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SUPPLEMENTAL FIG. S1 [see file Supplemental-figure-S1.xlsx]. **Distribution of ESP proteins between life stages of** *L. sigmodontis.* Interactive Venn diagram of the shared and stage-specific ESP proteins in each of the life stages examined.



SUPPLEMENTAL FIG. S2. Comparison of ESP protein abundance (iBAQ) in larval stages of *L. sigmodontis.* Proteins in each ESP preparation (A, vL3; B, iMf) are ranked by normalised iBAQ abundance (grey bars); the corresponding abundance in WBE is displayed for comparison (black bars) in stacked format. Individual protein abundance values were normalised by the summed total abundance per sample. An asterisk indicates proteins with a predicted signal peptide, while predicted secretion through the non-classical pathway is indicated by a plus sign.



SUPPLEMENTAL FIG. S3. **Domain organisation of protein nLs\_04059 from** *Litomosoides sigmodontis.* Linear representation of the amino-acid sequence highlighting the signal peptide (indigo box), six ShK toxin-like domains (open rectangles) containing six cysteine residues each (yellow), and a predicted propeptide cleavage site (red). Domain six at the C-terminus is unique in containing two lysyltyrosine dyads (cyan).

Consensus	1 10 <sup>-</sup> 20 30 <sup>-</sup> 40 50 <sup>-</sup> 60 70 80 MTTQRLQMVFIVAVVLTCLALNDIQAMRIKRDDAGQEDHKNQTDVNHDEHQEHGHEHQNDSSHEKHEHH-NCSGSHESHSKEHH
Identity	The second from the second of
Setaria labiatopapillosa Litomosoides sigmodontis Acanthocheilonema viteae Wuchereria bancrofti Brugia malayi (isoform c) Brugia malayi (isoform c) Loa loa Dirofilaria immitis Onchocerca ochengi Onchocerca gutturosa Onchocerca volvulus	MMNQ KLHVVFI VTMVLTCL TLNE IQAM RIKRNDA RPEDLKNQ TEL IQDQH QER QNDSSHER HEHHSNCS GNHEIHN KEHS MTTQ RLPMAFI VTVVVTCL VLND IQAM RIKRDDA GNEDQTNG TDVNRDEH QEHGDER RNDSTHEK HGHH-NCSENHN KEHH MTTR RLQMMFF VAVVLICL ALND IQAM RIKRDDA GQEDHRNE TDVNH DKH QEHGHEH QNDSNHEHH-NCS GSHESHS KEHH MTTH RSQMVFI VAVVLTCL ALHHI QAM RIKRDHS EQENRKNE TD INHGEH QEHGHEH QNDSSHEK HEHH-NCS GSHESHS KEHS MTTH RSQMVYI VAVVLTCL ALND IQAM RIKRDHS EQENRKNE TD INHGEH QEHGYEH QNDSGHEK HEHH-NCS SHESHS KEHS MTTH RSQMVYI VAVVLTCL ALND IQAM RIKRDHS EQENRKNE TD INQGKH QEHGYEH QNDSGHEK HEHH-NCS ENHESHS KEHS MTTH RSQMVYI VAVVLTCL ALND IQAM RIKRDHS EQENRKNE TD INQGKH QEHGYEH QNDSGHEK HEHH-NCS ENHESHS KEHS MTTQ RLQMVFI LAVVLTCL ALND IQAM RIKRDHS EQENRKNE TD INQGKH QEHGYEH QNDSGHEK HEHH-NCS SSHESHS KEHS MTTQ RLQMVFI LAVVLTCL ALND IQAM RIKRDHS EQEDHRKNE TD INQGKH QEHGYEH QNDSSHEK HEHH-NCS GSHESHS KEHS MTTQ RLQMVFI LAVVLTCL ALND IQAM RIKRDHS EQEDHRKNE TD INQGKH QEHGYEH QNDSSHEK HEHH-NCS GSHESHS KEHS MTTQ RLQMVFI LAVVLTCL ALND IQAM RIKRDD GQEDHKNQ TDVNHDEP QEHGHEH QNDSSHEK HEHH-NCS GSNESHS KEYS MTTQ RLRMMFV VAVILSCL ALNE IQAM RIKRSDA GQEEHKNQ TDVNHDEH DEHSHEH QNDSSHEK HEHH-NCS ESHESHS KEHH MTTQ RLRMMFV VAVILSCL ALNE IQAM RIKRSDA GQEEHKNQ TDVNHDEH DEHSHEH QNDSSHEK HEHH-NCS GSHESHS KEHH
	90 100 110 120 130 140 150 160
Consensus Identity	dedh hhekkmh yyckcrhh hdndtesh ehehehahendte thgd-yhhkgi hehlgnhsdsseynhzeckchch cpkh
