SUPPLEMENTARY MATERIAL

Table S1. Mean Ct (threshold cycle) of *Sra-hsp*-17.1 and *Sra-hsp*-17.2 compared to the housekeeping control gene, *Sra*-gapdh in iL3, parasitic and free-living *S. ratti* female stages. The data were expressed for two independent experiments. Ct values are means ± S.D.

Stage	*Sra*-gapdh	*Sra*-hsp-17.1	*Sra*-hsp-17.2
iL3	15,365±0,1341	20,5433±0,0273	26,8967±0,0103
PF	15,4±0,0782	15,6233±0,0121	19,1833±0,0288
FF	15,3767±0,304	18,04±0,041	22,06±0,0434

Table S2. List of nucleotide primers

Primer name	5′ - 3′ sequence
Oligo dT-T7I	GAGAGAGGATCCAAGTACTAATACGACTCACTATAGGGAGATT24
Oligo dT-T7II	GAGAGAGGATCCAAGTACTAATACGACTCACTATAGG
SL-1	GGTTTAATTACCCAAGTTTGAG
af1	ATGAACGACCGTTGGATGA
ar1	TTATTTTCTATATTCAATTGGGAC
bf1	ATGTTTGACAACCACATGATGACACC
br1	TTACTTAAACTTGATAGGAATATTTTTTCCC
af2	AACGACAAGGAATTCAGAGTCAA
bf2	CCATTCACTCGTATGCCACTT
ar2	ACGGACGAAACTTCTTTGGA
br2	TGGGTGGGTGTCAGCAAAT
af3	AACGACAAGGAATTCAGAGTCAA
ar3	ACGGACGAAACTTCTTTGGA
bf3	CCATTCACTCGTATGCCACTT
br3	TGGGTGGGTGTCAGCAAAT
af4	AAGCTTgatgatgatgataaaATGAACGACCG
ar4	GGATCCTTATTTTCTATATTCAATTGGGAC
bf4	CATATGgatgatgatgataaaATGTTTGACAAC
br4	GGATCCTTACTTAAACTTGATAGG
gapdhf	GTACCACTAACTGTTTAGCTCC
gapdhr	GCACCTCTTCCATCTCTCC
PJC45f	ATACGACTCACTATAGGGGAATTG

Fig. S1. (A) SDS-PAGE of excretory/secretory products from *S. ratti* PF after 250-fold concentration and mass spectrometric data analyses by ProteinPilot search engine v2.0.1, identifying *Sra*-HSP-17s peptides, in the respective 18-19 kDa-excised protein band. UPS= unused protein score. (B) SDS-PAGE of excretory/secretory products from *S. ratti* PF after inhibition of protein release by 70 µM cycloheximide.

