

1 *Supplementary Material*

2
3 **Profiling transcriptional regulation and functional roles of**
4 ***Schistosoma mansoni* c-Jun N-terminal kinase**

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14 **Supplementary Figure Captions**

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16 **Supplementary Figure S1. *In vitro* SmJNK knockdown effects in adult schistosome**
17 **movement.** Male (A) and female (B) movement units of adult worms knocked-down
18 for SmJNK normalized with untreated (●) or unspecific control (▲). The dotted line
19 represents normalized movement units in the control (N = 3).

20 **Supplementary Tables**

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22 **Supplementary Table S1. Primer sequences used in RT-qPCR validation of differentially expressed genes.**

Gene ID	Gene name	Forward	Reverse	Concentration (nM)	Slope	R ²	Efficiency (%)
Smp_089880	Putative fad oxidoreductase	TACGGTTTCTCTTCCAACC	CATGGACCTGCTGCATTAC	400	-3.32	0.996	100.1
Smp_093230	Actin-related protein 10, arp10	GAAGGCTTGGAAGGATTCTG	CAACTGCCAACTCTCGGATA	200	-3.27	0.999	102.2
Smp_153640	PDEase domain-containing protein	CTGGATGGCATGAATTTCTTC	GATGATGTTGACGACGACGA	400	-3.505	0.990	92.9
Smp_244480	putative ataxia telangiectasia mutated (atm)	GAAGAAGAGAAATTACAAGAAACGG	GTATCAGTGAATATAGGCAGAATGG	200	-3.342	0.993	99.2
Smp_303970	Coatomer subunit alpha	TATCACACAGTACCCTCTTCCC	TCAATGTGGACTGTAGTGTAAGC	400	-3.282	0.989	101.7
Smp_340860	Putative 26s proteasome non-ATPase regulatory subunit	TGGATCATTTGACAGTTGTGC	TTCCCACCATCATCATCAG	400	-3.447	0.994	95.0
Smp_009310	Putative plasminogen activator inhibitor 1 RNA-binding protein	TAGCTCCGACAGAAGCACCT	ACGACCTCGACCAAACATTC	900	-3.37	0.996	98.0
Smp_029820	Putative 60s acidic ribosomal protein P2	AGGCTTGACATCTGCTTGC	CCACAACCTGATTGCTGAAGG	1200	-3.383	0.994	97.5
Smp_041650	Putative 40s ribosomal protein S27	AACGTTTGGTTCCCTCACC	TGACATAGAATTCGGTCACATCC	800	-3.389	0.995	97.3
Smp_053390	Histone H4	GCGACGAATAGCAGGCTTAG	AAAGGTGGGAAAGGTCTTGG	400	-3.474	0.993	94.0
Smp_103610	Cathepsin B-like cysteine proteinase	ACTTGGTGGGCACGCTATAC	GGCTGTTACCTCGGATTCAA	200	-3.364	0.996	98.3
Smp_335990	Putative ubiquitin	CTGGTAAGCAGCTAGAAGATGG	GCTCAACTTCCAAAGTGATCG	1200	-3.332	0.984	99.6

23 **Supplementary Table S2. List of statistically significant DEGs from schistosomula exposed to SmJNK dsRNA.** Each table contains log₂
 24 Fold Change and padj values obtained by DESeq2 package.
 25 EXCEL FILE (TableS2.cvs)

26
 27 **Supplementary Table S3. List of enriched Gene Ontology categories and KEGG Pathways from downregulated genes in SmJNK**
 28 **knockdown schistosomula.** The analysis is separated into three GO categories (GO Biological Process, GO Molecular Function, and GO
 29 Cellular Component) and KEGG Pathways (padj < 0.05).

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Biological Process					
term_name	term_id	adjusted_p_value	term_size	query_size	intersection_size
translation	GO:0006412	1,56E-26	242	312	51
peptide biosynthetic process	GO:0043043	2,91E-26	245	312	51
peptide metabolic process	GO:0006518	1,44E-25	253	284	49
amide biosynthetic process	GO:0043604	1,74E-25	254	284	49
cellular amide metabolic process	GO:0043603	2,73E-24	269	284	49
organonitrogen compound biosynthetic process	GO:1901566	1,84E-21	427	284	57
cellular nitrogen compound metabolic process	GO:0034641	1,57E-14	1153	371	99
gene expression	GO:0010467	3,42E-16	863	371	86
cellular nitrogen compound biosynthetic process	GO:0044271	7,24E-15	740	361	75
cellular macromolecule biosynthetic process	GO:0034645	4,75E-14	748	361	74
macromolecule biosynthetic process	GO:0009059	6,85E-14	753	361	74
cellular biosynthetic process	GO:0044249	2,99E-12	920	346	78
biosynthetic process	GO:0009058	1,62E-12	950	319	76
cellular process	GO:0009987	1,92E-12	2960	341	166
organic substance biosynthetic process	GO:1901576	1,99E-12	933	319	75
cellular metabolic process	GO:0044237	2,07E-12	2073	371	139
protein metabolic process	GO:0019538	2,42E-10	1133	284	74
biological_process	GO:0008150	6,03E-11	3995	371	214

