

Supplementary Materials: De Novo Analysis of the Transcriptome of *Meloidogyne enterolobii* to Uncover Potential Target Genes for Biological Control

Xiangyang Li, Dan Yang, Junhai Niu, Jianlong Zhao and Heng Jian

Table S1. Statistically-significantly enriched GO terms in different categories of orthologous families.

GO_ID	Name	NSP	<i>p</i> -Value	Adj. <i>p</i> -Value	Pop. Count	Study Count	Category of Orthologous Families
GO:0040028	regulation of vulval development	B	5.46×10^{-6}	0.0049	38	5	Present in all <i>Meloidogyne</i> species
GO:0061062	regulation of nematode larval development	B	5.46×10^{-6}	0.0049	38	5	
GO:0048580	regulation of post-embryonic development	B	5.46×10^{-6}	0.0049	38	5	
GO:0048569	post-embryonic organ development	B	1.60×10^{-5}	0.014	80	6	
GO:2000026	regulation of multicellular organismal development	B	3.15×10^{-5}	0.028	90	6	
GO:0040025	vulval development	B	3.47×10^{-5}	0.031	55	5	
GO:0040027	negative regulation of vulval development	B	5.69×10^{-5}	0.051	31	4	Present in all <i>Meloidogyne</i> species
GO:0061064	negative regulation of nematode larval development	B	5.69×10^{-5}	0.051	31	4	
GO:0048581	negative regulation of post-embryonic development	B	5.69×10^{-5}	0.051	31	4	
GO:0002262	myeloid cell homeostasis	B	1.76169×10^{-5}	0.017	8	3	
GO:0048872	homeostasis of number of cells	B	2.62983×10^{-5}	0.026	9	3	
GO:0009719	response to endogenous stimulus	B	2.13189×10^{-5}	0.016	99	6	
GO:0030900	forebrain development	B	5.05432×10^{-7}	0.00063	19	5	Present in all <i>Meloidogyne</i> species
GO:0021545	cranial nerve development	B	6.92617×10^{-7}	0.00087	3	3	
GO:0021675	nerve development	B	2.75299×10^{-6}	0.0034	4	3	
GO:0042113	B cell activation	B	6.83907×10^{-6}	0.0086	5	3	
GO:0007420	brain development	B	1.09443×10^{-5}	0.014	34	5	
GO:0007270	neuron-neuron synaptic transmission	B	1.35919×10^{-5}	0.017	6	3	
GO:0042220	response to cocaine	B	3.75791×10^{-5}	0.047	8	3	Present in all <i>Meloidogyne</i> species
GO:0005261	cation channel activity	M	4.37561×10^{-5}	0.055	149	8	
GO:0014070	response to organic cyclic compound	B	5.21082×10^{-5}	0.065	76	6	
GO:0007612	learning	B	5.60136×10^{-5}	0.070	9	3	
GO:0060359	response to ammonium ion	B	7.95154×10^{-5}	0.099	10	3	

GO ID: the accession number of the GO term; Name: the name of the GO term.; NSP: the sub-ontology: biological process (B), cellular component (C) or molecular function (M); *p*-value: the nominal (uncorrected) *p*-value resulting from the observed overrepresentation of the GO term Adj. *p*-Value: the adjusted *p*-Value (adjusted by the MTC procedure chosen by the user); Pop. Count: the number of genes in the population set that are annotated to the GO term in question; Study Count: The number of genes in the study set that are annotated to the GO term in question.