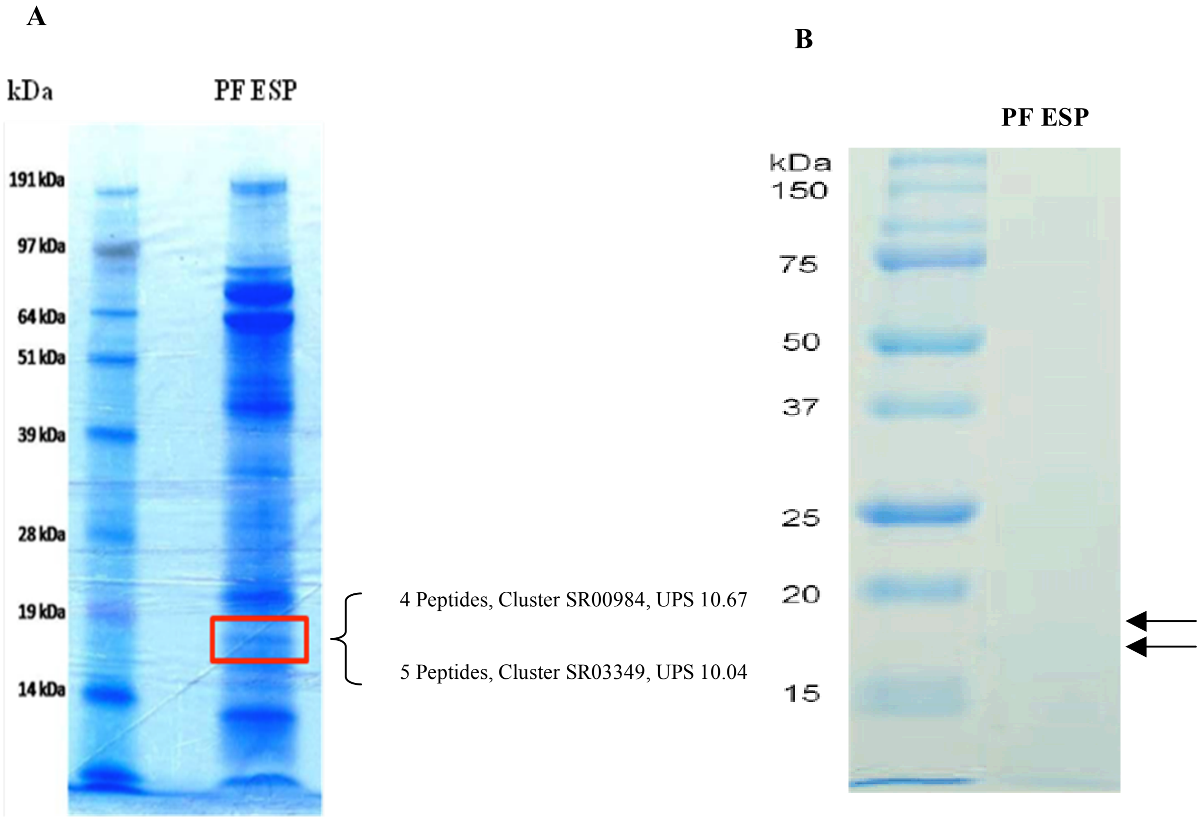
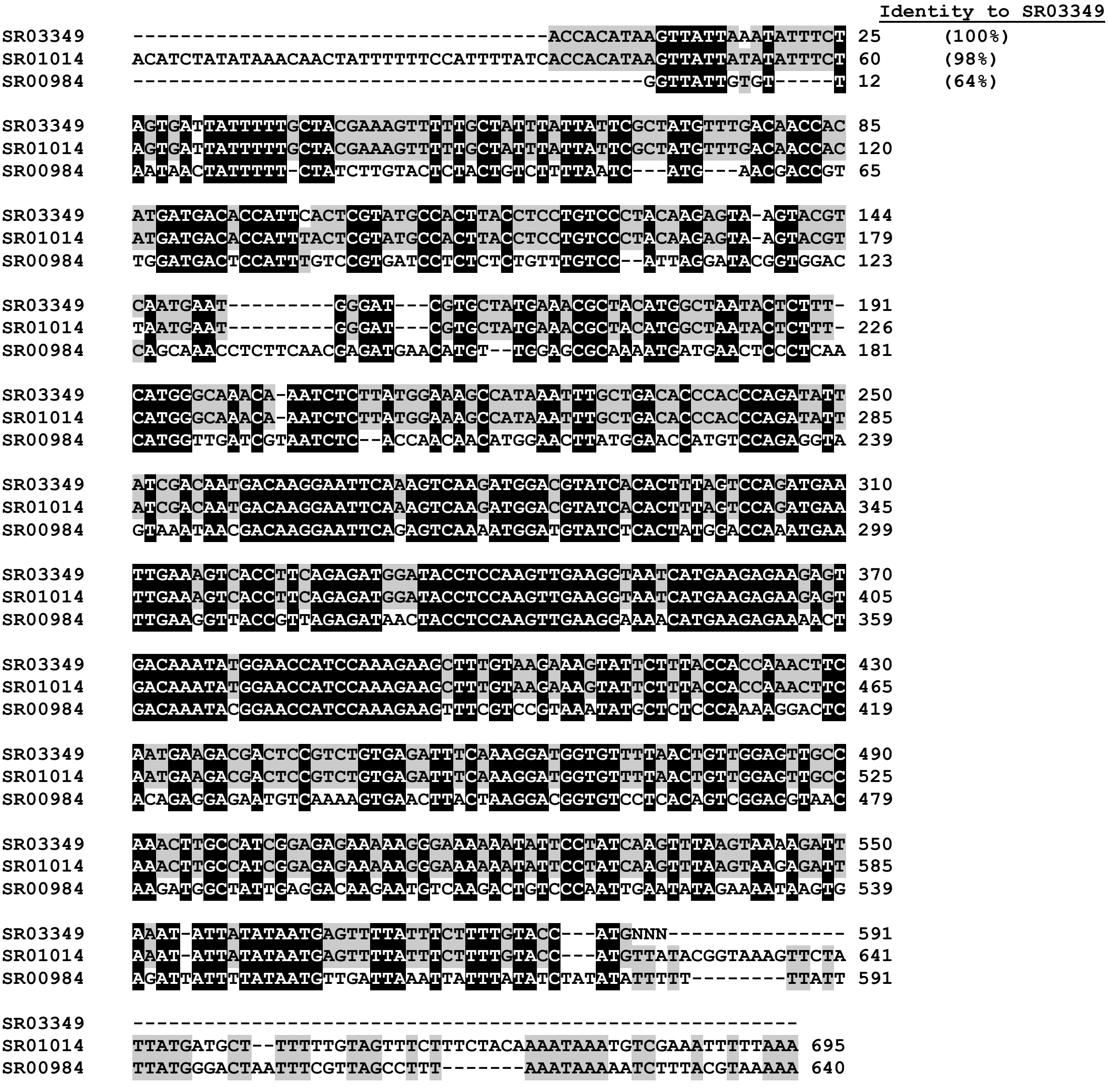


Fig. S2. Sequence identification. (A) Alignment of the two *hsp*-17 clusters identified by ProteinPilot search engine v2.0.1 from the ESP of the PF (SR03349 and SR00984) and a third alternative cluster SR01014. Sympols: identical residues are shaded in black blocks, conserved residues in two clusters are shaded in grey. (B) Alignment of *Cel-hsp*-17a (acc. No Q20660) and *Cel-hsp*-17b (acc. No Q7JP52) isoforms (differ nucleotides are in bounder). (C) Alignment of the identified full length cDNAs of *Sra-hsp*-17.1 and *Sra-hsp*-17.2. Identical residues underlined with asterisks.

