Supplemental TABLE 4. List of proteins found only in E/S products of parasitic females

N°	Cluster	BLAST Alignment	Species	Accession Number	E	SP	EST Lgt.	% Cov.	Pep. #	UPS
Anti-oxidants										
1	SR00399	Thioredoxin family protein	*Brugia malayi*	XP_001892562	$1e^{-43}$	no	152	15.8	2	5.15
Carbohydrate Metabolism										
2	SR02118	Phosphoribosyl transferase	*B. malayi*	XP_001895434	$2e^{-27}$	no	152	31.6	3	6.24
3	SR02411	Glycosyl hydrolase	*B. malayi*	XP_001901753	$3e^{-65}$	yes	181	16.0	2	4.17
4	SS02201	Glycosyl transferase	*B. malayi*	XP_001901721	$3e^{-99}$	no	218	11.0	2	5.22
5	SS00512	Glucosidase beta subunit	*B. malayi*	XP_001899874	$4e^{-37}$	no	137	12.4	2	4.00
Protein digestion and folding										
6	SR01641	Prolyl endopeptidase	*Treponema denticola*	NP_971802	$2e^{-12}$	no	126	31.0	4	11.26
7	SR03191	Prolyl endopeptidase	*Rattus norvegicus*	EDL99674	$3e^{-19}$	no	189	51.3	6	16.69
8	SR03587	Metalloprotease	*Nasonia vitripennis*	XP_001606489	$9e^{-06}$	yes	166	42.8	6	14.23
9	SR03310	mp1	*Onchocerca volvulus*	AAV71152	$2e^{-13}$	yes	189	39.2	5	11.64
10	SR03901	Aspartyl protease (asp-2)	*Caenorhabditis elegans*	NP_505384	$4e^{-43}$	no	191	56.5	5	13.20
11	SR00074	Aspartyl protease (asp-2)	*C. elegans*	NP_505384	$1e^{-59}$	no	222	11.7	2	4.70
12	SR00564	Calumenin	*C. elegans*	NP_001024806	$2e^{-134}$	yes	286	19.2	4	10.87
13	SS00575	Calcyclin binding protein	*Tribolium castaneum*	XP_967766	$8e^{-19}$	no	173	12.7	2	5.27
14	SR02954	Peptidase family M1 containing protein	*B. malayi*	XP_001901798	$5e^{-27}$	yes	171	14.0	2	4.00
15	SR02663	Metalloprotease precursor	*Strongyloides stercoralis*	AAK55800	$6e^{-12}$	trun-cated	182	19.2	3	6.91
16	SS00365	Ubiquitin family protein	*B. malayi*	XP_001902395	$6e^{-14}$	no	168	16.7	2	4.80
Structural proteins										
17	SR00945	Troponin T family member	*C. elegans*	NP_001024703	$3e^{-103}$	no	357	6.2	2	4.01
18	SR01499	Troponin family protein	*B. malayi*	XP_001898461	$5e^{-50}$	no	257	14.0	3	6.19
19	SS03220	Intermediate filament protein (ifa-3)	*C. elegans*	NP_510649	$6e^{-38}$	no	141	24.1	3	6.23
Heat shock proteins										
20	SR00984	Small heat shock protein	*Trichinella pseudospiralis*	ABJ55915	$9e^{-22}$	no	160	35.6	4	10.67
21	SR03349	Heat shock protein HSP17	*C. elegans*	NP_001023958	$2e^{-20}$	no	157	39.5	5	10.04

