial Rhabditida (formerly Secernentea), distinguished by the presence of a tail chemoreceptive sensillum, the phasmid. The Rhabditida and several clades of mostly free-living nematodes (e.g. Plectida, Monhysterida, Chromadorida) belong, in turn, to a deeper monophyletic group - the Chromadorea. Closer to the root of the nematode phylogeny are two clades, the Dorylaimia and the Enoplia that separated from other nematodes in the pre-cambrian. Historically, nematodes lacking sensilla (the Dorylaimia, Enoplia, and non-Secernentean Chromadorea) were classified as the clade Adenophorea, a grouping of mostly marine nematodes which are now proposed to be paraphyletic [4]. Along with marine species, the basal Dorylaimia clade includes several terrestrial parasites such as *Trichinella* spp. (Nematoda; Enoplea; Dorylaimia; Trichinellida; Trichinellidae), *Trichuris* spp. (whipworm parasites of humans and other mammals), Dorylaimida species (including viral-transmitting plant parasites such as the dagger nematode *Xiphinema index*, and *Mermis* spp. (insect parasites).

The life-cycle of *Trichinella spiralis*

The life cycle of *T. spiralis* (**Supplementary Fig. 2**) begins when an animal or person ingests muscle tissue containing encapsulated first stage muscle larvae (ML). The capsule dissolves during digestion in the stomach releasing the larvae which invade the columnar epithelium of the small intestine and migrate intracellularly [14]. Over 30 hours, the larvae molt four times, mature to the adult (Ad) stage, and begin mating. Each female can release upwards of 1,500 new born larvae (NBL) which penetrate the bloodstream and are distributed by general circulation throughout the body. A larva which reaches host striated skeletal muscle induces formation of a nurse cell where the worm may survive for the life of the host as an intracellular parasite. The radical transformation of a host differentiated muscle cell into a nurse cell occurs over several days and includes altered gene expression, loss of myofibrils, and cell cycle progression to G2/M [15-16]. *T. spiralis* excretory-secreted products are detected in the nurse cell including glycosylated proteins localized to the host cell nucleus [17-21].

Sequencing, assembly and genome characteristics

A total of 3,347,411 GSSs, 149,088 fosmid ends and 40,379 BAC ends were assembled using PCAP, as previously described [19]. 85.5% of the sequences (2,859,616 GSSs, 125,862 fosmid ends, 37,271 BAC ends) were assembled into 11,146 contigs (9,267 of which are with min size of 500bp and submitted to GenBank; the 1,086 contigs smaller than 500bp. Many unassembled reads and short contigs were identified as mitochondrial, ans assembled into 5 major contigs totaling 14.6 kb. Gene assessment only identifies 12 of 13 MT genes where NAD4L is missing.

All contigs, including the mitochondrion originated contigs are available at http://genome.wustl.edu/pub/organism/Invertebrates/, the mt originated contigs were reassembled and the mt genome submitted to GenBank), and subsequently into 8,795 supercontigs (**Supplementary Table 1**). Approximately 35 fold coverage of the nuclear genome was obtained. Several gene prediction algorithms, trained using *C. elegans* and *B. malayi*, and *T. spiralis* manually curated gene structures were used to generate the single set of gene predictions (version 1), which were used for subsequent analysis.

The total Q20 length of all sequences input to PCAP was 2,469,785,966 bp. The sources of Q20 sequences included: 2,238,615,150 bases of GSS sequence; 98,729,078 bases of fosmid ends; and 132,441,738 bases of BAC ends. The previously estimated size of the *T. spiralis* genome was 71.3 Mb. Therefore, the sequences obtained achieved an anticipated coverage of approximately 34.6X.

The total length of the scaffolds/supercontigs (which include spacers based on the expected seperation of contigs joined by read pairs of roughly known size) is 64.3 Mb. This assembled genome size was smaller than estimates that were published earlier [22], but was similar to recent genome size estimate of 1C = 71.3 +/1 1.2 Mb, based on flow sorted nuclei, stained with propidium iodide [23-24]. The average scaffold/supercontig length is 7,314 bp and the largest scaffold/supercontig is 9,955,697 bp. The N50 length of the scaffolds/supercontigs is 1,785,481 bp and the N50 number is 10. There were 8,461 orphan contigs (an orphan contig is the sole member of a scaffold/supercontig), and 334 scaffolds/supercontigs with 2 or more members. The total length of all orphan contigs was 9,788,023 bp, with the remainder of the 64.3 Mb being made up of scaffolds/supercontigs with multiple members.