primary metabolic process	GO:0044238	9,33E-10	2189	371	137
cellular protein metabolic process	GO:0044267	1,14E-11	928	284	68
organonitrogen compound metabolic process	GO:1901564	1,8E-11	1297	284	83
nitrogen compound metabolic process	GO:0006807	2,29E-09	2034	341	121
organic substance metabolic process	GO:0071704	4,9E-09	2260	371	138
cellular macromolecule metabolic process	GO:0044260	1,08E-08	1466	341	95
metabolic process	GO:0008152	1,11E-08	2518	371	151
macromolecule metabolic process	GO:0043170	1,46E-08	1871	341	112
protein folding	GO:0006457	5,37E-08	44	366	14
ATP hydrolysis coupled cation transmembrane transport	GO:0099132	0.00002036949264641862	24	368	9
proton transmembrane transport	GO:1902600	0.00005369077541597394	34	368	10
ATP metabolic process	GO:0046034	0.00017004833961436932	38	368	10
purine nucleoside triphosphate biosynthetic process	GO:0009145	0.003037670897198561	18	316	6
purine nucleoside triphosphate metabolic process	GO:0009144	0.003037670897198561	18	316	6
purine ribonucleoside triphosphate biosynthetic process	GO:0009206	0.003037670897198561	18	316	6
purine ribonucleoside triphosphate metabolic process	GO:0009205	0.003037670897198561	18	316	6
ATP synthesis coupled proton transport	GO:0015986	0.004856734136094929	12	316	5
ATP biosynthetic process	GO:0006754	0.004856734136094929	12	316	5
energy coupled proton transport, down electrochemical gradient	GO:0015985	0.004856734136094929	12	316	5
nucleoside triphosphate biosynthetic process	GO:0009142	0.006017155969374157	20	316	6
ribonucleoside triphosphate metabolic process	GO:0009199	0.006017155969374157	20	316	6
ribonucleoside triphosphate biosynthetic process	GO:0009201	0.006017155969374157	20	316	6
regulation of cellular catabolic process	GO:0031329	0.0060793489282895165	12	331	5
purine ribonucleotide metabolic process	GO:0009150	0.008363094556938505	53	316	9
positive regulation of proteolysis	GO:0045862	0.00889867157110456	7	327	4
positive regulation of protein catabolic process	GO:0045732	0.00889867157110456	7	327	4
positive regulation of proteolysis involved in cellular protein catabolic process	GO:1903052	0.00889867157110456	7	327	4

positive regulation of catabolic process	GO:0009896	0.00889867157110456	7	327	4
positive regulation of cellular protein catabolic process	GO:1903364	0.00889867157110456	7	327	4
positive regulation of proteasomal protein catabolic process	GO:1901800	0.00889867157110456	7	327	4
positive regulation of cellular catabolic process	GO:0031331	0.00889867157110456	7	327	4
nucleoside triphosphate metabolic process	GO:0009141	0.010989660932852382	22	316	6
purine nucleotide metabolic process	GO:0006163	0.01317340598199164	56	316	9
ribose phosphate metabolic process	GO:0019693	0.01317340598199164	56	316	9
ribonucleotide metabolic process	GO:0009259	0.01317340598199164	56	316	9
purine-containing compound metabolic process	GO:0072521	0.015914400720549757	63	357	10
regulation of proteasomal protein catabolic process	GO:0061136	0.01734643067712882	8	327	4
regulation of proteolysis involved in cellular protein catabolic process	GO:1903050	0.01734643067712882	8	327	4
regulation of cellular protein catabolic process	GO:1903362	0.01734643067712882	8	327	4
regulation of catabolic process	GO:0009894	0.021262053480788943	15	331	5
RNA splicing	GO:0008380	0.023264121690808364	59	322	9
protein import into nucleus	GO:0006606	0.02525493684655285	8	360	4
protein localization to nucleus	GO:0034504	0.02525493684655285	8	360	4
proteolysis involved in cellular protein catabolic process	GO:0051603	0.027637528021193663	73	327	10
cellular protein catabolic process	GO:0044257	0.03483520942918839	75	327	10
ATP hydrolysis coupled proton transport	GO:0015991	0.03512230510764226	15	368	5
ATP hydrolysis coupled ion transmembrane transport	GO:0099131	0.03512230510764226	15	368	5
ATP hydrolysis coupled transmembrane transport	GO:0090662	0.03512230510764226	15	368	5
energy coupled proton transmembrane transport, against electrochemical gradient	GO:0015988	0.03512230510764226	15	368	5
organic substance catabolic process	GO:1901575	0.035411496770635834	154	367	16
translational initiation	GO:0006413	0.041303296366220654	39	312	7
inorganic cation transmembrane transport	GO:0098662	0.044142864667227576	85	240	9
import into nucleus	GO:0051170	0.044191369106860286	9	360	4