A



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                                                                       Identity to SR03349
SR03349    -----------------------------------ACCACATAAGTTATTAAATATTTCT 25      (100%)
SR01014    ACATCTATATAAACAACTATTTTTTCCATTTTATCACCACATAAGTTATTATATATTTCT 60      (98%)
SR00984    -------------------------------------------GGTTATTGTGT-----T 12      (64%)

SR03349    AGTGATTATTTTTGCTACGAAAGTTTTTGCTATTTATTATTCGCTATGTTTGACAACCAC 85
SR01014    AGTGATTATTTTTGCTACGAAAGTTTTTGCTATTTATTATTCGCTATGTTTGACAACCAC 120
SR00984    AATAACTATTTTT-CTATCTTGTACTCTACTGTCTTTTAATC---ATG---AACGACCGT 65

SR03349    ATGATGACACCATTCACTCGTATGCCACTTACCTCCTGTCCCTACAAGAGTA-AGTACGT 144
SR01014    ATGATGACACCATTTACTCGTATGCCACTTACCTCCTGTCCCTACAAGAGTA-AGTACGT 179
SR00984    TGGATGACTCCATTTGTCCGTGATCCTCTCTCTGTTTGTCC--ATTAGGATACGGTGGAC 123

SR03349    CAATGAAT---------GGGAT---CGTGCTATGAAACGCTACATGGCTAATACTCTTT- 191
SR01014    TAATGAAT---------GGGAT---CGTGCTATGAAACGCTACATGGCTAATACTCTTT- 226
SR00984    CAGCAAACCTCTTCAACGAGATGAACATGT--TGGAGCGCAAAATGATGAACTCCCTCAA 181

SR03349    CATGGGCAAACA-AATCTCTTATGGAAAGCCATAAATTTGCTGACACCCACCCAGATATT 250
SR01014    CATGGGCAAACA-AATCTCTTATGGAAAGCCATAAATTTGCTGACACCCACCCAGATATT 285
SR00984    CATGGTTGATCGTAATCTC--ACCAACAACATGGAACTTATGGAACCATGTCCAGAGGTA 239

SR03349    ATCGACAATGACAAGGAATTCAAAGTCAAGATGGACGTATCACACTTTAGTCCAGATGAA 310
SR01014    ATCGACAATGACAAGGAATTCAAAGTCAAGATGGACGTATCACACTTTAGTCCAGATGAA 345
SR00984    GTAAATAACGACAAGGAATTCAGAGTCAAAATGGATGTATCTCACTATGGACCAAATGAA 299

SR03349    TTGAAAGTCACCTTCAGAGATGGATACCTCCAAGTTGAAGGTAATCATGAAGAGAAGAGT 370
SR01014    TTGAAAGTCACCTTCAGAGATGGATACCTCCAAGTTGAAGGTAATCATGAAGAGAAGAGT 405
SR00984    TTGAAGGTTACCGTTAGAGATAACTACCTCCAAGTTGAAGGAAAACATGAAGAGAAAACT 359

SR03349    GACAAATATGGAACCATCCAAAGAAGCTTTGTAAGAAAGTATTCTTTACCACCAAACTTC 430
SR01014    GACAAATATGGAACCATCCAAAGAAGCTTTGTAAGAAAGTATTCTTTACCACCAAACTTC 465
SR00984    GACAAATACGGAACCATCCAAAGAAGTTTCGTCCGTAAATATGCTCTCCCAAAAGGACTC 419

SR03349    AATGAAGACGACTCCGTCTGTGAGATTTCAAAGGATGGTGTTTTAACTGTTGGAGTTGCC 490
SR01014    AATGAAGACGACTCCGTCTGTGAGATTTCAAAGGATGGTGTTTTAACTGTTGGAGTTGCC 525
SR00984    ACAGAGGAGAATGTCAAAAGTGAACTTACTAAGGACGGTGTCCTCACAGTCGGAGGTAAC 479

SR03349    AAACTTGCCATCGGAGAGAAAAAGGAAAAAATATTCCTATCAAGTTTAAGTAAAAGATT 550
SR01014    AAACTTGCCATCGGAGAGAAAAAGGAAAAAATATTCCTATCAAGTTTAAGTAAGAGATT 585
SR00984    AAGATGGCTATTGAGGACAAGAATGTCAAGACTGTCCCAATTGAATATAGAAAATAAGTG 539

SR03349    AAAT-ATTATATAATGAGTTTTATTTCTTTTGTACC---ATGNNN--------------- 591
SR01014    AAAT-ATTATATAATGAGTTTTATTTCTTTTGTACC---ATGTTATACGGTAAAGTTCTA 641
SR00984    AGATTATTTTATAATGTTGATTAAATTATTTATATCTATATATTTTT--------TTATT 591

SR03349    --------------------------------------------------------
SR01014    TTATGATGCT--TTTTTGTAGTTTCTTTCTACAAAATAAATGTCGAAATTTTTAAA 695
SR00984    TTATGGACTAATTTCGTTAGCCTTT-------AAATAAAAATCTTTACGTAAAAA 640
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B