Setaria labiatopapillosa Litomosoides sigmodontis Acanthocheilonema viteae Wuchereria bancrofti Brugia malayi (isoform b) Brugia malayi (isoform c) Loa loa Dirofilaria immitis Onchocerca ochengi Onchocerca gutturosa Onchocerca volvulus	DEER HHGKKVH YYCKCHRH HDNDTDSH EH HVHENDTE ADGDNYHH HFDHKVV QEYQCNHS DI SEHDRN ECHCHCH CPKH DEDN HQLKKMH YYCKCRGG HENDTESH EQE-EHE HSHGNETE I HGDNYHH HHKDI HKHLSNHS DTSERDGD ECRCHCH CPRH DEDH HHEKKIH YYCKCRGH HDNDTESH EHEHE HTHKNDTE I HGDNYHHHKGT HEHLGNRS DSSEHNH QCCRCHCH CPKH DEDL H-EKKTH YYCKCRGH HDNDSESH EHD-EHE RVGENDTE THVHKGI HEHVGNNS DSSEYNHQ DCRCHCH CPKH DEDH H-EKKTH YYCKCRDH HDNDSESH EHD-EHD RAGENDTE THVHKGI HEHVGNNS DSSEYNHQ DCRCHCH CPKH DEDH H-EKKTH YYCKCRDH HDNDSESH EHD-EHD RAGENDTE THVHKGI HEHVGNNS DSSEYNHQ DCRCHCH CPKH DEDH H-EKKTH YYCKCRDH HDNDSESH EHD- HDR RAGENDTE THVHKGI HEHVGNNS DSSEYNHQ DCRCHCH CPKH DEDH H-EKKTH YYCKCRDH HDNDSESH EHD- HDR RAGENDTE THVHKGI HEHVGNNS DSSEYNHQ DCRCHCH CPKH DENH HHEKKTQ YYCKCHSH HDNTESQ EHEHEHK HAHENDTE THSHKGI HEHVGNNS DSSEYSHQ DCRCHCH CSKH DEDN HHEKKMH YYCKCHSH HDNTDNH DYEHAHENDTE THGHKNT HEHLGNYS DSSEHSDQ ECRCHCH CPKH DDDH QHGKKMH FHCKCRHH HDNDTDSH EHEHE HAPENGTE THGD-YHEHKDI HEHLGNHSEYNSE ECRCHCH CPKH DDDH QHGKKMH FHCKCRHH HDNDTDSH EHEHE RAPENGTE TH GD-YHEHKDI HEHLGNHSEYNSE ECRCHCH CPKH
Consensus Identity	170 180 190 200 210 220 230 240 251 KGSXNQEQERKKHKXKGSGEHCHCFCHHHGDE-EHKGSDQKERHDKEHXDKEXEHKKESEEKEXKEEKNQDQVMKLLF
Setaria labiatopapillosa Litomosoides sigmodontis Acanthocheilonema viteae Wuchereria bancrofti Brugia malayi (isoform b) Brugia malayi (isoform c) Loa loa Dirofilaria immitis Onchocerca ochengi Onchocerca gutturosa Onchocerca yalvulus	E-RNNQRKERKKNKHHETNEHCHCFCHSHGNE-EIKGSSQKEHHDSDKEQSKENKKESEEKEQGEEKHQDQVMKLLF KGRQDKKQERKEQKKKGSGKHCHCFCHEHGDE-EEKGPGQKERNHEGYHDKEDRQEHKKESDEKEHDEEKNQDQITKLLF KGSYDKEQEDKEHKKKGSGEHCHCFCHHHGDE-EQMESDQKEQHDKDQHVNEDSKEHKIKFQAKLEIIVTNLPMTLFCFS KESNNQEQKRRGHRKGSGEHCHCFCHHHGDE-EHKGSDQTERHDKEHSEEHKS KGNNNQEQKRRGHKKGSGEHCHCFCHHHGDE-EHKGSDQTERHDKEHSEEHKKEPEEKEHKEDKDQDQVMKLLF KGNNNQEQKRRGHKKGSGEHCHCFCHHHGDE-EHKGSDQTERHDKEHSEEHKKEPEEKEHKEDKDQDQVMKLLF KGNNNQEQKRRGHKKGSGEHCHCFCHHHGDE-EHKGSDQTERHDKEHSEEHKRGQRSRSGHETTVLKFQILCSMILAN KGSHAHKQKGSGEHCHCFCHHHGDE-EHKGSDQMEQQDKEDHDKEHKS KGTYDQKQEHKERKNEKHKGSGEHCHCFCHHHGD-EHKESNQKEYHDKEQDDKEHDNDYKKESEEKEQKEEKHQDLVMKLLF KGSHNHDQEHMKHRKNDRKVSGEHCHCFCHQHDDDDEHTGSKQKEHHDKKHGDIKKESEEKELKEEKVIFLLNNF KGSHNHDQEHMKHRKNDRKVSGEHCHCFCHQHDDDDEHTGSKQKE

SUPPLEMENTAL FIG. S4. Amino-acid sequence alignment of *L. sigmodontis* protein nLs\_03577 and its orthologues in other filarial nematodes. Homologues of nLs\_03577 were identified by BLASTP search of protein databases from sequenced nematode genomes and a transcriptome assembly for *Setaria labiatopapillosa* (G. Koutsovoulos, B. Makepeace, M. Blaxter; unpublished). No homologues were found outside the filarial nematodes. The protein sequences were aligned with ClustalOmega, and identity is indicated by a coloured scale (green, high; yellow, moderate; red, low).