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22	SS01231	Heat shock 70 kDa protein	*B. malayi*	XP_001892998	$2e^{-20}$	no	90	16.7	2	4.00
Cytoplasmatic										
23	SR00396	Endoplasmin	*B. malayi*	XP_001899398	$7e^{-98}$	yes	231	16.5	3	8.56
24	SS00604	Endoplasmin	*B. malayi*	XP_001899398	$7e^{-54}$	yes	179	11.2	2	4.49
Nucleic acid metabolism										
25	SR01055	Ribosomal protein (rpl-4)	*C. elegans*	NP_491416	$1e^{-132}$	no	341	9.1	2	4.41
26	SR01073	Ribosomal protein (rpl-5)	*C. elegans*	NP_495811	$2e^{-119}$	no	290	19.3	4	9.47
27	SR00991	Small subunit ribosomal protein	*Pristionchus sp. 3 CZ3975*	ABR87454	$5e^{-115}$	trun-cated	257	21.0	3	6.03
28	SR01039	Ribosomal protein L8 CG1263-PA	*Apis mellifera*	XP_393671	$2e^{-112}$	no	243	8.6	2	4.04
29	SR01021	Putative ribo-somal protein L	*Diaphorina citri*	ABG81972	$4e^{-85}$	no	204	10.3	2	4.00
30	SR01047	Ribosomal protein (rps-3)	*C. elegans*	NP_498349	$3e^{-100}$	no	242	8.7	2	5.57
31	SS01567	40S ribosomal protein S8	*B. malayi*	XP_001893693	$2e^{-91}$	no	209	20.1	3	6.00
32	SR01072	Ribosomal protein (rpl-13)	*C. elegans*	NP_001022017	$9e^{-69}$	no	213	13.1	2	5.62
33	SR01036	Ribosomal protein L6	*Strongyloides papillosus*	ABK55146	$4e^{-56}$	trun-cated	204	15.2	2	6.16
34	SS01551	40S ribosomal protein S9	*B. malayi*	XP_001894478	$1e^{-85}$	no	192	8.9	2	4.14
35	SR00979	Ribosomal protein L9	*S. papillosus*	ABK55147	$2e^{-73}$	trun-cated	166	21.7	2	6.47
36	SS01553	60S ribosomal protein L11	*B. malayi*	XP_001892371	$1e^{-88}$	no	197	16.2	2	5.42
37	SR01004	Ribosomal protein L18e	*Tribolium castaneum*	XP_968042	$6e^{-60}$	no	187	15.1	2	4.68
38	SR01002	Ribosomal protein (rps-18)	*C. elegans*	NP_502794	$5e^{-75}$	no	154	15.6	2	6.64
39	SR00943	Ribosomal protein (rpl-14)	*C: elegans*	NP_492576	$2e^{-36}$	no	134	20.9	2	4.07
Other function										
40	SS00866	EF hand family protein	*B. malayi*	XP_001901161	$2e^{-29}$	yes	177	13.6	3	6.01
41	SR01608	EF hand family protein	*B. malayi*	XP_001901161	$2e^{-37}$	yes	158	69.0	8	23.28
42	SR04713	Surface antigen BspA-like	*Trichomonas vaginalis*	XP_001315000	5.3	no	55	89.1	3	7.27
43	SR01156	Small nuclear ribonucleo-protein E	*B. malayi*	XP_001894662	$5e^{-24}$	no	88	33.0	2	5.40
44	SR04847	Acetylcholinester ase 2	*Ditylenchus destructor*	ABQ58116	$1e^{-44}$	no	192	36.5	5	12.4