Cellular Component

term_name	term_id	adjusted_p_value	term_size	query_size	intersection_size
cytoplasm	GO:0005737	7,96E-34	716	327	96
ribosome	GO:0005840	1,09E-30	143	311	44
intracellular	GO:0005622	3,88E-31	1535	367	148
intracellular part	GO:0044424	2,46E-30	1485	367	144
ribonucleoprotein complex	GO:1990904	7,35E-29	206	322	50
cell	GO:0005623	3,29E-28	1725	367	153
cell part	GO:0044464	7,7E-27	1674	367	148
protein-containing complex	GO:0032991	8,53E-27	880	372	104
cytoplasmic part	GO:0044444	1,26E-23	528	315	69
intracellular non-membrane-bounded organelle	GO:0043232	1,65E-21	455	301	60
non-membrane-bounded organelle	GO:0043228	1,65E-21	455	301	60
intracellular organelle	GO:0043229	3,18E-20	1211	364	111
organelle	GO:0043226	1,06E-20	1229	364	111
cellular_component	GO:0005575	3,62E-17	3007	368	189
ribosomal subunit	GO:0044391	9,87E-10	31	148	10
intracellular organelle part	GO:0044446	5,19E-09	691	361	60
small ribosomal subunit	GO:0015935	7,48E-09	15	54	6
organelle part	GO:0044422	9,89E-09	702	361	60
proton-transporting two-sector ATPase complex	GO:0016469	0.000033340414340879555	28	368	9
intracellular membrane-bounded organelle	GO:0043231	0.0003254368151697163	843	372	57
membrane-bounded organelle	GO:0043227	0.00042539893327894784	871	372	58
collagen trimer	GO:0005581	0.0008560587184345816	6	290	4
large ribosomal subunit	GO:0015934	0.000998150601320439	16	358	6
proteasome complex	GO:0000502	0.0010641972132517067	35	327	8
endopeptidase complex	GO:1905369	0.0010641972132517067	35	327	8
proton-transporting ATP synthase complex	GO:0045259	0.0017115059409485824	12	316	5
organelle membrane	GO:0031090	0.0022122525506626275	181	240	15

proton-transporting two-sector ATPase complex, catalytic domain	GO:0033178	0.0035717447354012195	12	368	5
mitochondrial envelope	GO:0005740	0.003847683226486142	65	203	8
peptidase complex	GO:1905368	0.005239484569349109	43	327	8
membrane protein complex	GO:0098796	0.008703524495472636	149	368	16
mitochondrial membrane	GO:0031966	0.00896532966217273	57	194	7
nucleosome	GO:0000786	0.012808504060448294	24	356	6
proton-transporting two-sector ATPase complex, proton-transporting domain	GO:0033177	0.016857577457431303	13	240	4
DNA packaging complex	GO:0044815	0.020648794787145514	26	356	6
protein-DNA complex	GO:0032993	0.020648794787145514	26	356	6
envelope	GO:0031975	0.02213081644347884	83	203	8
organelle envelope	GO:0031967	0.02213081644347884	83	203	8
proton-transporting ATP synthase complex, catalytic core F(1)	GO:0045261	0.026153877468782682	5	316	3
proteasome core complex	GO:0005839	0.03677935880748339	15	251	4
mitochondrial part	GO:0044429	0.03861625090962635	90	203	8
bounding membrane of organelle	GO:0098588	0.04261873163212783	85	275	9