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Cel-hsp-17a       ATGGATCGTCGTTTTCCACCATTCTCCCCATTCTTTAACCATGGCCGCAGATTCTTCGAT 60
Cel-hsp-17b       ATGGATCGTCGTTTTCCACCATTCTCCCCATTCTTTAACCATGGCC---GATTCTTCGAT 57
                  **********************************************   ***********

Cel-hsp-17a       GACGTCGACTTTGATCGCCACATGATCCGACCATACTGGGCCGATCAAACAATGCTCACT 120
Cel-hsp-17b       GACGTCGACTTTGATCGCCACATGATCCGACCATACTGGGCCGATCAAACAATGCTCACT 117
                  ************************************************************

Cel-hsp-17a       GGACACCGAGTAGGAGATGCTATTGATGTTGTGAACAACGATCAAGAATACAATGTATCT 180
Cel-hsp-17b       GGACACCGAGTAGGAGATGCTATTGATGTTGTGAACAACGATCAAGAATACAATGTATCT 177
                  ************************************************************

Cel-hsp-17a       GTAGATGTTTCACAGTTTGAACCAGAAGAGTTGAAAGTGAACATTGTTGATAATCAGCTA 240
Cel-hsp-17b       GTAGATGTTTCACAGTTTGAACCAGAAGAGTTGAAAGTGAACATTGTTGATAATCAGCTA 237
                  ************************************************************

Cel-hsp-17a       ATCATCGAAGGAAAGCATAACGAGAAGACTGATAAATATGGACAGGTAGAGCGTCACTTT 300
Cel-hsp-17b       ATCATCGAAGGAAAGCATAACGAGAAGACTGATAAATATGGACAGGTAGAGCGTCACTTT 297
                  ************************************************************

Cel-hsp-17a       GTCCGGAAGTATAACCTTCCAACAGGGGTCCGTCCAGAACAAATCAAGTCCGAATTGAGC 360
Cel-hsp-17b       GTCCGGAAGTATAACCTTCCAACAGGGGTCCGTCCAGAACAAATCAAGTCCGAATTGAGC 357
                  ************************************************************

Cel-hsp-17a       AACAATGGAGTGCTCACTGTCAAATATGAGAAGAATCAGGAACAGCAGCCAAAATCCATT 420
Cel-hsp-17b       AACAATGGAGTGCTCACTGTCAAATATGAGAAGAATCAGGAACAGCAGCCAAAATCCATT 417
                  ************************************************************

Cel-hsp-17a       CCAATCACAATTGTGCCAAAGAGAAACTGA 450
Cel-hsp-17b       CCAATCACAATTGTGCCAAAGAGAAACTGA 447
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C

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Sra-hsp-17.1     ATG---AACGACCGTTGGATGACTCCATTTGTCCGTGATCCTCTCTCTGTTTGTCC--AT 55
Sra-hsp-17.2     ATGTTTGACAACCACATGATGACACCATTCACTCGTATGCCACTTACCTCCTGTCCCTAC 60
                 ***    ** ***    ****** *****    ***   ** **  *    *****  *

Sra-hsp-17.1     TAGGATACGGTGGACCAGCAAACCTCTTCAACGAGATGAACATGTT--GGAGCGTAAAAT 113
Sra-hsp-17.2     AAGAGTA-AGTACGTCAATGAAT---------GGGAT---CGTGCTATGAAACGCTACAT 107
                 **  **  **    **   **          * ***   * ** *  * * **  * **

Sra-hsp-17.1     GATGAACTCCCTCAACATGGTTGATCGTAATCTC--ACCAACAACATGGAACTTATGGAA 171
Sra-hsp-17.2     GGCTAATACTCTTT-CATGGGCAAACA-AATCTCTTATGGAAAGCCATAAATTTGCTGAC 165
                 *   **  * **   *****   * *  ******  *   * * *    ** **   **

Sra-hsp-17.1     CCATGTCCAGAGGTAGTAAATAACGACAAGGAATTCAGAGTCAAAATGGATGTATCTCAC 231
Sra-hsp-17.2     ACCCACCCAGATATTATCGACAATGACAAGGAATTCAAAGTCAAGATGGACGTATCACAC 225
                  *    *****  *  *  * ** ************* ****** ***** ***** ***

Sra-hsp-17.1     TATGGACCAAATGAATTGAAGGTTACCGTTAGAGATAACTACCTCCAAGTTGAAGGAAAA 291
Sra-hsp-17.2     TTTAGTCCAGATGAATTGAAAGTCACCTTCAGAGATGGATACCTCCAAGTTGAAGGTAAT 285
                 * * * *** ********** ** *** * ******   ***************** **

Sra-hsp-17.1     CATGAAGAGAAAACTGACAAATACGGAACCATCCAAAGAAGTTTCGTCCGTAAATATGCT 351
Sra-hsp-17.2     CATGAAGAGAAGAGTGACAAATATGGAACCATCCAAAGAAGCTTTGTAAGAAAGTATTCT 345
                 *********** * ********* ***************** ** **  * ** *** **

Sra-hsp-17.1     CTCCCAAAAGGACTCACAGAGGAGAATGTCAAAAGTGAACTTACTAAGGACGGTGTCCTC 411
Sra-hsp-17.2     TTACCACCAAACTTCAATGAAGACGACTCCGTCTGTGAGATTTCAAAGGATGGTGTTTTA 405
                 * ***  *    ***  ** **  *   *    ****  ** * ***** *****  *