Integration of genome sequences into a physical map

A physical map was constructed for *T. spiralis* using 26,784 clones. Of those clones 23,755 had usable fingerprints. 3,029 clones were not used. 19,463 of those clones with usable fingerprints were in contigs, and 4,292 were 'singleton' clones. The clones resided in a total of 49 unique contigs with the following number of clones per contig: 22 contigs with over 200 clones each, 10 contigs with 100-200 clones, 5 with 50-100 clones, 7 with 25-50 clones per contig, 2 with 10-25 and 3 contigs with 3-9 clones. Using this physical map, we were able to construct 9 ultracontigs comprised of 69 large supercontigs. Supercontig were aggregated into ultracontigs when each supercontig had >= 6 BAC end sequences from fingerprinted clones which were properly arranged. Supercontigs with BAC end sequences in topologically problematic alignments were discarded. 103 supercontigs from our assembly had 6 or more BAC end sequences from fingerprinted clones, but 34 of them had to be discarded due to problematic topology, leaving 69 that could be arranged into ultracontigs. Those 69 supercontigs represent 48,574,849 bp of sequence out of the total 64,330,920 bp of all supercontigs. Thus 75.5% of the sequence was ordered into ultracontigs.

Repeat content and gene finding

Assessment of the repeat content in the *T. spiralis* genome was aided by a custom-built repeat library. A total of 18% of the genome occurred as repeat sequences (10,736,179 bp), of which 5.5% were low complexity and simple repeats (3,235,623 bp) 2.2% were identifiable mobile elements (1,276,787 bp), e.g. transposable elements based on similarities to the coding sequences in known transposons in other species, and 10.5% were species-specific and highly divergent repeats 6,223,769 bp). A total of 4.8% of the repeats were further characterized based on repeats represented in RepBase ([25]; release 12.09). We masked the repeats and called genes using a logical, hierarchical approach. The origin and numbers of genes in the final gene set by predictor/model is: SNAP (trained with *B. malayi*) 8398, SNAP (trained with *C. elegans*) 2005, EANNOT (EN) 911, FgenesH (trained with *C. elegans*) 4494 genes. Based on the identification of the core eukaryotic genes (CEGs; http://bioinformatics.oxfordjournals.org/content/23/9/1061.short) we have identified 91.5% of the *T. spiralis* genes.

Genomic analysis to identify possible T. *spiralis* operons

Many nematode genes are organized in operons in genomes from diverse species. Expression of those genes is achieved along with the *trans*-splicing of short, spliced leader (SL) RNAs onto the 5′ ends of mRNAs. Genes in the same operon also tend to have short intergenic spacing. All nematode species so far investigated utilize a characteristic, conserved spliced leader, SL1, on many mRNAs and then SL1-variant sequences that are added onto and appear to help resolve mRNAs from downstream genes in operons. These characteristics were utilized to assess potential operons in the *T. spiralis* genome. Genome organization was considered first:

1. Among the total of 15,808 *T. spiralis* genes, an estimated 5,800 have apparent orthologs in *C. elegans*, which were used to facilitate this analysis.
2. Analysis of approximately 8,000 supercontigs identified an estimated 12,000 neighboring gene pairs from the same strand in the *T. spiralis* assembly;
3. A total of 1,214 neighboring *T. spiralis* pairs have *C. elegans* orthologs for both neighboring *T. spiralis* genes;
4. Without any restrains on the length of intergenic regions, a total of only 16 *T. spiralis* neighboring pairs have their two *C. elegans* orthologs in a same operon in *C. elegans* (from a total of 1,138 *C. elegans* operons containing approximately 2,800 genes). The distance between genes in these 16 pairs ranged from 9 bp to 20 kb. This analysis provided no clear evidence for the occurrence of operons in the *T. spiralis* genome. Also, the smallest distance between *C. elegans* genes, has been reported as ‘0’where the 2 genes were on the same strand and the 5' UTR of the second gene started at the same position as the end of 3' UTR of the first gene.