Molecular Function					
term_name	term_id	adjusted_p_value	term_size	query_size	intersection_size
structural molecule activity	GO:0005198	6,98E-34	185	152	40
structural constituent of ribosome	GO:0003735	2,02E-28	128	301	40
molecular_function	GO:0003674	3,6E-18	5283	373	279
heterocyclic compound binding	GO:1901363	9,79E-18	1845	370	140
RNA binding	GO:0003723	1,62E-18	352	370	55
organic cyclic compound binding	GO:0097159	1,03E-17	1846	370	140
nucleic acid binding	GO:0003676	1,46E-13	1054	370	91
binding	GO:0005488	4,62E-12	3620	373	203
extracellular matrix structural constituent	GO:0005201	0.000006038829067217214	11	102	5
unfolded protein binding	GO:0051082	0.00005150980774374434	28	366	9

proton transmembrane transporter activity	GO:0015078	0.00005164345770840948	41	316	10
ion binding	GO:0043167	0.00008862333838870891	1509	369	90
purine ribonucleotide binding	GO:0032555	0.00038870566181245704	803	368	55
purine nucleotide binding	GO:0017076	0.0004355852488050613	806	368	55
small molecule binding	GO:0036094	0.00045698611524626543	911	368	60
ribonucleotide binding	GO:0032553	0.0004697202767809331	808	368	55
nucleoside phosphate binding	GO:1901265	0.0005424103025568984	874	368	58
nucleotide binding	GO:0000166	0.0005424103025568984	874	368	58
purine ribonucleoside triphosphate binding	GO:0035639	0.0005568939578934083	792	368	54
ATPase activity, coupled	GO:0042623	0.0006040045842672542	72	340	12
anion binding	GO:0043168	0.00064928849977488	900	368	59
carbohydrate derivative binding	GO:0097367	0.0007329760323595684	820	368	55
nucleoside-triphosphatase activity	GO:0017111	0.0023163089567947285	330	340	27
pyrophosphatase activity	GO:0016462	0.0035569348186957144	338	340	27
hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	GO:0016818	0.0043804768885977894	342	340	27
proton-transporting ATP synthase activity, rotational mechanism	GO:0046933	0.0044334894191827	7	316	4
structural constituent of cytoskeleton	GO:0005200	0.004633497481722036	16	121	4
proteasome-activating ATPase activity	GO:0036402	0.005073570955465585	7	327	4
hydrolase activity, acting on acid anhydrides	GO:0016817	0.005107551169497762	345	340	27
L-lactate dehydrogenase activity	GO:0004459	0.010793763431696754	2	87	2
lactate dehydrogenase activity	GO:0004457	0.010793763431696754	2	87	2
translation initiation factor activity	GO:0003743	0.014447137370812808	47	321	8
ATPase activity	GO:0016887	0.014647710830029931	98	340	12
ATPase coupled ion transmembrane transporter activity	GO:0042625	0.01902985354987977	17	316	5
active ion transmembrane transporter activity	GO:0022853	0.01902985354987977	17	316	5
cation-transporting ATPase activity	GO:0019829	0.01902985354987977	17	316	5
drug binding	GO:0008144	0.02569201274685189	672	368	43

adenyl ribonucleotide binding	GO:0032559	0.02657446646458657	652	368	42
adenyl nucleotide binding	GO:0030554	0.02747297309130325	653	368	42
peptidyl-prolyl cis-trans isomerase activity	GO:0003755	0.030141544695469886	19	308	5
cis-trans isomerase activity	GO:0016859	0.030141544695469886	19	308	5
ATP binding	GO:0005524	0.036997986471330804	641	368	41
ATPase activity, coupled to transmembrane movement of ions, rotational mechanism	GO:0044769	0.03786242193559343	11	316	4

KEGG Pathway					
term_name	term_id	adjusted_p_value	term_size	query_size	intersection_size
Ribosome	KEGG:03010	1,26E-26	83	152	26
Phagosome	KEGG:04145	0.000040246025285053825	41	368	11
Spliceosome	KEGG:03040	0.00011533198327651202	78	370	13
Oxidative phosphorylation	KEGG:00190	0.002152115462101306	51	368	9
ECM-receptor interaction	KEGG:04512	0.009036501095036616	8	187	3
Pyruvate metabolism	KEGG:00620	0.04343022668549986	18	295	4