Sra-hsp-17.1     ACAGTCGGAGGTAACAAGATGGCTATTGAGGACAAGAATGTCAAGACTGTCCCAATTGAA 471
Sra-hsp-17.2     ACTGTTGGAGTTGCCAAACTTGCCATCGGAGAGAAAAAGGGAAAAAATATTCCTATCAAG 465
                 ** ** **** *  ***  * ** ** *  ** ** ** *  ** * * * ** **  *

Sra-hsp-17.1     TATAGAAAATAA 483          Identity (64%)
Sra-hsp-17.2     TTTA---AGTAA 474
                 * **   * ***
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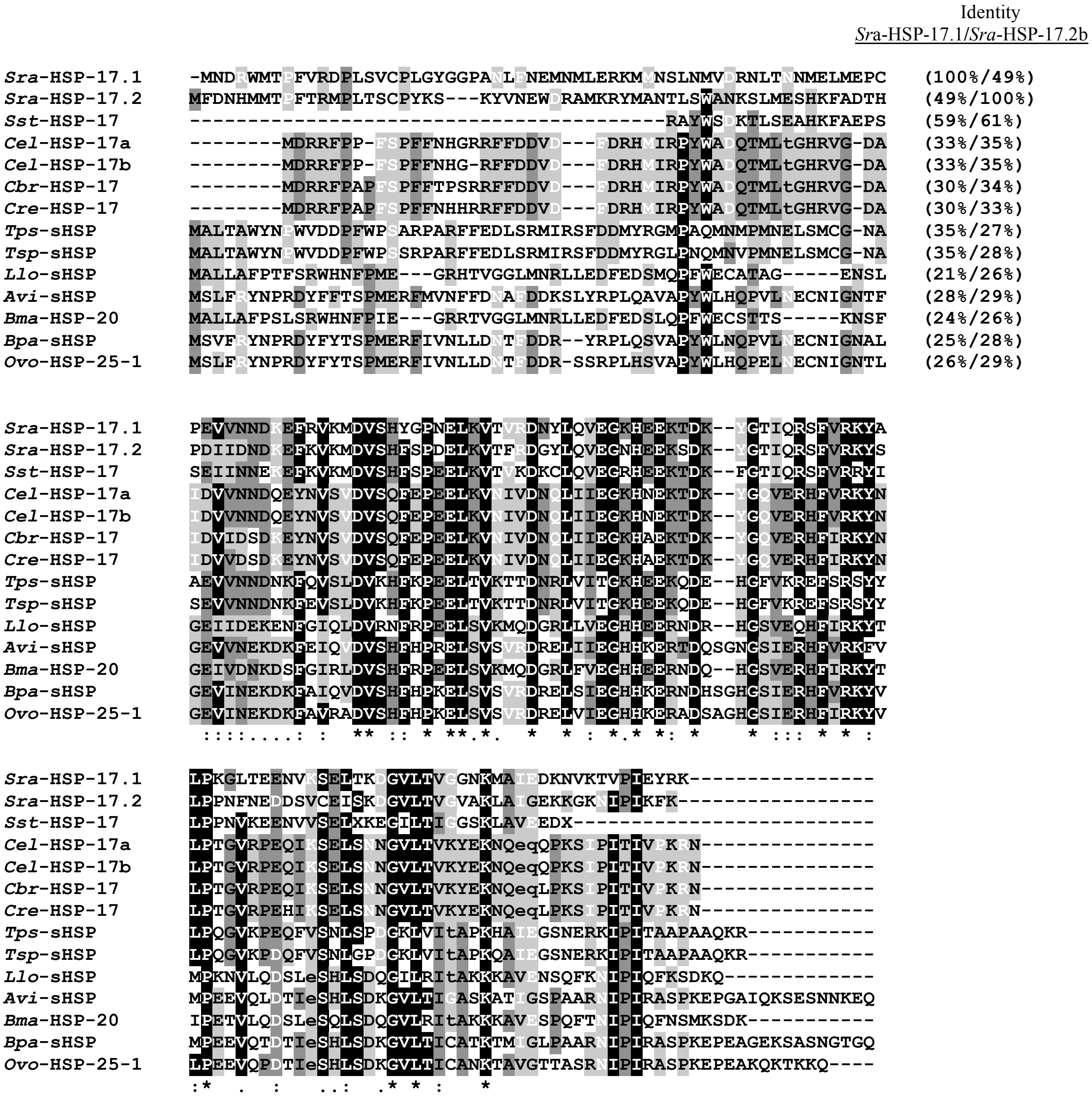
Fig. S3. Alignment of the *Sra*-HSP-17.1 and *Sra*-HSP-17.2 aa sequences with other 12 related nematodes sHSPs based on CLUSTAL W, neighbor-joining. Sympols: identical (asterisks), highly conserved residues (>10) are shaded in black blocks, median conserved residues (7-9) in dark grey, low conserved residues (4-6) in light grey, no amino acid residue (dashes), conservation of residue size and hydropathy (colons), conservation of size or hydropathy (periods). Accession numbers are listed in Fig. 2.