This approach did not uncover evidence for the general conservation of operonic gene constituents across the Nematoda, but does not exclude that operon organization is a genomic feature of the basal nematode *T. spiralis*. Intergenic-spacing could provide leads on this issue.

Spliced leader sequences were considered in published reports. Although a canonical SL1 sequence was not detected in the genome of *T. spiralis*, at least 15 distinct spliced leaders, encoded by at least 19 SL RNA genes, have been described [26]. The individual spliced leaders vary both in size and primary sequence, showing a much higher degree of diversity compared to other known *trans*-spliced leaders. These observations indicate that the use of spliced leader *trans*-splicing was an early characteristic in the Nematoda, and that the canonical spliced leader, SL1, found in *C. elegans*, evolved after the divergence of the major nematode clades. Nevertheless, the relationship between use of spliced leader addition and occurrence of operons in *T. spiralis* requires further clarification.

Alignment of *T. spiralis* genes, ESTs, cDNAs and the genome:

In total, 7,251 *T. spiralis* proteins (45%) shared homology to known proteins (cut-off e-05). For this protein search an extensive collection of proteins was built, containing all the proteins in the NR division of GenBank which was supplemented with proteins derived from nematode EST contigs (www.nematode.net). Work by our laboratory and others have generated the vast majority of sequences currently available for many parasites from the phylum Nematoda as expressed sequence tags (ESTs) and genome survey sequences (GSSs). For example, transcriptomes of 38 nematode species, 32 of which are parasites of vertebrates or plants, have been sampled to generate over 510,000 ESTs. However, putative nematode coding sequences among these ESTs and GSSs have never been explored systematically and have not been included in the NR.

There are 25,268 ESTs in dbEST of GenBank (as of 09/16/2008), totaling 12,788,240 bp. After removal of vector, poly-A, and low-complexity sequences, 25,083 ESTs (12,626,252 bp) were used in the BLAT analysis under default settings. BLAT results were further processed with pslReps to identify only highly confidence mappings with an empirical set of parameters for mRNA/genome mapping within the same species (-minAli=0.96 -nearTop=0.005). In summary, approximately 75% of the ESTs were mapped back to the *T. spiralis* gene set with high confidence, and the mapped regions account for approximately 57% of all the EST length. A total of 5,450 *T, spiralis* genes, 33.8% of all the 15,808 predicted gene models, have EST support. However, each EST was mapped to an average of 1.5 gene models. Using more stringent criteria, i.e. allowing a single mapping with the best high stringency nucleotide match, 4,688 loci were identified (29% of the total gene set).

The percentage of non-matching ESTs (**Supplementary Fig. 3**) indicates that the mappings are indeed high quality, in that 84% of all the EST-cDNA mappings have non-match ratios (defined as non-match bases/total bases of a mapped regions) of less than 0.5%. As expected, the percentage of query coverage is more dispersed. A total of 38.5% of all the EST-cDNA mappings cover less than 50% of the EST length (not including the UTRs). Such "short" coverage can contribute to mapping across multiple genes, although some of these mapping may be accurate if the ESTs include unspliced intronic or UTR sequences. For future use of these data, investigators might incorporate an empirical cutoff of coverage.

Amino Acid frequencies of *T. spiralis* and other nematode and non-nematode species.

The amino acid (AA) composition of predicted proteins in *T. spiralis* is similar to that observed in other nematodes and organisms where leucine (Leu) is the most common (9% of all codons) and tryptophan (Trp) the least common (1%). On average, seven AAs contribute more than 6% each to total AA content, confirming previous transcriptomic data [27]. These same AA are most common in other nematodes as well (**Supplementary Table 2**).

Generation of orthologous protein families

OrthoMCL [28] was used to predict orthologous groups of proteins among species to enable studies on gene/protein evolution and identification of taxonomically restricted sequences. Proteins were grouped based on the Markov Cluster algorithm to predict orthologs and paralogs. Complete proteomes were analyzed for four nematode species that span the Nematoda; the non-parasitic *C. elegans* (20,140 proteins), the plant parasitic *M. incognita* (19,212 proteins), the human filarial parasite *B. malayi* (11,407 proteins), the zoonotic basal nematode *T. spiralis* (15,808); and two outgroups, the arthropod *Drosophila melanogaster* (14,144 proteins) and the yeast *Saccharomyces cerevisiae* (6,696 proteins). Collectively these proteins were grouped into 12,163 orthologous groups (**Supplementary Table 3**).