No 5			No 8		
MSP3.txt	MPKLILLFYLIYGIILLTLEEFEGFGGGCGCPMFCQC	40	MSP6.txt	MATFFFTLLIIISIIATTEGMATNRSASTSDSLQCKDCK	40
NO.5.txt	MPKLILLFYLIYGIILLTLEEFEGFGGGCGCPMFCQC	40	MSP13.txt	MATFFFTLLIIISIIATTEGMATNRSASTSDSLQCKDCK	40
Consensus	mpklillfylliyygilll l e fgfgggcgcpmpapc		MSP23.txt	MATFFFTLLIIISIIATTEGMATNRSASTSDSLQCKDCK	40
			NO.8.txt	MATFFFTLLIIISIIATTEGMATNRSASTSDSLQCKDCK	40
			Consensus	matffftllliisiiat egm tnrstastsdsi qkdck	
MSP3.txt	IPQPPPIALPSLCFPQIQLECPFPSCGCCGRRKRRESGASA	80	MSP6.txt	VIYGMFVFPVAGSMHGDARSMKNNPSISNKLIVSGGNS	80
NO.5.txt	IPQPPPIALPSLCFPQIQLECPFPSCGCCGRRKRRESGASA	80	MSP13.txt	VIYGMFVFPVAGSMHGDARSMKNNPSISNKLIVSGGNS	80
Consensus	ipqpppialpqlcfpqiqlecpfpsscggcggrrkrresgasa		MSP23.txt	VIYGMFVFPVAGSMHGDARSMKNNPSISNKLIVSGGNS	80
			NO.8.txt	VIYGMFVFPVAGSMHGDARSMKNNPSISNKLIVSGGNS	78
			Consensus	viygmfvvpvags mhgdak m nnp n l vsqg s	
MSP3.txt	LLTVSTKSGIKRIGEEKNHCNNPHIKRIILKNLIIGDQV	120	MSP6.txt	KYSVTILQVENQPKCVAQNGCFVECCQIGDKLSGKLIYDI	120
NO.5.txt	LLTVSTKSGIKRIGEEKNHCNNPHIKRIILKNLIIGDQV	120	MSP13.txt	KYSVTILQVENQPKCVAQNGCFVECCQIGDKLSGKLIYDI	120
Consensus	llt vstksigikrigeeknhcnnphikriilknliligd v		MSP23.txt	KYSVTILQVENQPKCVAQNGCFVECCQIGDKLSGKLIYDI	120
			NO.8.txt	KYSVTILQVENQPKCVAQNGCFVECCQIGDKLSGKLIYDI	118
			Consensus	kysvtlqvenqpkcvaqn g pvecqi gdklsgkliydi	
MSP3.txt	GTRNAISSELRAKLGNYIINCAHPSFAYSGDSVIDYCV	160	MSP6.txt	ENGPSVNVFFKDTPIFVGNKCEIVEVDYKDHLTLIMN	159
NO.5.txt	GTRNAISSELRAKLGNYIINCAHPSFAYSGDSVIDYCV	160	MSP13.txt	ENGPSVNVFFKDTPIFVGNKCEIVEVDYKDHLTLIMN	159
Consensus	gtrnai selraklggnyiincah psfaysgdsvidy cv		MSP23.txt	ENGPSVNVFFKDTPIFVGNKCEIVEVDYKDHLTLIMN	159
			NO.8.txt	ENGPSVNVFFKDTPIFVGNKCEIVEVDYKDHLTLIMN	158
			Consensus	engpsv vpfkdtpifvgnk eiv yd kdhltil mn	
MSP3.txt	DGHQAITCAVFKI	173	MSP6.txt	KVKLMTPTKQIVKACGVKN...	180
NO.5.txt	DGHQAITCAVFKI	173	MSP13.txt	KVKLMTPTKQIVKACGVKN...	183
Consensus	dghqaitcavfki		MSP23.txt	KVKLMTPTKQIVKACGVKN...	180
			NO.8.txt	KVKLMTPTKQIVKACGVKN...	182
			Consensus	kvkltm pt kqivkacg kn	
No 10					
MSP4.txt	MKENLFKKSILIGLILLAFNFTKAGSGENTSLEASLKFI	40			
NO.10.txt	MKENLFKKSILIGLILLAFNFTKAGSGENTSLEASLKFI	40			
Consensus	mkenlfkksiligl illafnfteak sgentsleaslkp				
MSP4.txt	KSIENASLEEKNGKEENGVTFFAEGHEIVETKKEINSPEE	80			
NO.10.txt	KSIENASLEEKNGKEENGVTFFAEGHEIVETKKEINSPEE	80			
Consensus	ksienasleekngkeengvtffaegeheivetkkeinspee				
MSP4.txt	VITSTKGCDSSEDRKVTMNGDSEADKNNENVEGEERKA	120			
NO.10.txt	VITSTKGCDSSEDRKVTMNGDSEADKNNENVEGEERKA	120			
Consensus	v d tkg e sedrk t n sea k n enve eekka				
MSP4.txt	TENKNEVEEKEVLEKTKKEEDKISPEVKTKEKSTN	159			
NO.10.txt	TENKNEVEEKEVLEKTKKEEDKISPEVKTKEKSTN	160			
Consensus	tenkne veekevl ektkeeedkis epvktke kst				
MSP4.txt	NDREVEDLKEEKEVEKNGKDEEENKDEKDEKTRDE	198			
NO.10.txt	NDREVEDLKEEKEVEKNGKDEEENKDEKDEKTRDE	196			
Consensus	nd evedlkee ek ve k deeenk ekk kde				
MSP4.txt	KKVEFVIECEKKTPEKEHKSHWFMDRKFHAFCFITHYFF	238			
NO.10.txt	KKVEFVIECEKKTPEKEHKSHWFMDRKFHAFCFITHYFF	236			
Consensus	kk p vie ekktpk kehkshwfm d r k f h a f c f i t h y f f				
MSP4.txt	CPSNSAKCKESHGEGKESRGKRINSDFSSLSDEMI	278			
NO.10.txt	CPSNSAKCKESHGEGKESRGKRINSDFSSLSDEMI	272			
Consensus	cpsnsa k ke h egkes rgkrlnsd f s s l s s d e				
MSP4.txt	NFENAEHFSEEIEENGEFKAKMNVGATYFRAETDNSGRMR	318			
NO.10.txt		272			
Consensus					
MSP4.txt	GRIEKFNAEMH	329			
NO.10.txt		272			
Consensus					

Figure S1. Predicted protein sequence and homology of the candidate effectors. By the comparison using NCBI, No. 5 protein had high homology with the putative esophageal gland cell secretory protein 3 (*Meloidogyne incognita*); No. 8 protein had high homology with the putative esophageal gland cell secretory protein 13, putative esophageal gland cell secretory protein 6 and putative esophageal gland cell secretory protein 23 (*Meloidogyne incognita*); while No. 10 had high homology with the putative esophageal gland cell secretory protein 4 (*Meloidogyne incognita*).

Table S2. Different numbers of the KEGG Ontology (KO) predicted for *M. enterolobii*, *M. hapla* and *M. incognita*.