	Cluster	BLAST Alignment	Species	Accession Number	E	SP	EST Lgt.	% Cov.	Pep. #	UPS
45	SR02054	Scavenger receptor cysteine rich protein	*Culex pipiens quinquefasciatus*	XP_001866937	$3e^{-24}$	yes	328	14.6	4	10.44
46	SR04723	Abnormal nuclease family member	*C. elegans*	NP_509604	$8e^{-39}$	yes	187	20.3	2	4.84
47	SR01007	40S ribosomal protein S4	*B. malayi*	XP_001892792	$1e^{-117}$	no	262	7.6	2	5.51
48	SR01297	Immnunosuppressive ovarian message protein	*A. suum*	CAK18209	$2e^{-17}$	yes	324	19.8	4	8.15
49	SR03217	Immnunosuppressive ovarian message protein	*A. suum*	CAK18210	$6e^{-16}$	yes	193	10.9	2	4.00
50	SR00986	60S ribosomal protein L10	*B. malayi*	XP_001898297	$2e^{-85}$	no	189	17.5	3	8.26
51	SR00664	Pheromone biosynthesis-activating neuropeptide	*Heliothis virescens*	AAO20095	0.058	yes	229	15.3	2	4.19
52	SS03344	SPARC precursor	*B. malayi*	XP_001897784	$2e^{-74}$	yes	175	20.6	3	6.23
53	SR04821	PAZ domain containing protein	*B. malayi*	XP_001895198	$8e^{-08}$	no	175	12.6	2	5.40
54	SR01592	Ankyrin repeat domain containing protein	*Mus musculus*	CAQ51694	3.5	no	166	22.9	3	6.00
55	SR00441	SELD-1	*C. elegans*	NP_502604	$4e^{-54}$	no	179	15.1	2	5.40
56	SS01458	Beta-NAC-like protein	*B. malayi*	XP_001900247	$1e^{-59}$	no	156	20.5	2	4.01
57	SR04058	Nuclear movement protiein	*B. malayi*	XP_001892948	$4e^{-53}$	no	221	9.4	2	4.01
58	SR03161	Adenine phosphoribosyltransferase	*Loktanella vestofoldensis*	ZP_01000397 1	2.0	no	65	36.9	2	4.00
59	SR01308	Isochorismatase family protein	*B. malayi*	XP_001901766	$9e^{-19}$	no	117	29.1	2	5.70
Not assigned										
60	SR04455	Hypothetical protein CBG05204	*C. briggsae*	XP_001664881	2.0	yes	88	56.8	5	10.64
61	SR03561	Hypothetical protein CBG05204	*C. briggsae*	XP_001677019	$1e^{-49}$	yes	150	32.7	3	6.00
62	SS00845	C05D11.1	*C. elegans*	NP_001021145	$1e^{-46}$	no	209	11.0	2	4.15
63	SR03259	Hypothetical protein	*B. malayi*	XP_001896639	$1e^{-64}$	no	171	25.7	3	6.00
64	SR03153	Hypothetical protein CBG19978	*C. briggsae*	XP_001670997	$9e^{-82}$	no	192	15.6	2	5.70

N°	Cluster	BLAST Alignment	Species	Accession Number	E	SP	EST Lgt.	% Cov.	Pep. #	UPS
65	SS03048	Hypothetical protein CBG09854	*C. briggsae*	XP_001665147	$3e^{-53}$	yes	175	13.1	2	4.04
66	SR02153	Hypothetical protein CBG20335	*C. briggsae*	CAP37373	$2e^{-34}$	no	178	13.5	2	6.34
67	SR01296	Hypothetical protein CBG07632	*C. briggsae*	XP_001677777	$5e^{-59}$	yes	179	8.4	2	4.00
68	SR03570	Predicted protein	*Nematostella vectensis*	XP_001632220	0.001	no	33	72.7	2	5.22
69	SR00696	T20D3.2	*C. elegans*	NP_501640	$7e^{-19}$	yes	225	14.7	2	4.00
70	SR02281	Hypothetical protein CBG23452	*C. briggsae*	XP_001673551	$2e^{-26}$	no	112	28.6	2	5.40

Novel proteins that are not listed in one of the *Strongyloides ssp.* EST databases

N°	Acc. Number	BLAST Alignment	Species	SP	Fragment Length	% Cov.	Pep. #	UPS
71	gi|22759003	Acetylcholinesterase 1	*Necator americanus*	yes	594	1.2	2	4.02
72	gi|6754388	Intelectin 1	*Mus musculus*	yes	313	15.7	4	11.74
73	gi|3182894	Actin	*B. malayi*	no	376	22.3	5	15.55
74	gi|71992775	Y105E8A.19	*C. elegans*	no	722	3.0	2	4.55
75	gi|17534771	Heat shock protein (hsp-4)	*C. elegans*	yes	657	4.6	3	7.57
76	gi|71986328	F48E8.3	*C. elegans*	yes	493	4.5	2	4.02
77	gi|20163188	Aldolase	*H. glycines*	no	366	7.4	2	4.01
78	gi|17508209	Acylsphingosine Amidohydrolase	*C. elegans*	yes	393	9.4	2	5.06
79	gi|40388674	14-3-3b protein	*Meloidogyne incognita*	no	251	13.1	3	7.70

E, expectation value; SP, signal peptide; EST Lgt., EST length; % Cov., percentage coverage; Pep. #, number of peptides (#); UPS, unused protein scores