Gene duplication and deletion based on TribeMCL grouping

The tree used to map the protein family and protein events is based on amino acid subctitutions of a single member per core species orthologous families. The consensus tree is based on a total of 328 trees, constructed for each of the 328 single copy universal orthologous groups. The support for the tree was very strong for most of the branches ((Dme:100.0,Yea:100.0,(Tsp:100.0,(Bma:100.0,(Min:100.0,Cel:100.0):35.0):77.0):50.0)). Gene duplication and deletion analysis was investigated using both, TribeMCL (http://micans.org/mcl/) and OrthoMCL [28], to provide independent assessment of associations. These two methods, each used with default parameters, produced similar numbers of inter- and intraspecific groups: *T. spiralis* singletons, 33% or 32%; intra-specific families, 26% or 28%; and inter-specific families, 41% or 40%, respectively. The numbers of duplication and deletion events based on TribeMCL (data not shown) using the 1,147 families for which trees were successfully built (using tree reconciliation, from a total of 1,206 families) also revealed a higher number of events in nematodes compared to the arthropod representative, *Drosophila melanogaster*.

Trichinella spiralis specific gene (protein) family expansion

Gene duplication and deletion analysis among the four nematode species identify specific genes that reflect either lineage or species-specific genome evolution. A noteworthy example is the DNase II-like protein family (D2L) that has undergone remarkable expansion in *T. spiralis* by comparison to the other species. The p43 protein is a ML-expressed D2L that predominates in excretory-secretory products, generates a strong host antibody response, and has been suggested as a vaccine candidate [29]. Our analysis of ESTs [30] revealed a much larger *d2l* gene family that displayed relatively restricted diversity of genes expressed by ML, whereas extensive diversity was observed among *d2l* ESTs expressed by NBL. No *d2l* gene expression was detected for in that analysis. We have now detected 125 *d2l* genes in the *T. spiralis* genome, which reflects a marked expansion by comparison to other nematodes including *C. elegans* (**Supplementary Fig. 4**). Nearly half of the *T. spiralis* D2L genes were categorized as encoding secretory proteins (SP). The D2L ESTs were especially prevalent from NBL libraries; seven to nine times the number found in ML and Ad. The *T. spiralis d2l* gene family is therefore uniquely large compared to other parasitic and non-parasitic nematodes. The greatest level of the D2L protein diversity defined as the expansion of the number of genes, is found in the NBL stage where the parasite undergoes migration through host tissue. By analogy to the ML p43-D2L protein, which has been investigated extensively [29], other D2L proteins are likely to be released from ML and NBL where interactions with the host immune system are likely to occur. We hypothesize that the size and diversity of the D2L gene family is related to escape from host immune responses. The expression data coupled with the genomic inventory of *d2l* genes will provide tools necessary to test this hypothesis. While a role in digestion of host DNA to facilitate tissue migration has been suggested, the biochemical function of *T. spiralis* D2L proteins remains unknown. Preferential expansion of *T. spiralis* D2L genes resembles an expansion of cathepsin B-like cysteine (CBL) protease genes in the trichostrongylid parasite *Haemonchus contortus* [31] and several gene families in *B. malayi* (**Supplementary Table 4**). These gene expansions may provide important clues in host-parasite interactions and factors that figure decisively in evolution of nematode lineages.

Correlation among *T. spiralis* ultracontigs

The linear arrangement of genes along a chromosome can have important ramifications for regulation of gene expression, and in nematodes the occurrence of operons provides a functional example. Common chromosomal coordinates also provides one line of information to assess gene orthology. The *T. spiralis* genome sequence provided anchor points to assess this process across the phylum. *T. spiralis* genes organized on the six longest ultracontigs were compared to the predicted orthologs from *C. elegans;* non-random distribution was observed in several nematode species. In addition, the correlation supporting macrosynteny was improved when the orthologs from the *C. elegans* X chromosome were excluded from the analysis. This effect may reflect the different karyotypes between the two species (*C. elegans* has 2n=12, and *T. spiralis* has 2n=6 for the females and 2n=5 for the males). There was a strong correlation among *T. spiralis* ultracontigs (UC2/UC5=0.76; UC1/UC4=0.95; UC6/UC9=0.99), that was even higher when the X chromosome was excluded (UC2/UC5=0.97; UC1/UC4=0.97; UC6/UC9=0.99).