SUPPLEMENTAL FIG. S5. Rooted phylogenetic tree of *L. sigmodontis* protein nLs\_03577 and its orthologues in other filarial nematodes. Homologues of nLs\_03577 were identified by BLASTP search of protein databases from sequenced nematode genomes and a transcriptome assembly for *Setaria labiatopapillosa* (G. Koutsovoulos, B. Makepeace, M. Blaxter; unpublished). No homologues were found outside the filarial nematodes. The protein sequences were aligned with ClustalOmega and the alignment subjected to phylogenetic analysis using MrBayes version 3.2. Every 100<sup>th</sup> generation from the final 1 million generations of a 2 million generation analysis were combined to derive the consensus shown. Posterior probabilities are indicated by branch colouring (red: pp = 1) The tree is rooted with *S. labiatopapillosa*, in accordance with accepted systematics, and nuclear small subunit ribosomal RNA phylogeny.

SUPPLEMENTAL FIG. S6. Rooted phylogenetic tree of ShK domains among predicted proteins in filarial **nematodes.** The rooted subtrees for the six ShK domains from the nLs\_04059 orthologues are shown. Node support is indicated by colour on the branches (red: posterior probability = 1). In *B. malayi*, domain 1 is represented by two distinct isoform clusters, one of which (Bm1) is found only in this species and in *W. bancrofti*.



SUPPLEMENTAL FIG. S7 [see file Supplemental-figure-S7.pdf]. Unrooted phylogenetic tree of ShK domains among predicted proteins in filarial nematodes and Ascaris suum. The unrooted cladogram is the consensus of the last 1 million of 2 million generations of the analysis, sampled every 100 generations. Node supports are indicated by dots (width is proportional to support) and colour (red: posterior probability of 1). The clades containing the six nLs\_04059-like domains are highlighted.



SUPPLEMENTAL FIG. S8. Distribution of biotin in labelled and unlabelled specimens of adult *Litomosoides sigmodontis*. Fixed worm sections were incubated with streptavidin-FITC. *A*, Biotin-labelled worms. *B*, An unlabelled control specimen. Scale bars represent 20 μm.

SUPPLEMENTAL TABLE S1 [see file "Supplemental-table-S1.xlsx"]. Protein predictions from the *Litomosoides sigmodontis* genome, including *Brugia malayi* and *Dirofilaria immitis* orthologues and MS evidence. Tab 1, summary overview of nuclear-encoded proteins, including annotations, *Brugia* and *Dirofilaria* orthologues, and presence in ESP and/or WBE preparations; tab 2, summary overview of detected *wLs*-encoded proteins; tabs 3 – 7, protein inference data from ESP and WBE preparations for gAF, pgAF, AM, iMf and vL3, respectively; tab 8, protein inference data for adult nematode surface extracts; tabs 9 – 13, peptide assignment data from ESP and WBE preparations for gAF, pgAF, AM, iMf and vL3, respectively; tab 14, peptide assignment data for adult nematode surface extracts. On tab 1, "Updated description" in column P includes revised annotations for some ESP proteins following manual curation.

### ${\small {\sf SUPPLEMENTAL}} \ {\small {\sf TABLE}} \ {\small {\sf S2}}$

Homologues of abundant Litomosoides sigmodontis excretory-secretory proteins identified by DELTA-BLAST (National Centre for Biotechnology Information)