31 **Supplementary Table S4. List of enriched RNAi phenotypes in *C. elegans* orthologs**
 32 **from downregulated genes in SmJNK knockdown schistosomula.**
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Term	Overlap
sterile_WBPhenotype:0000688	137/1370
embryonic lethal_WBPhenotype:0000050	185/3015
maternal sterile_WBPhenotype:0000689	119/1002
larval arrest_WBPhenotype:0000059	141/1606
transgene subcellular localization variant_WBPhenotype:0000679	124/1182
slow growth_WBPhenotype:0000031	130/1858
avoids bacterial lawn_WBPhenotype:0000402	76/484
germ cell compartment expansion variant_WBPhenotype:0001980	70/437
RAB-11 recycling endosome morphology variant_WBPhenotype:0002094	61/353
pachytene region organization variant_WBPhenotype:0001951	55/274
lysosome-related organelle morphology variant_WBPhenotype:0002095	58/337
rachis narrow_WBPhenotype:0001941	55/292
RAB-11 recycling endosome localization variant_WBPhenotype:0002107	51/246
chromosome condensation variant_WBPhenotype:0001361	51/247
pleiotropic defects severe early emb_WBPhenotype:0000270	39/122
transgene expression increased_WBPhenotype:0001236	85/1038
gonad vesiculated_WBPhenotype:0001979	45/213
nuclei small_WBPhenotype:0001792	41/172
sister chromatid segregation defective early emb_WBPhenotype:0000772	34/103
protein aggregation variant_WBPhenotype:0001405	59/503
oocyte number decreased_WBPhenotype:0001944	50/333
oocyte morphology variant_WBPhenotype:0001260	48/325
larval lethal_WBPhenotype:0000054	68/770
locomotion variant_WBPhenotype:0000643	87/1347
apoptosis reduced_WBPhenotype:0000182	41/220
sick_WBPhenotype:0000032	62/651
cytoplasmic processing body variant_WBPhenotype:0001794	44/279
diplotene region organization variant_WBPhenotype:0001950	36/201
oocytes small_WBPhenotype:0001945	29/127
cell membrane organization biogenesis variant_WBPhenotype:0001982	42/344
diplotene absent during oogenesis_WBPhenotype:0001954	28/119
embryonic arrest_WBPhenotype:0000867	31/160
rachis morphology variant_WBPhenotype:0001940	39/300
cell corpse degradation variant_WBPhenotype:0010004	20/44
body elongation defective_WBPhenotype:0000242	20/48
accumulated cell corpses_WBPhenotype:0000241	22/65
pattern of transgene expression variant_WBPhenotype:0000961	62/929
gonad small_WBPhenotype:0001957	24/88
pharyngeal development variant_WBPhenotype:0000707	20/51
transgene expression reduced_WBPhenotype:0001278	55/760
receptor mediated endocytosis defective_WBPhenotype:0001425	54/737
anaphase bridging_WBPhenotype:0001875	21/70

extended life span_WBPhenotype:0000061	47/585
no induction of antimicrobial peptide expression after infection_WBPhenotype:0002460	36/340
germ cell compartment morphology variant_WBPhenotype:0001969	34/304
lethal_WBPhenotype:0000062	45/579
protruding vulva_WBPhenotype:0000697	51/763
pachytene progression during oogenesis variant_WBPhenotype:0001946	20/82
chromosome segregation variant_WBPhenotype:0000773	23/123
apoptosis fails to occur_WBPhenotype:0000184	20/83
no oocytes_WBPhenotype:0000291	28/213
intestinal degeneration_WBPhenotype:0002428	14/33
rachis absent_WBPhenotype:0001942	19/87
growth variant_WBPhenotype:0000030	28/244
germ cell compartment expansion absent_WBPhenotype:0001981	17/65
pathogen resistance increased_WBPhenotype:0001014	15/46
early larval arrest_WBPhenotype:0000055	24/188
nuclear appearance variant_WBPhenotype:0001028	25/225
oocyte septum formation variant_WBPhenotype:0001810	22/171
germ cell compartment anucleate_WBPhenotype:0001971	19/124
oocytes lack nucleus_WBPhenotype:0001956	18/121
germline nuclear positioning variant_WBPhenotype:0001952	25/274
molt defect_WBPhenotype:0000638	24/257
lima bean arrest_WBPhenotype:0000361	45/566
reduced brood size_WBPhenotype:0000154	47/1003
cell secretion variant_WBPhenotype:0000258	15/90
accumulated germline cell corpses_WBPhenotype:0001180	22/245
germ cell compartment size variant_WBPhenotype:0001973	19/176
nonsense mRNA accumulation_WBPhenotype:0000508	15/111
mRNA surveillance defective_WBPhenotype:0001538	15/112
organism morphology variant_WBPhenotype:0000535	27/420
body wall muscle myosin organization defective_WBPhenotype:0001569	16/155
apoptosis variant_WBPhenotype:0000730	17/182
shortened life span_WBPhenotype:0001171	26/444
gonad development variant_WBPhenotype:0000691	20/273
slow embryonic development_WBPhenotype:0000042	32/112
gonad morphology variant_WBPhenotype:0001355	16/182
multiple nuclei oocyte_WBPhenotype:0001955	28/065
excess intestinal cells_WBPhenotype:0001636	12/101
development variant_WBPhenotype:0000518	12/997
passage through meiosis defective early emb_WBPhenotype:0000776	24/016
cell proliferation increased_WBPhenotype:0000172	12/103
pathogen susceptibility increased_WBPhenotype:0001013	13/134
germ cell compartment multinucleate_WBPhenotype:0001972	15/184
germ cell partition morphology variant_WBPhenotype:0001977	34/639
meiotic progression during oogenesis variant_WBPhenotype:0000313	47/300
protein expression reduced_WBPhenotype:0000120	16/223
sterile progeny_WBPhenotype:0001037	31/763