KO_ID	Pathway	Mi_No.	Mh_No.	Me_No.
00760	Nicotinate and nicotinamide metabolism	8	8	12
00720	Carbon fixation pathways in prokaryotes	8	8	10
00561	Glycerolipid metabolism	12	14	17
00253	Tetracycline biosynthesis	0	0	1
00312	beta-Lactam resistance	0	0	1
00363	Bisphenol degradation	0	0	1
00550	Peptidoglycan biosynthesis	0	0	1
00791	Atrazine degradation	0	0	1
00984	Steroid degradation	0	0	1
01053	Biosynthesis of siderophore group nonribosomal peptides	0	0	1
05144	Malaria	0	0	1
00332	Carbapenem biosynthesis	2	0	0
00906	Carotenoid biosynthesis	1	0	0
00941	Flavonoid biosynthesis	1	0	0
00942	Anthocyanin biosynthesis	1	0	0
00945	Stilbenoid, diarylheptanoid and gingerol biosynthesis	1	0	0
05321	Inflammatory bowel disease (IBD)	0	1	0
05016	Huntington's disease	0	86	83
05169	Epstein-Barr virus infection	0	65	63
04932	Non-alcoholic fatty liver disease (NAFLD)	0	58	61
05166	Human T-Cell lymphotropic virus I (HTLV-I) infection	0	64	60
05168	Herpes simplex infection	0	35	38
05152	Tuberculosis	0	31	31
05034	Alcoholism	0	31	29
05100	Bacterial invasion of epithelial cells	0	32	29
05110	Vibrio cholerae infection	0	29	28
05120	Epithelial cell signaling in <i>Helicobacter pylori</i> infection	0	24	28
05161	Hepatitis B	0	27	26
05164	Influenza A	0	25	25
05132	Salmonella infection	0	23	23
05131	Shigellosis	0	25	21

Table S2. Cont.

KO_ID	Pathway	Mi_No.	Mh_No.	Me_No.
05160	Hepatitis C	0	18	19
05032	Morphine addiction	0	21	18
05162	Measles	0	15	18
05142	Chagas disease (American trypanosomiasis)	0	16	17
05145	Toxoplasmosis	0	17	17
05130	Pathogenic Escherichia coli infection	0	17	16
05146	Amoebiasis	0	16	16
05031	Amphetamine addiction	0	15	15
05134	Legionellosis	0	12	13
05030	Cocaine addiction	0	12	12
04930	Type II diabetes mellitus	0	9	11
05410	Hypertrophic cardiomyopathy (HCM)	0	10	11
05414	Dilated cardiomyopathy (DCM)	0	10	11
05412	Arrhythmogenic right ventricular cardiomyopathy	0	8	9
05020	Prion diseases	0	9	8
05133	Pertussis	0	8	8
05416	Viral myocarditis	0	7	7
04950	Maturity onset diabetes of the young	0	6	6
05033	Nicotine addiction	0	4	4
05140	Leishmaniasis	0	5	4
00290	Valine, leucine and isoleucine biosynthesis	0	2	3
04940	Type I diabetes mellitus	0	4	3
00300	Lysine biosynthesis	0	1	2
05143	African trypanosomiasis	0	3	2
00254	Aflatoxin biosynthesis	0	1	1
00626	Naphthalene degradation	0	1	1
01220	Degradation of aromatic compounds	0	1	1

Me: M. enterolobii; Mi: M. incognito; Mh: M. hapla.

Table S3. The numbers of CAZyme modules or domains in different nematodes.

CAZy Family	Bx	Ce	Gp	Me	Mh	Mi	CAZy Family	Bx	Ce	Gp	Me	Mh	Mi	CAZy Family	Bx	Ce	Gp	Me	Mh	Mi
AA3	1	1	1	1	1	2	GH20	5	5	2	2	3	4	GT24	2	2	0	1	1	0
AA4	2	3	0	1	1	2	GH22	0	0	0	0	0	1	GT25	1	1	1	1	1	1
AA7	1	0	8	0	0	1	GH25	3	10	1	10	5	5	GT26	2	0	0	0	0	0
CBM13	9	8	5	7	7	7	GH27	3	1	0	1	1	1	GT27	11	9	10	9	8	9
CBM14	19	46	20	27	22	8	GH28	0	0	0	0	4	4	GT28	1	1	1	0	1	4
CBM18	0	7	0	0	0	0	GH29	3	1	0	1	1	2	GT3	2	1	1	1	1	0
CBM2	0	0	12	4	4	13	GH3	0	0	1	0	0	0	GT31	35	31	33	10	17	22
CBM20	2	3	1	2	2	1	GH30	9	4	14	5	4	8	GT33	1	1	1	1	1	2
CBM21	1	2	5	1	1	2	GH31	4	4	5	3	3	1	GT34	1	2	2	3	1	4
CBM29	0	0	0	1	0	1	GH32	0	0	11	2	2	2	GT35	2	1	1	2	1	3
CBM32	7	4	5	5	4	3	GH35	1	2	2	2	1	4	GT39	2	0	0	0	0	0
CBM37	1	0	0	0	0	0	GH37	6	5	15	4	5	5	GT4	5	4	9	4	6	9
CBM40	0	0	0	0	0	1	GH38	5	3	3	3	3	1	GT41	2	3	1	1	3	1
CBM48	1	2	0	1	2	3	GH43	0	0	1	0	2	2	GT43	12	7	5	2	1	1
CBM49	1	0	0	0	0	0	GH45	11	0	0	0	0	0	GT44	0	0	1	1	0	0
CBM50	0	11	0	2	4	3	GH47	7	7	8	6	6	8	GT47	2	1	6	1	2	1
CBM52	0	0	0	0	1	0	GH5	0	0	15	8	10	31	GT49	11	10	0	0	0	0
CBM56	0	0	1	0	0	0	GH53	0	0	1	0	0	0	GT50	1	1	2	0	0	0
CBM57	0	1	0	0	0	0	GH56	3	1	0	0	1	2	GT54	1	0	1	0	1	0
CBM62	0	1	0	0	0	0	GH59	0	1	0	0	0	0	GT57	2	2	1	2	2	1
CBM63	0	1	1	0	0	0	GH63	1	1	0	2	1	3	GT58	1	1	1	0	2	0
CBM66	2	3	1	0	0	0	GH75	0	1	0	2	1	1	GT59	2	2	2	0	1	2
CE1	17	24	8	11	7	16	GH76	0	1	0	0	1	0	GT61	0	1	0	0	0	0
CE10	50	56	20	10	17	17	GH82	0	0	0	0	1	0	GT64	6	1	4	1	1	0
CE14	1	1	0	0	1	1	GH84	1	1	1	1	1	1	GT65	1	1	2	0	0	0
CE4	1	2	1	0	0	0	GH85	1	1	0	1	1	1	GT66	2	1	2	2	2	4
CE5	4	3	0	0	0	0	GH89	0	1	0	0	0	0	GT68	2	1	1	1	1	1
CE7	4	4	0	0	0	0	GH9	1	0	0	0	0	0	GT7	4	4	7	6	8	12
CE9	0	1	0	1	1	0	GH99	2	0	1	0	0	0	GT75	0	10	0	0	0	0
GH1	1	2	0	0	0	0	GT1	43	69	19	10	15	30	GT76	1	1	1	0	1	1
GH104	0	0	2	0	0	0	GT10	16	5	16	5	13	26	GT77	3	6	2	1	3	3