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                                                                                       Identity
                                                                              Sra-HSP-17.1/Sra-HSP-17.2b

Sra-HSP-17.1     -MNDRWMTPFVRDPLSVCPLGYGGPANLFNEMNMLERKMMNSLNMVDRNLTNNMELMEPC   (100%/49%)
Sra-HSP-17.2     MFDNHMMTPFTRMPLTSCPYKS---KYVNEWDRAMKRYMANTLSWANKSLMESHKFADTH   (49%/100%)
Sst-HSP-17       -----------------------------------------RAYWSDKTLSEAHKFAEPS   (59%/61%)
Cel-HSP-17a      --------MDRRFPP-FSPFFNHGRRFFDDVD---FDRHMIRPYWADQTMLtGHRVG-DA   (33%/35%)
Cel-HSP-17b      --------MDRRFPP-FSPFFNHG-RFFDDVD---FDRHMIRPYWADQTMLtGHRVG-DA   (33%/35%)
Cbr-HSP-17       --------MDRRFPAPFSPFFTPSRRFFDDVD---FDRHMIRPYWADQTMLtGHRVG-DA   (30%/34%)
Cre-HSP-17       --------MDRRFPAPFSPFFNHHRRFFDDVD---FDRHMIRPYWADQTMLtGHRVG-DA   (30%/33%)
Tps-sHSP         MALTAWYNPWVDDPFWPSARPARFFEDLSRMIRSFDDMYRGMPAQMNMPMNELSMCG-NA   (35%/27%)
Tsp-sHSP         MALTAWYNPWVDDPFWPSSRPARFFEDLSRMIRSFDDMYRGLPNQMNVPMNELSMCG-NA   (35%/28%)
Llo-sHSP         MALLAFPTFSRWHNFPME---GRHTVGGLMNRLLEDFEDSMQPFWECATAG-----ENSL   (21%/26%)
Avi-sHSP         MSLFRYNPRDYFFTSPMERFMVNFFDNAFDDKSLYRPLQAVAPYWLHQPVLNECNIGNTF   (28%/29%)
Bma-HSP-20       MALLAFPSLSRWHNFPIE---GRRTVGGLMNRLLEDFEDSLQPFWECSTTS-----KNSF   (24%/26%)
Bpa-sHSP         MSVFRYNPRDYFYTSPMERFIVNLLDNTFDDR--YRPLQSVAPYWLNQPVLNECNIGNAL   (25%/28%)
Ovo-HSP-25-1     MSLFRYNPRDYFYTSPMERFIVNLLDNTFDDR-SSRPLHSVAPYWLHQPELNECNIGNTL   (26%/29%)

Sra-HSP-17.1     PEVVNNDKEFRVKMDVSHYGPNELKVTVRDNYLQVEGKHEEKTDK--YGTIQRSFVRKYA
Sra-HSP-17.2     PDIIDNDKEFKVKMDVSHFSPDELKVTFRDGYLQVEGNHEEKSDK--YGTIQRSFVRKYS
Sst-HSP-17       SEIINNEKEFKVKMDVSHFSPEELKVTVKDKCLQVEGRHEEKTDK--FGTIQRSFVRRYI
Cel-HSP-17a      IDVVNNDQEYNVSVDVSQFEPEELKVNIVDNQLIIEGKHNEKTDK--YGQVERHFVRKYN
Cel-HSP-17b      IDVVNNDQEYNVSVDVSQFEPEELKVNIVDNQLIIEGKHNEKTDK--YGQVERHFVRKYN
Cbr-HSP-17       IDVIDSDKEYNVSVDVSQFEPEELKVNIVDNQLIIEGKHAEKTDK--YGQVERHFIRKYN
Cre-HSP-17       IDVVDSDKEYNVSVDVSQFEPEELKVNIVDNQLIIEGKHAEKTDK--YGQVERHFIRKYN
Tps-sHSP         AEVVNNDNKFQVSLDVKHFKPEELTVKTTDNRLVITGKHEEKQDE--HGFVKREFSRSYY
Tsp-sHSP         SEVVNNDNKFEVSLDVKHFKPEELTVKTTDNRLVITGKHEEKQDE--HGFVKREFSRSYY
Llo-sHSP         GEIIDEKENFGIQLDVRNFRPEELSVKMQDGRLLVEGHHEERNDR--HGSVEQHFIRKYT
Avi-sHSP         GEVVNEKDKFEIQVDVSHFHPRELSVSVRDRELIIEGHHKERTDQSGNGSIERHFVRKFV
Bma-HSP-20       GEIVDNKDSFGIRLDVSHFRPEELSVKMQDGRLFVEGHHEERNDQ--HGSVERHFIRKYT
Bpa-sHSP         GEVINEKDKFAIQVDVSHFHPKELSVSVRDRELSIEGHHKERNDHSGHGSIERHFVRKYV
Ovo-HSP-25-1     GEVINEKDKFAVRADVSHFHPKELSVSVRDRELVIEGHHKERADSAGHGSIERHFIRKYV
                  ::::....: :  ** :: * **.*.  *  * :*.* *: *    * ::: * * :