foraging behavior variant_WBPhenotype:0000662	13/149
embryonic morphology variant_WBPhenotype:0001136	13332
oocytes disorganized_WBPhenotype:0001925	26177
nuclei enlarged_WBPhenotype:0001567	34608
dauer lifespan extended_WBPhenotype:0002277	28/694
fat content reduced_WBPhenotype:0001183	20/423
paralyzed_WBPhenotype:0000644	11/135
embryonic lethal late emb_WBPhenotype:0001020	27242
variable cell division timing_WBPhenotype:0002390	27242
mitochondria alignment variant_WBPhenotype:0001577	10/125
diakinesis progression during oogenesis variant_WBPhenotype:0001948	28338
germ cell development variant_WBPhenotype:0000812	11/154
general pace of development defective early emb_WBPhenotype:0000126	21367
transgene expression variant_WBPhenotype:0000306	12/190
dead eggs laid_WBPhenotype:0000274	30529
nuclear fallout_WBPhenotype:0001953	22463
germ cell compartment small_WBPhenotype:0001974	23924
germ cell partition absent_WBPhenotype:0001978	42095
increased levels of reactive oxygen species_WBPhenotype:0002238	43619
diplotene progression during oogenesis variant_WBPhenotype:0001947	19146
ATP levels reduced_WBPhenotype:0001575	43191
germ cell morphology variant_WBPhenotype:0000900	28672
patchy coloration_WBPhenotype:0001029	8/106
diakinesis region organization variant_WBPhenotype:0001949	13271
small_WBPhenotype:0000229	15/344
thin_WBPhenotype:0000164	11/207
unfertilized oocytes laid_WBPhenotype:0000357	43711
L1 arrest_WBPhenotype:0000081	22433
motor neuron morphology variant_WBPhenotype:0001331	45383
synapse density variant_WBPhenotype:0002001	45383
exploded through vulva_WBPhenotype:0000038	15/372
mRNA levels increased_WBPhenotype:0000136	33786
life span variant_WBPhenotype:0000039	10/187
cell membrane morphology variant_WBPhenotype:0001399	43802
rachis wide_WBPhenotype:0001943	26451
embryo osmotic integrity defective early emb_WBPhenotype:0000365	8/130
organism development variant_WBPhenotype:0000531	18/527
peptide uptake by intestinal cell decreased_WBPhenotype:0002082	18749
adult lethal_WBPhenotype:0000060	28642
protein expression absent_WBPhenotype:0001410	41699
cell division precocious_WBPhenotype:0001495	41699
organism heat response variant_WBPhenotype:0001273	42430
late larval arrest_WBPhenotype:0000056	31199
clear_WBPhenotype:0001010	10/221
protein transport variant_WBPhenotype:0001864	43525
ectopic expression antibody_WBPhenotype:0001404	43525

protein subcellular localization variant_WBPhenotype:0000436	9/197
male gonad development variant_WBPhenotype:0001675	7/128
embryonic terminal arrest variable emb_WBPhenotype:0000051	43891
mitochondrial content increased_WBPhenotype:0002267	43618

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