Ancestrial orthologous regions

Our approach used a basic strategy in building homology maps, which uses exons that are orthologous in multiple genomes as map "anchors" (**http://www.biostat.wisc.edu/~cdewey/mercator/**). While the number of orthologous blocks maybe smaller than the real number due to the fragmented nature of two out of the three genomes (*C. elegans*, *B. malayi* and *T. spiralis*), the possible incorrect annotations are not likely to have significant alignments with other gene annotations therefore are not a problem. We identified 196 orthologous blocks (**Supplementary Table 7**). Among those identified, 155 were shared among *C. elegans* and *B. malayi* only; 5 were shared among *B. malayi* and *T. spiralis*, only. We also identified 36 segments that were shared among all three species and putatively defined as ancestral orthologous segments. No segments were shared exclusively among *C. elegans* and *T. spiralis***.** online). The genes pairs within the ancestral blocks accounted for ~50% of the genes in all segments for *C. elegans* and *B. malayi,* but 97% of all the genes in *T. spiralis*. The genes within the 36 ancestral blocks accounted for ~50% of the genes in all 196 blocks for *C. elegans* and *B. malayi* but as high as 97% of all the genes in *T. spiralis*. While 15% of the *C. elegans* operons had genes within the syntenic blocks, only 14 of the ancestral synteny blocks contained *C. elegans* genes organized into 26 *C. elegans* operons. This pattern was more pronounced in the syntenic blocks between *C. elegans* and *B. malayi*, where 68 syntenic blocks contained genes from 93 operons. Furthermore, over half of the ancestral syntenic blocks are located on chromosome III and IV. Overall, the ancestral syntenic blocks tended to be located in the center of the chromosomes compared to those restricted to any two species that were located predominantly on the chromosomal arms (**Supplementary Fig. 2b**).

Other characteristics of scNOGs. Available information, largely obtained from the *C. elegans* databases, supports the importance of NOGs in basic nematode functions (**Supplementary Table 9** contains annotation of the 274 NOGs, including the 85 scNOGs). Eighteen of the 85 scNOGs lacked homology to known proteins but did match IPR domains. As such, putative functions could only be inferred from information such as *C. elegans* RNAi phenotypes, anatomical expression and other annotations associated with *C. elegans*. For example, the *C. elegans* gene W08F4.6 encodes a novel protein having activity that is required for molting. It is expressed in hypodermal cells and in a single posterior neuron. We also evaluated InterPro (IPR) domains associated with scNOGs, and the remaining 67 scNOGs were collectively associated with 144 IPR domains. Five IPR domains for scNOGs from *T. spiralis* were statistically enriched compared to the IPR domains by comparison to the complete *T. spiralis* gene repertoire. Among the enriched IPRs were tetraspanin, Zinc finger C2H2 type, and calycin. Tetraspanin functions in the maintenance of epithelial cell integrity; a lethal RNAi phenotype in *C. elegans* during molting reflects disruption of the hypodermis [32]. Gene amplification of the tetraspanins has been recently documented in the genome of a flatworm [33], suggesting a critical role in helminth physiology beyond molting. The Zinc finger C2H2 type domain is enriched in *P. pacificus* genome compared to *C. elegans*. Calycins, largely represented by lipocalins, are expressed in body wall muscle, seam and somatic cells in *C. elegans* and are involved in locomotion. Thus, RNAi knockdown predictably causes abnormalities in locomotion, larval development and growth (e.g. [34]).

Finally, 11 of the 85 scNOG genes were associated with 12 IPR domains that were only represented once in the whole *T. spiralis* genome. Hence, functions related to these 12 IPR domains are singularly related to scNOGs. Predicted functions of these scNOGs include four TM proteins involved in metabolite transport, electron transport, DNA repair, and ergosterol biosynthetic process, and three SP proteins annotated as a metalloendoproteinase, selenium binding protein or a protein of unknown function.