Table S3. Cont.

CAZy Family	Bx	Ce	Gp	Me	Mh	Mi	CAZy Family	Bx	Ce	Gp	Me	Mh	Mi	CAZy Family	Bx	Ce	Gp	Me	Mh	Mi
GH109	7	0	2	3	1	1	GT11	2	25	6	5	11	16	GT8	3	6	4	4	1	2
GH116	1	2	0	0	0	0	GT13	2	4	2	0	2	5	GT83	0	0	2	0	0	0
GH120	0	0	0	0	1	1	GT14	15	20	16	12	10	7	GT84	1	0	0	0	0	0
GH128	0	1	0	0	0	0	GT16	2	1	2	2	1	0	GT87	0	1	0	0	0	0
GH13	5	5	2	2	4	3	GT18	1	1	0	0	0	0	GT92	14	61	18	1	2	1
GH15	2	2	0	0	0	0	GT2	4	5	4	3	4	3	PL14	0		1	0	1	0
GH16	8	0	0	0	0	0	GT20	1	2	3	1	1	8	PL22	1	1	0	0	0	0
GH18	12	39	11	6	9	3	GT21	1	3	1	1	1	0	PL3	15	0	8	11	20	33
GH19	2	4	2	0	1	4	GT22	3	3	3	2	3	2							
GH2	4	2	1	0	2	5	GT23	1	1	1	4	9	19	Total	475	606	393	249	310	418

Ce: *C. elegans*; Me: *M. enterolobii*; Mi: *M. incognito*; Mh: *M. hapla*; Gp: *G. pallida*; Bx: *B. xylophilus*. AA: auxiliary activities; CBM: carbohydrate binding module; CE: carbohydrate esterase; GH: glycoside hydrolases; GT: glycosyltransferase; PL: polysaccharide lyase.

Table S4. Comparison of the kinomes in selected nematode genomes.

Kinase-Group	Bx	Ce	Gp	Me	Mh	Mi
Total	376	456	229	169	238	374
AGC	28	30	19	17	20	26
CAMK	34	39	34	18	24	39
CK1	49	69	10	14	18	45
CMGC	40	49	34	23	30	40
Other	43	46	32	19	22	29
RGC	8	27	8	1	13	14
STE	25	24	16	11	14	22
TK	65	79	20	14	22	26
TKL	15	14	11	6	7	12
twilight	46	47	15	32	44	59
unclassified	20	26	26	12	20	52
Atypical	3	6	4	2	4	10

Ce: *C. elegans*; Me: *M. enterolobii*; Mi: *M. incognito*; Mh: *M. hapla*; Gp: *G. pallida*; Bx: *B. xylophilus*.

Table S5. Presence of *flp* and *nlp* neuropeptide-encoding genes in *M. enterolobii* and other nematodes.

Ce	Mi	Mh	Me	Gp	Bx
<i>flp</i> -1	+	+	+		+
<i>flp</i> -6		+	+	+	+
<i>flp</i> -11		+	+		+
<i>flp</i> -12	+	+	+	+	+
<i>flp</i> -13					+
<i>flp</i> -14	+		+		+
<i>flp</i> -16	+	+	+	+	
<i>flp</i> -17		+	+	+	+
<i>flp</i> -18		+	+		+
<i>flp</i> -22	+	+	+		+
<i>flp</i> -34	+	+		+	+
<i>nlp</i> -1	+	+	+		
<i>nlp</i> -2	+	+	+		+
<i>nlp</i> -3					+
<i>nlp</i> -10	+	+	+	+	+
<i>nlp</i> -12	+	+	+	+	
<i>nlp</i> -14					+
<i>nlp</i> -15	+	+	+	+	
<i>nlp</i> -21		+	+	+	+
<i>nlp</i> -37		+	+		+
<i>nlp</i> -40					+
<i>nlp</i> -42				+	+

Ce: *C. elegans*; Me: *M. enterolobii*; Mi: *M. incognito*; Mh: *M. hapla*; Gp: *G. pallida*; Bx: *B. xylophilus*.