Query	Filter <sup>a</sup>	Top annotated hit <sup>b</sup> [species] and accession	Max.	Identity	Query cover	E-value
			score	(%)	(%)	
nLs_00113	AT	PAN domain containing protein [ <i>Brugia malayi</i> ] <u>XP_001900239.1</u>	652	37	77	0.0
	FE	Flagellin [Salmonella enterica] WP_023208887.1	134	15	12	2 <sup>-28</sup>
	CO	Protein SRAP-1, isoform a [ <i>C. elegans</i> ] <u>NP_496398.3</u>	114	26	56	3 <sup>-24</sup>
nLs_01398	AT	Protein UNC-52, isoform m [ <i>Caenorhabditis elegans</i> ] <u>NP_001254444.1</u>	1848	52	97	0.0
nLs_02001	AT	KH domain-containing protein [ <i>Loa loa</i> ] <u>EFO27012.2</u>	513	75	58	2 <sup>-174</sup>
	FE	Far upstream element-binding protein 1-like [Setaria italica] XP_004972470.1	97.4	18	65	5 <sup>-18</sup>
	CO	RNA helicase GLH-2 [ <i>C. elegans</i> ] <u>AAB03337.1</u>	72.0	25	33	<b>2</b> <sup>-12</sup>
nLs_03577	AT	Hypothetical protein Bm1_38495 [ <i>Brugia malayi</i> ] <u>XP_001899152.1</u>	128	60	100	2 <sup>-32</sup>
	FE	Heavy metal translocating P-type ATPase [Dorea sp. 5-2] WP_016217557.1	63.5	29	74	2 <sup>-08</sup>
	CO	Protein THOC-2 [ <i>C. elegans</i> ] <u>NP_498392.2</u>	42.0	27	55	1 <sup>-03</sup>
nLs_04059	AT	Hypothetical protein LOAG_17826 [ <i>Loa loa</i> ] <u>EJD74931.1</u>	262	51	87	<b>7</b> <sup>-80</sup>
	FE	A disintegrin and metalloproteinase with thrombospondin motifs 3-like [Aplysia	52.0	29	68	<b>7</b> <sup>-04</sup>
		californica] <u>XP_005091919.1</u>				
	CO	_ <sup>C</sup>	-	-	-	-
nLs_05850	AT	Hypothetical protein LOAG_04060 [ <i>Loa loa</i> ] <u>XP_003139645.1</u>	269	54	94	1 <sup>-80</sup>
	FE	Chondroitin proteoglycan 2 [Ascaris suum] <u>ERG86992.1</u>	247	25	98	1 <sup>-68</sup>
	CO	CBR-CPG-2 protein [ <i>C. briggsae</i> ] <u>XP_002633936.1</u>	218	20	93	<b>8</b> <sup>-63</sup>
nLs_08836	AT	Apolipophorin [ <i>Ascaris suum</i> ] <u>ERG86007.1</u>	1535	42	99	0.0
	FE	Zonadhesin-like [Saccoglossus kowalevskii] XP_002738323.1	256	19	44	4 <sup>-65</sup>
	CO	Protein VIT-4 [ <i>C. elegans</i> ] <u>NP_508612.1</u>	97.1	21	8	9 <sup>-20</sup>
nLs_01626	AT	Animal heme peroxidase [ <i>Loa loa</i> ] <u>XP_003141164.1</u>	1367	84	98	0.0
	FE	Peroxidasin-like protein [Ascaris suum] <u>ERG87495.1</u>	1308	72	98	0.0
	CO	CBR-PXN-2 protein [ <i>C. briggsae</i> ] <u>XP_002644069.1</u>	1093	47	99	0.0

AT, all taxa; FE, Filarioidea excluded; CO, Caenorhabditis only.

<sup>*a*</sup> Filters were applied only where the top hit was to taxa other than *Caenorhabditis* spp.

<sup>b</sup> Only annotated hits are shown for non-filarial proteins.

<sup>c</sup> The only hits were to hypothetical proteins containing ShK domains.

## SUPPLEMENTAL TABLE S3

## Homologues of abundant Litomosoides sigmodontis excretory-secretory proteins identified by PSI-BLAST (Phyre<sup>2</sup>)

Query	Top annotated hit [species]	UniRef50 ID	Bits	Normalised identity (%)	E-value
nLs_02001	Transcription elongation factor SPT5 [ <i>Cryptococcus neoformans</i> var. <i>neoformans</i> serotype D]	POCR70	135	14.9	3 <sup>-30</sup>
nLs_04059	Sortilin-related receptor [Homo sapiens]	Q92673	210	10.0	1 <sup>-52</sup>
nLs_08836	SCO-spondin [Danio rerio]	B3LF39	351	10.4	1 <sup>-94</sup>

#### Extended narrative - Abundant proteins released by larval parasites

The dominant serum components identified in bMf ESP were fibronectin, complement C3, serum albumin, hemopexin, plasminogen and ceruloplasmin; while lower amounts of IgM were also detected (supplemental Table S4). Of the five quantifiable parasite-derived molecules, three were TTL proteins. Interestingly, the two most abundant parasite ESP proteins observed in bMf, a TTL protein and a nematode-specific uncharacterised protein (nLs 03443), were not present in iMf ESP (supplemental Table S4). Non-unique but proportionally enriched proteins in iMf included two galectins (βgalactoside-binding proteins 1 and 2), a fatty acid and retinoid-binding protein (FAR-1), and a nucleoside diphosphate kinase (supplemental Fig. S2b), all of which are known to be expressed throughout the filarial lifecycle (1, 2). In addition, Ls110, which is secreted from the uterine epithelium during embryonic development (3), was detected in iMf ESP but not iMf WBE. Conversely, the major sheath proteins Shp1a and Shp4 were found in iMf WBE but were not secreted (supplemental Table S1). Another distinctive feature of the iMf ESP was the overrepresentation of two proteoglycan core proteins: a perlecan-like protein that exhibited moderate similarity to UNC-52 from C. elegans (supplemental Table S2, supplemental Fig. S2b) (4); and a chondroitin proteoglycan (CPG) containing six peritrophin-A chitin-binding domains, which was distantly related to *C. elegans* CPG-2 (5) (supplemental Tables S1 and S2). However, a large (~250 kDa predicted mass) plasminogen-applenematode (PAN) domain protein, which displayed weak similarity (supplemental Table S2) to the predicted mucin SRAP-1 from C. elegans (6), was more abundant than either of the proteoglycans in iMf ESP (supplemental Fig. 2b). Finally, an apparently novel peroxidasin-like protein with orthologues in other filarial nematodes and more distant relatives in A. suum and Caenorhabditis briggsae (supplemental Table S2) was also identified in iMf ESP (supplemental Fig. 2b).