Sra-HSP-17.1     LPKGLTEENVKSELTKDGVLTVGGNKMAIEDKNVKTVPIEYRK----------------
Sra-HSP-17.2     LPPNFNEDDSVCEISKDGVLTVGVAKLAIGEKKGKNIPIKFK-----------------
Sst-HSP-17       LPPNVKEENVVSELXKEGILTIGGSKLAVEEDX--------------------------
Cel-HSP-17a      LPTGVRPEQIKSELSNNGVLTVKYEKNQeqQPKSIPITIVPKRN---------------
Cel-HSP-17b      LPTGVRPEQIKSELSNNGVLTVKYEKNQeqQPKSIPITIVPKRN---------------
Cbr-HSP-17       LPTGVRPEQIKSELSNNGVLTVKYEKNQeqLPKSIPITIVPKRN---------------
Cre-HSP-17       LPTGVRPEHIKSELSNNGVLTVKYEKNQeqLPKSIPITIVPKRN---------------
Tps-sHSP         LPQGVKPEQFVSNLSPDGKLVItAPKHAIEGSNERKIPITAAPAAQKR-----------
Tsp-sHSP         LPQGVKPDQFVSNLGPDGKLVItAPKQAIEGSNERKIPITAAPAAQKR-----------
Llo-sHSP         MPKNVLQDSLeSHLSDQGILRItAKKKAVENSQFKNIPIQFKSDKQ-------------
Avi-sHSP         MPEEVQLDTIeSHLSDKGVLTIGASKATIGSPAARNIPIRASPKEPGAIQKSESNNKEQ
Bma-HSP-20       IPETVLQDSLeSQLSDQGVLRItAKKKAVESPQFTNIPIQFNSMKSDK-----------
Bpa-sHSP         MPEEVQTDTIeSHLSDKGVLTICATKTMIGLPAARNIPIRASPKEPEAGEKSASNGTGQ
Ovo-HSP-25-1     LPEEVQPDTIeSHLSDKGVLTICANKTAVGTTASRNIPIRASPKEPEAKQKTKKQ----
                 :*  .  :   ..:  .* * :   *
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Fig. S4. Alignment of the cloned and sequenced PCR products amplified from the PF cDNA and gDNA. Sympols: identical (asteriks) and introns (underlined). (A) *Sra-hsp-17.1*. (B) *Sra-hsp*-17.2. A single intron in each sHSP located in the second third of the ACDs ORFs. Both introns are phase 0, their splice sites sequences followed the GU-AG convention.

A

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gSra-hsp-17.1         ATGAACGACCGTTGGATGACTCCATTTGTCCGTGATCCTCTCTCTGTTTGTCCATTAGGA 60
cSra-hsp-17.1         ATGAACGACCGTTGGATGACTCCATTTGTCCGTGATCCTCTCTCTGTTTGTCCATTAGGA 60
                      ************************************************************

gSra-hsp-17.1         TACGGTGGACCAGCAAACCTCTTCAACGAGATGAACATGTTGGAGCGTAAAATGATGAAC 120
cSra-hsp-17.1         TACGGTGGACCAGCAAACCTCTTCAACGAGATGAACATGTTGGAGCGTAAAATGATGAAC 120
                      ************************************************************

gSra-hsp-17.1         TCCCTCAACATGGTTGATCGTAATCTCACCAACAACATGGAACTTATGGAACCATGTCCA 180
cSra-hsp-17.1         TCCCTCAACATGGTTGATCGTAATCTCACCAACAACATGGAACTTATGGAACCATGTCCA 180
                      ************************************************************

gSra-hsp-17.1         GAGGTAGTAAATAACGACAAGGAATTCAGAGTCAAAATGGATGTATCTCACTATGGACCA 240
cSra-hsp-17.1         GAGGTAGTAAATAACGACAAGGAATTCAGAGTCAAAATGGATGTATCTCACTATGGACCA 240
                      ************************************************************

gSra-hsp-17.1         AATGAATTGAAGGTTACCGTTAGAGATAACTACCTCCAAGTTGAAGGAAAACATGAAGAG 300
cSra-hsp-17.1         AATGAATTGAAGGTTACCGTTAGAGATAACTACCTCCAAGTTGAAGGAAAACATGAAGAG 300
                      ************************************************************

gSra-hsp-17.1         AAAACTGACAAATACGGAACCGTAAGTTTACTTTATACCTCTAAGTATTTAACTGTGGTA 360
cSra-hsp-17.1         AAAACTGACAAATACGGAACC--------------------------------------- 321
                      *********************

gSra-hsp-17.1         AAATCTATTCCTTTTAATTTTTAGATCCAAAGAAGTTTCGTCCGTAAATATGCTCTCCCA 420
cSra-hsp-17.1         ------------------------ATCCAAAGAAGTTTCGTCCGTAAATATGCTCTCCCA 357
                                              ************************************

gSra-hsp-17.1         AAAGGACTCACAGAGGAGAATGTCAAAAGTGAACTTACTAAGGACGGTGTCCTCACAGTC 480
cSra-hsp-17.1         AAAGGACTCACAGAGGAGAATGTCAAAAGTGAACTTACTAAGGACGGTGTCCTCACAGTC 417
                      ************************************************************

gSra-hsp-17.1         GGAGGTAACAAGATGGCTATTGAGGACAAGAATGTCAAGACTGTCCCAATTGAATATAGA 540
cSra-hsp-17.1         GGAGGTAACAAGATGGCTATTGAGGACAAGAATGTCAAGACTGTCCCAATTGAATATAGA 477
                      ************************************************************

gSra-hsp-17.1         AAATAA 546
cSra-hsp-17.1         AAATAA 483
                      ******
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B