Structural annotation and comparison of the proteins of ORTHOMCL5157 and their interaction partners

To dissect the functional significance of nematode specific insertions in scNOGs, the three dimensional structure of the electron transfer complex, NADH dehydrogenase (ubiquinone) 1 beta sub-complex 4, which contains well defined insertions was modeled. NADH dehydrogenase (ubiquinone) 1 beta sub-complex 4 has very low homology to protein structures available in the PDB (less than 22% sequence identity, covering around half of the protein), so the *C. elegans* and *B. taurus* orthologs were modeled using the Rosetta3.0 software suite. The *ab initio* portion of the Rosetta3.0 software suite [35-37] was used to predict the structures of the *C. elegans* and *B. taurus* orthologs of NADH dehydrogenase (ubiquinone) 1 beta sub-complex 4. The Rosetta *ab initio* program was run using the AbinitioRelax option which combines an *ab initio* folding algorithm and refinement using the relax algorithm within Rosetta3.0. A total of 40,000 decoys were generated using the full-atom scoring method [38] for each sequence. Several of the decoys with a small radius of gyration and low all-atom energy (i.e. the bottom of the energy well) (**Supplementary Fig. 9**) were compared using two different structural genomics methods, TM-align [39] and MAMMOTH [40], to determine if a similar fold was present. One decoy from both *C. elegans* and *B. taurus* yielded a significant score with both TM-align (0.46) and MAMMOTH Z-score (4.9), indicating that the proteins have a significant degree of similarity in their folds, despite the large insertion regions in the *C. elegans* sequence. A TM-align score over 0.5 indicates the structures share the same fold, whereas a TM-score below 0.2 indicates no similarity between structures.

The position of the insertions were mapped onto the models generated (**Supplementary Fig. 10**) and are located predominately on the surface of the protein. The secondary structure predictions calculated for the Rosetta *ab initio* program were added to the sequence alignment which was generated by MUSCLE [41] to further dissect the functional importance of the insertion in the nematode proteins. The first insertion region in the *C. elegans* protein has a small amount of helical character based on the prediction from one of the secondary structure predictions. The other programs predicted a loop structure in this region (only one secondary structure prediction is shown in **Supplementary Fig. 10**). The other two insertion regions in *C. elegans* are toward the end of helices and are in the loop regions, as well.

The functional significance of the insertions in the electron transfer complex was further dissected by comparing interacting proteins. If the surface of a protein changes due to an insertion or deletion, it is likely the surface of an interacting protein will need to change as well. Two protein-protein interaction databases, IntAct [42] and MINT [43], were used to see if this protein or its orthologs were involved in a protein-protein interaction. The ortholog from *B. taurus* (UniProt ID: P48305) was annotated as involved in two protein-protein interactions within the IntAct database. One interaction was with the acyl carrier protein (UniProtID: P52505) and the other interaction was with Acadv bovine very long chain Acyl-CoA dehydrogenase (UniProtID: P48818). The mouse ortholog (UniProtID: Q9CQC7) interacted with a protein kinase C inhibitor protein (UniProtID: P63101). P48305 is part of a complex, and the complex interacts with P48818. BLASTP was used to find orthologs of these proteins, and MUSCLE was used to do the sequence alignments. P63101 and P52505 did not show significant differences between nematodes and other species. However, orthologs of P48818 in nematodes had deletions relative to non-nematode species (**Supplementary Fig. 10**); this protein-protein interaction was found via anti-bait coimmunoprecipitation [44]. The X-ray crystal structure is available for the *H. sapiens* ortholog of P48818. One of the deletions seen in nematodes is not resolved in the X-ray crystal structure and is likely to be unstructured, whereas the other deletion is in a more structured region and may play a role in the protein-protein interaction (**Supplementary Fig. 10**). Interestingly, this is the opposite of NADH dehydrogenase (ubiquinone) 1 beta sub-complex 4, which contains insertions in nematodes that are not present in non-nematodes. Evolutionarily, a sequence containing amino acid insertions in one protein interaction partner may be compensated by a deletion in the other protein interaction partner. This idea of compensation could provide a means of targeting a protein-protein interaction unique to one species for drug design.

Genes encoding predicted signal peptides for secretion (SP), transmembrane domains (TM) or both.