In many filarial nematodes, microfilariae are enclosed in a proteinaceous sheath comprising an inner layer that originates from the eggshell and an outer layer that is produced by secretions in the distal portion of the uterus. Five major structural proteins have been identified in the *L. sigmodontis* sheath, some of which are synthesised in the developing embryo and others in the uterine epithelium (7), but none of these were found in iMf ESP, indicating that they are stable components. Many host serum proteins were released from bMf in culture. These are likely to derive from specific interactions with the parasite surface, perhaps reflecting a tension between the nematode exploiting the host and the host immune system recognising the parasite. The finding of host material at the Mf surface is not new, as five serum components were the only proteins released by SDS extraction of *L. sigmodontis* Mf sheaths (8), and human serum albumin has been detected on the sheath surface of *W. bancrofti* Mf (9), but is generally not found on *Brugia* spp. Mf (10). The *L. sigmodontis* sheath is permeable to molecules of up to 70 kDa (11), and therefore might retain some host proteins after transfer to culture. However, several abundant serum proteins that we detected in bMf ESP are considerably larger than this (for

example, ceruloplasmin and fibronectin); therefore, they must be either adsorbed onto the sheath surface or proteolytically processed prior to uptake. Hemopexin and ceruloplasmin have roles in heme and copper transport (12), respectively. Hence, they might be exploited as a source of these essential cofactors by the parasite.

Several parasite-derived products were identified as secreted by iMf, including Ls110 [a protein localised in the uterine lumen and variably present on iMf, but absent from bMf (3)] and two putative proteoglycan core proteins. Accordingly, large glycoproteins (~200 kDa) have been described from B. malayi ESP (13). The closest C. elegans homologue of the perlecan-like proteoglycan, UNC-52, is a major component of the basement membrane of contractile tissues, including the pharynx and anus in developing embryos and subsequent stages (4). The L. sigmodontis iMf-derived CPG-like protein is predicted to have chitinbinding domains and may function in eggshell and sheath development. In C. elegans, CPGs form an inner layer that binds to the central chitinous layer of the eggshell, maintaining the perivitelline space around the embryo (14) and forming a barrier to prevent polyspermy (15). In L. sigmodontis, chitin has been detected in the oocytes and zygotes, although it is absent from the iMf sheath (16). The degradation of chitin during Mf sheath development in utero may release the underlying CPG, which is highly soluble (14), into the surrounding milieu. The origin and roles two of the other novel proteins that were enriched in iMf ESP is less clear. The closest homologue in C. elegans of the PAN domain protein is SRAP-1, which is expressed in the hypodermis, central nervous system and vulva of developing larvae and is secreted onto the cuticle surface during moulting (17). In *C. elegans*, peroxidasin PXN-2 is located in the extracellular matrix and is required for late embryonic elongation, muscle attachment, and motoneuron axon guidance choice (18).

The vL3 ESP was composed of previously characterised filarial proteins that are known to be uniquely expressed or enriched in this stage [such as ASP-1 (19), ALT-1 (20), and cathepsin-L-like protease (21)], alongside other antigens that were well represented in ESP from other stages (RAL-2, CPI-2, Ov16 and  $\beta$ -galactoside-binding proteins) (supplemental Fig. 2a). The nematode secreted protein 22U was moderately abundant in the *L. sigmodontis* vL3 ESP preparations (supplemental Fig. 2a), but apparently is not expressed in vL3 of other filarial species (22). This stage may be relatively quiescent in terms of secretory activity until they adapt to the mammalian host and undergo the third moult. Indeed, analysis of ESP from moulting L3 identified fivefold more proteins than from vL3 ESP in *B. malayi* (23).