Table S6. Presence of neurotransmitter biosynthesis, transport and metabolism genes in *M. enterolobii* and other nematodes.

	Gene Function	Ce	Mi	Mh	Me	Gp	Bx
Acetylcholine	choline acetyltransferase	<i>cha-1</i>	+	+		+	+
	synaptic acetylcholine transporter	<i>unc-17</i>		+	+	+	+
	choline transporter	<i>cho-1</i>		+	+	+	+
	post-synaptic transporter	<i>snf-6</i>	+	+	+	+	+
	acetylcholinesterase	<i>ace-1</i>		+	+	+	+
	acetylcholinesterase	<i>ace-2</i>	+	+	+	+	+
	acetylcholinesterase	<i>ace-3</i>	+	+		+	+
	acetylcholinesterase	<i>ace-4</i>					
Serotonin	tryptophan hydroxylase	<i>tph-1</i>		+		+	+
	GTP-cyclohydrolase I	<i>cat-4</i>		+	+	+	+
	aromatic AA decarboxylase	<i>bas-1</i>		+	+	+	+
	vesicular monoamine transporter	<i>cat-1</i>		+	+	+	+
	serotonin reuptake transporter	<i>mod-5</i>	+	+	+	+	+
	monoamine oxidase	<i>amx-1</i>					+
	monoamine oxidase	<i>amx-2</i>					
Dopamine	monoamine oxidase	<i>amx-3</i>					
	tyrosine hydroxylase	<i>cat-2</i>					+
	dopamine reuptake transporter	<i>dat-1</i>		+		+	+
Tyramine	tyrosine decarboxylase	<i>tdc-1</i>	+	+	+	+	+
Octopamine	tyramine β -hydroxylase	<i>tbh-1</i>	+	+	+		+
Glutamate	vesicular glutamate transporter	<i>eat-4</i>	+	+	+	+	+
	plasma membrane glutamate transporter	<i>glt-1</i>	+	+	+	+	+
GABA	glutamate decarboxylase	<i>unc-25</i>	+	+	+	+	+
	vesicular GABA transporter	<i>unc-47</i>	+	+	+	+	+
	GABA transporter	<i>snf-11</i>	+	+	+	+	+
	GABA transaminase	<i>gta-1</i>	+	+	+	+	+

Ce: *C. elegans*; Me: *M. enterolobii*; Mi: *M. incognito*; Mh: *M. hapla*; Gp: *G. pallida*; Bx: *B. xylophilus*.

Table S7. Comparison of genes involved in the RNAi pathway in *M. enterolobii* and other nematodes.

RNAi Pathway	Ce	Mi	Mh	Me	Gp	Bx
Small RNA biosynthetic proteins	<i>drh-3</i>	+	+	+	+	+
	<i>drsh-1</i>	+	+	+	+	+
	<i>xpo-1</i>	+	+	+	+	+
	<i>xpo-2</i>	+	+	+	+	+
	<i>dcr-1</i>	+	+	+	+	+
	<i>drh-1</i>	+	+	+		+
	<i>pash-1</i>	+	+	+	+	+
	<i>rde-4</i>					+
	<i>xpo-3</i>					
	<i>smg-2</i>	+	+	+	+	+
Amplification	<i>smg-6</i>	+	+	+	+	+
	<i>ego-1</i>	+	+	+	+	+
	<i>rrf-3</i>					+
	<i>rrf-1</i>	+	+	+	+	+
	<i>smg-5</i>					
	<i>rsd-2</i>					
Spreading	<i>rsd-3</i>	+	+	+	+	+
	<i>sid-1</i>					
	<i>rsd-6</i>					
	<i>sid-2</i>					

Table S7. Cont.

RNAi Pathway	Ce	Mi	Mh	Me	Gp	Bx
Argonautes	<i>alg-1</i>	+	+	+	+	+
	R06C7.1	+	+	+	+	+
	C04F12.1					
	F58G1.1	+	+	+	+	+
	<i>alg-4</i>					+
	<i>rde-1</i>					
	C16C10.3	+	+	+	+	+
	<i>ppw-1</i>					
	<i>csr-1</i>	+	+	+	+	+
	<i>ppw-2</i>	+	+	+	+	+
	<i>sago-1</i>					
	T22B3.2					+
	T22H9.3	+	+	+	+	+
	<i>alg-2</i>	+	+	+	+	+
	<i>ergo-1</i>					
	<i>prg-1</i>					
	F55A12.1					
	T23D8.7					
	<i>nrde-3</i>	+	+	+	+	+
	<i>sago-2</i>					
	T23B3.2					
	Y49F6A.1	+	+	+	+	+
	ZK1248.7	+	+	+	+	+
	<i>prg-2</i>					
Other RISC components	<i>tsn-1</i>	+	+	+	+	+
	<i>ain-1</i>					
	<i>vig-1</i>					+
	<i>ain-2</i>					

Table S7. Cont.