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gSra-hsp-17.2           ATGTTTGACAACCACATGATGACACCATTCACTCGTATGCCACTTACCTCCTGTCCCTAC 60
cSra-hsp-17.2           ATGTTTGACAACCACATGATGACACCATTCACTCGTATGCCACTTACCTCCTGTCCCTAC 60
                        ************************************************************

gSra-hsp-17.2           AAGAGTAAGTACGTCAATGAATGGGATCGTGCTATGAAACGCTACATGGCTAATACTCTT 120
cSra-hsp-17.2           AAGAGTAAGTACGTCAATGAATGGGATCGTGCTATGAAACGCTACATGGCTAATACTCTT 120
                        ************************************************************

gSra-hsp-17.2           TCATGGGCAAACAAATCTCTTATGGAAAGCCATAAATTTGCTGACACCCACCCAGATATT 180
cSra-hsp-17.2           TCATGGGCAAACAAATCTCTTATGGAAAGCCATAAATTTGCTGACACCCACCCAGATATT 180
                        ************************************************************

gSra-hsp-17.2           ATCGACAATGACAAGGAATTCAAAGTCAAGATGGACGTATCACACTTTAGTCCAGATGAA 240
cSra-hsp-17.2           ATCGACAATGACAAGGAATTCAAAGTCAAGATGGACGTATCACACTTTAGTCCAGATGAA 240
                        ************************************************************

gSra-hsp-17.2           TTGAAAGTCACCTTCAGAGATGGATACCTCCAAGTTGAAGGTAATCATGAAGAGAAGAGT 300
cSra-hsp-17.2           TTGAAAGTCACCTTCAGAGATGGATACCTCCAAGTTGAAGGTAATCATGAAGAGAAGAGT 300
                        ************************************************************

gSra-hsp-17.2           GACAAATATGGAACCGTAAGTTTTATGCTACTTACTTAGTGTTGTTATCTTATTCGTTTT 360
cSra-hsp-17.2           GACAAATATGGAACC--------------------------------------------- 315
                        ***************

gSra-hsp-17.2           TAAGATCCAAAGAAGCTTTGTAAGAAAGTATTCTTTACCACCAAACTTCAATGAAGACGA 420
cSra-hsp-17.2           ----ATCCAAAGAAGCTTTGTAAGAAAGTATTCTTTACCACCAAACTTCAATGAAGACGA 371
                            ********************************************************

gSra-hsp-17.2           CTCCGTCTGTGAGATTTCAAAGGATGGTGTTTTAACTGTTGGAGTTGCCAAACTTGCCAT 480
cSra-hsp-17.2           CTCCGTCTGTGAGATTTCAAAGGATGGTGTTTTAACTGTTGGAGTTGCCAAACTTGCCAT 431
                        ************************************************************

gSra-hsp-17.2           CGGAGAGAAAAAGGGAAAAAATATTCCTATCAAGTTTAAGTAA 523
cSra-hsp-17.2           CGGAGAGAAAAAGGGAAAAAATATTCCTATCAAGTTTAAGTAA 474
                        *******************************************
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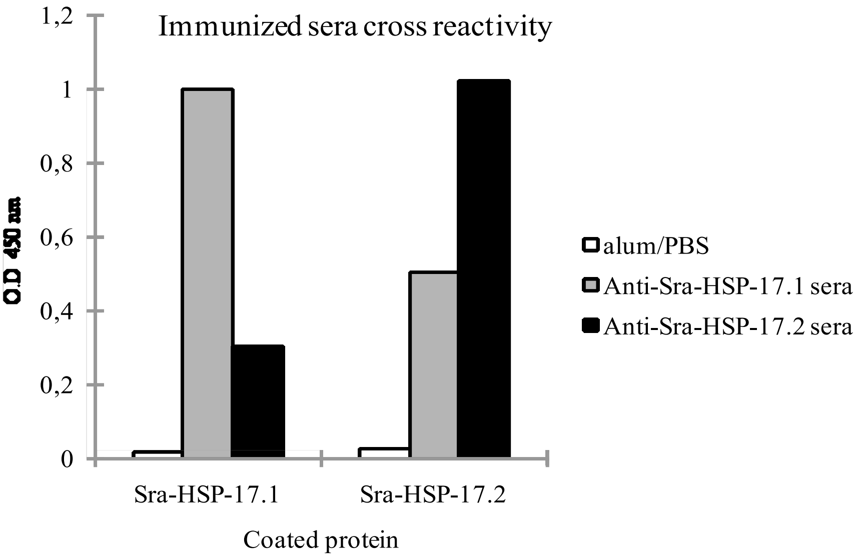
Fig. S5. Cross-reactivities in ELISAs titration of the (A) 1:3000 immune sera and (B) 1:300 purified antibodies against the respective *Sra*-HSP-17s, by using the recombinant *Sra*-HSP-17s as antigens. Sera from mock-immunized rats (1:50) served as controls.

A



B