## SUPPLEMENTAL TABLE S4

### Quantifiable proteins present in the excretory-secretory products of blood-derived microfilariae

Accession   Gene name	Peptides used for	Confidence	Description (species)	Normalised
	quantification	score		iBAQ
Q91X72 HEMO_MOUSE	7	898.19	Hemopexin (Mus musculus)	1.44 <sup>-01</sup>
Q8VCM7 FIBG_MOUSE	8	1040.62	Fibrinogen γ chain <i>(Mus musculus)</i>	1.15 <sup>-01</sup>
Q8K0E8 FIBB_MOUSE	9	1594.25	Fibrinogen β chain <i>(Mus musculus)</i>	9.56 <sup>-02</sup>
O35090 ALBU_MERUN	29	5013.66	Serum albumin (Meriones unguiculatus)	6.09 <sup>-02</sup>
P70274 SEPP1_MOUSE	3	203.64	Selenoprotein P (Mus musculus)	5.76 <sup>-02</sup>
Q61147 CERU_MOUSE	12	2215.19	Ceruloplasmin (Mus musculus)	5.56 <sup>-02</sup>
P29788 VTNC_MOUSE	6	1035.62	Vitronectin (Mus musculus)	5.43 <sup>-02</sup>
Q61702 ITIH1_MOUSE	7	1236.34	Inter- $lpha$ -trypsin inhibitor heavy chain H1 (Mus musculus)	5.32 <sup>-02</sup>
P11276 FINC_MOUSE	49	8184.33	Fibronectin <i>(Mus musculus)</i>	3.80 <sup>-02</sup>
P01027 CO3_MOUSE	28	3368.39	Complement C3 (Mus musculus)	3.63 <sup>-02</sup>
P01942 HBA_MOUSE	2	149.76	Hemoglobin subunit $lpha$ (Mus musculus)	3.60 <sup>-02</sup>
P97515 FETUA_MERUN	6	665.57	lpha-2-HS-glycoprotein (Meriones unguiculatus)	3.24 <sup>-02</sup>
P20918 PLMN_MOUSE	13	2062.8	Plasminogen (Mus musculus)	3.13 <sup>-02</sup>
P13020 GELS_MOUSE	5	1587.22	Gelsolin ( <i>Mus musculus</i> )	<b>2.83</b> <sup>-02</sup>
Q62577 AMBP_MERUN	6	1120.89	Protein AMBP (Meriones unguiculatus)	<b>2.33</b> <sup>-02</sup>
P01029 CO4B_MOUSE	11	1814.14	Complement C4-B (Mus musculus)	1.52 <sup>-02</sup>
P05367 SAA2_MOUSE	4	820.91	Serum amyloid A-2 protein (Mus musculus)	$1.34^{-02}$
Q61703 ITIH2_MOUSE	7	1223.42	Inter- $lpha$ -trypsin inhibitor heavy chain H2 (Mus musculus)	9.20 <sup>-03</sup>
nLs.2.1.2.t10069-RA	4	264.21	Transthyretin-like protein, partial (Litomosoides sigmodontis)	9.11 <sup>-03</sup>
P04186 CFAB_MOUSE	6	361.74	Complement factor B (Mus musculus)	8.08 <sup>-03</sup>
P52430 PON1_MOUSE	2	166.19	Serum paraoxonase/arylesterase 1 (Mus musculus)	<b>7.36</b> <sup>-03</sup>
Q02105 C1QC_MOUSE	2	292.88	Complement C1q subcomponent subunit C (Mus musculus)	6.31 <sup>-03</sup>
P06909 CFAH_MOUSE	2	156.16	Complement factor H (Mus musculus)	5.81 <sup>-03</sup>
P05017 IGF1_MOUSE	2	458.52	Insulin-like growth factor I (Mus musculus)	5.69 <sup>-03</sup>
P14106 C1QB_MOUSE	2	62.86	Complement C1q subcomponent subunit B (Mus musculus)	<b>3.94</b> <sup>-03</sup>
A6X935 ITIH4_MOUSE	4	301.36	Inter $lpha$ -trypsin inhibitor, heavy chain 4 (Mus musculus)	<b>3.94</b> <sup>-03</sup>
E7D4P4 E7D4P4_MERUN	9	1172.7	Apolipoprotein E (Meriones unguiculatus)	<b>3.78</b> <sup>-03</sup>
P97298 PEDF_MOUSE	5	420.63	Pigment epithelium-derived factor (Mus musculus)	<b>3.31</b> <sup>-03</sup>