RNAi Pathway	Ce	Mi	Mh	Me	Gp	Bx
RNAi inhibitors	<i>eri-1</i>	+	+	+	+	
	<i>xrn-2</i>	+	+	+	+	+
	<i>adr-2</i>					
	<i>xrn-1</i>					
	<i>adr-1</i>	+				+
	<i>lin-15b</i>					
	<i>eri-5</i>	+	+	+	+	+
	<i>eri-6</i>					
	<i>eri-7</i>					+
	<i>eri-3</i>					
Nuclear RNAi effectors	<i>mut-7</i>		+	+		+
	<i>cid-1</i>	+	+	+	+	+
	<i>ekl-1</i>	+	+	+	+	+
	<i>gfl-1</i>	+		+	+	+
	<i>mes-2</i>	+	+	+	+	+
	<i>ekl-4</i>	+	+	+		+
	<i>mes-6</i>		+	+	+	+
	<i>rha-1</i>	+	+	+	+	+
	<i>ekl-6</i>					+
	<i>zfp-1</i>					
	<i>mut-2</i>					
	<i>ekl-5</i>					
	<i>mes-3</i>					
	<i>mut-16</i>					
	<i>rde-2</i>					

Ce: *C. elegans*; Me: *M. enterolobii*; Mi: *M. incognito*; Mh: *M. hapla*; Gp: *G. pallida*; Bx: *B. xylophilus*.

Table S8. Presence of genes involved in immune signaling in *M. enterolobii* and other nematodes.

Immune signaling	Ce	Mi	Mh	Me	Gp	Bx
TGF- β signaling pathway	<i>dbl-1</i>	+	+	+	+	+
	<i>sma-2</i>	+		+	+	+
	<i>sma-3</i>	+	+	+		+
	<i>sma-4</i>	+		+		+
ERK MAPK signaling pathway	<i>lin-45</i>	+	+	+	+	+
	<i>mak-2</i>	+	+	+	+	+
	<i>mpk-1</i>	+	+	+	+	+
P39 MAPK signaling pathway	<i>nsy-1</i>	+	+	+	+	+
	<i>pmk-1</i>		+		+	+
	<i>sek-1</i>	+	+	+	+	+
	<i>tir-1</i>	+	+	+	+	+
Toll signaling pathway	<i>tol-1</i>	+	+	+	+	+
	<i>trf-1</i>					+
	<i>ikb-1</i>					
	<i>plk-1</i>	+	+	+	+	+

Ce: *C. elegans*; Me: *M. enterolobii*; Mi: *M. incognita*; Mh: *M. hapla*; Gp: *G. pallida*; Bx: *B. xylophilus*.**Table S9.** Putative secretory proteins of *M. enterolobii*.

Gene Name	E Value	ID	Function	Species
IK2WLD401ASNAP_5	3×10^{-33}	gb AAQ10016.1	putative esophageal gland cell secretory protein 2	<i>Meloidogyne incognita</i>
IK2WLD401BNOW1_7	4×10^{-24}	gb AAN08591.1	putative esophageal gland cell secretory protein 25	<i>Meloidogyne incognita</i>
IK2WLD401CC5IY_3	5×10^{-45}	gb AAF76925.1	AF159590_1 hypothetical esophageal gland cell secretory protein 11	<i>Heterodera glycines</i>
IK2WLD401CM1KN_10	1×10^{-16}	gb AAN08583.1	putative esophageal gland cell secretory protein 17	<i>Meloidogyne incognita</i>
IK2WLD401D16V8_8	1×10^{-33}	gb AAN08583.1	putative esophageal gland cell secretory protein 17	<i>Meloidogyne incognita</i>
IK2WLD401DDL8G_8	7×10^{-53}	gb AAF76926.1	AF159591_1 hypothetical esophageal gland cell secretory protein 12	<i>Heterodera glycines</i>
IK2WLD401DNW43_3	4×10^{-36}	gb AAF76925.1	AF159590_1 hypothetical esophageal gland cell secretory protein 11	<i>Heterodera glycines</i>
IK2WLD401DXTOX_7	1×10^{-53}	gb AAN08585.1	putative esophageal gland cell secretory protein 19	<i>Meloidogyne incognita</i>
IK2WLD401EBWBC_5	3×10^{-23}	gb AAQ10017.1	putative esophageal gland cell secretory protein 3	<i>Meloidogyne incognita</i>
IK2WLD402FVOYL_5	1×10^{-13}	gb AAQ10017.1	putative esophageal gland cell secretory protein 3	<i>Meloidogyne incognita</i>
IK2WLD402FXA8R_5	6×10^{-21}	gb AAN15808.1	putative esophageal gland cell secretory protein 28	<i>Meloidogyne incognita</i>

Table S9. Cont.