Identification and characterization of genes encoding proteins that harbor putative amino-terminal signal peptides (SP) and/or transmembrane domains (TM) are of importance in part because of their potential ability to directly interface with the host, hence promote parasites survival and growth by modulating host immunity and other biological functions. To this end, a subset of *T. spiralis* SP and TM containing proteins were identified [45], and these represent approximately 29% of 15,808 genes in the *T. spiralis* genome (SP 1,075; TM 3,315; SP+TM 329). Expression of these genes was investigated with a database of *T. spiralis* ESTs derived from three life cycle stages; newborn larvae (NBL, 14% of all ESTs), muscle larvae (ML, 71%) and adult parasites (Ad, 14%). Collectively, these ESTs mapped to 4,688 genomic loci, and 29% (370; 1,196; 138) of these loci encode proteins classified as SP, TM or SP+TM, respectively. Therefore, the relative representation of these three categories in the genome (29%) is congruent with genes expressed among the three life cycle stages (29%). A majority of *T. spiralis* SP genes (758/1089) were *T. spiralis*-specific. Among the nematodes, *C. elegans* had more SP and TM genes (~48%) compared to the parasitic nematodes (25-31%). Among the parasites, *M. incognita* had 50% more SP genes compared to the human parasites, and *T. spiralis* had the highest number of TM genes (**Supplementary Fig. 11**).

Based on EST representation, SP, TM, and SP+TM genes are highly expressed making up eight, eight, and seven of the ten most represented genes in the NBL, ML, and Ad EST collections, respectively. The most abundant transcript for NBL (567 ESTs) and ML (1106) mapped to a SP gene of unknown function, while the most abundant Ad transcript (321) was another SP gene of unknown function. Furthermore, 11 of the 14 excretory secreted proteins identified by proteomics analysis of the ML (e.g. [21]) were identified in the *T. spiralis* genes that had ML EST support. Interesting only the identified secreted serine protease [20,46] had orthologous proteins in the other nematode species and *D. melanogaster*, and 5' nucleotidase [47-48] with ortholog only in *D. melanogaster*. The SP genes are especially abundant among Ad ESTs, perhaps a reflection of its ability to adapt to most vertebrate hosts. Muscle larvae originated EST support was observed in 81 of the SP genes, and most of them were of unknown function as only 22% had GO associations. The most abundant ML-specific EST to which a function could be inferred was an aspartic-type endopeptidase (22 ESTs), known to facilitate hemogolobin digestion in the blood-feeding nematodes [49], or tissue degradation during the larvae migration in the host in non-blood-feeders (e.g. [30,50]).

Metabolic pathway analysis

The gene products were associated with a specific biochemical pathway using the KEGG pathway mappings [51]. WU-BLAST matches of the genes against KEGG database version 46.0 was used for pathway mapping with a filter of 1e-10. **Supplementary Table 13** online lists mappings for the top scoring and protein hits to the KEGG enzymes that meet the E-value filter. An example of the pan-phylum NemaPath viewer ([52]; http://nematode-dev/KEGGscan/cgibin/KEGGscan_pathway_tsp_4_species.cgi) is shown in **Supplementary Fig. 13**; and an example of the NemaCyc viewer (http://pathwaytools.wustl.edu) in **Supplementary Fig. 14**. The *C. elegans* NemaCyc viewer was generated by using the KEGG annotation of C. elegans genes (KEGG v.50), and parsed each GenBank chromosome file to add in the EC annotations. For the T. spiralis NemaCyc mapping a blastp alignment of the KEGG genesDB against the predicted T.spiralis genes was performed and e-value scores stronger than 1e-10 were considered. These genes were then annotated in SpirCyc based on that blastp alignment.

Detailed comparisons identified taxonomically restricted pathways. For example, pathways with more KOs in *T. spiralis* compared to *C. elegans* was the starch and sucrose metabolism (**Supplementary Fig. 13**). Of the 28 KOs associated with nematode enzymes in this pathway, 15 were CNKs, indicating sub-pathways that are taxonomically restricted. The glucose-6-phosphatase was only present in *T. spiralis*, and detailed analysis identified conservation of this enzyme only among Dorylaimia nematodes (e.g. the whipworm *Trichuris muris* and the plant-parasite *Xiphinema index*). A sub-pathway contained 4 enzymes specific only to the plant-parasitic nematode *M. incognita*, including a cascade of pectin-hydrolysis enzymes, endoglucanase and galacturonidase. All of these enzymes are known to facilitate invasion of the plant by the plant-parasitic nematodes through degradation of the main components of the plant cell wall [53].

IV – References for supplementary information:

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