P47878 IBP3_MOUSE	5	520.36	Insulin-like growth factor-binding protein 3 (Mus musculus)	3.10 <sup>-03</sup>
P46412 GPX3_MOUSE	3	275.46	Glutathione peroxidase 3 (Mus musculus)	2.99 <sup>-03</sup>
Q8BH35 CO8B_MOUSE	4	586.84	Complement component C8 $eta$ chain (Mus musculus)	2.99 <sup>-03</sup>
Q64118 A1AT_MERUN	3	183.98	lpha-1-antitrypsin (Meriones unguiculatus)	2.89 <sup>-03</sup>
Q06890 CLUS_MOUSE	5	427.41	Clusterin (Mus musculus)	1.91 <sup>-03</sup>
P70389 ALS_MOUSE	3	471.58	Insulin-like growth factor-binding protein complex acid labile subunit ( <i>Mus musculus</i> )	1.88 <sup>-03</sup>
P35441 TSP1_MOUSE	8	853.9	Thrombospondin-1 <i>(Mus musculus)</i>	1.81 <sup>-03</sup>
P68033 ACTC_MOUSE	2	978.66	Actin, $lpha$ cardiac muscle 1 (Mus musculus)	1.64 <sup>-03</sup>
Q00724 RET4_MOUSE	4	335.66	Retinol-binding protein 4 (Mus musculus)	1.63 <sup>-03</sup>
P26262 KLKB1_MOUSE	5	625.92	Plasma kallikrein (Mus musculus)	1.52 <sup>-03</sup>
Q61704 ITIH3_MOUSE	4	422.55	Inter- $\alpha$ -trypsin inhibitor heavy chain H3 ( <i>Mus musculus</i> )	1.52 <sup>-03</sup>
P19221   THRB_MOUSE	7	587.54	Prothrombin (Mus musculus)	1.45 <sup>-03</sup>
P33434 MMP2_MOUSE	3	283.7	72 kDa type IV collagenase (Mus musculus)	1.42 <sup>-03</sup>
Q9JHH6 CBPB2_MOUSE	3	367.6	Carboxypeptidase B2 (Mus musculus)	1.38 <sup>-03</sup>
P32261 ANT3_MOUSE	2	306.33	Antithrombin-III (Mus musculus)	1.30 <sup>-03</sup>
nLs.2.1.2.t03443-RA	3	366.35	Hypothetical protein, Bm1_50630 homolog ( <i>Litomosoides sigmodontis</i> )	1.18 <sup>-03</sup>
nLs.2.1.2.t01366-RA	2	269.78	Transthyretin-like protein, partial (Litomosoides sigmodontis)	9.56 <sup>-04</sup>
P11680 PROP_MOUSE	2	36.41	Properdin <i>(Mus musculus)</i>	9.27 <sup>-04</sup>
Q61646 HPT_MOUSE	3	236.91	Haptoglobin (Mus musculus)	8.65 <sup>-04</sup>
Q9JM99 PRG4_MOUSE	5	683.96	Proteoglycan 4 (Mus musculus)	8.57 <sup>-04</sup>
Q921I1 TRFE_MOUSE	4	728.55	Serotransferrin (Mus musculus)	8.09 <sup>-04</sup>
P28798 GRN_MOUSE	2	300.7	Granulins (Mus musculus)	7.86 <sup>-04</sup>
P26928 HGFL_MOUSE	4	375.93	Hepatocyte growth factor-like protein (Mus musculus)	7.43 <sup>-04</sup>
Q9JJN5 CBPN_MOUSE	3	219.53	Carboxypeptidase N catalytic chain (Mus musculus)	7.01 <sup>-04</sup>
P47879 IBP4_MOUSE	2	211.08	Insulin-like growth factor-binding protein 4 (Mus musculus)	$6.96^{-04}$
Q07968 F13B_MOUSE	3	410.66	Coagulation factor XIII B chain (Mus musculus)	6.89 <sup>-04</sup>
Q9DBD0 ICA_MOUSE	6	787.37	Inhibitor of carbonic anhydrase (Mus musculus)	5.99 <sup>-04</sup>
P97290 IC1_MOUSE	4	387.11	Plasma protease C1 inhibitor (Mus musculus)	5.94 <sup>-04</sup>
Q8K182 CO8A_MOUSE	2	332.91	Complement component C8 $lpha$ chain (Mus musculus)	5.78 <sup>-04</sup>
O70362 PHLD_MOUSE	2	100.85	Phosphatidylinositol-glycan-specific phospholipase D (Mus musculus)	4.92 <sup>-04</sup>
P01872 IGHM_MOUSE	2	174.92	Ig μ chain C region secreted form (Mus musculus)	4.48 <sup>-04</sup>

P06684 CO5_MOUSE	2	338.69	Complement C5 (Mus musculus)	4.07 <sup>-04</sup>
Q8K0D2 HABP2_MOUSE	2	60.74	Hyaluronan-binding protein 2 (Mus musculus)	3.53 <sup>-04</sup>
nLs.2.1.2.t01870-RA	2	196.87	ML domain-containing protein (Litomosoides sigmodontis)	3.44 <sup>-04</sup>
nLs.2.1.2.t01365-RA	2	188.68	Transthyretin-like protein, partial (Litomosoides sigmodontis)	<b>2.74</b> <sup>-04</sup>
P28665 MUG1_MOUSE	3	312.94	Murinoglobulin-1 (Mus musculus)	2.05 <sup>-04</sup>
Q08879 FBLN1_MOUSE	2	305.68	Fibulin-1 <i>(Mus musculus)</i>	$1.90^{-04}$
Q8CG16 C1RA_MOUSE	2	102.86	Complement C1r-A subcomponent (Mus musculus)	1.04 <sup>-04</sup>

iBAQ, intensity-based absolute quantification; AMBP,  $\alpha$ -1-microglobulin/bikunin precursor.