Gene Name	E Value	ID	Function	Species
IK2WLD402HJ8JG_9	2×10^{-7}	gb AAK94492.1	hypothetical esophageal gland protein scn1144	<i>Heterodera glycines</i>
IK2WLD402HQP79_5	5×10^{-63}	gb AAN52090.1	putative esophageal gland cell secretory protein 32	<i>Meloidogyne incognita</i>
IK2WLD402IGCSD_7	4×10^{-27}	gb AAN08591.1	putative esophageal gland cell secretory protein 25	<i>Meloidogyne incognita</i>
IKGN5RE01A3VIH_2	5×10^{-11}	gb AAN15809.1	putative esophageal gland cell secretory protein 29	<i>Meloidogyne incognita</i>
IKGN5RE01A74GJ_2	2×10^{-52}	gb AAF76926.1	AF159591_1 hypothetical esophageal gland cell secretory protein 12	<i>Heterodera glycines</i>
IKGN5RE01A81OV_8	4×10^{-47}	gb AAF76926.1	AF159591_1 hypothetical esophageal gland cell secretory protein 12	<i>Heterodera glycines</i>
IKGN5RE01A8FU5_7	2×10^{-10}	gb AAF76926.1	AF159591_1 hypothetical esophageal gland cell secretory protein 12	<i>Heterodera glycines</i>
IKGN5RE01AJLMG_1	2×10^{-7}	gb AAN15808.1	putative esophageal gland cell secretory protein 28	<i>Meloidogyne incognita</i>
IKGN5RE01AO2FR_2	2×10^{-52}	gb AAF76926.1	AF159591_1 hypothetical esophageal gland cell secretory protein 12	<i>Heterodera glycines</i>
IKGN5RE01AQNIQ_2	7×10^{-28}	gb AAN08585.1	putative esophageal gland cell secretory protein 19	<i>Meloidogyne incognita</i>
IKGN5RE01AXQ9P_9	4×10^{-30}	gb AAQ10020.1	putative esophageal gland cell secretory protein 6	<i>Meloidogyne incognita</i>
IKGN5RE01B2CCZ_7	3×10^{-38}	gb AAN08591.1	putative esophageal gland cell secretory protein 25	<i>Meloidogyne incognita</i>
IKGN5RE01BFIYU_5	4×10^{-39}	gb AAF76926.1	AF159591_1 hypothetical esophageal gland cell secretory protein 12	<i>Heterodera glycines</i>
IKGN5RE01BGZCY_2	6×10^{-25}	gb AAQ10020.1	putative esophageal gland cell secretory protein 6	<i>Meloidogyne incognita</i>
IKGN5RE01BLHBU_8	4×10^{-25}	gb AAN52095.1	putative esophageal gland cell secretory protein 31	<i>Meloidogyne incognita</i>
IKGN5RE01BSRIR_7	5×10^{-8}	gb AAF76926.1	AF159591_1 hypothetical esophageal gland cell secretory protein 12	<i>Heterodera glycines</i>
IKGN5RE01BV957_3	2×10^{-6}	gb AAN08587.1	putative esophageal gland cell secretory protein 21	<i>Meloidogyne incognita</i>
IKGN5RE01BV9AQ_6	2×10^{-40}	gb AAF76926.1	AF159591_1 hypothetical esophageal gland cell secretory protein 12	<i>Heterodera glycines</i>
IKGN5RE01C1JO4_2	5×10^{-29}	gb AAN08591.1	putative esophageal gland cell secretory protein 25	<i>Meloidogyne incognita</i>
IKGN5RE01C6CPD_6	1×10^{-52}	gb AAQ10020.1	putative esophageal gland cell secretory	<i>Meloidogyne incognita</i>
IKGN5RE01CANMP_10	6×10^{-63}	gb AAN08586.1	putative esophageal gland cell secretory protein 20	<i>Meloidogyne incognita</i>
IKGN5RE01CMMZB_1	9×10^{-24}	gb AAN15807.1	putative esophageal gland cell secretory protein 27	<i>Meloidogyne incognita</i>
IKGN5RE01CQVXJ_3	3×10^{-8}	gb AAF76926.1	AF159591_1 hypothetical esophageal gland cell secretory protein 12	<i>Heterodera glycines</i>
IKGN5RE01CUMWL_9	5×10^{-11}	gb AAN52095.1	putative esophageal gland cell secretory protein 31	<i>Meloidogyne incognita</i>
IKGN5RE01CYB5M_9	2×10^{-38}	gb AAN08586.1	putative esophageal gland cell secretory protein 20	<i>Meloidogyne incognita</i>
IKGN5RE01D01X1_3	2×10^{-15}	gb AAQ10017.1	putative esophageal gland cell secretory protein 3	<i>Meloidogyne incognita</i>

Table S9. Cont.

Gene Name	E Value	ID	Function	Species
IKGN5RE01D1FM5_5	6×10^{-8}	gb AAN15809.1	putative esophageal gland cell secretory protein 29	<i>Meloidogyne incognita</i>
IKGN5RE01D8493_3	1×10^{-14}	gb AAQ10017.1	putative esophageal gland cell secretory protein 3	<i>Meloidogyne incognita</i>
IKGN5RE01D9SN7_4	2×10^{-9}	gb AAN15809.1	putative esophageal gland cell secretory protein 29	<i>Meloidogyne incognita</i>
IKGN5RE01DC86S_1	0.0000004	gb AAR37369.1	putative esophageal gland cell secretory protein 38	<i>Meloidogyne incognita</i>
IKGN5RE01DHOKY_2	2×10^{-31}	gb AAN15809.1	putative esophageal gland cell secretory protein 29	<i>Meloidogyne incognita</i>
IKGN5RE01DT2MA_1	1×10^{-12}	gb AAN15808.1	putative esophageal gland cell secretory protein 28	<i>Meloidogyne incognita</i>
IKGN5RE01DV9U4_2	6×10^{-31}	gb AAQ10016.1	putative esophageal gland cell secretory protein 2	<i>Meloidogyne incognita</i>
IKGN5RE01DVQPH_5	5×10^{-31}	gb AAF76925.1	AF159590_1 hypothetical esophageal gland cell secretory protein 11	<i>Heterodera glycines</i>
IKGN5RE01DXDSG_8	4×10^{-30}	gb AAQ10020.1	putative esophageal gland cell secretory protein 6	<i>Meloidogyne incognita</i>
IKGN5RE01EDS56_3	2×10^{-39}	gb AAF76925.1	AF159590_1 hypothetical esophageal gland cell secretory protein 11	<i>Heterodera glycines</i>
IKGN5RE01EF5H1_2	7×10^{-25}	gb AAQ10020.1	putative esophageal gland cell secretory protein 6	<i>Meloidogyne incognita</i>
IKGN5RE01EFPLN_11	5×10^{-9}	gb AAN15809.1	putative esophageal gland cell secretory protein 29	<i>Meloidogyne incognita</i>
IKGN5RE01ELBUM_6	5×10^{-11}	gb AAN15809.1	putative esophageal gland cell secretory protein 29	<i>Meloidogyne incognita</i>
IKGN5RE01ENZFB_2	1×10^{-29}	gb AAN08585.1	putative esophageal gland cell secretory protein 19	<i>Meloidogyne incognita</i>
IKGN5RE01EQDR1_3	2×10^{-16}	gb AAQ10017.1	putative esophageal gland cell secretory protein 3	<i>Meloidogyne incognita</i>
IKGN5RE01ER4UR_8	5×10^{-53}	gb AAF76926.1	AF159591_1 hypothetical esophageal gland cell secretory protein 12	<i>Heterodera glycines</i>
IKGN5RE01EVNS1_9	7×10^{-15}	gb AAN15809.1	putative esophageal gland cell secretory protein 29	<i>Meloidogyne incognita</i>
IKGN5RE01EXQZU_3	3×10^{-15}	gb AAQ10017.1	putative esophageal gland cell secretory protein 3	<i>Meloidogyne incognita</i>
isotig01572	7×10^{-19}	gb AAR37369.1	putative esophageal gland cell secretory protein 38	<i>Meloidogyne incognita</i>
isotig05576	4×10^{-76}	gb AAN15808.1	putative esophageal gland cell secretory protein 28	<i>Meloidogyne incognita</i>
isotig05812	2×10^{-20}	gb AAR37368.1	putative esophageal gland cell secretory protein 37	<i>Meloidogyne incognita</i>
isotig07524	0	gb AAN08587.1	putative esophageal gland cell secretory protein 21	<i>Meloidogyne incognita</i>
isotig08163	1×10^{-29}	gb AAQ10024.1	putative esophageal gland cell secretory protein 9	<i>Meloidogyne incognita</i>
isotig08479	1×10^{-103}	gb AAQ10018.1	putative esophageal gland cell secretory protein 4	<i>Meloidogyne incognita</i>
isotig08832	5×10^{-19}	gb AAR37369.1	putative esophageal gland cell secretory protein 38	<i>Meloidogyne incognita</i>
isotig09791	3×10^{-36}	gb AAN15806.1	putative esophageal gland cell secretory protein 26	<i>Meloidogyne incognita</i>
isotig09833	2×10^{-16}	gb AAR37369.1	putative esophageal gland cell secretory protein 38	<i>Meloidogyne incognita</i>

Table S9. Cont.

Gene Name	E Value	ID	Function	Species
<i>isotig10273</i>	1×10^{-53}	sp Q9BN19.1	HSP6_HETGL RecName: full = putative esophageal gland cell secretory protein 6; flags: precursor gb	
<i>isotig10427</i>	2×10^{-44}	gb AAN08584.1	putative esophageal gland cell secretory protein 18	<i>Meloidogyne incognita</i>
<i>isotig10461</i>	5×10^{-42}	gb AAQ10018.1	putative esophageal gland cell secretory protein 4	<i>Meloidogyne incognita</i>
<i>isotig10924</i>	2×10^{-80}	gb AAQ10015.1	putative esophageal gland cell secretory protein 1	<i>Meloidogyne incognita</i>
<i>isotig11423</i>	2×10^{-43}	gb AAR37368.1	putative esophageal gland cell secretory protein 37	<i>Meloidogyne incognita</i>
<i>isotig11501</i>	2×10^{-52}	gb AAF76926.1	AF159591_1 hypothetical esophageal gland cell secretory protein 12	<i>Heterodera glycines</i>
<i>isotig11727.1</i>	7×10^{-60}	gb AAQ10020.1	putative esophageal gland cell secretory protein 6	<i>Meloidogyne incognita</i>
<i>isotig11727.2</i>	7×10^{-56}	gb AAN08579.1	putative esophageal gland cell secretory protein 13	<i>Meloidogyne incognita</i>
<i>isotig12059</i>	2×10^{-34}	gb AAN08586.1	putative esophageal gland cell secretory protein 20	<i>Meloidogyne incognita</i>
<i>IK2WLD402FRO9W_8</i>	2×10^{-22}	gb EJD74715.1	hypothetical protein LOAG_18005	<i>Loa loa</i>
<i>IK2WLD402G1OBP_3</i>	1×10^{-11}	ref XP_004888020.1	predicted: transcriptional activator GLI3 isoform X2	<i>Heterocephalus glaber</i>
<i>IK2WLD401D15KI_10</i>	5×10^{-38}	ref NP_498554.1	protein NHR-10	<i>Caenorhabditis elegans</i>