### SUPPLEMENTAL TABLE S5

Putative surface-associated proteins exhibiting >50-fold enrichment in biotin-labelled adult worm whole body extracts relative to unlabelled controls

Parasite stage	Treatment	Peptides used for quantification	Confidence score	Fold-difference	Locus tag	Annotation	Presence in ESP
AM	SDS	4	316.19	1,769.5	nLs_09715	Major sperm protein	Yes
	SDS	2	249.88	341.7	nLs_01747	Filarial antigen RAL-2	Yes
	SDS	6	873.95	62.2	nLs_06907	Adenylate kinase isoenzyme 1	No
	PBS	4	172.54	50.6	nLs_09625	Transthyretin-like protein 5	Yes
gAF	Urea	2	306.56	430.9	nLs_02969	Cysteine protease inhibitor-2	Yes
0	Urea	2	180.49	149.4	nLs_08458	Filarial antigen Ov16	Yes
	Urea	2	302.26	65.2	nLs_09625	Transthyretin-like protein 5	Yes
	OG	2	233.80	60,617.8	nLs_09890	Purine nucleoside phosphorylase	Yes
	OG	2	183.22	336.5	nLs_00852	Proliferating cell nuclear antigen domain protein	No
	OG	2	224.62	271.9	nLs_04749	60S ribosomal protein L18	No
	OG	2	191.67	168.3	nLs_01364	Transthyretin-like protein, partial	Yes
	OG	3	194.25	156.3	nLs_02023	Tetratricopeptide-repeat domain protein	Yes
	OG	2	159.32	139.9	nLs_02001	KH domain-containing protein	Yes
	OG	2	188.56	118.1	nLs_08084	Type I inositol-trisphosphate 5-phosphatase	Yes
	OG	3	367.83	79.9	nLs_02969	Cysteine protease inhibitor-2	Yes
	OG	3	367.26	66.6	nLs_02463	FKBP-type peptidyl-prolyl cis-trans isomerase	Yes
	OG	3	220.00	65.6	nLs_00523	KH domain containing protein	Yes
	OG	3	376.34	59.0	wLs_3910	Wolbachia surface protein	No
	OG	2	258.28	52.2	nLs_05241	Tetratricopeptide-repeat domain protein	No
	SDS	2	50.67	1,059.7	nLs_07759	Cyclophilin Ovcyp-2 homologue	Yes
	SDS	6	306.80	328.9	nLs_08458	Filarial antigen Ov16	Yes
	SDS	7	488.42	304.1	nLs_01747	Filarial antigen RAL-2	Yes
	SDS	4	156.74	262.8	nLs_05279	HSP20/ $lpha$ -crystallin family protein	No
	SDS	2	144.16	242.7	nLs_08696	Lysozyme protein 8, partial	Yes
	SDS	2	87.95	235.6	nLs_09890	Purine nucleoside phosphorylase	Yes
	SDS	7	432.37	216.4	nLs_09625	Transthyretin-like protein 5	Yes
	SDS	2	82.06	202.7	nLs_2001	KH domain-containing protein	Yes

SDS	6	332.26	193.2	nLs_08148	Papilin	Yes
SDS	2	122.31	162.4	nLs_06907	Adenylate kinase isoenzyme 1	Yes
SDS	2	44.96	162.1	nLs_00117	L-lactate dehydrogenase	Yes
SDS	3	144.30	148.4	nLs_05914	Pyruvate dehydrogenase E1 component, $lpha$ -	Yes
					subunit	
SDS	2	77.92	115.1	nLs_09750	Transthyretin-like protein 45	Yes
SDS	7	329.76	86.5	nLs_03034	p27 heat shock protein homologue	Yes
SDS	5	166.70	82.3	nLs_08836	von Willebrand factor type-d domain protein	Yes
SDS	3	138.70	71.7	nLs_03328	Myosin	No
SDS	2	89.16	67.5	nLs_01364	Transthyretin-like protein, partial	Yes
SDS	6	560.89	52.8	nLs_08415	Enolase	Yes
PBS	5	631.96	111.4	nLs_02378	Aldo/keto reductase family protein	No
PBS	2	309.24	104.0	nLs_03070	Atypical RIO/RIO2 protein kinase	Yes
PBS	3	372.59	93.5	nLs_00473	Aldehyde dehydrogenase 11	Yes
PBS	6	1058.57	89.2	nLs_06488	Acid phosphatase	Yes
PBS	9	1570.87	69.9	nLs_01747	Filarial antigen RAL-2	Yes
PBS	4	647.70	62.5	nLs_03174	Nematode secreted protein 22U	Yes

ESP, excretory-secretory products; AM, adult male; OG, octyl β-D-glucopyranoside; gAF, gravid adult female; FKBP, FK506-binding protein; HSP, heat-shock protein

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